EvolDir

June 1, 2019

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

Ankara EvolutionaryBiology Jul10-12

Dear All,

The 6th Ecology and Evolutionary Biology Symposium Turkey (EEBST), will be held from 10-12 July 2019 in Ankara, Turkey which is well-attended by diverse international faculty, post-docs and students from all around the world. The symposia aims to stimulate international collaborations and it offer great opportunity to interact other researchers.

Keynote Speakers;

-Douglas J. Futuyma, Stony Brook University, USA

-Olivia Roth, GEOMAR, Germany

-Dieter Ebert, Universität Basel, Switzerland

-Laurent Duret, Universitê Claude Bernard, France

-Lucie Zinger, Ãcole Normale Supérieure, France

You can visit our web site (http://eebst.org) to get updated information on the conference. The EEBST'19 call for early registration is now open and remain open until 19 Apr 2019.

Register now to secure your early registration discount -> http://eebst.org/registration There will be two panel, workshop and the photo contest (will be announced at website) during the EEBST'19.

EEBST'19 will be the sixth in a series of symposia organized annually by the Ecology and Evolutionary Biology Society of Turkey (www.ekoevo.org/en < http://-/www.ekoevo.org/en >) .

We look forward to welcoming you and your colleagues in Ankara!

EEBST Organizing Committee

Metehan Arıkan <arikanmetehan@gmail.com>

Berlin WildlifeConservation Sep30-Oct2 AbstDeadlineMay19

Dear colleagues,

We are happy that we have already received many great contributions for Wildlife Research and Conservation 2019. To also give the latecomers a chance to submit a contribution, we have extended the deadline for abstract submission and early bird registration to Sunday, May 19, 2019!

Submit your abstract now at: https://www.bayceer.uni-bayreuth.de/wrc2019/en/ DEADLINE for ABSTRACT SUBMISSION and EARLY BIRD REGISTRATION: SUNDAY, MAY 19, 2019 (midnight CEST)

Find all important information on abstract submission here: http://www.izw-berlin.de/abstract-submission-373.html CONFERENCE BANQUET: We will close the conference on Wednesday evening (October 2, 2019) with a banquet in the restaurant of the Berlin Zoological Garden. Enjoy an evening with a delicious buffet, beverages and great live music!

Regular banquet ticket: 50 Euro Student banquet ticket: 35 Euro

If you would like to join the conference banquet, please book a ticket during online registration for the conference: https://www.bayceer.uni-bayreuth.de/wrc2019/en/ Please circulate information about Wildlife Research and Conservation 2019 by email, twitter, facebook and other social media! For those who have twitter we ask you to use #WRC2019Berlin to refer to the conference. Many thanks!

We look forward to welcoming you and your colleagues in Berlin!

Sarah Benhaiem, Anne Berger, Oliver Honer, Conny Landgraf, Josepha Prugel and Viktoriia Radchuk

CONTACT: Conference Organisation Leibniz Institute for Zoo and Wildlife Research (IZW) Alfred-Kowalke-Str. 17 10315 Berlin Germany Phone: +49 (0) 30 5168 127 Fax: +49 (0) 30 5126 104 E-mail: symposium@izw-berlin.de Conference website: www.izw-berlin.de/welcome-234.html Online registration: www.bayceer.uni-bayreuth.de/wrc2019/en/ "Prugel, Josepha" <pruegel@izw-berlin.de>

Bristol SystematicsAssociation Jun17-19

We would like to invite you to the 10th Biennial Conference of the Systematics Association. The meeting will take place in the vibrant city of Bristol from 17th to 19th June 2019. The keynote speakers include Fredrik Ronquist, Tandy Warnow, and Tom Brooks. Abstracts can be submitted until 24th May.

More information can be found here: https://systass.org/events-2019/biennial-2019/ . You can also follow the Systematics Association twitter (@SystAssn) for update announcements.

Looking forward to welcoming you in Bristol!

The Systematics Association Biennial Organising Team

Jordi Paps <jordipaps@gmail.com>

BrownU MimulusEvolution Jun21

Mimulus Meeting 2019

June 21, 2019

Brown University, Providence, RI

Calling all Mimulus researchers and Mimulus-curious! This one-day meeting will be held in the Smith Buonanno Building at Brown University. The morning will feature four Discussion Sessions aimed at improving tools and resources for the Mimulus community. In the afternoon, we'll hear science updates during two Lightning-Talk Sessions. See this link for details:

http://mimubase.org/node/152 There is no registration fee, but, to attend, please sign up here:

https://docs.google.com/spreadsheets/d/-1tzyZlR6CHDeI_NHS7V4pjilj3goGtPPxy_XeyH5PrIw/-edit#gid=0 . We hope to see you there!

– Andrea L. Sweigart Department of Genetics 120 East Green Street Davison Life Sciences Building, C218 University of Georgia Athens, GA 30602-7223

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Andrea Sweigart <sweigart@uga.edu>

Lund, Sweden Jurriaan Ton ' University of Sheffield, U

jbrisso3@UR.Rochester.edu

Cambridge UK EvolIntergenChange Sep24-26

Registration is now open for Mechanisms and Evolution of Intergenerational Change, September 24-26, 2019, Wellcome Genome Campus, UK. https://dmtrk.net/-2SUU-V5PW-DA6U86R3F7/cr.aspx Recent observations strongly suggest that changes in maternal stress signalling can lead to altered development in offspring and changes in offspring physiology across evolutionary lineages. In mammals, studies suggest that maternal exposure to environmental stress during pregnancy can lead to an increased risk of a variety of pathologies in later life including diabetes, cardiovascular disease, depression and anxiety.

This new conference will bring together scientists working on foetal programming and developmental origins of health and disease in humans and animals, with ecologists and evolutionary biologists, to compare and contrast mechanisms of intergenerational change in diverse organisms, to help us understand how the maternal environment contributes to developmental programming and disease susceptibility.

Early Bird discount is available until 04 June 2019. A limited number of bursaries are available for PhD students to attend the meeting.

Scientific sessions include: Evolutionary modelling of intergenerational effects Evolutionary models of intergenerational change in plants Evolutionary models of intergenerational change in vertebrates and invertebrates Foetal programming models in mammals Foetal programming in humans

Keynote speakers: Pat Monaghan, University of Glasgow, UK Kent Thornburg, University of Oregon, USA

Confirmed speakers: Tracy Bale ' University of Maryland, USA Ryan Baugh ' Duke University, USA Kathleen Donohue ' Duke University, USA Anne Ferguson-Smith ' University of Cambridge, UK Dino Giussani ' University of Cambridge, UK Bram Kuijper ' University of Exeter, UK Cris Ledón-Rettig ' Indiana University, USA Kirsty MacLeod ' University of Lund, Sweden Susan Ozanne ' University of Cambridge,UK Andrew Pospisilik ' Max Planck Institute of Immunobiology and Epigenetics, Germany Tessa Roseboom ' University of Amsterdam, The Netherlands Karen Spencer ' University of St. Andrews, UK Tobias Uller ' University of

Debrecen Hungary Reproductive Strategies Nov7-10

Reproductive strategies in the 21st Century: University of Debrecens Official Symposium

To celebrate 30 years of research on reproductive strategies of plants and animals at the University of Debrecen (Hungary), we will host a three-day international symposium in November 2019. The Symposium will start with a welcome reception in the Universitys Aula at 7 pm on Thursday 7 November 2019.

The Symposium will provide a forum for researchers of reproductive behaviour of microbes, plants and animals including humans to consider the current state of science and where the field is going. World-leading speakers will overview their recent research and address the future challenges facing the field. The conference will close on Sunday 10 November with an optional excursion to nearby Hortobagy National Park, an UNESCO World Heritage Site.

The Symposium will be opened by Profs Rosemary and Peter Grant (Princeton), and followed by plenary speakers that will include Prof. Hans Hoffmann (University of Texas, Austin), Prof. Ruth Mace (University College London), Prof. Ran Nathan (Hebrew University of Jerusalem) and Dr Beata Oborny (Eotvos Lorand University, Budapest).

Speakers will cover various aspects of reproductive strategies in relation to life histories, neuroendocrinology, population demography, sexual dimorphism, mating systems and parenting, dispersal and biodiversity conservation. Keynote speakers will include Prof. Andy J. Green (Estacion Biologica de Donana, Sevilla), Prof. Zoltan Barta (University of Debrecen), Prof. Michaela Hau (Max-Planck-Institute for Ornithology, Seewiesen), Prof. Ferenc Jordan (Hungarian Academy of Sciences, Budapest), Prof. Andras Liker (University of Pannonia, Veszprem), Prof. Szabolcs Lengyel (Hungarian Academy of Sciences, Debrecen), Dr. Araxi Urrutia (University of Bath) and Prof. Bela Tothmeresz (University of Debrecen).

To facilitate the attendance of young scientists and to widen participation, costs will be kept at minimum. Debrecen is a one of the top tourist destinations in Hungary

with an international airport that has direct flights to several major European destinations. The city has a large international student community and offers an excellent selection of hotels, restaurants and sightseeing facilities.

Save the dates: registration and abstract submission will start in near future. Questions may be sent to reproductive.strategies2019@gmail.com .

Hope to see you in Debrecen.

Dr Orsolya Valko (University of Debrecen, valko.orsolya@science.unideb.hu)

Dr Zoltan Nemeth (University of Debrecen, nemeth-zoltan@science.unideb.hu)

Prof Tamas Szekely (University of Bath & Debrecen, T.Szekely@bath.ac.uk)

Zoltan Nemeth <znemeth05@gmail.com>

FrancisCrickInst London PhysicsofEvolution Jul8-10

Dear All,

Registration and abstract submission is open for the Physics of Life network workshop exploring the "The Physics of Evolution".

The aim of this workshop is to bring together physicists, biologists and experimentalists working on different aspects of evolution to explore new avenues and approaches that physics can bring to our understanding of evolution.

It will take place on 8-10 July 2019 at the Francis Crick Institute, London.

Abstract submission deadline: 12 June (contributed talks and posters)

Registration fee: pounds 110 (includes lunches and refreshments)

Registration deadline: 19 June

Register here: www.physicsoflife.org.uk/the-physics-of-evolution.html Themes: (with confirmed invited speakers)

Evolution of pathogens and cancer Rosalind Allen, University of Edinburgh

Emergence in genotype-phenotype maps Paulien Hogeweg, Utrecht University

Non-equilibrium statistical physics of evolution: analogies and beyond

Susanne Still, University of Hawaii ' "Thermodynamics of adaptive information processing"

Experimental evolution Santiago Elena, Universitat de València & Santa Fe Institute ' "Experimental evolution of RNA viruses in fluctuating fitness landscapes"

Regards,

Bhavin Khatri (bhavin.khatri@crick.ac.uk) Ard Louis Tom McLeish FRS

Dr Bhavin S Khatri Research Fellow in Statistical Genomics Dept of Life Sciences Imperial College London Silwood Park Campus Ascot, Berks SL5 7PY

http://bhavkhatri.io The Francis Crick Institute Limited is a registered charity in England and Wales no. 1140062 and a company registered in England and Wales no. 06885462, with its registered office at 1 Midland Road London NW1 1AT

Bhavin Khatri <Bhavin.Khatri@crick.ac.uk>

FrenchAlps GenomicsProbabilisticModeling Oct6-9

Dear Colleagues,

This is a second announcement for the ProbGen'2019 meeting. The deadline for early bird registration and for student/postdoc grant application is May 25.

We are pleased to announce the 5th Probabilistic Modeling in Genomics meeting (ProbGen19), to be held in Aussois, in the French Alps, Oct 6-9, 2019 (https://-probgen2019.sciencesconf.org/).

The goal of this meeting is to cover a wide variety of topics in genomics, ranging from population genomics to systems biology and cancer genomics, with a particular focus on the use of novel mathematical and computational models and inference methods to address timely and important biological questions. What makes the meeting special, in our view, is that it has substantial mathematical and theoretical depth yet remains well grounded in the practical and scientific concerns of modern genomics. We invite abstract submissions on a range of topics including functional genomics, molecular evolution, phylogenetics, epidemiology, methods for genome-wide association studies, quantitative genetics,

etc'

We will have three keynote speakers: Barbara Engelhardt (Princeton University) Gil McVean (Big Data Institute, University of Oxford) Caroline Colijn (Simon Fraser University, Vancouver)

Alongside invited speakers, oral presentations will be selected from submitted abstracts. We particularly encourage abstract submissions from junior investigators, including postdoctoral fellows and graduate students. A few grants will be available for students and postdocs.

Best wishes and hope to see some of you at the meeting,

Organizing committee: Laurent Duret, Michael Blum, Nicolas Lartillot & Franck Picard

ProbGen steering committee: Thomas Bataillon, Richard Durbin, Barbara Engelhardt, Anders Krogh, Gerton Lunter, Molly Przeworski, Adam Siepel, Yun S. Song

Laurent Duret Laboratoire Biomtrie et Biologie Evolutive UMR CNRS 5558, Universit Lyon 1 43 Bld du 11 Novembre 1918 69622 Villeurbanne cedex France

Phone : +33 (0) 4 72 44 62 97 e-mail : Laurent.Duret@univ-lyon1.fr Web page: http://-lbbe.univ-lyon1.fr/-Duret-Laurent-.html?lang=en Laurent Duret <Laurent.Duret@univ-lyon1.fr>

Kansas ArthropodGenomics Jun12-14

Early Registration Ends May 19 at 11:59 PM CT Poster Abstracts Due May 20 V June 12-14, 2019 V 12th Arthropod Genomics Symposium at KSU Manhattan, KS Hi All:

We look forward to you joining us in Manhattan, KS in a few short weeks. Visit our website at www.k-state.edu/-agc/ags for more details about the symposium.

IMPORTANT: + Early Registration ends May 19 at 11:59 PM CT + Registration Fee & On-Campus Cost automatically Increase on May 20 at 12:00 AM CT + Poster Abstracts Due May 20 + Hilton Garden Inn AGS room block available until May 21

REGISTRATION Register online for the symposium and for on-campus housing at the symposium website, www.k-state.edu/agc/ags POSTER SESSION Poster session will be scheduled for both Thursday and Friday of the symposium. This years sessions include:

i5K/Comparative Genomics, Stress Response, Microbiome, Evo/Devo, Vector Biology & Bioinformatics. If interested in submitting an abstract for the poster session, please visit the website at www.k-state.edu/-agc/ags. Abstracts are due for the Poster Session on Monday, May 20.

CURATION CLINIC: Gene Annotation using Apollo + Pre-symposium workshop in the afternoon on Wednesday, June 12 before the symposium opens that evening at the K-State Alumni Center in Manhattan, KS. +This pre-symposium workshop is designed to introduce researchers who are working with annotated arthropod genomes to the Apollo curation tool. This online genome browser allows users to check if their gene annotations are supported by the data and correct them if required. No prior knowledge of Apollo is needed. The practical parts of the workshop will require a laptop computer that can connect to the WiFi. + If interested in participating in this workshop, please complete the google form. < https://goo.gl/forms/9aoVnt9l1Sa8IQ0A2 > + More details will be provided as they become available on the symposium website, https://www.k-state.edu/-agc/ags/schedule/

OVERVIEW The symposium focuses on new insights gleaned from analyzing arthropod genomes and is designed for scientists interested in genomic studies of Arthropods, both model organisms and those of agricultural or health relevance. The program will include platform presentations, welcome reception and arthropod genomics-related poster sessions. A few poster abstract submissions will be selected for platform presentations. Postdoctoral, graduate, and undergraduate students are also encouraged to attend. Sessions begin Wednesday evening, June 12, with a Welcome Reception featuring our Keynote Speaker and conclude Friday evening, June 14, with a walk and dinner on Konza Prairie.

SPEAKERS Keynote Speaker: + Denise Montell, Duggan Professor and Distinguished Professor from University of California Santa Barbara

Invited Speakers Include: + Yehuda Ben-Shahar, Washington University in St Louis + Kerri Coon, University of Wisconsin-Madison + Nsa Dada, US Centers for Disease Control and Prevention + Conor McMeniman, John Hopkins Bloomberg School of Public Health + Shahideh Nouri, Kansas State University + Luisa Orsini, University of Birmingham + Mark Rebeiz, University of Pittsburgh + Stephen Richards, University of California Davis + Michelle Riehle, Medical College of Wisconsin + Stephane Rombauts, Ghent University + Surya Saha, Boyce Thompson Institute + Nick Teets, University of Kentucky + Yoshinori Tomoyasu, Miami University + Jamie Walters, University of Kansas

Abstract Speakers Include: + Welcome Bender, Harvard Medical School + Josh Benoit, University of Cincinnati + Romain Feron, University of Lausanne and Swiss Institute of Bioinformatics + Nick Grishin, University of Texas Southwestern + Liuqi Gu, University of Kansas + Sarah Kingan, Pacific Biosciences + Yiyuan Li, University of Texas at Austin + Olena Maiakovska, German Cancer Research Center (DKFZ) + Richard Meisel, University of Houston + Petr Nguyen, University of South Bohemia + Jan-Philip Warning: base64 decoder saw premature EOF! Oeyen, Zoological Research Museum Alexander Koenig + Livio Ruzzante, University of Lausanne and Swiss Institute of Bioinformatics + Maria Luisa Simoes, John Hopkins Bloomberg School of Public Health + Amanda Stahlke, University of Idaho + Kevin Sugier, CEA-Genoscope + Robert Waterhouse, University of Lausanne and Swiss Institute of Bioinformatics + Zixiao Zhao, University of Missouri + Jing Zhang, University of Texas Southwestern

QUESTIONS: Contact Symposium Coordinator, Kascha Johnson at kascha@k-state.edu

If you would like to join the ArthropodNews to ensure receiving future notices, please send an email with your name and email address

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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

Kew London Plants Sep4-5

Dear All,

Registration is now open for our inaugural Plants, People, Planet symposium, to be held at the Royal Botanic Gardens, Kew, 4-5 September 2019. All New Phytologist events are not for profit, and a number of grants are awarded to early career researchers in association with each meeting. Successful grant applicants will receive free registration as well as a contribution towards their travel and expenses.

Royal Botanic Gardens, Kew, London | 4-5 September 2019

Plants, People, Planet Symposium

The inaugural Plants, People, Planet symposium will highlight outstanding plant-based research in its broadest sense and celebrate everything new, innovative and exciting in plant sciences that is relevant to society and people's daily lives.

Leading scientists and invited early career researchers will give talks based on seven broad themes: engaging people with plants, plants and society, plant conservation, plant diversity, plant genomics applications, plants and global change, and plant natural assets. Defra's Chief Plant Health Officer, Nicola Spence, and the Director of the Arnold Arboretum of Harvard University, Ned Friedman, will both give keynote talks. Each session will conclude with an engaging Q&A panel, and there will be a poster session and symposium dinner on site at Kew.

Travel grant submission deadline: Friday 14th June 2019 < http://www.newphytologist.org/grants/index/51 >

Posters abstracts submission deadline: Monday 8th July 2019 < http://www.newphytologist.org/posters/index/-51 >

newphytologist.org/symposia/ppp2019

@plantspeopleplanet #PPP19

If you have any questions about the event, please contact us at np-symposia@lancaster.ac.uk, and we will be happy to help.

Best wishes, Freja

Freja Kärrman-Bailey Events and Promotions Coordinator, New Phytologist Trust

New Phytologist Trust, Bailrigg House, Lancaster University, Lancaster, LA1 4YE, UK Tel: +44 1524 594691; Fax: + 44 1524 594696 newphytologist.org Twitter: @NewPhyt Facebook: fb.com/NewPhytologist

The New Phytologist Trust, registered charity number 1154867

2017 Impact Factor 7.43

Events in 2019 Tropical vegetation structure and function < https://newphytologist.org/symposia/44 > | Plants, People, Planet Symposium < https://-www.newphytologist.org/symposia/ppp2019 >

"Karrman-Bailey, Freja" <f.karrman-bailey@lancaster.ac.uk>

Lausanne FishEvolution Jun2-6

We would like to invite you to the XVI European Congress of Ichthyology. The meeting will take place in the beautiful city of Lausanne, Switzerland from 2nd to 6th June 2019. Congress venue is the Aquatis Hotel at the Aquatis Aquarium, the largest freshwater aquarium-vivarium in Europe. The keynote speakers include Kevin Conway, Rajeev Raghaven, Bettina Reichenbacher, and Ole Seehausen.

NEW ABSTRACT SUBMISSION DEADLINE 31 MAY

More information can be found on our website: https://ecixvi.wixsite.com/ecixvi We are looking forward to welcoming you in Lausanne!

The XVI European Congress of Ichthyology Organising Team Lukas RÃÂ¼ber <lukas.ruber@nmbe.ch>

– Dr. Lukas RÃÂ¼ber Vertebrates Curator Ichthyology

+41 (0)31 350 72 82

NATURHISTORISCHES MUSEUM BERN Bernastrasse 15, CHÂ'Â3005 Bern www.nmbe.ch Eine Institution der Burgergemeinde Bern < https://www.bgbern.ch/ >

Ruber Lukas <lukas.ruber@nmbe.ch>

Lisbon 7thIberianPrimatological Oct9-11

7th Iberian Primatological Conference - "Empathy, Education and Conservation: Primates in a shared world"

Lisbon, Portugal, Sociedade de Geografia de Lisboa/Geographical Society of Lisbon (SGL) < http://www.socgeografialisboa.pt/en/ >

9th to 11th October 2019 (from Wednesday to Friday).

Website: https://7cip.apprimatologia.pt During the 7th edition of the Iberian Primatological Conference, the Associaçao Portuguesa de Primatologia (APP) < https://apprimatologia.pt/ > is responsible for organizing and hosting the congress in straight co-operation with the Asociación Primatológica Española (APE) < https://www.apespain.org/ >. This joint effort will combine the 7th Portuguese Primatology Conference (APP) with the 12th Congress of APE. This join conference aims to build a strong scientific bridge between the Portuguese and the Spanish primatologists by establishing network contacts and hopefully engaging researches, from both countries, in co-operative research activities. In spite of the name of the conference, other primatologists from all over the world are more than welcome to join us. More bridges can and should be created. Invited Speakers

Katherine Abernethy, University of Stirling, UK Inza Koné, CSRS (Centre Suisse de Recherches Scientifiques en Côte d'Ivore) Michael A. Huffman, Primate Research Institute, Kyoto University, Japan Conference official language

English is proposed as the conference language. All oral and poster communications must be presented in English, and abstracts must be submitted in English also.

Best wishes and hope to see some of you in Lisbon!

The organizing committee Tânia Minhós, PhD

Departamento de Antropologia Faculdade de Ciências Sociais e Humanas (FCSH) Universidade Nova de Lisboa (UNL) Av. Berna, 26-C 1069-061 Lisboa, Portugal Tel:+351 217908300 (Ext.1370)

Instituto Gulbenkian de Ciência (IGC) Rua da Quinta Grande, 6 P-2780-156 Oeiras, Portugal

taniaminhos@gmail.com

London MolluscComparativeGenomics Sep16-17

Pearls of wisdom: synergising leadership and expertise in molluscan genomics Monday 16 - Tuesday 17 September 2019 Kavli Royal Society Centre, Chicheley Hall, Newport Pagnell, Buckinghamshire, MK16 9JJ, UK Organised by Dr Angus Davison and Dr Maurine Neiman

I wanted to let you know that the Royal Society is holding a Theo Murphy meeting, Pearls of wisdom: synergising leadership and expertise in molluscan genomics, from 16 - 17 September 2019. The meeting is a 2-day event, held at Chicheley Hall, Buckinghamshire, and has a poster session for increased networking.

Although molluscs are ecologically, economically, and medically important, progress in understanding their biology has been limited by problems associated with genome sequencing and assembly. As technology breakthroughs overcome these challenges, this meeting will bring together experts in molluscan biology and genomics to share best practice in how to use these developments in elucidating the biology of this diverse and ill-understood phylum. More information on the speakers and programme is available on the website < https://royalsociety.org/science-events-and-lectures/-2019/09/pearls-of-wisdom/ >.

Registration for this meeting is free, but participants are required to register in advance of the meeting.

Sophia Coe Scientific Programmes Officer

T +44 20 7451 2503

The Royal Society 6-9 Carlton House Terrace London SW1Y 5AG royalsociety.org

Registered Charity No 207043

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

"Coe, Sophia" <Sophia.Coe@royalsociety.org>

Malawi SMBE EvolGenomics Sep18-22

SMBE Regional Meeting - Evolutionary genomics at the human-environment interface Malawi, Africa September 18-22, 2019.

https://smbe-malawi.org/ Abstract deadline extended. Register now. Travel awards for African researchers available.

Keynote speakers

Romulus Abila, Maasai Mara University Alex Cagan, Wellcome Sanger Institute Anne Charmantier, University of Montpellier Richard Durbin, University of Cambridge Sophie van der Heyden, University of Stellenbosch Cyprian Katongo, University of Zambia Peter Visscher, University of Queensland Naomi Wray, University of Queensland

Topics

- Genomics of invasive or alien species - Genomics of hybridization and introgression - Selection and adap-

tation - Population genetic inference - Meta-genomics - Genomics and resource management - The future of conservation genetics in Africa

Register now at https://smbe-malawi.org/ Abstract Deadline: June 30, 2019

Registration fee: 50/250 USD per person for African/international researchers

Travel grants available at https://smbe-malawi.org/ For the organising committee, Hannes Svardal

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

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

Hannes Svardal <hannes.svardal@uantwerpen.be>

Manchester SMBE Jul21-25 RegistrationAbstSubmission

SMBE 2019, 21-25 July 2019, Manchester, UK V Registration Early Bird Deadline Extension and Late Breaking Abstract Submission The SMBE 2019 registration early bird deadline has been extended, register by 23:59 (BST) on Wednesday 15 May in order to guarantee preferential registration rates. Information on the registration fees can be viewed at http://smbe2019.org/-registration/. SMBE 2019 is taking place in Manchester, UK on *21-25 July 2019* at the state of the art venue Manchester Central.

Full details on the symposia programme and confirmed keynote speakers can be viewed at http://-smbe2019.org/programme/ . Delegates can book your accommodation from a range of city centre properties within the registration system.

Delegates requiring a visa in order to attend SMBE 2019 can select this option within the registration system. The registration team will be able to assist in creating the documentation in order to support your visa application.

Carer Travel Awards (https://www.smbe.org/-smbe/AWARDS/AnnualMeetingTravelAwards/-CarerTravelAward.aspx) can be applied for as part of conference registration. SMBE will make available up to $2000 to SMBE members with children or dependent adults (including adult children with a disability or

elderly relatives) to spend as they wish to facilitate the members attendance at the annual SMBE meeting. Examples of eligible expenses include (but are not limited to) providing airfare for your child or for your caregiver to accompany you, flying a relative out to help with care at your home while youre at the meeting, or extra help paying for on-site daycare.

Late Breaking Abstract Submission V 1 May to 15 May V final chance to present your work The abstract submission portal will reopen for two weeks only. Abstracts are accepted for poster presentation only. The deadline for late breaking abstracts is 23:59 (BST) on Wednesday 15 May.

Abstracts should be no longer than 2500 characters (~250 words), with a title no longer than 300 characters. Full details on abstract topics, guidance and the submission portal can be found at http://smbe2019.org/-abstracts/ . Please note that individuals can only submit one abstract to SMBE 2019. If you have already submitted an abstract please do not submit another abstract as a late breaking abstract.

A range of sponsorship opportunities have been developed for the meeting, if interested please contact *SMBE2019@mci-group.com*

For any queries over abstracts or registration, please contact *SMBE2019@mci-group.com*

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

Manhattan Kansas ArthropodGenomics Jun12-14 deadline

Deadlines Quickly Approaching! V June 12-14, 2019 V 12th Arthropod Genomics Symposium at KSU Manhattan, KS Hi All:

We look forward to you joining us in Manhattan, KS in a little over a month. Visit our website at www.k-state.edu/agc/ags for more details about the symposium.

KEY DEADLINES Friday, May 10 V Hotel Blocks Expire Sunday, May 19 V Early Registration Deadline Monday, May 20 - Abstracts Due for Poster Sessions *abstracts received after May 20 may not be included in symposium abstract booklet

CURATION CLINIC: Gene Annotation using Apollo +

Pre-symposium workshop in the afternoon on Wednesday, June 12 before the symposium opens that evening at the K-State Alumni Center in Manhattan, KS. + This pre-symposium workshop is designed to introduce researchers who are working with annotated arthropod genomes to the Apollo curation tool. This online genome browser allows users to check if their gene annotations are supported by the data and correct them if required. No prior knowledge of Apollo is needed. The practical parts of the workshop will require a laptop computer that can connect to the WiFi. + If interested in participating in this workshop, please complete the google form. < https://goo.gl/-forms/9aoVnt9l1Sa8IQ0A2 > + More details will be provided as they become available on the symposium website, https://www.k-state.edu/agc/ags/schedule/-< https://www.k-state.edu/agc/ags/schedule/pre-symposium_workshop/index.html >

REGISTRATION Register online at the Symposium website, www.k-state.edu/agc/ags! OVERVIEW The symposium focuses on new insights gleaned from analyzing arthropod genomes and is designed for scientists interested in genomic studies of Arthropods, both model organisms and those of agricultural or health relevance. The program will include platform presentations, welcome reception and arthropod genomics-related poster sessions. A few poster abstract submissions will be selected for platform presentations. Postdoctoral, graduate, and undergraduate students are also encouraged to attend. Sessions begin Wednesday evening, June 12, with a Welcome Reception featuring our Keynote Speaker and conclude Friday evening, June 14, with a walk and dinner on Konza Prairie.

SPEAKERS Keynote Speaker: Denise Montell, Duggan Professor and Distinguished Professor from University of California Santa Barbara

Invited Speakers Include: + Yehuda Ben-Shahar, Washington University in St Louis + Kerri Coon, University of Wisconsin-Madison + Nsa Dada, US Centers for Disease Control and Prevention + Conor McMeniman, John Hopkins Bloomberg School of Public Health + Shahideh Nouri, Kansas State University + Luisa Orsini, University of Birmingham + Mark Rebeiz, University of Pittsburgh + Stephen ¥Fringy Richards, University of California Davis + Stephane Rombauts, Ghent University + Surya Saha, Boyce Thompson Institute + Nick Teets, University of Kentucky + Yoshinori Tomoyasu, Miami University + Jamie Walters, University of Kansas

Abstract Speakers Include: + Welcome Bender, Harvard Medical School + Josh Benoit, University of Cincinnati + Romain Feron, University of Lausanne and Swiss Institute of Bioinformatics + Nick Grishin, University of

Texas Southwestern + Liuqi Gu, University of Kansas + Sarah Kingan, Pacific Biosciences + Yiyuan Li, University of Texas at Austin + Olena Maiakovska, German Cancer Research Center (DKFZ) + Richard Meisel, University of Houston + Petr Nguyen, University of South Bohemia + Jan-Philip Oeyen, Zoological Research Museum Alexander Koenig + Livio Ruzzante, University of Lausanne and Swiss Institute of Bioinformatics + Maria Luisa Simoes, John Hopkins Bloomberg School of Public Health + Amanda Stahlke, University of Idaho + Kevin Sugier, CEA-Genoscope + Robert Waterhouse, University of Lausanne and Swiss Institute of Bioinformatics + Zixiao Zhao, University of Missouri + Jing Zhang, University of Texas Southwestern

POSTER SESSION Poster session will be scheduled for both Thursday and Friday of the symposium. This years sessions include: i5K/Comparative Genomics, Stress Response, Microbiome, Evo/Devo, Vector Biology & Bioinformatics. If interested in submitting an abstract for the poster session, please visit the website at www.k-state.edu/agc/ags. Abstracts are due for the Poster Session on Monday, May 20.

QUESTIONS: Contact Symposium Coordinator, Kascha Johnson at kascha@k-state.edu

If you would like to join the ArthropodNews to ensure receiving future notices, please send an email with your name and email address to kascha@k-state.edu.

2019 SYMPOSIUM ORGANIZING COMMITTEE:

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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

Marseilles EvolutionaryBiology Sep24-27

Dear All For the 23rd time we are organizing the Evolutionary Biology Meeting "at" Marseilles

The goal of the meeting is to gather together International scientists interested in the mechanisms of evolution that generate the incredible diversity of living things found on Earth .

The previous year programs are available on aeeb.fr Dates of the meeting : September : 24-27 2019. DL: 30 of June

web : aeeb.fr twitter :EvolBiolMeetingMarseilles

Best regards Pierre

< https://twitter.com/pontarotti >

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

Miami EvoDevoPanAm Jul30-Aug2

The Pan American Society for Evolutionary Developmental Biology 3rd Biennial Meeting July 30-August 2, 2019 University of Miami, Coral Gables

Abstract submission and meeting registration are now open!

Don't miss the opportunity to share your research with the evo-devo community, as a part of the 3rd Biennial Meeting of the Pan-American Society for Evolutionary Developmental Biology. We will meet July 30 to August 2, 2019, on the campus of the University of Miami, Coral Gables campus.

This year's invited speakers will include' - Kim Cooper - Karen Crow - Scott Gilbert - Manfred Laubichler - Vincent Lynch - Rajendhran Rajakumar - Patricia Schneider - Prashant Sharma 'with others to be announced soon.

The meeting will also feature a symposium honoring G'nter Wagner: ^{o}The Journal of Experimental Zoology (JEZ) and its role in the birth of Devo-Evo$\pm$.

Please visit http://www.evodevopanam.org/ for meeting updates and to register.

We look forward to seeing you in Miami!

- The PASEDB Executive Council

Dave Angelini <drangeli@colby.edu>

Montpellier DomesticationEvolution Jun3-7

Dear colleagues,

The detailed program for the Third Harlan Symposium, 3-7 June 2019, Montpellier is now out :

Please visit the website https://www.alphavisa.com/harlan/2019/ under the pre-program tab.

All speaker slots have been allocated, but posters are still welcome until the dates of the symposium (send abstract to harlan@alphavisa.com - inclusion in abstract book not garanteed).

Attendees still can register https://www.alphavisa.com/harlan/2019/registration.php We are looking forward to meeting you in June !

The organizing committee

Anne-Céline THUILLET <anne-celine.thuillet@ird.fr>

Padova Italy Evolution Sep1-4 ISEBawards

The Italian Society for Evolutionary Biology is pleased to announce the ISEB Awards that will be assigned during its 8th Congress to be held in Padova on 1-4 September 2019 (https://sibe2019.sibe-iseb.it)

Doctor Darwin Prize

Established by the Italian Society of Evolutionary Biology with the aim to stimulate interest and research related to the Evolutionary Medicine. The award consists in the amount of 1,000 granted to young researchers (up to 40 years old) members of the SIBE.

SIBE Prize

The Italian Society of Evolutionary Biology especially wants to promote the participation to the Congress of young researchers (younger than 40 years old), with a prize of 500 for the best published (or in press) article on Evolutionary Biology, in the period 2018-2019.

NEW!!! Best outreach project

The Italian Society for Evolutionary Biology decided to establish, for the first time, a prize of 500 for the best project of science communication, outreach, dissemination, and popularization in the fields of evolutionary biology, implemented in the period 2017-2019.

Best poster

The best poster will be voted by the congress attendees during the Congress,300 for the winner.

Best PhD student presentation

The best PhD presentation will be voted by the scientific committee of the Congress, 300 for the winner.

Please find all details about rules and procedures for assignment on SIBE 2019 website

https://sibe2019.sibe-iseb.it/awards.php We look forward to receiving your applications,

Lisa Locatello on behalf of the Organizing Committee

Department of Biology University of Padova, Italy

Italian Society for Evolutionary Biology: www.sibe-iseb.it Lisa Locatello <lisa.locatello@unipd.it>

Portland Oregon Sex Asex Jun2-4

If you were thinking about coming to a sexy meeting in a sexy city, register before it's too late!

The AGA has the friendliest symposia - small, good food and drink, lovely venues, great opportunities to interact with colleagues and hear wonderful speakers.

STUDENTS! (And post-docs). We have a couple of free registration slots. Email theaga@theaga.org if you'd like to attend.

https://www.theaga.org/program.htm Sex & Asex: The Genetics of Complex Life Cycles The American Genetic Association President's Symposium 2-4 June 2019, Portland, Oregon

Speakers: Key Distinguished Lecturer Sally Otto Rebecca Zufall, University of Houston Stacy Krueger-Hadfield, University of Alabama at Birmingham Matthew Hartfield, University of Edinburgh Laura Katz, Smith College Nadia Singh, University of Oregon Tanja Schwander, University of Lausanne, Switzerland Curt Lively, Indiana University Catherine Rushworth, UC Davis Solenn Stoeckel, INRA Rennes, France Jennifer Anderson, Uppsala University, Sweden Mercedes Burns, University of Maryland Jeannette Whitton, University of British Columbia

and – 8 oral presentations selected from student and early researcher abstracts.

Anjanette Baker <theaga@theaga.org>

theaga@theaga.org

Providence RI Evolution Jun21-25

EVOLUTION 2019 – Annual joint meeting of the ASN/SSB/SSE June 21-25, Rhode Island Convention Center in Providence, RI http://-www.evolutionmeetings.org **Poster sign-up closes 10 PM Eastern Daylight Time on MAY 15**

There is no selection process for posters; all those submitted by the deadline are accepted. Poster presenters will have access to our poster invite app just prior to the meeting; instructions will be sent by email. Contributed talks are full.

- Free professional childcare is available on-site. Bookings must be made by May 24 at the latest and are done as part of conference registration online.

- There are MANY optional events before and during the conference. Some required pre-registration. Details on the website.

- Hotel accommodations as filling but there are still single and double rooms at the Omni: https:-//www.evolutionmeetings.org/accommodation.html - Dorm accommodations are full.

- Talk and poster schedule will be posted in early June, as soon as it is available.

hrundle@uottawa.ca

Roscoff VirusEvolution Oct21-25 DeadlineJun21

Dear all,

this is a reminder for the Jacques Monod Conference entitled "Virus evolution on the mutualist - parasite continuum" that will be held in Roscoff (Britany, France) on October 21-25, 2019.

The deadline for abstract submision is June 21st.

More details about the conference can be found here: https://www.insb.cnrs.fr/virus-evolution-mutualist-parasite-continuum The list of invited speakers is the following:

Samuel Alizon (Montpellier, France), chairperson Raul

Andino (San Francisco, USA) Megan Baldridge (St Louis, USA) Monsef Benkirane (Montpellier, France) Ignacio Bravo (Montpellier, France) Siobain Duffy (Rutgers, USA) Christophe Fraser (Oxford, United Kingdom) Fernando Garcia-Arenal (Madrid, Spain) Clement Gilbert (Gif-sur-Yvette, France) Katia Koelle (Emory, USA) Eugene Koonin (Bethesda, USA) Philippe Lemey (Louvain, Belgium) Alice McHardy (Helmholtz, Germany) Yannis Michalakis (Montpellier, France) Marie-Agnes Petit (Jouy-en-Josas, France) Gwenael Piganeau (Banyuls, France) Thomas Pradeu (Bordeaux, France) Andrew Read (Penn State, USA) Roland Regoes (Zürich, Switzerland) Marilyn Roossinck (Penn State, USA) Carla Saleh (Paris, France) Rafael Sanjuan (Valencia, Spain) Pauline Scanlan (Cork, Ireland) Manuela Sironi (Bosisio Parini, Italy) Paul Turner (Yale, USA), vice-chairperson Stineke van Houte (Exeter, UK) Anne-Nathalie Volkoff (Montpellier, France) Lena Wilfert (Ulm, Germany)

Please do not hesitate to circulate this announcement!

- Samuel

– Samuel Alizon

samuel.alizon@cnrs.fr

MIVEGEC, CNRS, IRD, Université de Montpellier IRD, 911 Avenue Agropolis, BP 64501 34394 Montpellier Cedex 5, France

Phone: +33 4 48 19 18 67 Fax: +33 4 67 41 62 99

http://alizon.ouvaton.org/ Samuel.ALIZON@cnrs.fr

UChicago MidwestPopGen Aug16-17

Midwest Population Genetics Meeting 2019, August 16th-17th at the University of Chicago

[tl/dr] Info here: https://mwpg2019.wordpress.com/ Register here: https://docs.google.com/forms/d/e/-1FAIpQLSddJLtsd9G6zDFpaJng9f2y8zABLexPgBce7GNYO_jvLdt8SA viewform?usp=sf_link In order to continue to foster the sense of community for popgen groups in the Midwest, we are organizing the sixth annual Midwest PopGen conference. https://mwpg2019.wordpress.com/ The location and date this year will be The University of Chicago on August 16th-17th. The meeting will begin Friday at noon and continue to Saturday evening with a BBQ on Friday evening. If you would like to give an oral or poster presentation, please submit a title and

an abstract (talks only) by June 22nd. Submitters will be notified if their abstract is chosen for a talk by July 1st. We will select talks from submitted abstracts to balance the topics, career stage, etc. of the presenters. The meeting will be trainee-oriented, so students and postdocs are especially encouraged to present their work. There will be prizes awarded for best poster and best talk by a student and postdoc.

Registration is free [link https://docs.google.com/forms/d/e/-1FAIpQLSddJLtsd9G6zDFpaJng9f2y8zABLexPgBce7GNYiOEvuht36A/-viewform?usp=sf_link] please RSVP by August 1st (June 22nd for talk submissions). Registration will close earlier if capacity is reached.

Additional info / details / schedule etc. will be made available on https://mwpg2019.wordpress.com/ steinrue@uchicago.edu

steinrue@uchicago.edu

UK MolluscanGenomics Sep16-17 programme registration

Mollusks! Molluscs! Genomes and Long-reads!

The draft programme is now out for "Pearls of Wisdom", the first conference focused on molluscan genomics, at the Royal Society of London's Chicheley Hall, UK, 16th-17th September 2019. Co-organised by Dr Angus Davison, University of Nottingham (angus.davison@nottingham.ac.uk) and Dr Maurine Neiman, University of Iowa (maurine-neiman@uiowa.edu)

#pearls19

While all speaker slots have been allocated, we still have plenty of space for attendees. Posters welcome. Please request an invite via the Royal Society web page: https://royalsociety.org/science-events-and-lectures/2019/09/pearls-of-wisdom/ .There is no registration fee!

We anticipate that some funding may be available, especially to early-career scientists - email Angus for UK/EU-based scientists and Maurine for graduate students or postdocs who are US citizens or green-card holders.

Confirmed speakers:

Menno Schilthuizen @schilthuizen, Suzanne Saenko , Jeanne Serb @jeanne_serb, Mark Blaxter, Carrie

Albertin @CarrieOcto, Jin Sun, Matt Loose @mat-tloose, Andrew Calcino @AndrewCalcino, Marina Panova, Noriyuki Satoh, Marie-Agnes Coutellec, Peter Fields @peterdfields, Maurine Neiman @mneiman (co-organiser), Coen Adema, Otto Seppala @otto_seppala, Michael McCartney, Yale Passamanek, Kim Perry, Ximing Guo, Angus Davison @angus_davison (co-organiser)

Provisional programme: https://royalsociety.org/-science-events-and-lectures/2019/09/pearls-of-wisdom/ – Dr Angus Davison | Reader and Associate Professor in Evolutionary Genetics School of Life Sciences | University Park | University of Nottingham | NG7 2RD +44 (0) 115 8230322 | angus.davison@nottingham.uk | @angus_davison | angus.davison.org

Angus.Davison@nottingham.ac.uk

Zurich EvolutionAndMedicine Aug13-16

THE FIFTH ANNUAL MEETING OF THE INTERNATIONAL SOCIETY FOR EVOLUTION, MEDICINE, AND PUBLIC HEALTH

Just a few more days to register at the early bird discounted rate! Full information at https://-isemph.org/2019-Meeting All 134 talks are now listed with abstracts. https://isemph.org/ISEMPH-2019-Presentations-Card-View The Fifth Annual Meeting of the International Society for Evolution, Medicine, and Public Health will be in Zurich, Switzerland, August 13-16. Students, researchers and clinicians from medicine, nursing, evolutionary biology, ecology, genetics, anthropology, psychology, behavioral ecology and epidemiology are all welcome.

KEYNOTE SPEAKERS

Prof. Dario Valenzano, Max Planck Institute for Biology of Ageing, Germany: African killifishes shed light on the genomic basis of life history trait evolution in vertebrates.

Prof. Verena Schunemann, University of Zurich, Switzerland: Ancient DNA and pathogens: uncovering the past of human diseases

Prof. Bernard J. Crespi, Simon Fraser University, Canada: How evolutionary biology can frame a unified theory for understanding human mental illness.

Prof. Kayla King, University of Oxford, UK: Protectors vs. killers: microbes within the host as drivers of

pathogen evolution.

PLENARY TALKS BY PRIZE WINNERS

G.C Williams $5000 Prize winner: Dr. Jessica Marie Hoffman: Is antagonistic pleiotropy ubiquitous in aging biology?

Gilbert Omenn $5000 Prize winner: TBA (Nominate your paper now!)

SYMPOSIA

The Normal and the Pathological: Paul Griffiths

Translational and clinical applications of evolutionary medicine: Nicole Bender

Human Animal Health: Barbara Natterson-Horowitz and Nicole Bender

How does the microbiome affect the brain to moderate neurological disease risk and aetiology? :Molly Fox

Using evidence from the learning sciences to develop effective evolutionary medicine resources: Jay Labov

Palaeopathology and Evolutionary Medicine: Kimberley Plomp, Gillian Bentley, Charlotte Roberts & Sarah Elton

PRECONFERENCE WORKSHOP Oxytocin and so-cial disorders: from evolutionary perspectives to clinical applications

SOCIAL PROGRAM

Tuesday August 13, afternoon: Individual visit of several museums in the near of the University main building, for example the museum of wax moulages https://-www.moulagen.uzh.ch/en.html, the zoological museum https://www.zm.uzh.ch/en.html, or the anthropological museum https://www.uzh.ch/cmsssl/en/outreach/-museums/anthropologisches-museum.html . Tuesday August 13, evening: Welcome reception with bratwurst and beer (and vegetarian alternatives) on the University main building terrace

Wednesday August 14, evening: Make your own Swiss chocolate! Chocolate factory on the University main building terrace

Thursday August 15, evening: Conference Dinner

Friday August 16, evening: Farewell Dinner

Friday August 16, late evening: Guided night city tour

Saturday August 17, all day: Individual excursions in the surroundings of Zurich. Please visit the Zurich Tourism website https://www.zuerich.com/en . Randolph Nesse <nesse@asu.edu>

GradStudentPositions

Barcelona AncientGenomics

MSc and PhD positions in Biological Anthropology:

PhD/Master in Ancient Genomics of Iberians (Ironage) PhD/Master in Anthropological analysis of Iberian infants (Ironage)

For more information: http://grupsderecerca.uab.cat/-greab/node/173 Interested candidates please write to Cristina Santos (cristina.santos@uab.cat) and Assumpció Malgosa ([assumpcio.malgosa@uab.cat]assumpcio.malgosa@uab.cat) with a motivation letter and academic record. The evaluation of applications will begin immediately and will continue until a suitable candidate was found.

Cristina Maria Pereira Dos Santos <Cristina.Santos@uab.cat>

Barcelona ComputationalGenomics

PhD fellowship Barcelona

The group of Mar Albà (evolutionarygenomics.upf.edu) is seeking a candidate to do a PhD in Computational Genomics in our group at the Barcelona Biomedical Research Park (PRBB). The funding is available from Oct 2019, through a grant from the Spanish Science Ministry which includes an FPI PhD fellowship. The student will be enrolled in the Universitat Pompeu Fabra Doctorate Programme in Biomedicine and is expected to complete the PhD in 4 years.

The PhD project involves using genomic and high throughput RNA sequencing data to investigate the mechanisms of formation of new genes in different groups of organisms. The student is expected to have a degree in Biological Sciences or a related subject. Experience with the statistical package R and a programming language will be an advantage.

We are part of the Research Programme in Biomedical Informatics (GRIB) at Universitat Pompeu Fabra (UPF) and Hospital del Mar Reserach Institute (IMIM). The lab is located in the fourth floor of the Barcelona Biomedical Research Park (PRBB), a vibrant Research Center that includes a large community of researchers working in bioinformatics and genomics.

Interested candidates please write to Mar Albà (mar.alba@upf.edu) with a short motivation letter and academic record. The evaluation of applications will begin immediately and will continue until a suitable candidate has been found.

Representative publications:

Ruiz-Orera, J., Albà, M.M. (2019) Translation of small ORFs: roles in regulation and evolutionary innovation. Trends in Genetics, Vol. 35, 186-198.

Ruiz-Orera, J., Grau-Verdaguer, P., Villanueva-Cañas, J-L., Messeguer, X., Albà, M.M. (2018) Translation of neutrally evolving peptides provides a basis for de novo gene evolution. Nature Ecology and Evolution, vol. 2: 890 - 896.

thank you!

Mar

M.Mar Albà ICREA Research Professor Fundacio IMIM Universitat Pompeu Fabra, Barcelona +34933160516

"Albà Soler, Maria Del Mar" <MAlba@imim.es>

Bergen NeuronEvolution

PhD position There is a vacancy for a 4-year PhD student position at the Sars International Centre for Marine Molecular Biology in the research group of Dr. Pawel Burkhardt (www.sars.no < https://www.uib.no/en/-sarssenteret/114773/burkhardt-group >). The position is funded by Sars Centre core funding. The Sars Centre belongs to the University of Bergen and is partner of the European Molecular Biology Laboratory (EMBL) (www.embl.de). The place of work will be at the Sars Centre. The starting date is flexible, but should be no later than 01 October 2019.

About the project/work tasks: The goal of the Burkhardt group is to reconstruct the evolutionary origin of synapses and neurons. The group is particularly interested in studying synaptic protein homologs in choanoflagellates, sponges and ctenophores. We are looking for a highly self-motivated and enthusiastic PhD student with interests in evolutionary biology, neurobiology or cell biology. The successful candidate will undertake research with the possibility to use a variety of techniques, ranging from various biochemical methods to X-ray crystallography, super resolution immunofluorescence and electron microscopy, to study synaptic protein homologs in choanoflagellates and sponges (for examples see: Burkhardt et al, 2011 PNAS; Burkhardt et al, 2014 Mol Bio Evo; Bhattacharyya et al, 2016 eLife; Laundon et al, 2019 PLoS Biology). The PhD project will focus on when protein signalling complexes required for synaptic activity first evolved and how they functioned at a molecular level.

Qualifications and personal qualities:

* The applicant must hold a master's degree or the equivalent or must have submitted his/her master's thesis for assessment prior to the application deadline. It is a condition of employment that the master's degree has been awarded. * Routine experience in standard molecular and cellular biology techniques is required * Practical experience in a variety of biochemical techniques (e.g. protein expression & purification, Co-IPs, mass spec)

and with different fluorescence imaging techniques is highly desirable * Specific experience with choanoflagellates is beneficial, but not essential. * The ability to work both independently and to cooperate with others and a high motivation/enthusiasm is essential. * Proficiency in both written and oral English

About the PhD position: The duration of the PhD position is 4 years, of which 25 per cent of the time each year comprises required duties associated with research, teaching and dissemination of results. The employment period may be reduced if you have previously been employed in a recruitment position.

About the research training: As a PhD Candidate, you must participate in an approved educational programme for a PhD degree within a period of 4 years. A final plan for the implementation of the research training must be approved by the faculty within three months after you have commenced in the position. It is a condition that you satisfy the enrolment requirements for the PhD programme at the University of Bergen.

We can offer:

* A professional, challenging and international working environment. * Well-equipped, modern laboratories and facilities * Salary at pay grade 51 (Code 1017/Pay range 20, alternative 9) in the state salary scale. Currently equal to NOK 449.400. Further promotions are made according to qualifications and length of service in the position * Enrolment in the Norwegian Public Service Pension Fund. * A position in an inclusive workplace (IA enterprise). * Good welfare benefits < https://-www.uib.no/en/foremployees/30808/welfare >

Your application in English must include:

* A brief account of the applicant's research interests and motivation for applying for the position * The names and contact information for two reference persons. One of these must be the main advisor for the master's thesis or equivalent thesis * CV * Transcripts and diplomas showing completion of the bachelor's and master's degrees, or official confirmation that the master's thesis has been submitted * Relevant certificates/references * List of published papers and pre-prints or other relevant scientific work.

Please note that the entire application and relevant appendices with certified translations into English or a Scandinavian language must be uploaded at Jobbnorge. Applications submitted without required information or applications sent as e-mails will not be considered. Only submitted documents will be subjected to an expert assessment.

Application Deadline: 26 May 2019

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Berlin PopulationGeneticsGeneRegulation SingleCell

I have an open PhD position on an ERC-funded project looking at the impact of regulatory sequence variation on developmental gene expression using a combination of single-cell genomic data sets and evolutionary modelling. www.garfieldlab.org The position is for 3 years (with a 4th year extension possible) and is offered at the standard 66% TV-L 13.

The Garfield lab is based at the IRI for Life Sciences, a collaboration between Humboldt University, the Charité Medical Centre, and the Max Delbrück Centre for Molecular Medicine. As members of the IRI, researchers have access to facilities and training opportunities at all three institutions located on a common campus in central Berlin, including computational resources associated with the Berlin Institute of Health. Grad Students are affiliated with both the HU and the Systems Biology program at the MDC-BIMSB. We're also walking distance to the Museum for Natural History with its associated seminars and research efforts.

If you are interested, please send a CV and a cover letter to dagarfield@garfieldlab.org. Applications (and expressions of interest) will be accepted until June 1st, though start dates are negotiable.

Questions prior to application are, of course, most welcome.

David Garfield, PhD

Research Group Leader IRI Life Sciences Humboldt-Universität zu Berlin Philippstr. 13 (Haus 18, Rm. 108) 10115 Berlin, Germany

Office: +49 (0)30 2093-92382 Fax: +49 (0)30 2093-47908 info: www.garfieldlab.org email: david.garfield@hu-berlin.de

David Garfield <david.garfield@hu-berlin.de>

BielefeldU BirdBehaviouralEvolution

2 PHD positions on the behaviour ecology of shorebirds in Madagascar

1) Behavioural ecology meets disease biology and immuno-ecology 2) The scent of Madagascar plovers: communication or concealment?

2 PhD positions (3 years), Bielefeld University (Germany), Universities of Bath and Bristol (UK)

Supervisors: 1) Prof Oliver Kruger, Prof Tamás Szekely and 2) Dr Barbara Caspers, Prof Innes Cuthill

Mating systems and parental behaviour are among the most diverse social behaviours, and recent research suggests that the social environment influences these behaviours. Small plovers (Charadrius spp.) exhibit highly variable breeding systems, between and within species, making them an ideal model system for studying the causes and consequences of sex ratio variation. The objective of these studentships is to investigate these fundamental issues by means of fieldwork in three plover populations in Madagascar. The research builds on the results from previous successful studentships working with these birds.

We seek two bright and highly motivated students with strong interests in evolutionary ecology and behavioural ecology. Willingness to carry out fieldwork in a harsh tropical environment is essential for this position. The students will search for nests, trap birds and take blood and preen gland samples and record their behaviour. In addition, they will use molecular methods and chemical analysis in the laboratory. Previous experience with avian field biology or any other field experience in the tropics is very important.

Fieldwork will be in a remote and pristine location in SW Madagascar. Facilities are extremely basic, the weather can be very harsh, and a great deal of walking and cycling are required. Opportunities for outside communicate on are very limited. You must be physically fit, hard-working and meticulous, and have a proven ability to work independently. You must have a positive attitude and an ability to look after yourself (i.e. cook your own meals, deal with logistics and organise your own work over extended periods). Speaking French or Malagasy is advantageous, but not a requirement.

Project 1. Behavioural ecology meets disease biology and immuno-ecology. Supervisors: Oliver Kruger, Joe Hoffman, Nayden Chakarov, Tamás Székely. The aim of this project is to study the immune-ecological causes of sex ratio bias in three sympatric species of plovers with varying mating systems at one site in Madagascar. At which stage of the life cycle do mortality differences between the sexes emerge and what are the demographic consequences of these differences? We aim to experimentally manipulate parasite infection and load in plovers but also monitor the populations closely to find the proximate causes of the adult sex ratio biases previously described. In addition, the student will test hypotheses of mating system evolution, and develop demographic models to estimate key demographic properties of natural populations., statistical modelling and/or immunological techniques is advantageous. Strong quantitative skills are essential, and willingness to programme is a must.

Project 2. The scent of Madagascar plovers: communication or concealment? Supervisors: Barbara Caspers, Innes Cuthill, Tamás Székely. The aim of this project is to investigate the function of preen gland secretion variation in three sympatric species of plovers with varying mating systems at one site in Madagascar. Within the last decades various hypothesis have emerged, which will be tested using this unique study system. Using state of the art chemical analysis techniques together with behavioural experiments and molecular techniques we will investigate whether plovers change their preen gland composition to protect themselves, their chicks or eggs against microbes, or olfactory hunting predators, or in order to communicate with conspecifics.

These projects will provide cutting edge training in evolutionary biology, behavioural ecology and disease biology. In addition, the student will be involved in biodiversity conservation impact of the projects by working with local conservationists and training Malagasy students in field biology and conservation.

The students will be based at the Department of Animal Behaviour at Bielefeld University (www.uni-bielefeld.de/biologie/animalbehaviour.html). The Department is the oldest of its kind in Germany and currently hosts 6 Principal Investigators, 7 Postdocs and 20 PhD students. It offers a stimulating international environment and an excellent research infrastructure with access to state-of-the-art techniques. The working language of the Department is English. The students will also spend some of their time at the Universities of Bath (www.bath.ac.uk/bio-sci/biodiversity-lab/index.htm) and Bristol

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Budweis Czechia CichlidAdaptiveRadiation

Adaptive radiation of cichlid fish in rivers: Evolutionary genomics of replicated diversification in Neotropical pike cichlids

PhD position at the University of South Bohemia in Ceske Budejovice (Budweis, Czech Republic) available from: July 2019 (negotiable) application deadline: May 31st

More information: https://zoo.prf.jcu.cz/wp-content/-uploads/2019/05/PhD-position-at-USB-Adaptive-radiation-of-cichlid-fish-in-rivers.pdf   Project background: Adaptive radiations are often too rapid for the emergence of new relevant mutations between successive speciation events and are thus more likely to utilise standing genetic variation. Hybridization between species can instantaneously boost genetic diversity and create novel phenotypes, and thus facilitate speciation and adaptive radiation. On the other hand, the question whether interspecific hybridization is important as a mechanism that generates biological diversity is a matter of some controversy due to the argument that reduced fitness would typically render hybrids an evolutionary dead end.

The model system: Our research group has recently discovered and introduced an outstanding evolutionary model of replicated diversification that includes two independent riverine lineages of a South American cichlid genus, Crenicichla, inhabiting adjacent river basins (of the La Plata River) with similar geomorphology. Both clades show an extremely wide range of morphologies and coloration patterns tied closely with trophic ecology, in which the corresponding (and strikingly similar) ecomorphs from different basins have evolved independently. We have recently demonstrated, based on morphological tests of similarities, ancestral states and rates of evolution that the replicated ecomorphs arose via parallel processes of phenotypic and trophic diversification.

Goal of the project: The aim of this project is to bring new resolution into the study of microevolutionary processes of diversification based on whole-genome sequencing and RAD-seq genotyping. Phylogenomic and mor-

phological analyses will be used to better understand the biological and environmental factors underlying rapid speciation with special focus on the role of hybridization. To achieve full employment of the WGS/RAD data we will also sequence and assemble a reference genome of an appropriate congeneric species.

Research team: The student will work in a small team supervised by Lubomir Pialek and Oldrich Rican. The project will be conducted in close collaboration with Jorge Casciotta and Adriana Almirn (National University of La Plata, Argentina), Edward Burress (University of California, USA), and Milan Malinsky (University of Basel, Switzerland).

Time and place: The PhD position is available for three years, starting in July 2019 (starting date negotiable) at the Dept. of Zoology, Faculty of Science, University of South Bohemia, Czech Republic.

Applicant's desired qualification: Master's degree in biological sciences Understanding of the basic principles of population genetics and molecular evolution

See more details about the position and how to apply: https://zoo.prf.jcu.cz/wp-content/uploads/2019/05/-PhD-position-at-USB-Adaptive-radiation-of-cichlid-fish-in-rivers.pdf

Lubomir Pialek University of South Bohemia, Dept. of Zoology Branisovska 31, Ceske Budejovice, Czech Republic email: lubomir.pialek@prf.jcu.cz

Lubomr Pilek <lpialek@yahoo.com>

CharlesU PlantSpeciation

An interdisciplinary PhD project is available under the joint supervision of the Plant Repro Evo Lab (http://-plantreproevo.natur.cuni.cz) and Machac Lab (https:-/machac.weebly.com) at Charles University & Czech Academy of Sciences in Prague.

How sexual selection generates new species remains among the fundamental puzzles in evolution. Classic theory postulates that sexual selection produces divergence in sexual traits which, eventually, translates into reproductive barriers and large-scale speciation. Plants present excellent opportunities to test and extend the theory, given that sexual selection has been studied extensively at the gametic level in plants (competition between male pollen grains and female choice mediated by the flower stigmas and ovules). However, the genomic basis of sexual selection and its large-scale influence on plant speciation have yet to be examined.

The PhD project will bridge these gaps in current knowledge by integrating research from micro- and macroevolution. The microevolutionary research will involve developmental biology, transcriptomics and population genomics. Specifically, the student will evaluate genetic and phenotypic differentiation in sexual traits across several *Arabidopsis* species*, *using laboratory techniques. The macroevolutionary research will examine whether sexual traits (floral traits, pollination mode, etc.) translate into large-scale speciation in plants, using statistical techniques. By bridging two traditions in evolutionary research (micro- and macro-), the project will produce an integrative perspective on sexual selection and speciation. In the process, it will equip the PhD student with theoretical and practical skills currently in high demand in academia and private sector (plant reproduction biology, genomic techniques, statistics, programming).

We are looking for PhD student with interest in multi-disciplinary approaches, involving plant reproduction, genomics, and macroevolution. Previous experience in any of these fields is not required but will be beneficial. The project is supported jointly by the Department of Botany and the Center for Theoretical Studies (Charles University, Prague, Czech Republic) and combines the expertise from two related fields, under the supervision of Clment Lafon Placette (plant reproduction biology, genomics; http://plantreproevo.natur.cuni.cz) and Antonin Machac (macroevolution, macroecology; https://-machac.weebly.com/).

The project is expected to start on October 1, 2019. It will be financed for four years. The salary together with the doctoral stipend provided by the university (starting Ö 800 EUR, with significant raise over the years) is equivalent to the average salary within Prague, which represents currently one of the most vibrant cities in Europe, with rich social life, large international community, and opportunities for collaborative research across multiple institutes and universities located in the city. If you are interested, please send us an email explaining your motivations and your CV at lafonplc@natur.cuni.cz.

Clment Lafon Placette <lafonplc@natur.cuni.cz>

CIBIO InBio Portugal 4 EvolutinaryBiology

OPEN POSITIONS @ CIBIO-InBIO

2 PhD holder positions | Evolutionary Biology

CIBIO-InBIO, Portugal

Application deadline: May 29, 2019

< https://cibio.up.pt/open-positions-careers/details/-iceta-2019-47-48 > Click here for more information and to know how to apply

PhD holder position | Human Population Genomics, Quantitative Linguistics, Statistical Inference

CIBIO-InBIO, Portugal

Application deadline: May 29, 2019

< https://cibio.up.pt/open-positions-careers/details/-iceta-2019-49 > Click here for more information and to know how to apply

PhD holder position | Evolutionary Biology

CIBIO-InBIO, Portugal

Application deadline: May 29, 2019

< https://cibio.up.pt/open-positions-careers/details/-iceta-2019-52 > Click here for more information and to know how to apply

IT Specialist

CIBIO-InBIO, Portugal

Application deadline: June 10, 2019

< https://cibio.up.pt/open-positions-careers/details/-iceta-2019-54 > Click here for more information and to know how to apply

CIBIO-InBIO's Office for Science Communication and Outreach CIBIO - Research Center in Biodiversity and Genetic Resources InBIO Associate Laboratory University of Porto, Vairao Campus Rua Padre Armando Quintas 4485-661 Vairao Portugal

t: +351 252 660 400

e: divulgacao@cibio.up.pt

w: http://cibio.up.pt | http://www.inbio-la.pt

f: https://www.facebook.com/cibio.inbio

CIBIO-InBIO Divulgaçao

CNRS SorbonneU RedAlgaeEvolution

We have a PhD position to fill. The PhD subject (funded 100% by the CNRS) concerns the study of interactions that might favour the encounter of gametes in red algae of the genus /Gracilaria/. We are looking for students with an interest in Evolutionary Ecology and Genetics. The PhD will be co-supervised by Marie-Laure Guillemin (marielaure.guillemin@gmail.com), University of Valdivia, Chile; and Myriam Valero (valero@sb-roscoff.fr), Station Biologique de Roscoff, France. Applications must be submitted by July 15th, 2019. The description of the subject can be downloaded at: http://www.sb-roscoff.fr/en/2019/04/-19/phd-position-how-maximize-gametes-encounters-absence-flagellum?lab_ids&group_id=All – Myriam Valero UMI EBEA 3614, Evolutionary Biology and Ecology of Algae CNRS, Sorbonne Université, PUCCh, UACH Station Biologique de Roscoff CS 90074, Place Georges Teissier 29688 Roscoff cedex

Tel : (+33) 2 98 29 23 28 E-mail: valero@sb-roscoff.fr site web: http://www.sb-roscoff.fr/en/valero-myriam/-202 Valero Myriam <myriam.valero@sb-roscoff.fr>

DeakinU BirdEvolutionClimateChange

I am looking for an enthusiastic and motivated student to take up a PhD scholarship at Deakin University in Melbourne, Australia, as part of a project called 'Shape-Shifting Birds'.

The goal of this Australian Research Council-funded Project is to determine whether changes in body shape are an evolutionary response to climate change. Birds in warmer climates tend to have large extremities (bills and legs), increasing their surface area and enabling loss of excess heat. Increases in extremity size may therefore be a predicted consequence of climatic warming. The student will undertake an extensive comparative analysis of Australian birds, designed to identify a) which bird species are showing changes in body shape (bill and leg

morphology); b) what ecological (life-history, behaviour, habitat) factors determine such responses; c) whether these changes relate to fitness/survival and d) whether such changes are linked to long-term populations trends in Australian birds.

The project will involve extensive work in Australian museum collections, measuring bird morphology using traditional and modern (3D-scanning) techniques. There is also a strong analytical component, involving use of long-term field data on Australian bird species as well as phylogenetic comparative analysis of large-scale ecological data sets for Australian birds.

Applicants must enrol full time and hold an Honours degree (First Class) or an equivalent standard Master's degree with a substantial research component. Applicants will have good English-writing skills and preferably have experience with handling large data sets and appropriate techniques for analysing them (e.g. phylogenetic comparative analysis, linear models, model selection). Experience with R would be advantageous. Previous experience of either of working with museum specimens, or research experience with birds is desirable but not essential. PhD students receive a stipend of AU\$27,596 per annum tax exempt (2019 rate) plus a tuition fee waiver. A relocation allowance from \$500 to \$1,500 (for single to family) is awarded to students who are moving from interstate or overseas in order to study at Deakin. For international students only: you will also receive health coverage for the duration of the tuition fees offset (Duration is 3 years for stipend and 4 years for the tuition fees offset). Application letters (or inquiries) should sent, together with a CV to Dr Matthew Symonds (matthew.symonds@deakin.edu.au). Closing date for applications is 7th June 2019.

Dr Matthew Symonds Senior Lecturer in Ecology School of Life and Environmental Sciences Deakin University Burwood, VIC, 3125 Australia

Matthew Symonds <matthew.symonds@deakin.edu.au>

EstonianMarineInst AdaptationOncogenicEnv

APPLY FOR A PHD POSITION IN AN INTERNATIONAL PROJECT!

Pollution and cancer in aquatic environment

We invite candidates to apply for a PhD student position in an international research project focusing on pollu-

tion and cancer in aquatic environment. The applicant can have a background in either Evolutionary biology, marine biology, genetics, veterinary science or zoology. The project will involve field work on the Baltic Sea, laboratory analyses, work with captive fish, and many opportunities for international collaboration and travel. The PhD position will be host by the Estonian Marine Institute, but with tight collaboration with the Zoology Department at the University of Tartu. Main work will be conducted in Tartu, some work will also take place in Montpellier, France.

For more information and applying, please contact Tuul Sepp (tuul.sepp@gmail.com) and Mathieu Giraudeau (giraudeau.mathieu@gmail.com).

Deadline for applying is June 1st.

*Title of the project: *Natural adaptations to oncogenic aquatic environments: a study of contemporary evolution in Baltic Sea, using flounders and their cell lines

Supervisors: dr. Tuul Sepp (Department of Zoology, University of Tartu), dr. Lauri Saks (Marine Institute, University of Tartu), dr. Mathieu Giraudeau (CNRS; France)

*Description of the project: *All multicellular organisms have developed mechanisms to supress malignant processes. Our knowledge of these natural defence mechanisms against cancer is so far limited. A better understanding of adaptations to avoid cancer is crucial for building our understanding of evolution of cancer and finding novel possibilities for the treatment of cancer.

Human activities have resulted in large-scale environmental modifications. This unintentionally creates possibilities for using polluted environments as "natural laboratories" for studying the evolution of cancer defence mechanisms. While it is known that organisms that are naturally exposed to environmental pollutants can evolve specific adaptations to cope with pollutants and their adverse effects on fitness, almost no attention has been focused on contemporary natural adaptations to environmental oncogenic factors.

Hypothesis: In polluted habitats, local adaptation have developed in flounders to overcome the negative physiological effects of environmental oncogenic factors.

Methods: Baltic Sea is one of the most polluted marine areas in the world. Pollutant levels vary between localities, creating a gradient of more and less polluted habitats. Previous studies have indicated that cancerous lesions are common in flounders (*Platichthys flesus*) living in the Baltic Sea. Flounder is the main target species for monitoring health effects of contamination in

North Sea and Baltic Sea since the species is abundant, benthic, and inhabits shallow waters.

Stage 1. We will start with an assessment of the prevalence of tumors in flounders from 10-15 Baltic Sea localities differing in pollutant levels. We will conduct histological analyses for confirming cancers. We will assess cellular defence mechanisms against pollution along the gradient of polluted local habitats, using tissue samples collected from the field (immune defences, antioxidant defences and DNA damage).

Stage 2. Based on the data collected from the first stage of the project, we will conduct a captive study with flounders originating from differently polluted habitats to assess the plasticity and genetic background of investment in antioxidant and anti-tumor mechanisms in a common garden environment.

Stage 3. We will develop cell lines from wild fish to assess the effects of various environmental oncogenic factors on cell functioning and defence mechanisms on the level of gene expression.

giraudeau.mathieu@gmail.com   giraudeau.mathieu@gmail.com

EstonianU PikeGeneticsParasites

PhD position on northern pike genetics and parasites

A 4-year Ph.D. position is available focusing on population genetics and parasite fauna in northern pike (Esox lucius) at Estonian University of Life Sciences (Chair of Aquaculture) under the supervision of Prof. Anti Vasemägi and Dr. Veljo Kisand. More specifically, the project aims to i) develop and test the performance of DNA-based approaches for estimation of pike abundance and recruitment success in coastal Baltic Sea; ii) characterize inter- and intra-specific parasite diversity in pike using next-generation sequencing (NGS) approaches. This PhD project is a component of a larger project examining the alternative molecular genetic methods to estimate northern pike abundance (e.g. using environmental DNA and mark-recapture for quantification of biomass/abundance, sib-ship analysis for estimating effective number of breeders) and characterize parasite fauna (NGS for characterization of the trematode species in the family Diplostomidae). The PhD student will work with other PhD students focused on eDNA and mark-recapture analysis of pike.

Declining trends in the abundance of many fish species illustrate the urgent need to implement more informative monitoring programs and improve the efficiency of ongoing management and conservation actions. The northern pike (Esox lucius) is one of few abundant predatory fish species in Baltic Sea coastal areas. Declines of pike populations have been related to trophic cascades (an increase of mesopredators) and eutrophication symptoms. In addition, pike is a much-appreciated target for growing recreational and small-scale coastal commercial fisheries and thus has a significant socio-economical value. Over the last decades, severe local declines of Baltic pike have been reported, and although pike is not regarded as threatened in the Baltic Sea, there is still reason for conservation concern for many populations.

The PhD will join research groups of Vasemägi at the Chair of Aquaculture (Estonian University of Life Sciences) and Kisand at Institute of Technology (University of Tartu). The molecular work is jointly carried out in the labs of Riho Gross (https://www.researchgate.net/-lab/Riho-Gross-Lab) and Veljo Kisand (https://-www.tuit.ut.ee/en/research/veljo-kisand).

Duties: You will be part of our teams working with molecular ecology of fishes their parasites (https:-//www.researchgate.net/profile/Anti_Vasemaegi) and microbial symbionts and commensals (https://-www.researchgate.net/profile/Veljo_Kisand). You will carry out field-work, laboratory work, bioinformatics, and population genetic analyses. The principal responsibilities include phenotyping, sample collection, DNA extraction, microsatellite analysis, estimation of the effective number of breeders, NGS library preparation, analyses of NGS data, analysis of inter-and intraspecific diversity of parasites, writing manuscripts and keeping detailed notes and logs of the analyses.

Qualifications: The qualification requirement is the completion of a master's degree. Candidates should have a strong background and interest in ecology, population genetics and evolution, and motivation for highly collaborative team-based fieldwork. Suitable applicants have a strong background in next-generation sequencing data analysis and/or host-parasite interactions. Previous experience working with fish would be useful but is not required. The starting date for this position is Sept-Oct 2019. Excellent communication skills in both oral and written English are expected. Candidates should be able to work both independently and as part of a collaborative team.

Place of work: Tartu, Estonia. Form of employment: Fixed-term employment of 4 years. Extent: 100%. Starting date: By agreement; the position is available from Sept-Oct 2019, initial fieldwork will start in June-July 2019.

Application: The application should include a motivation letter, curriculum vitae, copies of degrees and transcripts of academic records, one copy of the dissertation for masters or undergraduate degree, a list of at least two references familiar with the applicant's qualifications and certified knowledge of the English language.

Please submit your application no later than 31th of May 2019 to anti.vasemagi@slu.se and kisand@ut.ee. For more information, please contact by email to anti.vasemagi@slu.se and kisand@ut.ee.

Contact persons: Prof. Anti Vasemägi anti.vasemagi@slu.se

Dr. Veljo Kisand kisand@ut.ee

När du skickar e-post till SLU så innebär detta att SLU behandlar dina personuppgifter. För att läsa mer om hur detta går till,

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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

ETH Zurich FungalPopGenetics

Title: Global population genetics of Cercospora beticola, cause of cercospora leaf spot on sugar beets

Summary: Cercospora beticola causes the most important fungal disease on sugar beets worldwide. A global collection of ~1000 strains of C. beticola will be assayed for 20 SSR markers. Population genetic analyses of these neutral loci will be used to elucidate global population structure and infer effective population size, reproductive mode, and extent of gene flow. 150 of the strains will be used to conduct an FST/QST analysis to determine the importance of local adaptation in selected populations. Using complete genome sequences from these 150 strains, a GWAS will be conducted to identify candidate genes underlying each trait.

Description: Cercospora leaf spot (CLS) caused by the fungus Cercospora beticola (Cb) is an important disease on sugar beets. CLS is typically controlled with fungicides, but resistance has become a problem in many locations and there would be economic and ecological benefits associated with using genetic resistance instead of fungicides to control CLS. Cb populations in Europe

and North America have already shown their ability to evolve resistance to fungicides, but it is unknown how they will respond to deployment of CLS resistant cultivars.

Pathogen population genetic structure has proven to be one of the best predictors of pathogen evolutionary potential. The core of this project is oriented around obtaining a detailed understanding of the population genetics of Cb to provide insight into the distribution of gene and genotype diversity within and among Cb populations sampled from different regions around the world. The results will enable quantitative assessments of the importance of sexual recombination, gene flow and effective population size, all of which affect a pathogen's evolutionary potential. This comprehensive population genetic analysis can be used to develop an overall risk assessment model for Cb that would consider both the evolution of virulence against resistance genes and the emergence of fungicide resistance. The analysis will also consider the potential for long-distance gene and genotype flow and the likely importance of sexual recombination.

In the first phase of the project, the student will obtain completely assembled PacBio genome sequences for 2 European strains of Cb and Illumina genome sequences for 10 additional strains of Cb. These genome sequences will be used to identify 20 robust SSR loci that can be assayed in ~1000 global strains of Cb, with 30-50 strains coming from each sugar beet field. The SSR data will be collected from all global strains and used to conduct detailed population genetic analyses.

In the second phase of the project, the student will identify ~150 global Cb strains to use in an FST/QST analysis. FST/QST analyses provide a powerful approach to identify quantitative traits that are under selection for local adaptation, as shown in our earlier work with three other fungal plant pathogens. In the framework of the FST/QST analysis, we will collect phenotypic data for a series of in vitro traits, including melanization, and growth rates at different temperatures, in the presence or absence of fungicides and in the presence or absence of reactive oxygen stress provided by hydrogen peroxide. For each trait, we will partition the phenotypic variance into components reflecting variance within field populations and between field populations (i.e. QST) and compare this to the distribution of neutral genetic variance for SNP markers (i.e. FST) distributed among the same populations. The SNP markers will be based on complete genome sequences obtained from each of the 150 strains used in the FST/QST analysis.

In the third phase of the project, the student will use the phenotype data collected in the FST/QST analysis and

the SNP data obtained from the 150 genome sequences to conduct a genome-wide association study (GWAS) aiming towards determining the genetic architecture of each quantitative trait and identifying candidate genes underlying each trait.

Qualifications of the applicants: Applicants should have a masters degree in bioinformatics, biology, microbiology or a similar qualification. Previous experience in population genetics, evolutionary biology, plant pathology or mycology will offer an advantage. We seek individuals who possess good collaboration skills, can take their own initiative, and work independently.

Research fields covered by this project include: Plant pathology, Population genetics, Population genomics, Microbiology, Ecology, Evolutionary biology, Quantitative genetics

The Plant Pathology Group in the Institute of Integrative Biology at the ETH: Our major areas of research are population genetics and genomics, evolutionary biology, evolutionary ecology, experimental evolution, phylogeography and molecular biology. Our primary experimental

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FUBerlin EcoEvo InsectImmunity

Freie Universitaet Berlin, Germany Open PhD position: Eco-evo-immunity of Drosophila ' bacteria interactions Application deadline: 10th June 2019

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 PhD position (TV-L E13, 50%) for the research project: Eco-evo-immunity of Drosophila ' bacteria interactions. The position is fixed-term and available for 3.5 years and it will start in August 2019, or as soon as possible thereafter.

Project background Our research lies in the field of eco-evo-immunology, focusing on host resistance and tolerance to infection (https://armitagelab.com/). Pathogens can have substantial negative fitness effects on their hosts. This creates a strong selection pressure on a host to have efficient immune defences. A host can counteract an infection by directly reducing its pathogen load, i.e., resistance, or by reducing the harm that the infection does to its fitness, i.e., tolerance. Given that resistance can be costly and involve autoimmune damage, a more resistant host is not always the fittest. Tolerance is therefore an interesting concept because it describes how well hosts are able to ameliorate the fitness costs of a given pathogen load. Resistance and tolerance are predicted to give contrasting perspectives on host-pathogen evolution and infectious diseases, therefore it is important to understand infection in the light of these two concepts. The project will involve studying the interaction between the host (Drosophila melanogaster) and bacterial pathogens during the infection process, with the objectives to understand how fitness parameters interrelate with each other and describe host sickness trajectories and the effects that defences have upon the evolution of the pathogen. The project will follow the progression of the infection within the host (resistance), and it's longitudinal effect on host fitness parameters such as health-, behaviour- and fecundity-tolerance.

Requirements 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. - Ability to work independently. - Good team-working and communication skills. - Laboratory experience with either bacteria or insects. - Good basic knowledge of statistics and experimental design. - Proficient in spoken and written English. - Experience: 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 with a short statement of motivation to join the research project (no more than one page), (2) a CV including details of your research experience 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: 21245101/22/19. The deadline for applications is the 10th June 2019. Interviews will take place as soon as possible after this date. The working language of the group is English. Please note that the position requires participation in teaching (2 hours per week during University semester time).

For further information, please don't hesitate to contact Sophie Armitage.

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

Iceland 2 SticklebackEvolution

Two PhD positions on ECO-EVO-DEVO dynamics in threespine stickleback of lake Mývatn, Iceland

Hólar University, Iceland, seeks two PhD students for a Grant of Excellence (RANNIS) project to study the dynamics of *Ecological (ECO), Evolutionary (EVO) and Developmental (DEVO) processes*

The phenotype is an important determinant of the dynamic interactions between ecological and evolutionary processes (eco-evolutionary dynamics) and the processes that shape biological diversity in face of global change. This project will study the interplay among ECO, EVO and DEVO to understand 1) the dual role of ecology in evolution (as driver of natural selection and phenotypic plasticity), 2) the molecular mechanisms underlying phenotypic variation, and 3) the feedbacks between phenotypic change and ecosystem function. The project uses threespine stickleback (*Gasterosteus aculeatus*) from lake Mývatn, Iceland, as a model. The project is led by Prof. Bjarni K. Kristjánsson (lead PI, Hólar University, Iceland) and Dr. Katja Räsänen (Swiss Federal Institute of Aquatic Sciences, Eawag, Switzerland). It is part of a large collaboration across Hólar University (Prof. Skúli Skúlason), Eawag (Dr. Blake Matthews), Univ. of Wisconsin-Madison, USA (Prof. Anthony R. Ives), Univ. of Iceland (Prof. Zophonías O. Jónsson) and the Mývatn research station (Dr. Árni Einarsson).

We are looking for two excellent PhD students to work on two complementary aspects of the project: *i) the determinants of phenotypic variation and ii) consequences of phenotypic and genetic variation for ecosystem processes. *Which of these aspects each student specifically focuses on will depend on their interests as well as expertise (to be stated in application, see below). These student projects are an integral part of research that includes long-term field data, laboratory, mesocosm and field experiments, genomics and mathematical modelling. We are an international research team dedicated to high quality training. The students will have the opportunity to conduct part of their research at the collaborative institutions.

Location: The students will be based at the Dept. of Aquaculture and Fish Biology (DAFB - http://holar.is/-en/department_of_aquaculture_and_fish_biology) at Hólar University (North Iceland) and registered at the Univ. of Iceland (Reykjavik). HU is situated in the beautiful Hjaltadalur (Skagafjordur), with offices and research laboratories in the nearby town Sauárkrókur. DAFB is an active research centre and the students will become part of a dynamic international team of graduate students and faculty. The beautiful natural setting and central location in North of Iceland offer both outdoor and cultural activities.

*Requirements: *The candidates must hold a MSc degree in a relevant field (e.g. Ecology, Molecular Biology, Evolution, or Development). The ideal candidates have a strong interest in *evolutionary ecology, *enjoy working in a dynamic group, and have experience from fieldwork and laboratory work (with relative importance depending on the project specifics). Expertise and interest in *molecular genetics (transcriptomics and/or genomics) is preferable.* Peer-reviewed publication(s), previous experience with animal experiments (fish in particular) will be a plus.

The working language is English. A valid driving license is a requirement.

This is a 100% position for three years. Salary is in accordance with the agreement between HU and Rannis. Rights and obligations follow the Act 70/1996 on the Rights and Obligations of Civil Servants.

Applicants should send an application letter, with a statement of research interests (incl. statement on favoured topic of PhD) and relevant experience (max. 2 pages), *curriculum vitae* with a list of publications, copies of academic qualifications and the names and e-mail addresses of three referees, *as a single pdf* to ecoevodevo@holar.is The positions are open until filled and suitable candidates will be interviewed on regular basis until the position is filled.

For further information contact Bjarni K. Kristjánsson (Head of the Dept. of Aquaculture and Fish Biology, Hólar Univ. College) (bjakk@holar.is) or Dr. Katja Räsänen (katja.rasanen@eawag.ch).

– Dr. Bjarni K. Kristjánsson, Prófessor Hólaskóli - Háskólinn á Hólum/ Hólar University College Hólar íHjaltadal Iceland bjakk@holar.is Phone: +354 4556300 holar.is

Bjarni Kristófer Kristjánsson <bjakk@holar.is>

Israel EvolutionHonestSignalling

Hi Brian,

Yes, this is an evolutionary project. I reworded the ad to stress that aspect:

The evolution of honest signalling: a test case using rock hyrax We are looking for an enthusiastic and fit graduate student (MSc or PhD) for a multidisciplinary project on the evolution of honest communication in wild rock hyrax. The project involves capturing, marking, sampling, observing, recording, and carrying out manipulation experiments in the Ein Gedi Nature Reserve, near the Dead Sea, Israel. The ideal applicant has a strong background in behavioural ecology and vocal communication, field experience handling wildlife, and an ability to work both independently, and as part of a team. Experience with sound analysis is an asset. Financial support includes a scholarship from Bar Ilan University, tuition, and TAship. For more information, please contact Dr. Lee Koren (Lee.Koren@biu.ac.il). Please include a CV and a cover letter with field experience and interests. Start date: November 2019.

Thanks and best wishes, Lee

Lee Koren, PhD The Mina and Everard Goodman Faculty of Life Sciences Bar-Ilan University Ramat Gan, 5290002 Israel

Institute of Nanotechnology and Advanced Materials (Building 206) Office B-940; Lab B-935 (9th floor) Telephones: office +972-3-7384371 lab +972-3-7384372 Skype: leezik Lee.Koren@biu.ac.il https://-leekoren.wixsite.com/korenlab Lee Koren Lab (Facebook page) @LeeKoren2 (Twitter)

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

JagiellonianU Poland InsectMicrobiomes

Ph.D. Student position: The diversity and dynamics of insect microbiomes

The new Symbiosis Evolution research group at the Institute of Environmental Sciences of Jagiellonian University in Krakow, Poland is seeking a motivated Ph.D. Student to join the project "The insect microbiome dynamics in time and space", recently funded by the Polish National Science Centre (NCN) OPUS grant.

Insects frequently associate with microbes, forming different types of symbiotic associations that often play major roles in the insect biology. We know that the microbiome abundance, composition, and roles vary among insect species, but they also often differ among populations, sampling dates, and among individuals sampled from a population at the same time. However, our understanding of the microbiome diversity patterns across insects, and factors that influence them, remains limited. Our team's goal is a broad, comprehensive survey of microbial symbioses across the diversity of Swedish insects. We will do this in close collaboration with Insect Biome Atlas, an international project sampling flying insect communities at hundreds of sites. We will use large numbers of insects carefully selected from that collection for the microbiome characterization using high-throughput next-generation sequencing. This approach will allow us to understand the microbiome composition across the taxonomic diversity of insects, as well as to describe the seasonal changes, geographic variation, and the effects of environmental factors on microbiomes of selected, broadly distributed species.

The Ph.D. Student will primarily focus on the study of the diversity of microbes across thousands of insect species, addressing the question of how the microbiomes vary across the insect phylogeny. Initially, the Student will work with Swedish partners on preparing and curating large numbers of insect specimens for the microbiome characterization, while learning the relevant bioinformatic techniques. They will also participate in high-throughput next-generation sequencing library preparation. However, their main task is going to be the bioinformatic analysis of large amounts of insect microbiome composition and metagenomics data. The Student will be encouraged to work closely with other team members and project collaborators, including Insect Biome Atlas consortium members in Sweden and Dr. Brandon Cooper at the University of Montana, U.S.A.

The Student will be based at one of the top research institutes in the fields of Ecology and Evolution in Central Europe, in a medieval city known as the cultural capital of Poland, with good access to outdoor recreation opportunities and well-connected to the rest of Europe. They will be supported by a 36-month, tax-free research stipend, starting at 3500 PLN (~800 EUR) per month and increasing during subsequent years to 4500 PLN (~1050 EUR) per month. This stipend may be combined with the standard Ph.D. program scholarship. Note that

in Poland, the living costs are relatively low (check out a cost-of-living calculator such as www.numbeo.com), and these amounts suffice for taking the full advantage of what Krakow has to offer. Generous funding is available for research and research travel.

The successful candidate will have an M.Sc. degree in a relevant field by July 2019; a demonstrated interest in Evolution, Entomology, Microbiology, and/or Genomics; experience with, or a keen interest in learning, Bioinformatics and Computational Biology; and strong English language, communication, and organizational skills. Previous experience with insect diversity, ecology, evolution, and especially symbioses, molecular biology, microbiome surveys, phylogenomics and/or comparative genomics, as well as willingness to travel are advantageous.

The candidates are asked to e-mail a cover letter explaining their background, skills, and interest in the project, a CV, and contact details of two academics who can provide a confidential reference, to Dr. Piotr Lukasik (p.lukasik@gmail.com). The review of applications is ongoing; please apply by 11th June 2019 to ensure full consideration. The selected candidate or candidates will be assisted with a formal application to the Ph.D. program at Jagiellonian University.

For more information, please check the group website (www.symbioses.pl), the Institute website (www.eko.uj.edu.pl/en_GB), or e-mail Piotr Lukasik directly. Candidates interested in the current position may also consider a Ph.D. opportunity in our team within a different project, focusing on the evolution of heritable nutritional endosymbionts of hemipteran insects: http://evol.mcmaster.ca/˜brian/evoldir/GradStudentPositions/-JagiellonianU_Poland.InsectSymbioses Piotr Lukasik

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JustusLiebigU ComparativeVenomic

PhD Position in Comparative Venomics

In the interdisciplinary Animal Venomics group based at the Institute for Insect Biotechnology, Justus-Liebig-University Gießen, a PhD position is available as soon as possible for three years (Experience depending the salary band will be TV-H 13, 65%) within the German Science Foundation funded project:

Venom evolution in solitary and eusocial aculeate hymenopterans

Tasks - Working in the project that focuses on comparative venomics and toxin evolution of social and solitary bees and wasps. One aim is to understand better processes that drive toxin evolution in hymenopterans. Genomes will be complementary analyzed to proteomics and transcriptomics data to tackle this major aspect. - Proteomics is in parallel conducted via collaborations, depending on the results activity tests and assays are planned for some interesting toxin candidates. - The project-work allows to conduct a PhD within this project.

Demanded skills and profile: - Applicants should hold a Diploma/Master degree in Biology or related natural sciences - Candidates should be highly motivated and should have a background in evolutionary biology, trait evolution and/or venomics - Proven background in transcriptomics and genomic work and analyses is necessary - Bioinformatics skills are important, experience in Perl or Python of advantage - Candidates should be self-organized but as well team players, good communication and English skills are important, the major tongue in the Animal Venomics group is English. - Fieldwork experience and taxonomic knowledge of hymenopterans is a further asset - Laboratory experience in RNA extraction, library reconstruction and/or HMW DNA extraction and general knowledge in proteomic work (HPLC, and MassSpec) is an advantage.

We offer a unique opportunity to grow and participate in an integrative environment within the new Animal Venomics group creating workflows comprising genomics, transcriptomics, proteomics, and protein characterization with evolutionary and applied perspectives. The main PI in this project is Dr. Björn M. von Reumont.

Gießen is a vibrant student town at the river Lahn in the green heart of the State Hessen, very central in Germany. Other, old university cities like Marburg or Wetzlar are located within 20 km. The metropolis Frankfurt with its large international airport is roughly 50 km away and its center can be reached from Gießen within 40 minutes by regional trains.

Please send applications without photograph and without date of birth as single PDF file including a CV (with two references), certificates, motivation letter (â1 page) with additionally a short summary of previous work and applied methods (â 1 page), and one reference letter to: Bjoern.Von-Reumont@agrar.uni-giessen.de.

The JLU Gießen promotes equal opportunities and diversity in its employment relations. Women are expressly encouraged to apply and given priority in accordance with the Equal Opportunities Act. We expressly welcome applications from individuals with severe disabilities or people of equivalent status. Severely disabled applicants of equal merit and qualifications will be given priority.

Application deadline is the 07.06.2019

Dr. Björn M. von Reumont

Research Associate LOEWE Center Translational Biodiversity Genomics University of Gießen & Fraunhofer IME Animal Venomics Winchesterstr 2 35394 Gießen Germany Tel +49 (0)641-99-39503

mob +49 (0) 151-61997924 www http://www.reumont.net Björn Marcus von Reumont <bmvr@arcor.de>

LeedsU EvolutionaryGenomics

4 year Faculty funded PhD studentship at the University of Leeds in Evolutionary Genomics of Galapagos Iguanas. Open to UK and EU students only.

This project provides a unique opportunity to examine adaptation and evolutionary history in an the marine (Amblyrhynchus cristatus) and land iguanas (Conolophus sp) of the Galapagos archipelago. Both genera of Galapagos iguanas originate from the same common ancestor, diverging around 4.5-10.5 million years ago, with both groups subsequently spreading across the archipelago. Land iguanas diversified to form 3 species - Conolophus subcristatus, native to six islands, and Conolophus pallidus, which is restricted to Santa Fe. The third species Conolophus marthae, known as the pink iguana, is only found on Volcan Wolf at the northern end of Isabela. It was only recently recognised as forming a genetically and ecologically distinct species and is now considered endangered due to its small population size and restricted distribution.

The process of divergence and diversification among these iguanas has generated many novel adaptations over relatively short evolutionary timescales V most strikingly adaptation to diving and the marine environment in Amblyrhynchus cristatus, which is the worlds only fully marine lizard. Land iguanas have their own adaptations to the harsh terrestrial environment in the Galapagos, including diet, tolerance of arid conditions and fluctuating resources, as well as various differences in morphology and pigmentation. This provides an amazing natural model system for evolutionary biologists to characterise the genomic basis of adaptation and novel phenotypes; the process of speciation, including mechanisms that prevent hybridization and genetic introgression; as well as characterising the origins and history of iguana populations. These can be linked with palao- and present environmental data to yield a better understanding of the environmental and ecological conditions which drove the evolution of these species.

The project is a part of a collaborative iguana genome and evolution consortium led by Dr Gabriele Gentile at the University of Rome Tor Vergata. Dr Gentile has been pioneering the study and conservation of pink iguanas for many years. The student will spend time working in both Leeds and Rome.

Multiple genome sequences for all land and marine iguana species are currently being generated, as a result of a collaboration between the University of Rome Tor Vergata and the Universiti Kebangsaan Malaysia (Prof. Mohd Firdaus Raih) and will be completed shortly.

This is essentially a bioinformatics/computation project, but there may be opportunities to gain hands on laboratory experience of associated DNA sequencing techniques. The project will use data from a range of Next Generation Sequencing (NGS) approaches including de novo sequencing on Illumina and other platforms to build and annotate de novo assemblies of iguana genomes. Data will be then be analysed with a range of bioinformatics, population genomics and molecular evolution tools in high performance computing environments, as appropriate to the research questions.

An interest in working at the interface of ecology, biodiversity and population/evolutionary genomics is desirable. Prior experience of bioinformatics is helpful but not essential. However interest in developing skills in bioinformatics and computing is important. This project is part of a consortium involving researchers from the University of Leeds, University of Rome, Tor Vergata, and Universiti Kebangsaan, Malaysia. The student will join the Ecology and Evolution group in the School of Biology, Leeds, and will be integrated with the LIDA and Leeds Omics, virtual institutes which encompass a large group of researchers working on genomics and bioinformatics related projects. The student will also spend significant time working with Dr Gentile in Rome, and visiting other collaborating institutions across Europe and further afield.

Please contact Dr Simon Goodman (s.j.goodman@leeds.ac.uk) or Dr Gabriele Gentile (gabriele.gentile@uniroma2.it) for more information

about the project.

Apply online here: https://-
biologicalsciences.leeds.ac.uk/dir-record/research-
opportunities/398/fbs-studentships-school-of-biology
Closing date for applications 31st May 2019

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

Leipzig
SeaCowComparativeGenomics

PhD student (m/f/d) (TV-L E13, 65%)

Location: Rudolf Schönheimer Institute of Biochemistry
(Faculty of Medicine) and the Max Planck Institute for
Evolutionary Anthropology Leipzig, Germany

Starting date: Spring/Summer 2019

Project: We are looking for a highly motivated PhD
student for a 3-year position. The main project deals
with comparative genomics of the ancient Steller's Sea
Cow Genome. This project aims to identify pathways
and genes involved in body size and energy storage by
comparing the genomes of the ancient Steller's sea cow,
possibly the largest recent non-cetacean mammal, to
the ones of the modern smaller sirenians, the dugong
and the manatee. We also intend to detect how climate
adaptation may shape genetic data by selection since un-
like the modern sirenians, which are adapted to a warm
climate, the Steller's sea cow inhabited arctic environ-
ments. Additionally, we will build the phylogenetic tree
of the sirenians, including genomic data of the hyraxes
as a more distant outgroup than the African elephant.
A second running project deals with gene expression pro-
files of lipomas. By analyzing the differential expression
of genes in lipoma versus matched normal subcutaneous
adipose tissue we intend to identify genetic networks
that are involved in lipid accumulation with a long-term
goal of better understanding mechanisms of obesity. At
the Rudolf Schönheimer Institute of Biochemistry (Fac-
ulty of Medicine) we aim to understand medicine in the
context of evolution. Leipzig University developed a
major research focus in obesity. The two projects the
PhD student is involved in inquires the same question
using different perspectives and techniques.

Collaboration Partners: The project offers stimulating
interactions and training opportunities including the
Human Genetics Institute in Leipzig, the Institute for
Biochemistry and Biology, Department of Mathematics
and Natural Sciences, Potsdam University, and the De-

partment of Bioinformatics and Genetics of the Swedish
Museum of Natural History.

Profile of candidate's qualifications: If you are highly
motivated, fascinated by evolution and translating the
findings to modern medicine, this may be the right po-
sition for you. Programming experience in R, python,
and C++, as well as working in Linux environment will
be of benefit.

Our offer: - a supportive and international working
environment - access to cutting edge genomics, com-
puting, and research facilities - the chance to pursue
fundamental research of medical relevance - enrollment
and graduation within the International Max Planck
Research Schools (IMPRS) Programme

Interested? Please send your full application as a PDF
to diana_leduc@eva.mpg.de

– Diana Le Duc, M.D./Ph.D. Max Planck Institute for
Evolutionary Anthropology Department of Evolutionary
Genetics Deutscher Platz 6 D-04103 Leipzig

Phone +49 (0)341-3550-544 Email:
diana_leduc@eva.mpg.de Gabriela-
Diana.LeDuc@medizin.uni-leipzig.de

Diana LeDuc <diana_leduc@eva.mpg.de>

LMU Munich Paleobiology

*Applications invited for the Master's program "Geo-
biology and Paleobiology" (MGAP) at the Ludwig-
Maximilians-Universität (LMU) Munich (Germany) for
EU students until 31 May 2019*

The Master's program "Geobiology and Paleobiology"
(MGAP) is a consecutive, research-focussed, two-year
Master of Science program at the Faculty of Geosciences
of the Ludwig-Maximilians-Universität (LMU) Munich,
in collaboration with researchers of the Bavarian Natu-
ral History Collections and the GeoBio-Center @ LMU.
MGAP aims to provide students with a comprehensive
introduction into the interdisciplinary research fields of
geobiology and paleobiology.

The MGAP program is based on interdisciplinary,
research-oriented courses in geo- and biosciences that ad-
dress patterns and processes of evolutionary and environ-
mental geobiology and paleobiology. The module-based
curriculum provides an integrative approach facilitated
by experts in different areas of expertise. Students will
learn and acquire routines with a wide range of scien-

tific methods such as modern techniques in molecular biology, fieldwork, collection management, comparative morphology, phylogeny, bioinformatics, statistics and (paleo-) biodiversity assessments. Students will learn independent scientific work in individual and intensively supervised research projects at early stages of the curriculum.

MGAP in brief

- International Master's program in Geobiology and Paleobiology (Master of Science, M.Sc.) at the LMU Munich

- 2 years, 4 semesters, start in October (winter semester)

- All courses taught in English

- Course total: 120 credit points (ECTS)

More information is available on the program's website: < http://www.mgap.geo.uni-muenchen.de >

Applications have to be submitted via our online submission portal:

<   https://www.efv.verwaltung.uni-muenchen.de/-mageopal >

PD Dr. Oliver Voigt

mgap@geo.lmu.de

Mainz Germany 14 GeneRegulationInEvolution

Dear colleagues,

14 PhD positions can be offered in Mainz as part of a new, DFG funded Research Training Group:

"Gene Regulation in Evolution: From Molecular to Extended Phenotypes" (GenEvo < https://www.imb.de/-about-imb/joint-research-initiatives/genevo/ >).

PhD projects are carried out at the Biology department of Johannes Gutenberg University Mainz or at the Institute of Molecular Biology (IMB).

We offer to our students

* The possibility to work on exciting, interdisciplinary projects at the interface between gene regulation and evolution * A team of dedicated advisors from several disciplines * Numerous opportunities for advanced professional training in scientific knowledge, techniques and professional skills * Fully-funded researcher positions (EG 65% contracts) * Use of state-of-the-art technology

in highly motivated research teams * A lively and very international student community

The following projects are available in GenEvo groups:

Joachim Burger, Falk Butter, Miguel Andrade: A genome-wide view of human adaptation to novel selective environments using ancient genome data

Julian Konig, Joachim Burger, Thomas Hankeln: The molecular evolution of Alu

Thomas Hankeln, Miguel Andrade: Gene expression regulation in the adaptive evolution of the hypoxia-tolerant rodent Spalax

René Ketting, David Rosenkranz, Hans Zischler: Systematic comparative analysis of nematode small RNA pathways

René Ketting, Falk Butter, Susanne Gerber: Comparative analysis of evolutionary changes in the transcriptome and proteome in nematodes

Petra Beli, René Ketting, Thomas Hankeln: Evolution of gene regulation induced by the ultraviolet radiation stress response

Eva Wolf, Miguel Andrade, Susanne Foitzik: Structural insights into the evolution of circadian gene regulation

Helen May-Simera, Martin Kaltenpoth, Susanne Gerber: Evolution of 'cilia' proteins in gene regulatory mechanisms

Peter Baumann, Romain Libbrecht: Epigenetic diversity and adaptation in parthenogenetic lizards

Romain Libbrecht, René Ketting: Gene regulatory mechanisms modulating reproductive activity in ants

Susanne Foitzik, Peter Baumann, Susanne Gerber: The role of gene regulation in the division of labour in ants

Susanne Foitzik, Peter Baumann, Falk Butter: Parasite interference in regulation of host gene expression

Martin Kaltenpoth, Christof Niehrs: Evolution of molecular mechanisms regulating mutualism establishment

During the application process, one to several projects can be chosen. Please select in the online application form for each project you are interested in (up to 5) the adviser listed in bold. For further details, please visit our GenEvo page < https://www.imb.de/about-imb/joint-research-initiatives/genevo/ > and read more about all projects < https://www.imb.de/students-postdocs/international-phd-programme/apply-to-ipp/-projects-offered/ >.

We appreciate your help in spreading the word among your colleagues and master students who may be inter-

ested to apply.

With kind regards Susanne Foitzik

Prof. Dr. Susanne Foitzik Evolutionsbiologie Institut fur Zoologie Johannes Gutenberg Universität Mainz Johannes von Muller Weg 6 55099 Mainz

Tel: +49 (0) 6131 39 27 840 Fax: +49 (0)6131 39 27 850 Email: foitzik@uni-mainz.de

"Foitzik, Susanne" <foitzik@uni-mainz.de>

Mainz Germany 3 SocialInsectEvolution

3 PhD positions in evolutionary biology of social insects at the Johannes Gutenberg University of Mainz, Germany The Institute of Organismic and Molecular Evolution is seeking candidates for 3 PhD positions (starting October 1st 2019) to study the molecular regulation of ant social life within the Research Training Group GenEvo.

Position 1 ' Molecular regulation of reproduction in insect societies (co-supervised by Romain Libbrecht and René Ketting). The main feature of social insects is the reproductive division of labour, whereby queens monopolize reproduction while sterile workers perform other tasks to maintain the colony. Investigating the molecular mechanisms regulating reproduction and division of labour in ants is necessary to understand the evolution and ecological success of insect societies. The clonal raider ant O. biroi has emerged as a powerful study system to investigate gene regulatory processes and the molecular regulation of reproduction (Chandra et al. 2018, Libbrecht et al. 2016, Libbrecht et al. 2018). This project will identify putative gene regulatory mechanisms associated with reproduction, and investigate the functional link between social cues (presence of larvae), regulatory mechanisms, gene expression, and reproduction. It will thus shed light on the regulation and evolution of reproductive division of labour in insect societies, as well as on how gene regulation can translate social cues into physiological changes.

Position 2 ' Gene regulation and division of labour (co-supervised by Susanne Foitzik, Peter Baumann, Susanne Gerber). Social insect workers specialise in specific tasks and this division of labour contributes to the ecological success of insect societies. Task specialisation is mostly neither genetically determined nor rigid, but changes with age and colony needs. Typically, young workers takeover brood care, whereas older workers focus on risky tasks. The expression of behavioural genes shifts with the tasks of workers and histone acetylation can regulate task-specific gene expression (Simola et al. 2016). Our preliminary work revealed division of labour, the expression and functions of task-specific genes (Feldmeyer et al. 2014; Kohlmeier et al. 2018; 2019), and the importance of histone acetylation for their expression in the ant Temnothorax longispinosus. This projects aims to understand how different regulatory processes respond to external cues, the expression of which genes they alter and how fast they can change gene expression. It will thus give insights into the molecular regulation of worker division of labour in social insects.

Position 3 ' Parasite interference with gene regulation of a social host (co-supervised by Susanne Foitzik, Peter Baumann, Falk Butter). Parasites with complex life cycles often manipulate the behaviour of their intermediate hosts to increase transmission to the definite host and we hypothesise that they do so by interfering with host gene regulation. Infection of Temnothorax nylanderi ant larvae with the parasitic cestode Anomotaenia brevis strongly alters the adult phenotype. Parasitized workers exhibit altered behaviour, morphology, chemical profile and a lifespan extension (Scharf et al. 2012, Beros et al. 2015), and these changes are linked to transcriptomic alterations (Feldmeyer et al. 2016). The cestode, residing in its cysticercoid stage in the ants' gaster is transcriptionally active and releases many proteins into the host. The aim of this project is to demonstrate that parasite-induced changes in host phenotype are actively promoted by the parasite. We therefore will study how the cestode parasite interferes with the hosts' gene regulation, which gene-regulatory mechanisms are utilised and whether these alterations are permanent or have to be actively maintained. This project will reveal genetic and epigenetic underpinnings of behaviour and longevity in social insects and will uncover the mechanisms of across-species interference in gene regulation.

We are looking for highly motivated students with a Master degree (or equivalent) in biology, good English skills, and a keen interest in evolutionary biology. Previous experience with social insects, statistics and bioinformatics is advantageous, but not required. Successful applicants will join an international, interactive, dynamic and English-speaking scientific environment in a brand new building with access to state-of-the-art, newly equipped laboratories and climate-controlled rooms. The JGU of Mainz hosts many excellent scientific institutions, and Mainz is a historic city located on the Rhine River with a large student population and a rich social and cultural life.

Interested candidates should apply to the IPP summer

call 2019. They will have to register before May 22nd 2019 and complete their application before May 27th 2019. Informal enquiries should be sent to Dr. Romain Libbrecht (romain.libbrecht@uni-mainz.de) for position 1 and Dr. Susanne

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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

Marseille MasterProgram CompMathBiology

Dear EvolDir Community,

I'd like to bring to your attention a new international Master program on "Computational and Mathematical Biology" at the Turing Center for Living Systems in Marseille, France. While not strictly evolutionary, the program might still be of interest for quantitatively-oriented students. For more information, see http://centuri-livingsystems.org/cmb/ . Michael Kopp, Aix-Marseille University http://-www.i2m.univ-amu.fr/perso/michael.kopp/ Michael Kopp <michael.kopp@univ-amu.fr>

MonashU MitonuclearEcol

PhD projects in mitonuclear ecology, genetics, and behaviour

TWO fully-funded Ph.D. positions are available for projects that will seek to understand how genetic variation within the mitochondrial genome influences organism performance, life history, and evolution.

The projects will involve testing emerging hypotheses from the rapidly growing field known as "mitonuclear ecology," which explores how mitochondrial genetics and biochemistry (driven by interacting mitochondrial and nuclear genomes) influence fundamental behavioural, ecological, and evolutionary processes-from the complex pre-copulatory behaviours associated with mating to reproductive outcomes to ageing.

Project 1 will address the physiological and behavioural consequences of variation in mitochondrial performance. The project will test new hypotheses for how mitochondrial function affects individual "quality" and thereby mating behaviour; depending on student experience and interests, the project can test these hypotheses from the bottom up (biochemistry/physiology) and/or the top down (evolutionary/behavioural ecology).

Project 2 will address the genotypic contributions of mitochondrial and nuclear genomes (and their interactions) to sex differences in organismal life history, from reproductive performance to longevity. This project will explore the functional consequences of mito-nuclear genetic variation, with a focus on testing an evolutionary hypothesis known as "Mother's Curse" $\frac{3}{4}$i.e, that maternal inheritance of mitochondria has led to the accumulation of mutations within the mitochondrial DNA sequence that confer harm to males, but which are benign or beneficial in effect to females.

Both projects will integrate techniques and experimental designs drawn from evolutionary biology, ecology, genetics, and physiology. A key tool will be genetic strains of fruit flies (Drosophila melanogaster) in which different mitochondrial DNA haplotypes have been introgressed alongside a diverse set of nuclear DNA backgrounds. This system offers the invaluable opportunity to separate mitochondrial and nuclear genetic effects on organismal function, exploring the downstream consequences of mitochondrial variation on individual behaviors and physiology. There will be full flexibility for the successful applicants to pursue their own academic ideas and interests within the scope of their projects.

We are seeking students who are highly motivated and passionate about evolutionary biology, the mechanistic bases of animal behaviour, and/or mitonuclear ecology; applicants should be familiar with the fundamentals of evolutionary theory and behavioural ecology. The successful candidates will be supervised by A/Prof. Damian Dowling (damiandowlinglab.com) and Dr. Rebecca Adrian (rkadrian.com) within the Experimental Evolutionary Biology Lab at Monash University's School of Biological Sciences $\frac{3}{4}$a vibrant group comprising other PhD students, postdoctoral associates, and undergraduate researchers, with access to state-of-the-art technology platforms for the study of evolutionary genetics, physiology, and behaviour.

The successful applicant will be awarded a scholarship that covers salary (current rate is $27,872 AUD tax-free per year), a waiver of student fees, and the option to supplement salary through teaching assistance during undergraduate lab courses. The position includes funding for international and national conference visits and

for all research costs.

Monash and the School of Biological Sciences Monash University is a member of Australia's "Group of Eight"-a coalition of research-intensive universities-and is internationally recognized for excellence in research and teaching. The School of Biological Sciences (http://monash.edu/science/about/schools/-biological-sciences/) is home to a collegial and world-class research environment, with key strengths in evolutionary ecology and genomics.

Melbourne Monash University is located in the suburbs of Melbourne, Australia, a vibrant cultural and recreational centre that is consistently rated one of the world's most liveable cities (http://en.wikipedia.org/-wiki/World's_most_livable_cities).

Application process

Interested candidates should send their CV, a copy of their academic transcript, and a cover letter outlining their research interests to rebecca.adrian@monash.edu and damian.dowling@monash.edu. Enquiries prior to application are welcome.

For further information on Ph.D. scholarships and Monash application procedures, please visit http://monash.edu/science/about/schools/biological-sciences/postgrad rebecca.adrian@monash.edu

Montpellier EcologyButterflyInversions

PhD studentship on the ecology of inversions and balancing selection in butterflies, CNRS Montpellier France

A fully-funded 3-year PhD studentship is available at the CNRS Center for Evolutionary and Functional Ecology (CEFE) in Montpellier, France, under the supervision of Mathieu Joron, on the ecology of balancing selection.

Closing date. 12/06/2019. Application portal: http://-bit.ly/2JV8AyB The project focuses on deciphering the evolution of a complex of polymorphic inversions forming a supergene in an Amazonian butterfly (Heliconius numata). The supergene controls switches in wing pattern elements, whose linked variation produces distinct morphs shaped by natural selection favouring mimicry with other defended species. Inversion polymorphism is promoted by negative assortative (or 'disassortative') mate preferences among mimetic morphs. Yet we ignore why and how these preferences have evolved, or how

inversion polymorphism has become associated with a diversity of wing patterns. The PhD project will help decipher the selective factors (viability trade-offs, deleterious variation, etc.) and the mating cues associated with the maintenance of inversion polymorphism, and will improve our understanding of the stability of complex polymorphisms involving the covariation of multiple traits.

The project will largely rest on insectary and field experimental data. Diverse approaches to characterise trait variation associated with inversions may be developed during the PhD (e.g. morphometrics, chemical ecology, physiology...). The project allows for much flexibility in the direction taken, depending on the student's interests and ideas. By collaborating with team members focused on the genomics of inversions, the student will also be able to tackle the link between natural and sexual selection and the underlying genetic architecture of traits.

The student will join a lively consortium of teams whose research combines experimental approaches with population genomics (CEFE Montpellier), bioinformatics (Claire Lemaitre, INRIA Rennes), and evolutionary theory (Violaine Llaurens, MNHN Paris).

The student will receive first-class education in biology bridging many disciplines from behavioural ecology to evolutionary genomics and bioinformatics. The student will attend advanced courses, workshops and conferences, will interact with other team members working on related projects, and will report his/her results in progress meeting, international conferences, publications, and a written thesis in French or in English which should be completed within three years.

The student must have a degree in ecology/evolution, a keen interest in ecology and evolution and excellent understanding of the underlying theory, outstanding academic achievement, a background in experimental or field-based research, and must not be afraid of working with caterpillars. Independence and motivation are essential to successfully carry out challenging field and experimental work overseas in the Amazon, as well as with collaborating teams in French Guiana and Panama.

The CEFE is the largest ecology lab in France and is a major institute for evolutionary ecology and genetics. Within CEFE, our team comprises 12 researchers whose research combines genetics and evolutionary ecology to address a diversity of topics on adaptation and natural variation. Our group focuses on butterfly wing patterns as a model to decipher how diversity is shaped by natural selection and other processes at the phenotypic and genomic level. Montpellier is a major hotspot for evolutionary and environmental research worldwide and

has a vibrant research community with several hundred researchers in this domain, and highly praised graduate programmes. The University of Montpellier ranked 1st in the 2018 Shanghai ranking in Ecology. Montpellier lies near the Mediterranean region in the South of France and enjoys pleasant weather, fantastic nature and great cultural and city life.

Starting date should be in September or October 2019. Net salary is around 20.5Keuro /year, including social benefits and public health insurance.

Applications should be done through the CNRS portal. See http://bit.ly/2JV8AyB. Applicants should upload a letter of application explaining their motivation and achievements, a paragraph on the preferred questions they would like to address or focus on during the project, a full CV, academic transcripts, and the names and contact details of two references. Closing date. 12/06/2019.

For information and informal enquiry, please contact Mathieu Joron (Mathieu.joron@cefe.cnrs.fr). Website : http://joron.cefe.cnrs.fr

NewCaledonia MSc FieldAssist

M.Sc. students/ field assistants

We are looking for 2-3 field assistants to conduct research on avian behavioural ecology in New Caledonia. M.Sc. students interested in conducting a field project for their thesis are particularly encouraged to apply. The main project is part of a long-term study on the co-evolutionary arms race between the Fan-tailed Gerygone and the Shining Bronze-cuckoo in New Caledonia. There are several possible secondary projects for a M.Sc. thesis:

- frontline of the arms race between Shining Bronze-cuckoo and Fan- tailed Gerygone - spatial ecology of the Fan-tailed Gerygone - breeding ecology of small passerines in New Caledonia - vocal repertoire and communication of the Fan-tailed Gerygone

Period: 2-3 months, from October to December 2019 (exact dates to be agreed).

Location: fieldwork will be conducted at several field sites on the main island of Grande Terre, New Caledonia. These include tropical wet forest, secondary forest and dry savannah habitats with abundant birdlife.

Duties: main duties include searching for and monitoring nests during the breeding season, behavioural observations, mist-netting and banding, video analysis, maintenance of field equipment. Additional experimental work will vary depending on the secondary project chosen by the applicant in agreement with the project leader. Field activities will require on average 10-12 working hours a day plus commute to the field sites (max 2 hours drive), at least 5 days a week (6-7 days a week during the peak of the breeding season) and an early morning start.

Experience: behavioural observation of banded birds, nest searching, mist-netting, banding and use of photo traps desired. Additional training will be provided. Previous experience of working in a tropical environment is also desirable. Physical fitness, enthusiasm and self-motivation are required as fieldwork will be physically demanding and conducted in a variety of environments sometimes in extreme weather conditions (UV exposure, heat, humidity, rain). Ability to work independently or as part of a group and to share living spaces are a necessity. A driving license is also required.

Selected applicants will need to cover their travel expenses to and from New Caledonia. The project will offer a monthly wage of 80000 XPF (670 EUR) for food costs and living expenses. Accommodation will be provided. To apply, please email a single PDF file containing CV, a brief description of relevant field work/research experience and potential project (or projects) of choice to attisano@miiz.waw.pl (deadline 30/06/2019). Selected applicants will be contacted within one week from the deadline to arrange a Skype interview. For informal enquiries and more information please contact: Alfredo Attisano (attisano@miiz.waw.pl) or Jörn Theuerkauf (jtheuer@miiz.eu).

Alfredo Attisano <attisano@miiz.waw.pl>

NHM Bern FishPhylogenomics

Call for a PhD Student in Comparative Genomics and Phylogenomics of Miniature Fishes

Natural History Museum Bern, Switzerland Start in August 2019

We are seeking to fill a PhD position funded by the Swiss National Science Foundation (SNSF) in the group of Lukas RÃÂ¼ber to look at comparative genomics and phylogenomics of miniature fishes. This is a joint placement between the Department of Vertebrates, Natural History Museum Bern (NMBE) and the Institute

of Ecology and Evolution (IEE), University of Bern.

The zebrafish, Danio rerio, is one of the most important vertebrate models for studies of development, genome evolution, and disease. This project aims to investigate the evolutionary consequences of miniaturization in close relatives of the zebrafish, including some of the most striking examples of miniaturization in vertebrates. We recently sequenced the genome of the dwarf minnow genus Paedocypris, comprising the smallest fish species, to investigate for the first time the genomic consequences of miniaturization in vertebrate species. We discovered drastic genome size reduction and extensive loss of Hox and other developmental genes in Paedocypris (MalmstrÃÂm et al. 2018, https://doi.org/10.1093/gbe/evy058). In the PhD project, we will use whole genome data for an in-depth exploration of the evolutionary consequences of miniaturization in a broader comparative framework by providing a robust phylogenetic framework of zebrafish relatives. We will examine whether genome size reduction and extensive loss of developmental genes are general features of miniaturization in these fishes.

We are looking for a committed and enthusiastic candidate with an MSc or an equivalent university degree in biology/bioinformatics and a strong background/interest in evolutionary biology, phylogenetics, genomics and bioinformatics. Experience in tropical fieldwork and knowledge of fish systematics is an advantage. The PhD candidate will conduct demanding fieldwork in Southeast Asia collecting miniature cyprinid fishes, carry out whole genome sequencing of the collected material, and conduct phylogenomic analyses and comparative genomic analyses focusing on the evolution of genome size and Hox genes in the group. Our working language is English and excellent communication and writing skills in English are essential.

The project involves several partners including Ralf Britz (Natural History Museum, UK), Richard Durbin (University of Cambridge, UK), Kerstin Howe (Wellcome Sanger Institute, UK), Catherine Peichel (University of Bern, Switzerland) and Walter Salzburger (University of Basel, Switzerland). During the duration of the project, there will be opportunities for short-term visits to the laboratories of the project partners. Lukas RÃÂ$\frac{1}{4}$ber (NMBE and IEE) will supervise the PhD student with co-supervision provided by Catherine Peichel and Walter Salzburger.

Salary for this four-year project is at SNSF PhD Fellowship level and the position is available from August 1st, 2019.

Bern is a vibrant city with a beautiful historic old town that has been declared a UNESCO World Heritage Site offering excellent quality of life. The nearby majestic Bernese Alps invite for a variety of outdoor activities.

Please email your complete application in a single pdf file containing the following: 1) your CV and publication list, 2) a letter of motivation, 3) a copy of your MSc or an equivalent university degree with grades, and 4) contact details of three referees to Lukas RÃÂ$\frac{1}{4}$ber (lukas.ruber@nmbe.ch). Review of applications starts on May 31, 2019 and continues until the position is filled. Please direct further inquiries to Lukas RÃÂ$\frac{1}{4}$ber (lukas.ruber@nmbe.ch).

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Dr. Lukas RÃÂ$\frac{1}{4}$ber Vertebrates Curator Ichthyology

+41 (0)31 350 72 82

NATURHISTORISCHES MUSEUM BERN Bernastrasse 15, CHÂ'Â3005 Bern www.nmbe.ch Eine Institution der Burgergemeinde Bern < https://www.bgbern.ch/ >

Ruber Lukas <lukas.ruber@nmbe.ch>

NorthDakotaStateU GrapeColdAdaptation

Cold tolerance in North Dakota grape cultivars

Two MS positions are available to study the mechanisms contributing to cold adaptation in North Dakota grape cultivars with Jill Hamilton (Biological Sciences) and Harlene Hatterman-Valenti (Plant Sciences) at North Dakota State University in Fargo, North Dakota available starting August 2019 or January 2020.

The ability to grow competitively, while reducing the risk of winter injury represents a critical trade-off mediated by environmental cues for many species. In grapevines, sensitivity to environmental cues, particularly temperature and photoperiod, which may accelerate or delay development of dormancy, will impact cultivar health and consequent fruit production. This project aims to comprehensively assess the interaction between temperature cues, phenology, and cold hardiness across multiple growing seasons in North Dakota grape cultivars. This project will systematically assess the fine-scale relationship between temperature and the induction and breakup of dormancy and dormancy-related traits for six grape cultivars replicated four times across two distinct environments. The graduate student will (i) monitor temperature, (ii) phenological shifts over time

in response to environmental cues, and (iii) estimate development of cold hardiness using electrolytic leakage or differential thermal analysis. Data developed through this research will be used to test and optimize models that simulate life history transitions in response to environmental cues for North Dakota grape cultivars. Results from this work will provide valuable information for varietal development and may be used for risk-management to predict winter injury.

The ideal MS student will be prepared to lead field-based research monitoring phenological shifts in response to shifting environmental (temperature) cues and testing for cold hardiness using different experimental approaches, including electrolytic leakage and differential thermal analysis. In addition, the student will test an established model using North Dakota grape cultivars that predicts shifts in cold hardiness associated with the induction and breakup of dormancy. There is plenty of room to pursue particular interests in adaptive trait variation depending on the interest and experience of the candidate. The student will also be involved in outreach activities associated with the project engaging with local state agencies, grape growers, and wine producers in the region. Ability to work independently in the field, alongside basic botanical and plant physiology expertise is required. Some experience in quantitative analysis and modeling in R and previous experience evaluating physiological trait variation is preferred.

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

Interested students are encouraged to contact Dr. Hamilton (jill.hamilton@ndsu.edu). Please include a brief description of your research interests, experience, and a CV in your email. This position is funded via a USDA Specialty Crop Block Grant and includes a full tuition waiver plus $18,000/year stipend. Options are available for both US and international students.

Tentative start date is August 15, 2019, although a January start date is possible. Applications are being accepted now and the position will remain open until filled.

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

Paris ReproductiveSuccessFromGenomicData

Application should be made through this link

https://emploi.cnrs.fr/Offres/Doctorant/UMR7206-TAOLAH-001/Default.aspx?lang=EN   TransIA: Machine Learning based Inference of Cultural Transmission of Reproductive Success using Genomic Data

General information

Reference : UMR7206-TAOLAH-001 Workplace : PARIS 16 Date of publication : Friday, May 10, 2019 Scientific Responsible name : HEYER Evelyne Type of Contract : PhD Student contract / Thesis offer Contract Period : 36 months Start date of the thesis : 1 October 2019 Proportion of work : Full time Remuneration : 2 135,00 €gross monthly

Description of the thesis topic

Abstract Due to the access to large amounts of genomic data and the recent advancements in IA, several machine learning based methods are currently being developed in the population genetics field, among which a few aim at reconstructing the demographic history of populations. A challenge is to integrate in the studies of human populations cultural phenomena such as the cultural transmission of reproductive success. This transmission exists when the reproductive success of individuals depends on a cultural trait (wealth, social status, network of knowledge) that is itself transmitted from one generation to the next. This process strongly influences the evolution of genetic diversity and we have previously designed a statistic that detects unilinear transmission based on the unbalance of coalescence trees (through women with mitochondrial DNA or through men with the Y chromosome). The objective of this PhD is to focus on an entirely different scale thanks to large sets of genomic data and develop machine learning and deep learning methods capable of detecting this transmission when it affects the entire genome as a result of transmission by both men and women.

Aims Developing methods that can detect the existence of transmission of reproductive success in large genomic data sets by combining a set of signals. Machine learning approaches make it possible to jointly use multiple patterns, whether computed based on expert knowledge, or detected automatically. However, these methods,

and in particular the ones based on deep learning, have never been used for the inference of cultural traits and have been emerging only recently in population genetics. Methods (1) Simulations of whole genome genetic data under different scenarios, with or without transmission of reproductive success (based on forward simulations in which one can integrate complex processes such as a reproduction success depending on the number of siblings) (2) Implementation of several statistics related to the transmission of reproductive success, demography and selection (tree shape, Fst, shared haplotype length, allele frequencies) and exploration of their distribution along the genome for extreme scenarios. These generated data and statistics will be used to train or test the following statistical learning approaches. (3) Semi-automatic inference. Methodological development for classification (predict whether or not there is a transmission of reproductive success) and inference (estimate of transmission factor) from the summary statistics proposed in step (2) using Approximate Bayesian Computation and Random Forest (Pudlo et al., 2016, Raynal et al., 2017) or deep MLP networks (Multi Layer Perceptron, Sheehan and Song 2016). This approach will allow the use of a large number of summary statistics, hence a better coverage of the characteristics of the transmission process. (4) Automatic inference. Replacing the task of designing and choosing expert statistics with the automatic detection of signals characterizing the transmission of the success of the reproduction. To do this, the same set of simulated genetic data can be used to train a more complex neural network. In particular, it has been shown very recently that demography, selection and recombination signals (at the population level) can be detected using convolutional neural networks (work in progress at LRI, Sanchez et al. JDSE2017, Chan et al., 2018, Flagel et al., 2018). These methods need to be extended to the estimation the transmission of reproductive success. (5) Applications to modern human genetic data

Skills Python and / or R programming, bash Machine learning / Applied statistics Knowledge in population genetics

Keywords IA - Big Data Genomics - Cultural Transmission - Human Evolution Work Context

Assigned to the Musée de l'Homme (Paris) at the Eco-anthropology laboratory - UMR7206, attached to the team Genetic anthropology (AGène)under the direction of Pr Evelyne HEYER, and co-direction of Frédéric AUSTERLITZ (Directeur de recherche,Eco-anthropology) and Flora JAY (Chargée de recherche, Laboratoire de Recherche en Informatique (LRI), Orsay/Saclay - UMR8623)

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QueenMaryLondon AfricanCattleEvolution

Queen Mary University of London Funded PhD position: Genomics of African indigenous cattle Deadline: 23rd June 2019

We are currently seeking highly motivated PhD student for a fully-funded project to start in September 2019. The project will focus on analysing molecular data from modern and museum cattle samples to unravel their population histories in Sub-Saharan Africa.

Sub-Saharan Africa is home to a rich but poorly understood diversity of indigenous cattle breeds. Many of the regions ~150 indigenous breeds show unusual resistance to extremes of climate and disease, and these traits are likely to become increasingly important in the face of climate change and mixing of stocks. Despite this, many of these local cattle breeds are endangered, facing threats from uncontrolled crossbreeding, as well as from replacement by exotic yet ill-adapted European breeds. There is a now an urgent need to identify and characterise the genomic diversity of African cattle, to better manage and retain genetic diversity and avoid the permanent loss of desirable traits.

Genetically-varied African cattle breeds have evolved from a complex history of artificial and natural selection. The student will use genomic methods to reconstruct these processes. These analyses will be able to address key questions concerning African cattle, such as the origin and number of introductions of zebu cattle. The student will also perform analyses to quantify genetic diversity available in African cattle populations, and identify key genetic markers for disease, fertility and drought resistance in the genome of specific populations.

This studentship is fully-funded by Queen Mary University of London (QMUL) and is aligned to the UKs overseas development strategy. The PhD student will be trained in population genetics, genomics and bioinformatics by the supervisory team. Data collection, generation, and analyses will be funded by our non-academic partner SilverStreet Capital.

The successful candidate is expected to have a strong academic background with a at least a 1st class or

2.1 Bachelors degree (or equivalent). An MSc in a relevant field (genomics, evolutionary biology, bioinformatics), and an interest in animal domestication, evolutionary genetics, and/or conservation issues, would also be advantageous. Candidates can contact either Laurent Frantz (laurent.frantz@qmul.ac.uk), Stephen Rossiter (s.j.rossiter@qmul.ac.uk), or Chris Faulkes (c.g.faulkes@qmul.ac.uk) for further details.

Send you application via https://www.qmul.ac.uk/-sbcs/postgraduate/phd-programmes/projects/display-title-654499-en.html laurent.frantz@gmail.com

QueensU
SeabirdGenomicAdaptation

I am looking for a Canadian citizen or landed immigrant to fill a PhD position studying genomics of adaptation in arctic seabirds (abstract below). The student will be part of an NSERC Strategic project to aid conservation and management of several species. Applicants must have a background in evolutionary genetics. Practical experience with genomics and bioinformatics is an asset. Field work on remote islands will be required. The successful applicant will join a dynamic group of faculty and students studying ecology and evolution at Queen's University. Please send a resume or curriculum vitae, informal transcript, and contact information for two academic references to Dr. Vicki Friesen (vlf@queensu.ca). The deadline for completed applications is June 12 2019, so please contact me asap.

Dr. Vicki Friesen, Professor Department of Biology, 4443 Biosciences, 116 Barrie Street, Queen's University, Kingston, ON K7L 3N6, Canada Tel: 613-533-6156 Fax: 613-533-6617 Email: vlf@queensu.ca Website: http://-post.queensu.ca/˜birdpop/index.html As numerically dominant apex predators, seabirds are key components of Canada's arctic marine ecosystem. Seabirds and their eggs also are important to the culture and diet of indigenous Arctic peoples. However, Arctic seabird populations are facing multiple simultaneous direct and indirect threats from climate change, shipping and industrial development. Unsurprisingly, many populations are showing signs of stress such as reduced reproductive success or declining numbers. To avoid extinction, wildlife populations must adapt through (1) changes in behaviour or physiology, (2) dispersal, or (3) genetic changes. The capacity for seabirds to adapt through these three avenues is virtually unknown, but it is criti-

cal to maintenance of healthy populations. New genomic methods, especially when combined with on-going studies of behaviour and physiology, provide powerful opportunities to determine the long-term sensitivities of Arctic seabirds to climate change and industrial development. We will use genomic, behavioural and ecological data in a landscape context to estimate levels of phenotypic plasticity, dispersal, and genomic variation for seven seabird species that Canada has a global responsibility to protect. Results will help Environment and Climate Change Canada (ECCC) develop science-based policies for Arctic stewardship. The students will be responsible for analysis of one species, and will gain training in population and landscape genomics, bioinformatics, population modeling and arctic ecology.

vlf@queensu.ca

Tours France
InsectPlantInteractions

Tours.France.InsectInteractionNetworks.PhD

We are looking for a candidate to do a PhD on Temporal dynamics of insect assemblages and interactions in oilseed rape crops the general conditions are:

Contract Period : 36 months Start date of the thesis : 1 October 2019 Remuneration : 2 135,00 gross monthly

Scientific Background Among the potential solutions for a sustainable agriculture, the concept of ecological intensification is particularly promising. It hinges on the hypothesis that by acting on populations and diversity of service providers, it is possible to increase the multi-functionality of ecosystems. To fully deploy an ecological intensification strategy and ensure optimum delivery of ecosystem services, a better understanding of the underpinning mechanisms shaping not only biodiversity but also interaction networks and their associated services is needed. In agroecosystems, regulatory services such as animal pollination and biological control of pests are particularly important because they have the potential to maintain or increase crop production while reducing chemical inputs. These services are based not only on key species but also on their trophic interactions. Food webs are traditionally described as stable states while they are intrinsically dynamic. This is particularly true in agricultural landscapes of annual crops where resources vary considerably throughout the season until the almost complete disappearance of the base of the food web (the primary producer). When harvesting an

annual crop, the sudden disappearance of the resource and habitat leads to a drastic reduction of invertebrate populations and consequently a collapse of the food webs. Yet these networks are re-built every year from a limited number of early colonisers coming from neighbouring "refuge" habitat (e.g. natural or semi-natural habitat), or emerging directly from the field when they manage to survive winter and soil handling (e.g. tillage). In theory, the first individuals that manage to colonise early in the season are likely to determine the make-up of the future populations within a given year and in a given field.

Aim The aim of this PhD project is to describe of the temporal dynamics of species assemblages and interaction networks involving key species of regulatory services in oilseed rape (OSR) crops. The three services selected for the project are 1) predation of insect pests by ground beetles, 2) impact of parasitoid wasps on aphids and 3) pollination by wild and domestic bees. This PhD project will use innovative environmental genomics tools to describe the spatial and temporal dynamics of insect trophic interactions. A DNA metabarcoding approach will be applied to the stomach contents of ground beetles caught in Barber traps, parasitized aphids (mummies) collected on the OSR and pollen pellets collected by wild and domestic bees.

Methods High throughput DNA sequencing and field observations will help decipher trophic interactions and quantify regulatory services (predation, parasitism, pollination) provided by predatory beetles, parasitoids and pollinators. These regulatory services will be studied in rape crops through the analysis of food web dynamics on a very fine time scale (monthly surveys) and wide spatial scale (from the plot to the landscape). For this, about thirty fields of rapeseed will be sampled each year on the Zone Atelier Plaine and Val de Sévres. This study site includes 19,000 agricultural parcels covering 450 km2, and offers a quasi-experimental context where it is possible to test the impact of agricultural practices and landscape heterogeneity on the structuring and dynamics of interaction networks. Plots selected for the study will be distributed along gradients of interest such as agricultural intensification or distance to semi-natural areas. In addition, an existing research partnership between farmers and the CEBC AGRIPOP team will lead to controlled experiments in the field.

Prerequisites This project will be based at the Insect Biology Research Institute (IRBI) in Tours and will include sample collection campaigns at the Chizé Biological Study Center (CEBC). Samples will be analyzed by DNA metabarcoding (on Illumina platform) and the dynamics of interaction networks will be analysed in relation to spatial distribution, environmental hetero-

geneity and agricultural practices. - The candidate will be comfortable in the field and in a molecular biology laboratory - Experience in basic molecular methods (DNA extraction, PCR, electrophoresis) is essential - Basic knowledge in bioinformatics for genetic data analysis is needed - Use of R - Skills in the use of GIS tools would be a plus - Driver's license would be a plus

Skills acquired during the PhD During the thesis, the doctoral student will design an innovative approach to study complex and dynamic multi-trophic networks. The student will develop various skills related to field ecology, advanced molecular

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TU Munich EvolutionaryGenomicsTomato

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

hires a PhD Student to study

Molecular genomics of secondary metabolite pathways in wild tomato species.

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

Therefore, we are looking for an enthusiastic PhD student to investigate the diversity of secondary metabolites in S. chilense and the effects thereof on plant defence mechanisms in an evolutionary context. The applicant must have a very good MSc in biology, biotechnology or (bio)chemistry with an interest in evolutionary biology. Knowledge and practical experience in biochemistry, molecular plant sciences and an interest in bioinformatics and population genetics are required. English skills, both written and spoken, are essential.

The project will be carried out in the group of Dr. Remco Stam at the Chair of Phytopathology (Prof. Dr. Ralph HÃÂ¼ckelhoven). The chair hosts several research groups studying molecular biology of plant pathogens and is well equipped to study pathogen defence responses on different levels. The project will be carried out in collaboration with the Bavarian Center for Biomolecular Mass Spectrometry (BayBioMS) and the Chair for Experimental Bioinformatics, both located on campus. The project is integrated into the SFB924 "Molecular mechanisms regulating yield and yield stability in plants", allowing direct access to state of the art technology for cell biological and biochemical analysis, next generation sequencing etc.

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

More information about the department can be found on http://pp.wzw.tum.de More information about the research group cab be found on http://www.remcostam.com Informal queries about the project are highly encouraged.

Please send your comprehensive application including a letter of motivation highlighting how your interests and expertise match this position (1-2 pages), your CV, certificates and names of 2 potential referees as a single pdf file by email to: stam@wzw.tum.de

Related publications

The wild tomato species Solanum chilense shows variation in pathogen resistance between geographically distinct populations. R Stam*, D Scheikl, A Tellier (2017) PeerJ 5, e2910 https://doi.org/10.7717/peerj.2910 Pooled enrichment sequencing identifies diversity and evolutionary pressures at NLR resistance genes within a wild tomato population. R Stam*, D Scheikl, A Tellier (2016) Genome biology and evolution 8 (5), 1501-1515 https://doi.org/10.1093/gbe/evw094 The de novo reference genome and transcriptome assemblies of the wild tomato species Solanum chilense. R. Stam*%, T. Nosenko%, A.C. Horger, W. Stephan, M. Seidel, J.M.M. Kuhn, G. Haberer ç, A. Tellier ç (2019) BioRxiv https://doi.org/10.1101/612085 A small subset of NLR genes drives local adaptation to pathogens in wild tomato R. Stam*, G.A. Silva-Arias, T. Nosenko, D. Scheikl, A.C. Horger, W. Stephan, G. Haberer, A. Tellier (2017) BioRxiv https://doi.org/10.1101/210559 stam@wzw.tum.de

UCalgary WildQuantitativeGenetics

PhD position in wildlife parasitology and evolutionary ecology at the University of Calgary

Title: Evolutionary ecology of mixed parasitic infections in wild horses

I am seeking a motivated graduate student interested in evolutionary ecology of host-parasite interactions, quantitative genetics and wildlife biology to join my group at the University of Calgary. Research in my laboratory uses molecular and evolutionary ecology approaches to improve our understanding of the processes modulating variation in fitness-related traits and adaptive evolution in free-living wildlife populations.

I am currently recruiting a PhD student to study the genetic basis and fitness consequences of variation in complex gastro-intestinal parasitic nematode infections in natural environments using the Sable Island horse long-term population study as a model. The project will involve characterising complex strongyle infections in >500 horses over multiple years using DNA metabarcoding, and applying pedigree-based multivariate quantitative genetics and selection analyses to study the evolution of resistance to mixed infections. Interactions between nematode infections and the bacterial microbiome will also be investigated. For additional information about the study system see: Debeffe et al. 2016. Negative covariance between parasite load and body condition in a population of feral horses. Parasitology 143:983-997.

Gold et al. 2019. Quantitative genetics of gastrointestinal strongyle burden and associated body condition in feral horses. International Journal for Parasitology: Parasites and Wildlife 9:104-111. Ideal candidates will have demonstrated skills or interest in parasitology, molecular ecology, quantitative genetics, wildlife biology or evolutionary ecology.

The student will be based at the University of Calgarys Faculty of Veterinary Medicine or the Department of Biological Sciences, and receive a minimum stipend of $CA23,000/year. Start date is flexible but would ideally be between September 2019 and September 2020. More information about the lab is available at https://sites.google.com/site/jocelynpoissant/home . Interested students should send a brief email outlining research interests along with a CV and unofficial copies of tran-

scripts to jocelyn.poissant@ucalgary.ca.

Jocelyn Poissant Assistant Professor Dept. of Ecosystem and Public Health, Faculty of Veterinary Medicine University of Calgary, Calgary, AB Office: TRW 2D24

Web: https://sites.google.com/site/jocelynpoissant/- Twitter: @jocelynpoissant @SI_Horses

Jocelyn Poissant <Jocelyn.Poissant@ucalgary.ca>

UCanterbury SexualSelection

PhD Project on how sexual selection contributes to trait evolution and population differentiation

I seek a PhD candidate for a fully-funded 3-year PhD scholarship in the School of Biological Sciences, University of Canterbury, Christchurch, New Zealand.

Project description: This PhD position offers the flexibility for the PhD student to decide on the direction of the doctoral studies within the framework of my research program. Possible projects include theoretical studies of how the genetic architecture of traits can influence variation; comparative genomics and transcriptomics of sexually selected traits; and/or empirical studies of behavioral ecology, sexual selection, and drivers of variation. The PhD position has the opportunity to include theoretical, computational, laboratory-based, and/or field-based research. The successful candidate will be fully funded, including research costs, with a stipend for three years plus payment of tuition fees and associated service charges.

The Flanagan lab: My group studies how and why complex traits and behaviors evolve, with a focus on sexually selected traits. We use a number of different methods to address these broad questions: studies of relevant traits and selection on those traits; genomic studies of signatures of selection; and theoretical simulation studies. For more information, please see the lab website: https://flanagan-lab.github.io/ . My lab is inclusive, welcoming, and committed to advancing diversity; I welcome everyone regardless of their nationality, ethnicity, color, socioeconomic background, gender identity, sexual orientation, religion, and age. I especially encourage members of historically underrepresented groups including (but not limited to) people of color, women, veterans, and people from socioeconomically disadvantaged communities to inquire about opportunities and apply to join my group.

Eligibility: I seek a PhD candidate with a demonstrated high level of academic achievement at the undergraduate and/or postgraduate level. The candidate is required to have a BSc with Honors (or equivalent) or a Masters degree to enroll as a PhD candidate at the University of Canterbury. See the University's eligibility requirements for more detail: https://www.canterbury.ac.nz/- enrol/doctoral/apply/ The ideal candidate will have research experience in behavioral ecology, evolutionary biology, and/or population genetics and genomics. Previous experience with programming (e.g., R, C/C++, python), analysis of genomic or transcriptomic data, and/or molecular techniques is preferred.

The University: The University of Canterbury is located in Christchurch, the largest city in New Zealand's South Island. The University has approximately 13,000 students and 2,000 postgraduate students enrolled. The University's modern and well-equipped facilities are spread across a spacious suburban campus, with easy access to the city and the cultural and recreational facilities it provides. There is also good access to the scenic and recreational resources of the Southern Alps and Banks Peninsula.

Application and contact: Applications should include a letter of application (cover letter), CV, academic transcripts, and the email addresses of two scientific referees. In the cover letter please describe your relevant research experience and include your specific research interests with potential project ideas. The review of applications will begin 15 July 2019.

For more information or to apply please contact me by email: Dr Sarah Flanagan, School of Biological Sciences, University of Canterbury, Christchurch, New Zealand, sarah.flanagan@canterbury.ac.nz

sarah.flanagan@canterbury.ac.nz

UCologne SpiderEvolution

PhD position in evolutionary biology analyzing body-axes formation in the spider Parasteatoda tepidariorum

The laboratory of professor Prof. Dr. Siegfried Roth, at the Institute of Zoology of the Albertus-Magnus University of Cologne, Germany, is offering a 3-year PhD position. Salary according to German TV-L E13 (65%).

Background: Chelicerates are the most basally branching clade of the arthropods, and include horseshoe crabs, sea spiders and arachnids (e.g. spiders and scorpions).

Embryonic development of this group of animals is of special interest as they have evolved a very interesting mode of setting up the dorsoventral body axis. This mode involves the establishment of an organizer (called the cumulus) that is analogous to the organizers that can be found in vertebrate embryos (e.g. Spemann organizer of amphibian embryos). Similar to organizer transplantations in vertebrate embryos, transplantation of the cumulus is able to induce axis duplication in spider embryos. The projects aims to better understand anteroposterior and dorsoventral body-axis formation in chelicerates as well as the formation, patterning and migration of the cumulus. The project will involve next generation sequencing, antibody generation, knockdown and overexpression studies in the common house spider Parasteatoda tepidariorum.

Your profile: We are looking for a committed, talented and highly motivated PhD candidate with a MSc or an equivalent university degree in biology or a related discipline. The candidate should have a strong background/interest in evolutionary biology. Excellent communication and writing skills in English are essential. Experience in handling and imaging embryos of arthropod species as well as being experienced in molecular biological techniques like gene cloning, performing protein overexpression and Western Blots would be beneficial. Bioinformatic skills to analyse next generation sequencing data would be beneficial but are not mandatory.

How to apply: Applications should include: (1) Letter of motivation (relevant skills, experience and research interests) (2) Curriculum vitae (3) Official MSc certificates (4) Contact details of academic references

Please submit your application electronically as a single PDF file until June 16th, 2019 to Dr. Matthias Pechmann (Email: pechmanm@uni-koeln.de).

The University of Cologne is an equal opportunities employer. Applications of women are especially encouraged. Handicapped candidates will be given priority in case of equal professional qualification.

Contact Information: Dr. Matthias Pechmann (AG Prof. Dr. Siegfried Roth) University of Cologne; Institute for Zoology; Biocenter Zulpicher Straße 47b; D-50674 Cologne; Germany http://www.zoologie.uni-koeln.de/15922.html Email: pechmanm@uni-koeln.de

Matthias Pechmann <pechmanm@uni-koeln.de>

UDuisburgEssen AquaticMolecularBiodiversity

About the position A position as a PhD Research Fellow in aquatic ecology is avilable at the Faculty for Biology, Department Biodiversity, led by Prof. Jens Boenigk. The focus of this group is on the evolution and taxonomic and functional diversity of aquatic microorganisms. Expertise of the members within the group covers a broadness of methods ranging from classical plankton ecology and limnology to molecular amplicon diversity, transcriptomics and genomics further to metatranscripomics and Vgenomics including the bioinformatics tools for dealing with such data.

The fellowship will be for a period of 3 years. Scholarship amount: 1500£á / month Starting date: between 01.06.-01.07.2019 Application deadline: 15.05.2019

Job description The candidate will work on a project entitled "Differential potential of metabarcoding, metatranscriptomics, and metagenomics for the assessment of lake water quality", financed by the Bauer und Stemmler foundations. The overall objective of this project is to assess the potential of molecular data from microbial communities (metabarcoding, metagenomics and metatranscriptomics) to act as indicators of water quality. This work will be based on an existing dataset comprising samples from 250 european lakes and further field sampling and laboratory work is planned within the project to extend the dataset. The project entails field sampling, molecular lab work, bioinformatic analyses of amplicon/metabarcoding, metagenomic and transcriptomic data, as well as statistical analysis of gradients in the data (both in terms of taxonomic and functional diversity), and correlations between these gradients and environmental (physicochemical) variables. The focus of the PhD-thesis will be on the bioinformatics and statistical analyses, while the sampling and molecular work will be a joint effort with another PhD project. The main emphasis can be adjusted according to the research interests and qualifications of the successful candidate. Further description of the project can be provided upon request.

Qualifications A masters degree or equivalent in biology, ecology, bioinformatics or related fields Experience with (statistical) programming languages such as R or Python, and/or experience with bioinformatic processing of amplicon/metabarcoding, metagenomic- or

metatranscriptomic data is a requirement Experience with field sampling and molecular lab work (DNA/RNA isolation, PCR) is an advantage Fluent English or German

How to apply Interested candidates should send a brief statement of research interests/motivation, CV, certificates/transcripts of grades and names and contact information of two references, as one pdf file to Elianne Egge (elianne.egge@uni-due.de).

Elianne Dunthorn Egge <elianne.egge@uni-due.de>

UInnsbruck SnailEvolution

University Assistant ' PhD Position (Code BIO-10559)

University Assistant ' PhD Position (20 hours per week, with the submission of the dissertation agreement the working hours will be 30 hours per week), University of Innsbruck, Research Department for Limnology, Mondsee, Austria, starting on 1st September 2019, duration 4 years.

In this position, you will conduct experimental research on the evolutionary ecology of the responses of freshwater snails to changing environmental conditions under climate change. The main goal of the project is to learn to understand the relative importance of different genetic and non-genetic factors in determining snails' responses to high temperature in a quantitative genetic framework. Additionally, the fitness consequences of snails' responses will be described to predict their evolutionary change. Details of the project will be planned together with Prof. Seppälä. Available resources include, for example, tens of inbred Lymnaea stagnalis lines as well as transcriptomic tools.

Qualifications:

Master in Biology

- Experience in laboratory work

- Experience in carrying out experimental research

- Statistical knowledge in the evaluation of experiments

- Communicative personality

- Social skills and ability to work in a team, as well as flexibility, are essential

- Please attach a written idea to your dissertation project (max. 5 pages)

Job profile: The description associated with this job du-

ties and requirements can be found at www.uibk.ac.at/-karriere, Code BIO-10559. We are looking forward to receiving your online application by 23rd May 2019. For questions or more information concerning research, please contact Prof. Seppälä: otto.seppaelae@eawag.ch Travel costs cannot be reimbursed.

Salary: The minimum gross salary for this position amounts to €1.432,00 per month (14 times). Furthermore, the university has numerous attractive offers.

Kind regards, [cid:image003.jpg@01D45CBA.C883A490] Universität Innsbruck Forschungsinstitut für Limnologie, Mondsee Sonja Burggraf Institutssekretariat Mondseestraße 9, A-5310 Mondsee Telefon +43 512 507-50201 Fax +43 512 507-50299 E-Mail sonja.burggraf@uibk.ac.at, office-ilim@uibk.ac.at Bürozeiten: Dienstag ' Freitag 8:00-16:00

"Burggraf, Sonja" <Sonja.Burggraf@uibk.ac.at>

UKoblenzLandau ArthropodEvolution

Job announcement

University of Koblenz-Landau, Institute for Integrated Natural Sciences

PhD Position in Animal Ecology / Biodiversity Research

Application deadline: 02.06.2019

A PhD position is available at the Institute for Integrated Natural Sciences, University of Koblenz-Landau, Campus Koblenz. Starting date is as soon as possible; duration: 3 years; salary scale: TV-L 13, 50%. We invite applications from highly motivated candidates with passion for and experience in research related to the biodiversity of agricultural ecosystems. Specifically, we will investigate the effects of different management regimes on arthropod communities. The successful applicant will (1) hold a M.Sc. degree (or equivalent) in biology or another relevant discipline, (2) have solid experience with at least one relevant taxon (e.g. butterflies, carabid beetles etc.), (3) have a solid background in (field) ecology, (3) experience with experimental designs in ecology and according statistical analyses, and (4) an excellent command of the English language.

To apply please send an email to bewerbung-k21@uni-koblenz.de <mailto:bewerbung-k21@uni-koblenz.de> before June, 3rd 2019 and refer the following reference number: Ko 25/2019. Please attach a single PDF file

to this email including a (1) cover letter, (2) scientific CV including copies of all degrees, (3) motivation letter including personal research interests, (4) contact details of two academic referees, and (5) the abstract of the latest thesis.

The University of Koblenz-Landau is an equal opportunity employer. Application expenses cannot be refunded. The official version of this advertisement is published on the university's homepage: https://www.uni-koblenz-landau.de/de/uni/-organisation/stellen/wissenschaftli che-stellen.

For any enquiries please contact: Prof. Dr. Klaus Fischer; e-mail: klausfischer@uni-koblenz.de

Prof. Dr. Klaus Fischer Institut fur Integrierte Naturwissenschaften

Abteilung Biologie Universität Koblenz-Landau Universitätsstraße 1 D-56070 Koblenz

klausfischer@uni-koblenz.de

Phone: +49-261-287-2238

Klaus Fischer <klausfischer@uni-koblenz.de>

UMuenster
WaspEvolutionaryGenetics

Open PhD position in Evolutionary Genetics & Analytical Chemistry

The Molecular Evolutionary Biology and Chemical Communication group at the Institute for Evolution and Biodiversity at the University of M'nster, Germany, are looking to fill a PhD Position (TV-L E13, 65%) for the research project:

Genetic, chemical and behavioral investigation of sexual signaling evolution in parasitoid wasps

The fixed-term position is available for three years and will begin on the 1st of September 2019 or as soon as possible. One of the most important questions in evolutionary biology is how new species potentially originate. The development and maintenance of barriers to interspecific reproduction has been postulated to be the major driving force of speciation. Variations in sexual signaling have the potential to greatly contribute to keep species reproductively isolated through species-specific communication and recognition mechanisms. In the insect model system Nasonia, a closely related species complex of parasitoid jewel wasps, we could demonstrate that female cuticular hydrocarbons (CHC) function as species-specific sex pheromones distinguishable by the males, hinting at their profound role in reproductive isolation. Curiously though, in one particular Nasonia species (N. giraulti), an apparently recent evolutionary leap shifted the female CHC profile out of the males' perceptive range, which, in turn, still retain a potentially ancestral attraction to CHC profiles of females from other species. In this PhD project, the successful candidate will have the unique opportunity to track this highly unusual evolutionary shift genetically, chemically and behaviorally with the ultimate goal to unravel the key compounds responsible for maintaining the sexual signaling function in Nasonia CHC profiles. The PhD candidate will establish female sipship lines based on Nasonia hybrids to enable the performance of haploid genetics on Nasonia males to assess differential phenotypic traits in the diploid Nasonia females. The sexual attractiveness of the resulting hybrid female sibship lines will be simultaneously accessed by our established male mate choice assays as well as gas-chromatographic coupled with tandem mass spectrometric analysis of their corresponding CHC profiles, utilizing our new, state-of-the-art GC-MS/MS set-up. Furthermore, the successful candidate is expected to generate a high-density genomic map based on novel Restriction-site Associated DNA (RAD) sequencing for localizing quantitative trait loci (QTL) governing CHC variation in the hybrid female sipship lines. To confirm their function, the unraveled candidate gene regions co-localizing with our predicted QTL for CHC variation and female attractiveness will be selectively knocked down in the parental Nasonia females utilizing double-stranded RNA interference (dsRNAi). Lastly, the successful knockdown in the Nasonia females needs to be confirmed behaviorally (male mate choice assays), chemically (GC-MS/MS) and genetically (qPCR), for unambiguously revealing the crucial components and mechanisms governing the sexual signaling function in Nasonia CHC profiles. The successful PhD candidate will be supervised by Dr. Jan Buellesbach and integrated into the newly established Chemical Communication within the larger framework of Molecular Evolutionary Biology headed by Prof. Dr. J'rgen Gadau. The PhD student will also have the chance to join the M'nster Graduate School of Evolution, one of the largest graduate programs in evolutionary biology in Germany.

Requirements: Applicants are required to have a master's or equivalent degree in biology, chemistry or a related field. Applicants are also expected to show a strong interest in evolutionary biology, functional genetics and genomics as well as analytical chemistry. Experience with genomic mapping techniques, particularly RAD-sequencing and QTL mapping as well as func-

tional genetics approaches such as dsRNAi and qPCR are highly desirable. Furthermore, high motivation to be trained in state-of-the-art gas-chromatography coupled with tandem mass spectrometry (GC-MS/MS) analysis and behavioral mate choice assays will be expected from the potential candidates as well. Other requirements are the capacity to effectively integrate several multi-variate datasets, formulate and solve individual research questions, motivation to conduct research independently and finally, fluency in written and spoken English.

The University of M'nster is an equal opportunity employer and is committed to increasing the proportion of women in academics. Consequently, we actively encourage applications by women. Female candidates with equivalent qualifications and academic achievements will be preferentially considered within the framework of the legal possibilities. We also welcome applications from candidates with severe disabilities. Disabled candidates with equivalent qualifications will be preferentially considered.

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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

UNewSouthWales
PhenotypicPlasticityAgeing

We have a PhD position (or two) at the Evolution & Ecology Research Centre at UNSW (http://www.eerc.unsw.edu.au/)

Title: Phenotypic plasticity and aging in a changing world

Abstract: Human-induced changes such as clmate change threaten many populations. Evidence suggests that for many organisms, an increase in temperature expedites aging. Importantly, aging is often associated with the loss of phenotypic plasticity, key for population viability in a changing world. Surprisingly, we know very little about how plasticity changes as organisms age. This project will fill this knowledge gap on age-dependent plasticity using both theoretical and empirical approaches. Our project will reveal not only how phenotypic plasticity can dampen the effect of climate change, but also how, in turn, climate change itself can affect phenotypic plasticity.

Candidate: We are looking for a candidate with a background in ecology and evolution, so they are familiar with the theory and literature, although a candidate with a background in mathematics, statistics and computer sciences is also suitable. Ideally, a candidate should have some experience in empirical work (e.g. having conducted a field or lab experiment of their own) and good quantitative and computational skills (e.g. basic knowledge of linear algebra, competence in R). Also, we seek a demonstrated ability in academic communication in the form of journal publications and/or conference presentations.

Supervisory team: Prof Shinichi Nakagawa (http://www.i-deel.org/) Prof Tracey Rogers (https://www.bees.unsw.edu.au/tracey-rogers) Dr Szymon Drobniak (https://szymekdrobniaken.wordpress.com/)

APPLICATION PROCEDURE:

(1) DISCUSS: Email letter with CV, academic record, and details of two academic referees, to Prof Shinichi Nakagawa (s.nakagawa@unsw.edu.au). Your letter should explain how your results are sufficient to allow application for a SCHOLARSHIP at UNSW (see below). At this point we cannot provide funding for a PhD from other sources, so you need to qualify for a scholarship (see below) or bring your own funding to work with us. Note that we do have funding to cover all lab work.

(2) PhD CANDIDACY APPLICATION: Requirements for PhD are BSc (Hons 1), MSc, or equivalent along with solid research and communication skills. For application timing and details, see: https://research.unsw.edu.au/how-apply-enrol-research-degree (3a) PhD SCHOLARSHIP APPLICATION - LOCAL: Citizens or permanent residents of Australia/NZ, apply for APA, UPA & Scientia at UNSW. You will need to have completed a research degree (e.g. MSc or BSc Honours research year), with results which are equivalent to 85% or higher, in order to be competitive for these scholarships. Publications in ISI-listed international journals will also help. For application timing and details see: https://research.unsw.edu.au/postgraduate-research-scholarships (3b) PhD SCHOLARSHIP APPLICATION V INTERNATIONAL: Applicants who are NOT citizens or permanent residents of Australia/NZ, can apply for IPRS, UIPA & Scientia at UNSW. In order to be competitive for these scholarships, you will need to have completed a research degree (e.g. a full year of research in either MSc or BSc-Honours), with results which are equivalent to 95% or higher for the research component of the degree. Note that a coursework MSc is NOT acceptable.

Professor Shinichi Nakagawa Deputy Director of Research, Evolution & Ecology Research Centre, EERC

(Visiting Scientist at Garvan Institute of Medical Research) Room 5102, Biological Sciences Building (E26) School of Biological, Earth and Environmental Sciences, BEES The University of New South Wales Randwick NSW 2052, Sydney, Australia Mobile: 0422 655 854 Office: 0293 859 138 Website: http://www.i-deel.org/ Shinichi Nakagawa <s.nakagawa@unsw.edu.au>

UParis13 TermitePhylogeography

A PhD position is available for 3 years at the Laboratory of Experimental and Comparative Ethology (LEEC, University Paris 13, France).

Phylogeography of the Neotropical soil-feeding termite Embiratermes neotenicus (Termitidae, Syntermitinae) in South America

Soil-feeding species occur in several lineages of Termitidae (most evolved termite family) and represent over one-third of all described termite species. Soil feeders are especially abundant and diversified in humid tropical forests, where they largely contribute to the soil humification process. It was proposed that soil feeders were poor passive dispersers over water gaps because their colonies are usually located in the soil or soil-made nests and are unlikely to raft over water gaps, contrary to wood feeders frequently drifting in wood pieces. Up to date, only two genetic study investigated the dispersal potential of alates in soil feeders in pristine habitats, i.e. Fournier et al. (2016) in Cavitermes tuberosus and Fougeyrollas et al. (2018) in Embiratermes neotenicus and Silvestritermes minutus. Beside their typical soil-feeding ecology, our interest in these two last species was further prompted by their unusual breeding system: asexual queen succession. In this system, the founding primary queen is replaced by numerous neotenic daughters arising through thelytokous parthenogenesis. The neotenics then take over the reproduction of the colony and mate with the founder king. While the breeding system of E. neotenicus is now well known, the reproduction of colonies, i.e. the dispersal and mating strategies, remain to be investigated at a large scale, i.e. in South America where this species occurs. Therefore, we aim to study population genetics and phylogeography (i.e. study of the principles and processes governing the geographical distributions of genealogical lineages, including those at the intraspecific level) of Embiratermes neotenicus in South America. Molecular analyses will be performed on samples collected in many different countries from South America. This will allow us: (1) to determine whether it includes genetically and geographically distinct lineages, (2) to elucidate its demographic history (diversification events), (3) to infer biogeographic scenarios.

We are seeking a highly motivated candidate with a Master degree in a relevant area (ethology, behavioral ecology, genetics or entomology). We expect successful candidates to write scientific papers on the project in internationally peer-reviewed journals, and to present the research at national and international meetings. Working language is French or English. Possibility of doing teaching in French only.

Please submit your application (CV + motivation letter + contacts of two potential referees, pdf format) to both D. Sillam-Dussès (sillamdusses@univ-paris13.fr) and V. Roy (roy@upec.fr) until May 20th, 2019. Relevant publications

Fougeyrollas R, DolejÅová K, Sillam-Dussès D, Roy V, Hanus R, Roisin Y (2015) Asexual queen succession in the higher termite Embiratermes neotenicus. Proc R Soc Lond B Biol Sci 282:20150260.

Fougeyrollas R, KÅivánek J, Roy V, DolejÅová K, Frechault S, Roisin Y, Hanus R, Sillam-Dussès D (2017) Asexual queen succession mediates an accelerated colony life cycle in the termite Silvestritermes minutus. Mol Ecol 26:3295'3308.

Fougeyrollas R, DolejÅová K, KÅivánek J, Sillam-Dussès D, Roisin Y, Hanus R, Roy V (2018) Dispersal and mating strategies in two neotropical soil-feeding termites, Embiratermes neotenicus and Silvestritermes minutus (Termitidae, Syntermitinae). Insectes Sociaux. 65:251-262.

Fournier D, Hellemans S, Hanus R, Roisin Y (2016) Facultative asexual reproduction and genetic diversity of populations in the humivorous termite Cavitermes tuberosus. Proc R Soc Lond B Biol Sci 283:20160196

David SD <sillamdusses@univ-paris13.fr>

UppsalaU AnimalEvolution

PhD-position in Animal Evolution at Uppsala University, Sweden

A 4-year PhD-position in evolutionary genetics is available in the research group of Dr. Richard Svanbäck at the Department of Ecology and Evolution, Animal Ecol-

ogy in Uppsala, Sweden. Starting date in September 2019 or as agreed upon.

Project description: Earth is permeated by a remarkably rich flora and fauna, from the highest mountains to the deepest seas and lakes. Unfortunately, biological diversity is disappearing at a fast and accelerating pace. To preserve the biological diversity it is important to understand the two ways that underlie changes in species diversity: extinction and speciation. So far, most studies have been focused on understanding mechanisms of extinction, since speciation traditionally has been seen as a slow process that 'only adds new species to the existing ones'. Recent research efforts challenge this picture and require that we reassess the roles of both speciation and extinction in generation and maintenance of biodiversity. Speciation can occur quickly, especially when the process acts in reverse ' i.e. where a new species develops from two parental species through hybridization. In this project, we aim to characterize and quantify mechanisms that affect how species boundaries dissolve in freshwater lakes. Particular focus will be on the common bream and the white bream (Abramis sp.), two closely related freshwater fish species that currently hybridize to some extent and that run the risk of collapsing into a single unit (gene-pool). The PhD project will contain a range of approaches including genetic studies, field and lab experiments and mathematical modelling. A major aim will be to derive a risk analysis for loss of biodiversity in Swedish freshwater lakes.

The project is a collaboration between Richard Svanbäck (richard.svanback@ebc.uu.se) och Nicklas Backström (niclas.backstrom@ebc.uu.se) at Uppsala University and Ske Brännström at UmeÃ¥ University (ake.brannstrom@umu.se)

The Evolutionary Biology Centre (http://-www.ebc.uu.se/?languageId=1) is one of the world's leading research institutions in evolutionary biology. It is part of Uppsala University, which has been ranked very high among all European Universities in the subject of animal ecology and evolutionary biology. Our lab is part of the Program of Animal Ecology that excels in many aspects of genetics and evolution and offers an inspiring international atmosphere. There are ample opportunities for interaction with PhD-students, PostDocs and 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.

For further information about the position please contact: Senior Lecturer, Richard Svanbäck,

richard.svanback@ebc.uu.se, +46-18-471 2938.

You are welcome to submit your application no later than June 12, 2019, UFV-PA 2019/1829. Formal applications should be made using our online application form: https://uu.mynetworkglobal.com/en/what:job/-jobID:271078/ Richard Svanbäck Animal Ecology Program Department of Ecology and Genetics Uppsala University, Sweden Email: richard.svanback@ebc.uu.se

När du har kontakt med oss pÃÂ¥ Uppsala universitet med e-post sÃÂ¥ 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 richard.svanback@ebc.uu.se

UppsalaU
AnimalEvolutionaryGenetics

PhD-position in Animal Evolution at Uppsala University, Sweden

A 4-year PhD-position in evolutionary genetics is available in the research group of Dr. Richard Svanbäck at the Department of Ecology and Evolution, Animal Ecology in Uppsala, Sweden. Starting date in September 2019 or as agreed upon.

Project description: Earth is permeated by a remarkably rich flora and fauna, from the highest mountains to the deepest seas and lakes. Unfortunately, biological diversity is disappearing at a fast and accelerating pace. To preserve the biological diversity it is important to understand the two ways that underlie changes in species diversity: extinction and speciation. So far, most studies have been focused on understanding mechanisms of extinction, since speciation traditionally has been seen as a slow process that Âonly adds new species to the existing ones'. Recent research efforts challenge this picture and require that we reassess the roles of both speciation and extinction in generation and maintenance of biodiversity. Speciation can occur quickly, especially when the process acts in reverse ' i.e. where a new species develops from two parental species through hybridization. In this project, we aim to characterize and quantify mechanisms that affect how species boundaries dissolve in freshwater lakes. Particular focus will be on

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You are welcome to submit your application no later than June 12, 2019, UFV-PA 2019/1829. Formal applications should be made using our online application form: https://uu.mynetworkglobal.com/en/what:job/-jobID:271078/ Richard Svanbäck Animal Ecology Program Department of Ecology and Genetics Uppsala University, Sweden Email: richard.svanback@ebc.uu.se

När du har kontakt med oss pÃÂ¥ Uppsala universitet med e-post sÃÂ¥ 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 Richard Svanbäck <richard.svanback@ebc.uu.se>

USBohemia Czechia ParasitePopulationGenomics

Call for a PhD student in population genomics of parasites is open to apply by May 22, 2019:

A four year grant-supported phd position is available in the Laboratory of Molecular Ecology and Evolution (at the Biology Centre CAS and University of S. Bohemia in Ceske Budejovice, Czechia). http://jstefka.info The phd applicant will work on two related projects, studying patterns of population genomic diversity modulated by adaptation to parasitism.

- we seek for a candidate interested in population genetics and demography, evolution of pesticide resistance and the role of selection in host-parasite co-evolution. The candidate will work closely with a collaborator in Prague (at the Czech Univ. of Life Sci. https://-bedbugs.fzp.czu.cz/). - we seek for a person willing to pick up new skills and apply them to solving wetlab and bioinformatic problems as they emerge. The candidate will be encouraged to use his/her own creativity to shape the topic according to their own interests. Upon starting the position, the candidate should hold a master degree in biology (or a related field). Previous bioinformatic and wetlab experience is desirable but not compulsory.

Come to study and do research at a highly international research facility, located in a charming historical city in the south of Czechia within an easy reach of Prague and Vienna, whilst with great outdoors nearby! The offered stipend and salary covers all living costs with a comfortable margin!

To apply, send a motivation (cover) letter and a CV to stefka@paru.cas.cz Applications are welcome until May 22. Ideal position start is July 2019, but later date is negotiable.

For more information go to: http://-jstefka.info/Homepage_of_Jan_Stefka/Welcome_files/-2019_newPHD.pdf Jan Stefka, PhD Associate professor Laboratory of Molecular Ecology and Evolution Institute of Parasitology, Biology Centre, CAS & Faculty of Science, Univ. S. Bohemia Branisovska 31, Ceske Budejovice 37005, CZ

tel.: +420 387 775 409 e-mail: jan.stefka@gmail.com web: www.jstefka.info jan.stefka@gmail.com

USherbrooke EcolEvolMountainUngulates

Graduate position: Two MSc programs on ecology and conservation of mountain ungulates.

MSc 1: Effects of age of ancestors on bighorn sheep fitness. Using the long-term study and pedigree at Ram Mountain, this student will examine lifelong effects of the ages of parents and grandparents on growth, survival and reproduction. Starting September 2019 or January 2020, this research will include one or two summers of fieldwork at Ram Mountain.

MSc 2: Mountain goat horn growth. In collaboration with BC Wildlife Biologists, this student will examine regional and temporal variability in annual horn increments of harvested goats, to look for evidence of changes in age of first reproduction in females, investigate the effects of weather and determine whether early horn growth is correlated with age at harvest. Data on horn growth of marked individuals at Caw Ridge, Alberta, will also be available. Starting September 2019 or January 2020, this research will include one summer of fieldwork at Caw Ridge.

Both projects are fully funded and scholarships of $ 17,000/yr will be available for 2 years. Note that the Université de Sherbrooke is a francophone institution, and there are substantial extra tuition fees for most non-Canadians. Please consult http://marco.recherche.usherbrooke.ca/advice.htm before applying. Deadline: August 1, 201/9.

Candidates should be fluent in English and have a strong quantitative background. Previous field and research experience (such as an undergraduate research project) will be major assets. If you are interested send me your CV, a statement of interest, unofficial transcripts and the names and e-mails of 2 people able to assess your research potential. m.festa@USherbrooke.ca

For more information see http://marco.recherche.usherbrooke.ca/marco.htm and http://marco.recherche.usherbrooke.ca/advice.htm Marco Festa-Bianchet <Marco.Festa-Bianchet@USherbrooke.ca>

USunshineCoast SocialEvolution

USC. Social plasticity and Adaptation

PhD projects available in Celine Frere's Lab around the themes of social evolution, social plasticity and adaptation to urbanisation using four long-term behavioural, ecological and genetic (SNPs) datasets on iconic Australian native species including bottlenose dolphins (+36 years), kangaroos (+6 years), koalas (+ 6 years) and eastern water dragons (+9 years).

I am primarily interested in building and exploiting long-term, individual-based genetic and behavioural empirical information to answer questions about evolutionary processes in nature (with a focus on social evolution and adaption). My research also has strong applied outcomes delivering ecological data and analysis on vulnerable species to government and industry (through the Detection Dogs for Conservation (DDC) Research and Consultancy which I established with Dr Romane Cristescu in 2015).

My research lab currently comprises 4 post-doctoral fellows, 7 PhD candidates, 3 honours candidates and one part-time Research Assistant. Our values are that of team work, kindness and hard work.

I am looking to support students' application for HDR/PhD scholarships available at the University of the Sunshine Coast and developed fundamental/applied research projects to match both Dr Celine Frere and that of future prospect students research interests. Please see www.celinefrerelab.com for more information. Applicants will need to have an extremely competitive academic record and obtain an Australian Postgraduate Award or International Research and Fee Remission Scholarships. The RTP Scholarship Round will open on Monday 3 June. More information about the application process and internal deadlines for prospective students can be found on the Applying for a Research Training Program web page (for details and scholarship application forms https://www.usc.edu.au/research-and-innovation/research-students/hdr-scholarships/-applying-for-a-research-training-program-scholarship). The main application deadlines for these scholarships are 13th of October 2019 (Domestic and International), but application to the HDR/PHD programs must be processed prior to the 13th of October 2019.

Interested students are invited to email their CV to

Celine Frere (cfrere@ usc.edu.au).

Celine Frere PhD #SuperstarsofSTEM Senior Research Fellow Office: KDM2 Faculty of Science, Health, Education and Engineering University of the Sunshine Coast 90 Sippy Downs Drive Sippy Downs Queensland 4556 Australia mobile: 0423312893 work: 0754565415 celinefrerelab.com [cid:image002.jpg@01D0D8E1.DA4153E0] [Signature block logos]

USC, Locked Bag 4, Maroochydore DC, Queensland, 4558 Australia. CRICOS Provider No: 01595D Please consider the environment before printing this email.

Celine Frere <cfrere@usc.edu.au>

UVictoria ProtistEvolutionaryCellBiol

Graduate position (M.Sc/Ph.D): Evolution and Cell Biology of Microbial Eukaryotes in the Department of Biology at the University of Victoria.

I am looking for an enthusiastic candidate for either a M.Sc. or a Ph.D research project in the Department of Biology at the University of Victoria (https://www.uvic.ca/science/biology/), commencing in September 2019, or as soon as possible thereafter.

Our lab focuses on questions related to the origin and evolution of mitochondria, and the genetic diversity of microbial eukaryotes (???protists???). A wide variety of potential projects are available, ranging from proteomic investigations of protist mitochondria, to development of molecular genetic tools in an emerging model protist, and single-cell genomics of wild-caught marine microbes. Depending on the student???s interest, the project would include a combination of next generation sequencing, molecular biology, microscopy, and bioinformatics.

These projects are ideal for a student with a strong background in cell and molecular biology and an interest in the application of the techniques in understanding eukaryotic evolutionary cell biology. Previous experience with protists is not required. The student will be supervised by Dr. Ryan Gawryluk (https://protistlab.weebly.com), and will have opportunities to interact with other researchers at the University of Victoria.

Preference will be given to a student with an excellent academic standing, and an appropriate background. Applications are open to international candidates as well as Canadian citizens or permanent residents of Canada.

Interested applicants should submit a CV, copies of university transcripts (undergraduate and graduate as appropriate ??? unofficial copies are adequate) and a brief statement of scientific and academic interests to Dr. Ryan Gawryluk (ryangawryluk@uvic.ca).

Ryan Gawryluk Assistant Professor Department of Biology University of Victoria Email: ryangawryluk@uvic.ca Website: https://protistlab.weebly.com Ryan Gawryluk <ryangawryluk@uvic.ca>

UWyoming WildlifePopGenetics

PhD student assistantship position for Fall 2019 is available for research and training in wildlife population genomics, conservation genetics, and disease ecology at the University of Wyoming (UW) in Laramie. The position will be mentored within two labs: the Holly Ernest Wildlife Genomics and Disease Ecology Lab http://www.wildlifegenetichealth.org/ and the Jennifer Malmberg Wildlife Pathology and Genomics Lab https://www.uwyo.edu/vetsci/department-directory/faculty-members/malmberg-jennifer.html in the Department of Veterinary Sciences https://www.uwyo.edu/vetsci and the UW Graduate Program in Ecology (PiE; http://www.uwyo.edu/pie/). Research will use genomic, genetic and diagnostic methods to study wildlife population ecology and disease ecology in the Rocky Mountain West and/or California, with project either in large mammal or avian species.

Information and application instructions: http://www.wildlifegenetichealth.org/grad-wildlife-genomics/ The Ernest and Malmburg Labs are dynamic and highly collaborative and maintain affiliations with Colorado State University, University of California Davis and other academic institutions, as well as state, federal, and non-governmental agencies. There are many opportunities to work with recognized leaders who apply excellence in science toward wildlife conservation and management. There are opportunities for an added academic minor in Environment and Natural Resources: http://www.uwyo.edu/haub/. In addition to research and course work, responsibilities may include teaching (TA-ing), lab maintenance tasks, and mentoring other students. Quality mentorship of trainees is a priority for us. University of Wyoming hosts excellent wildlife and ecology science and a collegial academic atmosphere.

Laramie is a wonderful college town of ~ 30,000 and offers easy access to the Rocky Mountains and outdoor activities including skiing, hiking, climbing, birding, and fishing & hunting.

To apply for this position please do two things: 1) email a cover letter of introduction and C.V. to Holly.Ernest@uwyo.edu and 2) submit an electronic application to UW and note that your application is directed to Dr. Ernest and Dr. Malmburg: http://www.uwyo.edu/admissions/graduate/ then click "Graduate Application" to arrive at: http://www.uwyo.edu/admissions/apply-online.html. Applicants can temporarily upload documents without the need to pay the $50 application fee until notified that they are finalists for the position. At the UW application site, please upload your cover letter, C.V., unofficial transcripts for all college work, and everything you can upload short of paying the application fee. Finalists for the position will be notified and asked to finalize their UW online application with 3 letters of recommendation, and official transcripts, official GRE's, etc. as well as $50 application fee.

The application cover letter should include educational and research background, PhD research and study interests as regards to wildlife population genomics, ecology, and disease ecology; career goals, specific interests in our labs, GPA (overall and science/math) and GRE (raw and percentile scores), your address, email, cell phone, and names for at least three research/academic-related references including MS adviser, with their contact information (name, position, email, phone, institutional affiliation, website, and research area). GRE's must have been taken after Sep 2014, (within 5 years) and please include both percentiles and raw scores for all GRE's taken. Applications reviews will begin as soon as received, position may remain open until filled. If a candidate is not identified for Fall 2019, we may consider a start date of January 20, 2020. We are sorry but this position is not available for students outside the US and Canada. Feel free to email Dr. Ernest (Holly.Ernest@uwyo.edu) with inquiries - we look forward to your application!

Information and application instructions: http://www.wildlifegenetichealth.org/grad-wildlife-genomics/ Holly Ernest DVM PhD Professor, Wildlife Genomics and Disease Ecology Excellence Chair in Disease Ecology University of Wyoming http://www.wildlifegenetichealth.org/ Holly.Ernest@uwyo.edu

Holly.Ernest@uwyo.edu

Vienna PopulationGenetics

Call for PhD students in Population Genetics is open: apply by May 13, 2019

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

We invite applications from highly motivated and outstanding students with a background in one of the following disciplines: bioinformatics, statistics, biomathematics, evolutionary genetics, functional genetics, theoretical and experimental population genetics. Students from related disciplines, such as physics or mathematics are also welcome to apply.

Topics include:

- Complex trait dissection in conifers. - Dissecting the genetic basis of co-selected traits during thermal adaptation in Drosophila simulans. - Efficient detection of variants of polygenic adaptation in Drosophila experimental evolution. - Evolution of gene expression. - Functional characterization of beneficial alleles in Drosophila. - Genomic architecture of reverse selection. - Incipient speciation during adaptation to a new environment. - Inference of selection parameters using whole genome data. - Long-term dynamics of adaptive alleles. - Microbiome evolution in Drosophila. - Multi-measurement experimental evolution: How to combine evidence from different sources? - Polygenic adaptation: The roles of pleiotropy and epistasis. - The genetics of local adaptation in Arabidopsis thaliana. - The role of a nascent sex chromosome on interspecific patterns of allele sharing. - Transposon polymorphism in Arabidopsis thaliana. - Within-species consequences of genomic interactions in ecologically important species.

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by May 13, 2019 will be considered. Two letters of recommendation need to be sent directly by the referees. Accepted PhD students will receive a monthly salary based on currently EUR 2.162,40 before tax according to the regulations of the Austrian Science Fund (FWF).

All information about the about available topics, the training program and the application procedure can

be found at www.popgen-vienna.at – Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator

www.popgen-vienna.at   https://twitter.com/-PopGenViennaPhD   c/o Institut fÃÂ¼r Populationsgenetik Veterinärmedizinische Universität Wien (Vetmeduni Vienna) Veterinärplatz 1, 1210 Wien

T +43 1 25077 4338 F +43 1 25077 4390

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

Vienna TreePathogenInteractions

PhD position in tree breeding and genomics of tree-pathogen interactions

We are seeking a highly motivated PhD candidate with background in evolutionary biology and genetics having a special focus on tree-pathogen interactions. The position is for 3 years (full-time) and the working place will be the Federal Research and Training Centre for Forests (BFW) in Vienna, Austria.

Project description: Diplodia sapinea or Diplodia tip blight is an important pathogen affecting economically valuable pine species around the world. As an endophyte in many pines, it can quickly develop into a severe disease especially when trees become drought stressed in summer. Hence, it is considered an important biotic disturbance agent under climate change. However, the genomic architecture of resistance against Diplodia tip blight is largely unexplored yet. The aim of the project is i) to get a better understanding of the underlying mechanisms leading to resistance and ii) to find genetic variants and phenotypes that can be employed in breeding programs in order to produce more resilient seed material. The candidate will work on whole-genome sequencing information (Exome-capture) as well as on metabolomic data. The model tree species is Black Pine (Pinus nigra), which is occurring in an area of 20,000ha in eastern Austria. In the project, we will combine infection experiments of clonal copies of Black Pine trees with field sampling and landscape genomic approaches.

Requirements: The candidate should have a completed Master degree in biology, genetics or plant biotechnology with outstanding rating. Experience with tree and/or fungal DNA is an advantage. Knowledge of programming in R or other related software languages is also beneficial. A high level of reliability and an accurate mode of working is absolutely desirable for this project

The Federal Research and Training Centre for Forests (BFW) is located in the heart of Vienna close to the castle of Schönbrunn in a nice and green working environment. The candidate will work in an international team and will also partly work in the labs of collaborating partner institutions in Vienna. We offer a gross monthly salary of €2.718,90 (14 times per year).

The position will start in October 2019 and applicants should send their CV together with a Letter of motivation (all in one pdf-document named as Surname_Name_CV.pdf) until July 31st to jan-peter.george@bfw.gv.at Contact details of two academic reference persons should also be given in the CV. Candidates selected for a Skype interview will be informed latest until beginning of September.

george <jan-peter.george@bfw.gv.at>

AlabamaMNH CuratorOfPaleontology

Curator of Paleontology, Alabama Museum of Natural History (ALMNH)

The Department of Research and Collections of the University of Alabama Museums is seeking a highly-motivated researcher in the area of paleontology. The paleontology collections at the Alabama Museum of Natural History date back to the mid 1800's and include over 25,000 specimens. The collection is made up of vertebrate, invertebrate and paleobotanical specimens and boasts many unique and important specimens including several holotypes and arguably the most complete Clidastes propython mosasaur specimen known (Artemis). The ALMNH also maintains an extensive collection of extant vertebrates that are useful for comparative studies (osteological specimens, study skins, and wet specimens). This position will oversee a fully functional fossil preparation laboratory adjacent to the collection as well as a 130-acre paleontological field station in Dallas County, AL. Areas of research focus could include but are not be limited to: systematics, functional or evolutionary morphology, paleoecology, and biomechanics. The ALMNH is also interested in connecting paleontological research with our visitors and the local community.

The Curator of Paleontology is responsible for managing the paleontological collections including, in conjunction with the Director, Research and Collections, developing plans for maintenance and expansion. Writing proposals to fund the collection and create synergies with faculty and other researchers promoting deposition of specimens in the ALMNH collections. Creating and maintains an active research program focused on the paleontology collections. Managing a budget for paleontological activities and administering grants and proposals for paleontology collections. Managing Harrell Station, ALMNH's paleontological field station. Oversees the recruitment and coordination of ALMNH paleontological assistants and volunteers. Teaches one course per year in paleontology, geology or a related field. Assists with development of policies and processes conforming to best practice standards for the long-term preservation and conservation of specimens within the collections.

Qualifications and Required Application Materials: Ph.D. in Geology or Biology with specialization in Paleontology and one (1) year of college level teaching experience. Job close date 5/31/2019. Visit UA's employment website at staffjobs.ua.edu (job no. 508814) for more information and to apply. The University of Alabama is an equal-opportunity employer (EOE) including an EOE of protected vets and individuals with disabilities. http://staffjobs.ua.edu/cw/en-us/job/508814/curator-of-paleontology-508814 Kevin M. Kocot Assistant Professor, Department of Biological Sciences Curator of Invertebrates, Alabama Museum of Natural History The University of Alabama < https://www.ua.edu/ > 307 Mary Harmon Bryant Hall 500 Hackberry Lane Tuscaloosa, AL 35487 office 205-348-4052 <tel:205-348-4052> fax 205-348-4039 kmkocot@ua.edu | www.kocotlab.com [The University of Al-

abama] < https://www.ua.edu/ > [Facebook] < https://-www.facebook.com/kmkocot > [Twitter] < https://-twitter.com/kmkocot >

"Kocot, Kevin" <kmkocot@ua.edu>

CenterNaturalHistory Hamburg 3 Curators

Dear Colleagues!

In behalf of the Center of Natural History, Hamburg (CeNk) and in the name of its director Prof. Dr. Matthias Glaubrecht, I am pleased to announce two research and collection curation positions in Entomology and a research position/curatorship in Ornithology as part of our ongoing strategic development of collection based research at the CeNak.

1. RESEARCH ASSOCIATE Curator Ornithology - SALARY LEVEL 13/14 TV-L - 2. RESEARCH ASSOCIATE Curator of Entomology (Mecopteroidea: Lepidoptera, Trichoptera, etc.)- SALARY LEVEL 13/14 TV-L - 3. RESEARCH ASSOCIATE Curator of Entomology (Neuropteriformia: Coleoptera, Neuroptera, etc.) - SALARY LEVEL 13/14 TV-L -

Please find the details for each of the positions in the pdf documents provided under Centrum fur Naturkunde at

https://www.uni-hamburg.de/uhh/-stellenangebote.html Please circulate these job offers widely in pertinent community circulars and specialist groups. We hope to reach as many researchers as possible, nationally an internationally.

Thank you very much for your consideration and support!

Kind regards, Martin Husemann

– Martin Husemann, PhD

Head of Entomology Centrum fur Naturkunde (CeNak) - Center of Natural History Universität Hamburg - Zoological Museum Martin-Luther-King-Platz 3, Room 131 20146 Hamburg, Germany P: +49 40 42 838 2373

Email:martin.husemann@uni-hamburg.de

Web: https://www.cenak.uni-hamburg.de/forschung/-zoologie/entomologie.html https://www.uni-hamburg.de/humboldt-lebt Martin Husemann <martin.husemann@uni-hamburg.de>

ClemsonU VertebrateEvolution

Clemson University: College of Science: Biological Sciences *Lecturer - Vertebrate Organismal Biology, Ecology and/or Evolution*

Location: *Clemson University - Clemson, SC*

The Department of Biological Sciences at Clemson University is seeking a full-time, 9-month Lecturer in Vertebrate Organismal Biology, Ecology and/or Evolution to begin Fall 2019 who will contribute innovative teaching and student-centered learning in our BA and BS degrees in Biological Sciences and online MS in Biological Sciences. This is a renewable, non-tenure track position with opportunity for promotion. Salary level will be commensurate with education and experience and a benefits package is included.

Undergraduate teaching responsibilities will include lecture and lab courses such as vertebrate biology, behavioral ecology, evolution, and/or other courses and labs within the candidate's area(s) of expertise. Teaching in the online MS program will include ecology, evolution, and/or animal biology. There are summer salary opportunities available for teaching on-campus, online, or study abroad classes. The Department supports faculty development at all ranks, and promotion through instructional ranks will be expected for this renewable position.

For more information about the department, visit the Department's website at http://www.clemson.edu/-science/departments/biosci/. The Department is committed to building a culturally diverse faculty and strongly encourages applications from women and underrepresented groups.

QUALIFICATIONS

Successful candidates will have a Ph.D. in biological sciences or a related discipline at the time of appointment. Ideal candidates will demonstrate successful experience teaching university-level biology lecture and laboratory courses, as well as strong interest in online teaching and undergraduate study abroad experiences.

APPLICATION INSTRUCTIONS

Applicants should submit the following items through http://apply.interfolio.com/63040: (1) cover letter, (2) curriculum vitae, (3) statement of teaching philosophy, experience, and interests, (4) course evaluations or other

evidence of past teaching performance, (5) statement describing teaching strategies currently used or planned to use to foster diversity and inclusion, and (6) names and contact information for three professional references.

Inquiries should be directed to BiolSci@clemson.edu.

For full consideration, applications should be submitted by May 29, 2019. Review will continue until the position is filled.

* Clemson University is an AA/EEO employer and does not discriminate against any person or group on the basis of age, color, disability, gender, pregnancy, national origin, race, religion, sexual orientation, veteran status or genetic information. Clemson University is building a culturally diverse faculty and staff committed to working in a multicultural environment and encourages applications from minorities and women.*

– Richard Blob Alumni Distinguished Professor Department of Biological Sciences Clemson University rblob@clemson.edu Web: https://sites.google.com/site/-richardbloblab/ Richard Blob <rblob@clemson.edu>

CSIRO Hobart AustNatlFishCollection

JOB TITLE: CSIRO Science Leader - Fish, Food and Humans

* Help secure the Australian National Fish Collection's continued vitality * Provide scientific leadership and pursue new ideas and approaches * Contribute to how specimens held in biological collections are used as tools for research

As the CSIRO Science Leader with the Australian National Fish Collection (ANFC), your Priority Area will address diverse gaps in our knowledge of the biology and population structure of fish. Integrating current and new strands of knowledge, your research will lead to improved evolutionary biology of fish, management of human food and health, and marine biodiversity conservation.

ANFC comprises 157,000 specimens representing 3000 species of Australia's unique marine fish fauna. Still growing, this vital resource of marine biodiversity underpins understanding of iconic ecosystems such as the Great Barrier Reef and the Southern Ocean.

Overall, the work to be undertaken in your Priority Area will heighten the impact of ANFC, and deliver

key outcomes to marine science, industry sustainability and biodiversity conservation. Using a collaborative approach across CSIRO's Business Units, research in this area will strengthen CSIRO as a global leader in collections-based, applied research of profound economic, cultural and scientific significance.

The program is directed towards mid-career researchers who have ˜10 to 15 years of post PhD experience, and:

* have established expertise and knowledge aligned to the strategic priority areas; * bring novel capability into CSIRO; and * develop cutting edge technology platforms not already in CSIRO.

As part of this key leadership role, you will

* Develop an integrative research program in the Priority Area's theme supported by two postdoctoral fellows and two PhD students. * Develop individual performance plans and oversee general day to day operations of the team. * Use professional expertise, knowledge of other disciplines and research experience to formulate, develop and complete an approved research program. * Communicate research results to the scientific community through oral and written reports. * Provide advice to policy makers and inform and transfer knowledge to non-scientific audiences. * Ensure that experiments are established in accordance with the research design and are completed within agreed timeframes and budget.

Location: Hobart, Tasmania Salary: Attractive salary package offered Tenure: Indefinite with an initial five years specific science leader funding Reference No.: 61584

A successful science leader will:

* be recognised by their peers as making a significant contribution in their field of science or engineering; * have a track record of translating scientific outcomes into impact; * demonstrate the ability to collaborate at the intersection of disciplines; * bring an extensive network which they will actively share across the whole organisation, engaging and satisfying multiple stakeholders; and * have the ability to mentor a team of talented postdoctoral fellows and postgraduate students and attract distinguished visiting researchers.

To discuss this pivotal role in more detail, call the contact person on the brochure at the link below.

https://jobs.csiro.au/job/Hobart%2C-TAS-CSIRO-Science-Leader-Fish%2C-Food-and-People/557636400/ About CSIRO: At CSIRO you can be part of helping to solve big, complex problems that make a real difference to our future. We spark off each other, learn from each other, trust each other and collaborate to achieve more than we could individually in a supportive, rewarding,

inclusive and truly flexible environment - CSIRO

CSIRO's Commitment to Diversity: We're working hard to recruit diverse people and ensure all our people feel supported to do their best work and empowered to let their ideas flourish. D&I Strategy

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

Apply Online: Before applying, please call/email the contact person indicated in the brochure at the link above.

Applications Close: Sunday 7 July, 2019 (11:59pm AEST)

"Hink, Helena (HR, Kensington WA)" <Helena.Hink@csiro.au>

Hobart
AustralianNatlFishCollection

Hello all

I write in my capacity as Group Leader of the Vertebrate Collections at CSIRO's National Research Collections Australia.

We have today advertised for a prestigious position of Science Leader in the Australian National Fish Collection (ANFC), Hobart, Tasmania. The web link to the position is https://jobs.csiro.au/job/Hobart%2C-TAS-CSIRO-Science-Leader-Fish%2C-Food-and-People/-557636400/ and I attach the electronic brochure for the position. For the first five years the position comes with two PhDs and two Postdoctoral Fellowships fully funded by CSIRO. I stress that the Science Leader will of course be instrumental in choosing the successful candidates for these four positions in the Science Leader's program. To reiterate, they are funded in the first five years by CSIRO as part of the Science Leader program. You may wish to apply yourself for the Science Leader position or you may know someone who would be eligible. Most of all, please feel free to share as widely as possible as we are very excited about this opportunity. The position is open until July 7, 2019.

ANFC (https://www.csiro.au/en/Research/-Collections/ANFC) is of course one of our major biological collections in CSIRO. We will be especially interested in a collections-based ichthyologist with a grounding in areas such as systematics and evolution. This could include, but by no means be confined to, fields such as phylogenomics, molecular and/or morphological systematics, population genetics or population ecology, for example. We will welcome and encourage integration of your research with biologists working in other disciplines such as but again by no means confined to endocrinology, genomics, population modelling, evolutionary biology, phylogeography, satellite tracking and so on. Collaborations might be with researchers elsewhere in CSIRO or in universities and industry. We require only that the research program that the Science Leader develop fall under the theme of Fish, Food and Humans. It is stated in the formal advertising material that the position is aimed at mid-career researchers but I encourage anyone interested in the position to apply.

The Australian National Fish Collection (ANFC) is part of CSIRO's National Research Collections Australia (https://www.csiro.au/en/Research/Collections). Also in Hobart where this position is based is the Australian National Algal and Culture Collection and our colleagues in CSIRO's Oceans and Atmosphere research hub (https://www.csiro.au/en/Research/OandA). The University of Tasmania is also based in Hobart. Opportunities for building collaborations with biologists in CSIRO's other Collections or indeed in Oceans and Atmosphere and at University of Tasmania are many.

The other CSIRO Collections are in Canberra. There we have the Australian National Wildlife Collection (terrestrial vertebrates), the Australian National Herbarium, Australian National Tree Seed Centre, and the Australian National Insect Collection.

Again, please feel free to share this position with colleagues far and wide. Do not send applications to me, however. They must be lodged online as per the instructions at the link above and repeated here: https://jobs.csiro.au/job/Hobart%2C-TAS-CSIRO-Science-Leader-Fish%2C-Food-and-People/557636400/ Kind Regards

Leo

Dr Leo Joseph Director Australian National Wildlife Collection National Research Collections Australia, CSIRO GPO Box 1700 Canberra ACT 2601 Australia Phone: + 61 (0)2 6242 1689 Fax: + 61 (0)2 6242 1688 Email: Leo.Joseph@csiro.au Web: http://-people.csiro.au/J/L/Leo-Joseph "Joseph, Leo (NCMI, Crace)" <Leo.Joseph@csiro.au>

ImperialCollegeLondon 8 EvolutionaryAdaptation

The Life Sciences Department at Imperial College London is recruiting 8 open-rank positions.

The successful candidate will join a dynamic group of 30 researchers working to address global challenges using evolutionary and ecological approaches (http://-www.imperial.ac.uk/ecosystems-and-environment). The candidate will be expected to lead a research programme and research group and to enthuse and inspire students at both undergraduate and graduate level. Silwood Park has over 100 hectares of grounds for conducting large scale experiments and several long-term experiments which may be of interest (https://www.imperial.ac.uk/-silwood-park/research/silwood-lte/). Depending research focus, there is also scope for working closely with the Grantham Institute (https://www.imperial.ac.uk/-grantham/).

For more information please see: http://-www.imperial.ac.uk/jobs/description/NAT00452/-lecturer-senior-lecturer http://www.imperial.ac.uk/-jobs/description/NAT00454/reader-or-chair For questions please contact Dr. Lauren Cator (l.cator@imperial.ac.uk).

"Cator, Lauren J" <l.cator@imperial.ac.uk>

KSR Toronto FieldResearchStationAssistant

Summer position: *Reserve Operations Assistant at the Koffler Scientific Reserve*

We will be hiring a Reserve Operations Assistant to work at the Koffler Scientific Reserve (KSR) at Joker's Hill (https://ksr.utoronto.ca/) in a full time position from May 21 ' August 30, 2019. The Reserve Operations Assistant will work under the KSR Station Manager to facilitate the research and education programming by 1) performing routine maintenance and cleaning of housing, laboratories, grounds, roads, and storage facilities, 2) providing general research support services including GPS mapping, meteorlogical monitoring and data entry, and 3) organizing housing for visiting students and researchers. This individual will support and be guided by both the Station Manager and the Facilities Manager during the course of the day to complete the expected duties.

The Koffler Scientific Reserve is an internationally recognized site for cutting-edge research and education in biodiversity, ecology, evolution and conservation biology. It is located on the Oak Ridges Moraine in King Township, north of Toronto. Housing can be made available on the reserve.

QUALIFICATIONS

- Minimum of two years of instruction in biological sciences at the university or college level.

- A Valid class "G" driver's license is mandatory.

- Some experience in field research or similar working environment.

- Excellent communication skills.

- Ability to operate and maintain landscaping machinery (e.g. lawnmowers, tillers, all-terrain vehicles).

- Understand the risks posed by working outdoors (e.g. uneven terrain, gravel roads, wildlife, insects such as bees, dehydration, weather conditions).

- Basic knowledge of safety protocols related to outdoor work and working with machinery.

- Ability to perform routine physical tasks involved in field station operations.

- Strong work ethic and initiative with a "can do" attitude.

- Demonstrated ability to work both independently and as part of a team.

- Ability to work variable hours.

This position is open, and we will accept applicants until it is filled.

*Applicants must be legally entitled to work in Canada. *

To apply: email ksr.temporary@gmail.com with a copy of your resume and a brief cover letter stating your background and interest in the position. The email subject should read "Reserve Operations Assistant Application"

KSR Manager <koffler.manager@gmail.com>

KULeuven EcolEvolGenomics

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

The Division 'Ecology, Evolution and Biodiversity Conservation' at the Department of Biology at the KU Leuven (Belgium) is seeking candidates for a faculty position in Ecological and Evolutionary genomics starting 1 October 2020.

We encourage applications by outstanding candidates with a research program at the intersection of ecology and evolution which addresses fundamental research topics using a genomics toolbox with aquatic organisms. The successful candidate will be expected to build her/his own independent research group and further integrate and strengthen collaborations across research groups within the Division. The new faculty member will also have responsibility for part of the teaching in ecology, evolution and genomics. After a pre-selection step by the Division, the successful candidate will be expected to continue the selection procedure at the university level for one of the two 'BOFZAP' categories of research professorships: junior BOFZAP for a researcher with high research potential proven by internationally recognized scientific publications, or Senior BOFZAP for a highly internationally recognized researcher in the field. Key selection criteria for BOFZAP positions is excellence in research reflected in both the scientific achievements and the research plan for the next five years. We aim for candidates with a research profile at the level of successful ERC applicants. Candidates should master up-to-date molecular and bioinformatic methods. Candidates are expected to teach students at all academic levels, including supervision of PhD students and postdocs. Candidates will be appointed in an academic staff position (ZAP) with a rank depending on the candidate's qualifications. BOFZAP researchers receive a BOF start-up grant < https://www.kuleuven.be/-onderzoek/gedocumenteerd/index_en.html#details/-ac6a8115c765a8699ea4db628cd50a1dd0f61bed > of 100,000 euro for the first two years. In addition the department of Biology provides a PhD fellowship of 4 years.

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

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

Questions can be directed to the Head of the Division, Professor Robby Stoks (robby.stoks@kuleuven.be). The application must be sent as a single PDF by email to Conny.coeckelberghs@kuleuven.be with as subject 'Eco-Evo Genomics faculty position'. The closing date for applications is June 25th 2019.

Robby Stoks <robby.stoks@kuleuven.be>

MichiganStateU FieldTech PlantEvolution

Open Field Technician Position

The Lowry Lab in the Plant Biology Department at Michigan State University is currently looking for 1-2 field technicians to conduct research on genetics of evolutionary adaptations in the bioenergy crop switchgrass. The successful applicants will work with a team of other technicians, undergraduate students, and postdocs. Applicants should send their resume/CV and contact information for at least two references to David Lowry at dlowry@msu.edu. The starting wage will be $15.50 per hour, with the opportunity to work up to 40 hours per week. The successful applicant will be located at the fantastic Kellogg Biological Station (http://www.kbs.msu.edu/) in western Michigan. This position is available now with the opportunity to continue at least through November 15th. More information about research in the Lowry Lab can be found at: https://davidbryantlowry.wordpress.com/ – David B. Lowry Assistant Professor Plant Biology Department Michigan State University Plant Biology Labora-

tories Room 268 Cell: 908-723-3534 Office: 517-432-4882
http://davidbryantlowry.wordpress.com/ David Lowry
<davidbryantlowry@gmail.com>

NorthCarolina MNS MammalogyCurator

NC Museum of Natural Sciences: Collections Manager, Mammalogy

The North Carolina Museum of Natural Sciences is searching for a new Collections Manager for Mammalogy to join our scientific team. This position will be primarily responsible for the management and maintenance of the Museum's Mammalogy Research Collection and associated curatorial duties (databasing, specimen inventory and management, managing loan activity, collection expansion, participating in funded collections grants, seeking additional collections stewardship funding, etc.). This position will be responsible for coordinating, training, and supervision of volunteers and others who are associated with the Mammalogy Research Collection. The Collections Manager of Mammalogy will be expected and encouraged to participate in research projects in mammal biology, systematics, conservation, and/or ecology, leading to publication of results in peer-reviewed scientific journals and popular media outlets. The CM will participate in various educational and outreach activities of the Museum, including (but not limited to): annual events, public science presentations, and 'behind-the-scenes' tours of the Collections facilities. This position might also be called upon by other state agencies or external organizations to provide collections information, training and other assistance.

More details and application instructions can be found at:

https://www.governmentjobs.com/careers/-
northcarolina/jobs/2269195/collections-manager-
mammalogy?keywords=Mammalogy&pagetype=-
jobOpportunitiesJobs Jason R. Cryan, Ph.D. Deputy
Director Chief, Research & Collections NC Museum of
Natural Sciences

11 West Jones St., Raleigh, NC 27601 USA jason.cryan@naturalsciences.org 919.707.9933

"Cryan, Jason R" <Jason.Cryan@naturalsciences.org>

NTNU Norway ManagerMolecularLaboratory

The NTNU University Museum wishes to develop an internationally leading academic environment in the field of molecular biodiversity.

The Department of Natural History has a vacant permanent 100% position as a Senior Engineer/Head Engineer at the Department's molecular laboratory and cleanlab. The Department of Natural History has a special responsibility for building and maintaining scientific collections and long-term series of objects, biological data and environmental data. The institute conducts active research within the field of biodiversity (biosystematics, biogeography, and ecology with particular emphasis on conservation biology). A central part of the department's activities is focused on molecular biodiversity, especially molecular analyzes of scientific collections and long-term series.

This Senior Engineer/Head Engineer position is central for realizing the Department for Natural History's ambitious goals for outstanding research in this field.

Job description Work tasks include, besides daily operation of laboratories (orders, HSE work, updating the chemical register, running various types of analyzes, maintenance of analytical instruments), also participation in the development of research methodology, development of the laboratories and participation in research projects. Guidance and training of students is also included in the position.

Qualification requirements For the position, it is required that the candidate has relevant education from university or college, at minimum a master degree in biology (molecular biology, evolutionary biology or similar), biotechnology or other relevant subject areas. Relevant work experience is required, as well as good oral and written communication skills in English.

Desirable qualifications It is desirable that candidates for this position have a good knowledge of state-of-the-art laboratory methodology (development of NGS libraries, in-situ hybridization, DNA / RNA extraction, PCR, qPCR, electrophoresis, metagenomics) and analyses of large-scale sequence data (mapping, bash/python/R, genome assembly). Experience in population genomics and/or phylogenomics is also desirable.Experience with modern analytical instruments is an advantage (for ex-

ample: Agilent BioAnalyzer/TapeStation, BluePippin, Qubit, BioRuptor, Illumina platforms, or similar).

Desired personal characteristics - A genuine interest in research - Positive and cooperative - Systematic and hard-working - Structured and responsible - Ability to work independently and in teams - Personal suitability, initiative and ability to familiarize yourself with new methods will be emphasized.

The NTNU University Museum and the Department of Natural History are undergoing rapid growth and development. We want a Senior Engineer/Head Engineer with great ability and willingness to adjust.

In other words, we seek you, a candidate who is sociable, self-reliant, and who takes initiative to solve tasks accurately, and take prides in the tasks to be done. You are pleasant, learn quickly and are interested in the type of tasks we work with.

Questions about the position can be directed to Mike Martin, phone number + 47 901 51 850, e-mail mike.martin@ntnu.no

Application deadline: 24.05.2019

For more information and to apply, please see: https://www.jobbnorge.no/en/available-jobs/job/169170/-senior-engineer-head-engineer-molecular-laboratory Mike Martin <sameoldmike@gmail.com>

NTNU Trondheim Metabarcoding eDNA

The Department of Natural History, NTNU University Museum, Norwegian University of Science and Technology, invites applications for a researcher position within the field of:

Molecular analyses of environmental DNA and bulk organismal samples (metabarcoding, metagenomics).

The NTNU University Museum is aiming to be a leading international institution within the field of molecular biodiversity.

The city of Trondheim is a modern European city with a rich cultural scene, and easy access to breath-taking natural landscapes. The Norwegian welfare state, including healthcare, schools, kindergartens and overall equality, is among the best of its kind in the world.

The position is permanent and financed by external project funding.

The person hired will conduct research within DNA metabarcoding/metagenomics on environmental DNA (eDNA). The person will:

- Obtain externally funded projects

- Do project management

- Do field work

- Process collected material

- Do molecular lab work

- Analyse data

- Publish in scientific journals

- Qualification requirements

- Application deadline: 24.05.2019.

For more information, please see https://www.jobbnorge.no/en/available-jobs/job/169869/-researcher-in-metabarcoding-and-edna Prof. Hans K. Stenoien Head of Department, Dept. Natural History, NTNU University Museum http://www.ntnu.edu/employees/hans.stenoien "Hans K. Stenøien" <hans.stenoien@ntnu.no>

OklahomaStateU 2 1yr EvolGenetics

Candidates taking evolutionary approaches to problems in genetics or genomics are encouraged to apply for these positions.

Visiting Assistant Professor in Integrative Biology

The Department of Integrative Biology at Oklahoma State University (http://integrativebiology.okstate.edu) invites applications for two Visiting Assistant Professors. We seek applicants with a Ph.D. in a life sciencesfield, demonstrated excellence in undergraduate teaching, and a commitment to meeting the needs of a diverse undergraduate population. The successful candidate will teach two courses each semester, supervise laboratory sections, and contribute to departmental governance and outreach activities. The appointment is for one year with the possibility to apply for a continuing tenure-track position. The position offers a competitive salary and an excellent benefits package. Our department has a growing and diverse body of over 900 undergraduates majoring in biology, zoology, and physiology.

Faculty prepared to teach introductory courses in genetics, genomics, or conservation genetics are especially encouraged to apply. Stillwater is located in north-

central Oklahoma, and offers a high quality of life in a thriving college community with a low cost of living, many restaurants, a local airport served by American Airlines, and close proximity to both natural and major metropolitan areas (Tulsa and Oklahoma City).

To apply, please submit the following items via https:/-/apply.interfolio.com/62743 : cover letter, curriculum vitae, teaching statement, and contact information for three professional references. Application review will begin May 20, 2019 with employment starting August 2019 or as negotiated.

Bruce Waldman <bw@bronze.lcs.mit.edu>

OmahaZoo GeneticsLabTech

Omaha's Henry Doorly Zoo and Aquarium

Laboratory Technician- Genetics

Summary:

The Laboratory Technician will participate in ongoing molecular and next generation sequencing research as well as conservation-focused investigations by performing the following duties. The start date for this position will be on or after August 1, 2019

Duties and Responsibilities (include but not limited to):

* Carry out experiments and perform required tasks well both under supervision and when operating independently. * Perform molecular and biological experiments. * Practice aseptic technique. * Prepare solutions and media for molecular biology applications. * Perform proper sample handling for molecular analyses. * Compile thorough and accurate lab documentation, paying attention to detail. * Be a proactive communicator, with the ability to read, understand and follow lab protocols and Standard Operating Procedures. * Maintain cleanliness and sanitation while complying with safety procedures in their employed laboratories. * Utilize arithmetic for the performance of daily experiments. * Have a clear understanding of the metric system of weight and volume as well as conversion between various weight measures, and chemical calculations (molarities and pH). * Assist in ordering, care, maintenance, and utilization of department equipment, supplies, and inventories. * Responsible for troubleshooting as necessary and be proactive in resolving problems regarding essential laboratory equipment such as automated sequencers, thermocyclers, and spectrophotometer. * Contribute to grant preparation efforts, literature searches and

manuscript writing, as needed. * Assist in running field-based volunteer program in Madagascar by managing e-mail correspondence, conducting interviews with potential volunteers and coordinating the logistics with personnel in Madagascar. * Efficiency and ability to use computers and related programs is imperative.

Knowledge, Skills and Abilities Required:

* A thorough knowledge of molecular genetics and related techniques, and have a good understanding of biological sciences. Experience with next-generation sequencing is highly preferred. * 1+ years of experience * Strong people skills * Detailed oriented * Willingness to learn and contribute * Follow directions * Meets deadlines

Education

* A Bachelor's degree in the Biology, Genetics, Environmental Science, or related field is required. An equivalent combination of further education and experience may be substituted.

DISCLAIMER

The information presented indicates the general nature and level of work expected of employees in this classification. It is not designed to contain, nor is it to be interpreted as, a comprehensive inventory of all duties, responsibilities, qualifications and objectives required of employees assigned to this job.

Omahas Henry Doorly Zoo & Aquarium is an Equal Employment Opportunity Employer as defined by the EEOC.

VISA SPONSORSHIP IS NOT AVAILABLE

We can only accept applications through this link: https://www.paycomonline.net/v4/ats/web.php/jobs/-ViewJobDetails?job093&clientkeywB425C21C6E28F6E3B0849B4A14F IwAR2zI8M_wY9KohN4O_VoHGmaTvSDeKVxxJZNCetS5AH5bbqoD E-w4 Genetics Department <genetics@omahazoo.com>

QueenMaryULondon BioinformaticsEvolutionGenomics

QueenMaryULondon.FacultyPosition.BioinformaticsEvolutionGenomics

Permanent Lectureship in Bioinformatics

We are seeking a Lecturer (Assistant Professor) with a strong background in bioinformatics, ideally within the context of evolutionary or ecological science. The successful candidate will contribute to developing the

core research themes of the department and be expected to develop a world-leading research programme and lead an active research group. Additionally, the Lecturer will be expected to teach on our growing MSc-level Bioinformatics courses, as well as contribute to some teaching at undergraduate level.

For full details and instructions on how to apply, see: https://webapps2.is.qmul.ac.uk/jobs/-job.action?jobIDB87   For the departmental website: http://www.sbcs.qmul.ac.uk/ The permanent full-time position will start in September 2019.

Closing date for applications is 20th June 2019. Interviews will be held over the summer. Informal enquires to Dr. Christophe Eizaguirre: c.eizaguirre@qmul.ac.uk

SJ Rossiter <s.j.rossiter@qmul.ac.uk>

StateCollectionMunich CuratorDeptEntomology

Here comes a job opportunity as a curator in the Department of Entomology of the Zoological State Colletion Munich. This is one of the larger entomological collections in the world, with strong specimen based research programs in all aspects of systematic zoology, biogeography and evolutionary biology. ZSM is part of the SNSB. The Bavarian Natural History Collections (Staatliche Naturwissenschaftliche Sammlungen Bayerns, SNSB) are a research institution for natural history in Bavaria. They encompass five state collections (zoology, botany, paleontology and geology, mineralogy, anthropology). Our research focuses mainly on the past and present bio- and geodiversity and the evolution of animals and plants. To achieve this we can in part rely on our large scientific collections (ca. 35,000,000 specimens). ZSM and SNSB are very well equipped with modern research infrastructure required for state-of-the-art research. Interactions with two top universities in Munich are manifold. Munich offers an exceptionally high quality of life. Posted by Michael Balke, balke.m@snsb.de

JOB OFFER We offer as soon as possible a job as a Curator (Zoology, Entomology) (m/w/d) at the Zoologische Staatssammlung MÃÂ¼nchen (ZSM; www.zsm.mwn.de), part of the Staatliche Naturwissenschaftliche Sammlungen Bayerns (SNSB). We are looking for an excellent entomologist as Head of Section ÂHemiptera". The collections at ZSM comprise several 100.000 specimens of about 13.000 species, among them

ca. 60% Heteroptera, 40% Auchenor- and Sternorrhyncha, Saltatoria, Phasmatodea und Mantodea. The main focus of research of the applicant may also be outside this field of entomology. Required is an academic education with zoological focus including PhD or adequate, expert knowledge in entomological systematics and European faunistics, fluent knowledge of German and English. Preferred candidates have knowledge in modern methodologies (morphological or molecular techniques, imaging, data-basing) and have experience with large entomologcal collections. We expect high-level papers, acquirement of private collections and of research grants, integration into our PR-activities, engagement in the societies associated with our house, and also providing oral expertise concerning species protection subjects or mid-European insects in general.

Half-time contracts are possible, but we would prefer a full-time scientist. If all preconditions are fulfilled salary will follow the rules of 13 TV-L or A13 of Germany. A first contract will be for two years, but a permanent employment afterwards is possible as is habilitation at LMU Munich. Applicants with handicaps are preferred, if otherwise equally profiled. To raise the percentage of women in science we are particularly interested in applications of women. Applications with letter of intent, CV, list of publications and maximally five selected papers (also via email as pdf-files or CD-ROM or USB-stick) should be sent

Until 7th June 2019 to Prof. Dr. Gerhard Haszprunar Zoologische Staatssammlung MÃÂ¼nchen, Direktion MÃÂ¼nchhausenstr.   21   D-81247   MÃÂ¼nchen GERMANY.   Tel.:   ++48-89-8107-104,   email: haszprunar@snsb.de

Please note that after finishing the competition your data will not returned. Travel expenses for the journey to a possible interview will not be accepted. All your data will be safed for one year after finishing the competition and fully deleted afterwards.

Michael Balke <michael_balke@yahoo.de>

StonyBrookU EvolutionaryBiology

Endowed Full Professor Laufer Center for Physical & Quantitative Biology Stony Brook University

Responsibilities & Requirements: We seek an outstanding senior scientist for a tenured endowed full professor position. We want a bold innovator working at the

interface between the life sciences and physical sciences. We seek expertise in the physical biology of cell actions – principles, mechanisms, adaptation/evolution. Examples include – but are not limited to – cellular networks, single-cell experiments, fitness landscapes and stochastic dynamics. We focus on basic research, but are cognizant of the impacts on challenges such as aging, amyloid diseases, cancer, or drug resistance. We prefer an experimentalist, but we welcome applications from theorists.

This is a basic-research position, with minimal teaching. It has attractive resources, including a Laufer Endowed chair that provides some annual research support. The successful individual will have considerable freedom to choose his or her departmental affiliation. Preference will be given to a candidate with leadership skills who can help guide the Center's future.

The Laufer Center is an exciting collaborative cross-disciplinary place for physical and quantitative biology at Stony Brook University, just minutes from Stony Brook Medicine, comprising the Renaissance School of Medicine and the Stony Brook Cancer Center. We have researchers from Biomedical Engineering, Chemistry, Physics, Applied Mathematics and Statistics, Computer Science, Pharmacology, Molecular Genetics and Microbiology, and Ecology and Evolution, and close ties to our neighbors at Cold Spring Harbor Laboratory and Brookhaven National Laboratory. Stony Brook is in a beautiful mid-Long-Island location on the LI Sound with outstanding local schools, 70 miles from New York City.

This is a basic-research position, with minimal teaching.

Required Qualifications: PhD and a strong record of research productivity in relevant field.

Special Notes: This is a tenure track position. FLSA Exempt position, not eligible for the overtime provisions of the FLSA. Internal and external search to occur simultaneously. Eligibility for tenure will be based upon applicants' qualifications and experience. To qualify for tenure and/or a senior faculty appointment, the candidate must meet the criteria established by Stony Brook University. Anticipated Start Date: Spring 2020.

Pursuant to Executive Order 161, no State entity, as defined by the Executive Order, is permitted to ask, or mandate, in any form, that an applicant for employment provide his or her current compensation, or any prior compensation history, until such time as the applicant is extended a conditional offer of employment with compensation. If such information has been requested from you before such time, please contact the Governors Office of Employee Relations at (518) 474-6988 or via

email at info@goer.ny.gov.

Stony Brook University is 100% tobacco-free as of January 1, 2016. See our policy and learn more at stony-brook.edu/tobaccofree.

The selected candidate must successfully clear a background investigation.

Application Procedure: Those interested in this position should submit a State Employment Application , cover letter, resume/CV, a two- to three-page description of research plans, and arrange to have at least three letters of reference uploaded to AJO by clicking Apply. Alternately, you may submit your application package to the departmental address below. Please also fill out an online Applicant Information Survey . Do not submit this survey to the department. Applications should be sent to: https://academicjobsonline.org/ajo/jobs/-13401 Campus Description: Stony Brook University, home to many highly ranked graduate research programs, is located 60 miles from New York City on Long Island's scenic North Shore. Our 1,040-acre campus is home to 24,600 undergraduate, graduate, and doctoral students and more than 13,500 faculty and staff, including those employed at Stony Brook Medicine, Suffolk County's only academic medical center and tertiary care provider. The University is a member of the prestigious Association of American Universities and co-manager of nearby Brookhaven National Laboratory (BNL), a multidisciplinary research laboratory supporting world class scientific programs utilizing state-of-the-art facilities such as the Relativistic Heavy Ion Collider, the National Synchrotron Light Source, and the Center for Functional Nanomaterials, and the New York Blue IBM BG/L+P supercomputer, owned by Stony Brook and managed by BNL. Stony Brook is a partner in managing the Laboratory for the Department of Energy, and is the largest institutional scientific user of BNL facilities. As such, many opportunities exist for collaborative research, and in some cases, joint appointments can be arranged.

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UCaliforniaLosAngeles LabTech UrbanConservationGenomics

The UCLA La Kretz Center for California Conservation Science (http://www.environment.ucla.edu/lakretz/) and the UCLA Sustainable LA Grand Challenge (https://grandchallenges.ucla.edu/sustainable-la/) invite applications for a lab technician to work on a Molecular Urban Ecology and Bioinformatics project. The work is embedded in an ongoing project on the impact of urbanization on a suite of 22 plant, invertebrate and vertebrate species spanning the Urban/Wildland interface of the Los Angeles basin. Our overarching goal is to determine such issues as the contribution of protected lands to the conservation of genetic diversity, the ability of species to traverse the urban landscape, and genetic resilience to future climate change.

We are looking for a highly motivated individual with experience in the collection of genomic (RADseq, and possibly de novo genome assembly) data. The candidate would work collaboratively with Dr. Joscha Beninde (https://www.ioes.ucla.edu/person/joscha-beninde/), an urban landscape geneticist already working on the project.

The appointment is for one year, and with a strong possibility of extending for additional time. Our preferred start date is summer, 2019. Salary is commensurate with experience.

Interested candidates should submit 1) cover letter, 2) current CV/resume, 3) maximum 2-page description of their molecular genetic experience, and 4) names and contact details of two referees, all as a single PDF file.

Deadline for completed applications is July 1, 2019.

E-mail questions and application materials to Brad Shaffer (Director of the La Kretz Center) at brad.shaffer@ucla.edu or Joscha Beninde (postdoc in this project) at beninde@ucla.edu.

Brad Shaffer brad.shaffer@ucla.edu Phone: (310) 825-3836

H. Bradley Shaffer Distinguished Professor Department of Ecology and Evolutionary Biology www.eeb.ucla.edu/Faculty/Shaffer/ Director UCLA La Kretz Center for California Conservation Science Institute of the Environment and Sustainability University of California, Los Angeles https://www.ioes.ucla.edu/lakretz/ hbshaffe@g.ucla.edu

UCBerkeley ResAssoc EvolutionaryGenetics

Staff Research Associate, PMB (9612C) http://jobs.berkeley.edu Job ID# 26825

About Berkeley The University of California, Berkeley, is one of the world's most iconic teaching and research institutions. Since 1868, Berkeley has fueled a perpetual renaissance, generating unparalleled intellectual, economic and social value in California, the United States and the world. Berkeley's culture of openness, freedom and acceptance-academic and artistic, political and cultural-make it a very special place for students, faculty and staff.

Berkeley is committed to hiring and developing staff who want to work in a high performing culture that supports the outstanding work of our faculty and students. In deciding whether to apply for a staff position at Berkeley, candidates are strongly encouraged to consider the alignment of the Berkeley Workplace Culture with their potential for success at http://jobs.berkeley.edu/why-berkeley.html . Application Review Date The First Review Date for this job is: May 17, 2019

Departmental Overview

The Blackman Laboratory in the Department of Biology is seeking a Staff Research Associate to assist with research in evolutionary and ecological developmental genetics using sunflower and monkeyflower as study systems. Research in the lab focuses on how and why plant developmental responses to environmental cues evolve during domestication, adaptation, and speciation.

Responsibilities Planning and Carrying Out Expriments: includes planning and executing greenhouse, growth chamber, and field studies; carrying out DNA/RNA extractions, PCR or qRT-PCR amplification, sequencing library construction and sequencing Assist in evaluating research methods, procedures, and techniques, based on established objectives. Provide basic assistance to researchers in manipulating, computing, and analyzing data using specialized statistical computer software. Assist with training other staff members on procedures; may supervise students or volunteers. Assist Principal Investigators and other researchers in developing new strategies and techniques for experimentation. Provide routine, technical, and administrative support to research projects. Managing Datasets and

Seed Stocks: Record/enter, proofread, organize, and summarize datasets in Excel or other database software; ensure the integrity of large datasets, samples, and notes so they are easily accessible to the Principal Investigator and other lab members; organize and maintain lab seed stocks. Maintaining and Collecting Data on Experiments in Controlled or Field Conditions: take responsibility for daily observations of germination and flowering of plants in greenhouse, growth chamber, or field facilities; measure additional traits as necessary, including image capture of floral development; perform genetic crosses to develop new mapping populations or inbred lines as well as perpetuate existing germplasm General Laboratory Administration: assist with training other staff members on procedures; supervise students or volunteer personnel and coordinate their work schedules; fulfill the lab's purchasing needs, ensuring supplies are well stocked and communicating with fiscal staff as needed; keep the lab's chemical inventory and compliance with safety regulations up to date

Required Qualifications The specialist must be able to be able to work in the field and in a greenhouse, manage data sets utilizing Excel, perform sterile techniques, prepare media, carry out basic procedures associated with DNA amplification and sequencing, and follow research protocols and regulatory guidelines with exactness. Must be able to train and supervise student workers and coordinate student work schedules. Good baseline knowledge of genetics, plant biology, and evolutionary biology is essential. The specialist must have strong organizational, computer, and communication skills, including familiarity with Microsoft Office tools. Excellent oral and written communication in daily interactions is necessary in order to work independently and as part of a team and provide direct support to leaders as needed; and to assist in training, provide work direction, prepare reports, and keep records.

Preferred Qualifications Experience using packages relating to statistics, image analysis, phylogeny, sequence alignment, and bioinformatics. Experience building libraries for next-generation sequencing. Research experience working with sunflower and/or monkeyflower. Associate's degree and at least 2 years of lab experience which may include student experience; or Bachelor's degree in related science; or an equivalent combination of education and experience.

Salary & Benefits This is an exempt, monthly paid position. Salary is commensurate with experience within the range of \$47,100.00 - \$58,560.00.

For information on the comprehensive benefits

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UCopenhagen 3yr HumanPalaeogenomics

Research Assistant, Human Palaeogenomics The Section for Evolutionary Genomics is looking for a skilled research assistant to fill a 3-year position, as part of a recently funded project that will investigate the population genomic history of Northern Europe. This project is a collaboration with multiple international partners, and is funded by the Carlsberg Foundation. The overall aim of the grant is to generate full genomic data from skeletal materials that span the last 1000 years from multiple European locations, for use in analyses to look at how the populations at these sites have changed through time, and what pathogen challenges they faced. This research assistant position will in particular be charged with extracting DNA from skeletal material, conversion of this DNA into NGS libraries for deep sequencing, sampling skeletal elements and maintaining a well-organized database of the samples and results. It is likely the candidate may be required to travel to visit other partners for certain periods to assist them in their data generation. Thus, we are looking to hire a research assistant who has prior relevant experience, and who is dedicated to the generation of high-quality data. The position would be co-supervised by Prof Tom Gilbert, Asst. Professor Ashot Margaryan, and Dr. Sshild VÃ¥gene (Section for Evolutionary Genomics, Dept Biology).

Main Tasks

- Subsample skeletal material for subsequent DNA extraction - Organise samples into a sample database - Extract DNA from the samples, following standard palaeogenomic protocols - Generate shotgun sequencing libraries and data from the samples - Implementation of roboticised pipelines for DNA extraction and library construction

Mandatory Qualifications

- Relevant scientific background ' at least MSc level in a topic related to Biology and/or Genetics. - Prior experience in the extraction of nucleic acids from ancient skeletal materials - Prior experience in the generation of NGS data from ancient skeletal materials - Highly

organized, and able to work both as part of a team but also under their own initiative. - Excellent teamwork and communication skills, both verbal and written - Fluency in English (written, reading, spoken)

Other Qualifications of Considerable Interest

- Knowledge of the principles of palaeogenomic data generation.

This advertisement can also be found on the University of Copenhagen's job portal: https://employment.ku.dk/all-vacancies/?show=9584 Further information on the Department is linked at http://www.science.ku.dk/english/about-the-faculty/organisation/ .Inquiries about the position can be made to Prof Tom Gilbert (tgilbert@snm.ku.dk).

The position is open from 1 September 2019 or as soon as possible thereafter.

The University wishes our staff to reflect the diversity of society and thus welcomes applications from all qualified candidates regardless of personal background.

Terms of employment

The position is covered by the Memorandum on Job Structure for Academic Staff. Terms of appointment and payment accord to the agreement between the Ministry of Finance and The Danish Confederation of Professional Associations on Academics in the State. The starting salary is currently at a minimum DKK 349,819 including annual supplement (+ 17.1 % pension). Negotiation for salary supplement is possible.

The application, in English, must be submitted electronically by clicking APPLY NOW below.

Please include

- Curriculum vita, including clear documentation of above listed mandatory skills requirement. - Diploma and transcripts of records (BSc and MSc) - Complete publication list

The deadline for applications is Sunday 16 June 2019, 23:59 GMT +2.

After the expiry of the deadline for applications, the authorized recruitment manager selects applicants for assessment on the advice of the Interview Committee.

You can read about the recruitment process at http://employment.ku.dk/faculty/recruitment-process/ . Interviews will be held at the end of July and beginning of August (week 31-32).

Ashild Vagene <ashild.v@googlemail.com>

UGroningen 6 EvolutionaryBiology

Dear EvolDir community,

The University of Groningen is recruiting candidates for its Rosalind Franklin programme: tenure-track positions for talented women who aspire to become full professor. There are in total 27 fellowships available at the Faculty of Science and Engineering; six positions are open for candidates from the Life Sciences - including evolutionary biology. For evolutionary research at FSE, see https://www.rug.nl/research/gelifes/gelifes . (Under European jurisdiction it is lawful to specifically recruit underrepresented groups. Since 2002 the university has welcomed over 100 Rosalind Franklin Fellows, see https://www.rug.nl/about-us/work-with-us/rff/rosalind-franklin/overview-rff-all)

The deadline for applications is 3 June.

For information and application, see: https://www.rug.nl/about-us/work-with-us/job-opportunities/?details Martine Maan

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Martine E. Maan Associate Professor and Rosalind Franklin Fellow Groningen Institute for Evolutionary Life Sciences (GELIFES) University of Groningen PO Box 11103 9700 CC Groningen The Netherlands +31 (0)50 363 2196

Visiting address: Nijenborgh 7 9747 AG Groningen The Netherlands building 5171, room 01.42

http://www.rug.nl/staff/m.e.maan — This email has been checked for viruses by Avast antivirus software. https://www.avast.com/antivirus "m.e.maan@rug.nl" <m.e.maan@rug.nl>

UIdaho ResearchSpecialist InsectEvolution

The Arthropod Molecular Systematics laboratory (PIs Marek Borowiec & Chris Hamilton) at the University of Idaho is seeking a full-time Research Specialist to assist in research on a broad range of topics, from taxonomy and phylogenetics to bioinformatics. The laboratory

is located in Moscow, Idaho. The town offers a small and lively community with a range of outdoor activities nearby in the lovely Palouse region of Idaho and Washington. This position is contingent upon work and/or funding. However, there are three years of initial funding available for the position.

The candidate will be tasked with handling and curating insect and other arthropod specimens, live, mounted or otherwise preserved, participating in field work, performing data management, photographing specimens, designing experiments, performing wet laboratory work including DNA extraction, amplification, genomic library preparation, and data analysis. The candidate will assist in ordering and organizing lab equipment and supplies. They will also be responsible for facilitating training students and postdocs in laboratory techniques and the use of specialized equipment. The candidate will also assist in outreach and in communicating the lab's research. The possibility exists for the candidate to be a coauthor on resulting publications. Importantly, the candidate will help foster a safe, productive, inclusive, and collegial lab environment.

For more details and how to apply see here: https://uidaho.peopleadmin.com/postings/26591

"Borowiec, Marek (mborowiec@uidaho.edu)" <mborowiec@uidaho.edu>

UManchester Genomics

The University of Manchester

Faculty of Biology, Medicine and Health

School of Biological Sciences

Division of Evolution and Genomic Sciences

Senior Lecturer / Reader / Chair in Genomic Sciences

Salary commensurate with experience

The School of Biological Sciences are seeking to appoint an outstanding scientist to enhance our strengths in genomic science, in areas allied to sequencing, analysis, evolution, systems and computational biology and its applications in biology and clinical medicine.

You will be appointed to an academic teaching and research position (commensurate with your track record) and will be able to seize on the opportunities available from the unique environment offered in Manchester for collaboration with colleagues working in basic biology through to translational therapies.

You will contribute to the development and delivery of our undergraduate and postgraduate programmes and will participate in the successful mentoring and supervision of our cohort of postgraduate researchers and junior academic staff.

You will be supported in establishing your lab and research programme at the University of Manchester from which you will enhance your international reputation in the field. You will benefit from joining an established community of collegiate researchers including the Manchester Centre for Genomic Medicine.

You will have a PhD and established publication record in the genomic sciences field as well as the ability to communicate your research successfully to a wide audience. A commitment to teaching and learning is essential in addition to the drive to progress and develop in your career. We would particularly welcome applications from those who have a previously attracted significant external funding for their research.

The University of Manchester is committed to equality of opportunity for all our staff and holds Athena Swan and Race Charter Marks from the ECU (the School of Biological Sciences is proud to hold an Athena Swan Silver Award), was ranked #20 in the Stonewall Top 100 Employers in 2019 and is a Disability Confident Employer.

We welcome qualified applicants from all backgrounds and are happy to discuss part-time or flexible working opportunities in respect to this post.

The University of Manchester values a diverse workforce and welcomes applications from all sections of the community.

Please note that we are unable to respond to enquiries, accept CV's or applications from Recruitment Agencies

Enquiries about the vacancy, shortlisting and interviews:

Professor Simon Hubbard Professor of Computational Biology Head of Division, Division of Evolution and Genomic Sciences Simon.Hubbard@manchester.ac.uk / +44(161) 306 8930

Professor Simon Lovell Professor of Molecular Biology Domain Director for Evolution, Systems and Genomics Simon.Lovell@manchester.ac.uk

General enquiries: Email: hrservices@manchester.ac.uk Tel: 0161 275 4499

Technical support: Email: universityofmanchester@helpmeapply.co.uk Tel: 01565 818 234

This vacancy will close for applications at midnight on the closing date.

Reinmar

Dr Reinmar Hager Evolution and Genomic Sciences |
School Lead for International Postgraduate Research

School of Biological Sciences | Faculty of Biology,
Medicine and Health | Michael Smith Building |
The University of Manchester | Manchester M13
9PT, UK Tel.   ++44 (0)161-275-1550 | http://-
hagerlab.lab.manchester.ac.uk/

Reinmar Hager <Reinmar.Hager@manchester.ac.uk>

UManchester GenomicsEvolution

Senior Lecturer / Reader / Chair Division of Evolution
and Genomic Sciences School of Biological Sciences Fac-
ulty of Biology, Medicine, & Health The University of
Manchester

Job Reference: BM&H-13927 Location: Oxford Road,
Manchester Closing Date: 10/06/2019 Salary: Senior
Lecturer/Reader (£51,630-£67,317), or Chair (Professo-
rial Scale according to experience) Employment Type:
Permanent Hours Per week: Full Time

For further particulars and full details, please visit:

https://www.jobs.manchester.ac.uk/-
displayjob.aspx?jobid=285   The School of Biological
Sciences is seeking to appoint an outstanding scientist
to enhance our strengths in genomic science, in areas
allied to sequencing, analysis, evolution, systems and
computational biology and its applications in biology
and clinical medicine.

You will be appointed to an academic teaching and re-
search position (commensurate with your track record)
and will be able to seize on the opportunities available
from the unique environment offered in Manchester for
collaboration with colleagues working in basic biology
through to translational therapies.

You will contribute to the development and delivery of
our undergraduate and postgraduate programmes and
will participate in the successful mentoring and supervi-
sion of our cohort of postgraduate researchers and junior
academic staff.

You will be supported in establishing your lab and re-
search programme at the University of Manchester from
which you will enhance your international reputation
in the field. You will benefit from joining an estab-
lished community of collegiate researchers including the
Manchester Centre for Genomic Medicine.

You will have a PhD and established publication record
in the genomic sciences field as well as the ability to com-
municate your research successfully to a wide audience.
A commitment to teaching and learning is essential in
addition to the drive to progress and develop in your
career. We would particularly welcome applications
from those who have a previously attracted significant
external funding for their research.

The University of Manchester is committed to equality
of opportunity for all our staff and holds Athena Swan
and Race Charter Marks from the ECU (the School of
Biological Sciences is proud to hold an Athena Swan
Silver Award), was ranked #20 in the Stonewall Top
100 Employers in 2019 and is a Disability Confident
Employer.

We welcome qualified applicants from all backgrounds
and are happy to discuss part-time or flexible working
opportunities in respect to this post.

The University of Manchester values a diverse work-
force and welcomes applications from all sections of the
community.

Please note that we are unable to respond to enquiries,
accept CV's or applications from Recruitment Agencies

Enquiries about the vacancy, shortlisting and interviews:

Professor Simon Hubbard Professor of Computational
Biology Head of Division, Division of Evolution and
Genomic Sciences Simon.Hubbard@manchester.ac.uk /
+44(161) 306 8930

Professor Simon Lovell Professor of Molecular Biology
Domain Director for Evolution, Systems and Genomics
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Tel: 0161 275 4499

Technical support: Email: universityofmanch-
ester@helpmeapply.co.uk Tel: 01565 818 234

This vacancy will close for applications at midnight on
the closing date.

Danna Gifford <danna.gifford@manchester.ac.uk>

UNAM Mexico ModellingBiodiversity

The Universidad Nacional Autonoma de Mexico (UNAM) invites applications to fill a tenure-track position at a level equivalent to Assistant Professor at the Departamento de Ecologia de la Biodiversidad, Instituto de Ecologia.

The successful candidate will be required to develop an independent research program on Theoretical Ecology. It will be expected that she/he develops collaborations, primarily but not exclusively with members of the Institute and the University. Lecturing regularly at undergraduate and graduate levels is compulsory.

Candidates should hold a PhD in Biology or Ecology and have a background in theoretical ecology and modelling of ecological/evolutionary processes to understand biodiversity patterns at different scales and levels of organization. As part of a University program to rejuvenate the academic workforce, the youngest candidates will be favoured. The successful candidate will have a strong publication record (Ý 10 high-impact peer-reviewed papers in the relevant area), a track record of securing competitive funds, and verifiable experience teaching and supervising students. Fluency in Spanish to perform lecturing is a requirement.

Selection will be based on 1) the strength of the candidate's Curriculum vitae, 2) a written research proposal (less than 10 pages) following the profile outlined above 3) a brief outline of the research activities for the first year including teaching and student supervision, and 4) a two-page proposal outlining the candidate's strategy to increase the scientific and social impact of his/her research project.

The application should include a letter addressed to the director of the Institute, Dr Constantino Macas Garcia stating the candidate's reasons to apply, the Curriculum vitae, a brief description of current and future research interests, the documents indicated in numbers 2 to 4 (above), a copy of the PhD official diploma, a copy of birth certificate, and the documents supporting the CV (only the first page of published papers, letters/e-mails indicating that papers have been accepted for publication, and evidence of teaching and theses supervision).

All documents should be sent electronically as a single PDF file to secacad@iecologia.unam.mx. The closing date is Jun 23rd, 2019. Shortlisted candidates will be required to send the documents by post to: Instituto de Ecologa, UNAM, Ap. Postal 70-275, Ciudad Universitaria, Ciudad de Mxico, CP 04510, Mxico.

Dr. Juan Fornoni Secretario Acadmico Instituto de Ecologa, UNAM

Constantino Macias Garcia Director Instituto de Ecologia, UNAM (http://web.ecologia.unam.mx/)

maciasg <maciasg@unam.mx>

UOttawa CRC Chair Genomics

Tier 1 Canada Research Chair in Genomics and the Environment

The University of Ottawa invites applications for a Tier 1 Canada Research Chair (CRC) in Genomics and the Environment. Applicants with expertise in genomics, bioinformatics, DNA technologies, with applications in toxicology or evolutionary biology will be considered. However, the preference will be given to candidates whose research aligns with the Strategic Areas of Development in Research https://research.uottawa.ca/-about/strategic-areas-development at the University of Ottawa. This includes, but is not limited to, Molecular and Environmental Sciences; Health. The successful candidate should be recognized internationally and demonstrate evidence of ongoing international collaborations. Contributions to the field of regulatory science will be an asset.

The Faculty of Science is one of the most research intensive science faculties in Canada and is recognized for its world-class programs and infrastructure within its five departments in the following domains: Biology, Chemistry and Biomolecular Sciences, Earth and Environmental Sciences, Mathematics and Statistics, and Physics. The Department of Biology, has ~ 40 faculty members with particular expertise in comparative physiology, evolutionary biology (genetics, ecology), and ecotoxicology. The Department is part of the Ottawa-Carleton Institute of Biology, and contributes significantly to graduate programmes in Chemical and Environmental Toxicology, Bioinformatics, and Environmental Sustainability.

Tier 1 Chairs, tenable for seven years and renewable once, are for outstanding researchers acknowledged by their peers as world leaders in their fields. For each Tier 1 Chair, the institution receives $200,000 annually for seven years. Nominees for Tier 1 Chair positions must be

full professors or associate professors who are expected to be promoted to the full professor level within one or two years of the nomination. Alternatively, if they come from outside the academic sector, nominees must possess the necessary qualifications to be appointed at these levels. New CRC nominees are also eligible for infrastructure support from the Canada Foundation for Innovation (CFI) https://www.innovation.ca/ to help acquire state-of-the-art equipment essential to their work.

Preferential Hiring: The University of Ottawa strongly supports a workplace environment that removes disparities experienced by the designated groups in Canada: women, Indigenous peoples, persons with disabilities and members of visible minorities, as defined in the Employment Equity Act https://laws.justice.gc.ca/-eng/acts/e-5.401/page-1.html. In a preferential hiring, only applications from members of those groups are considered and assessed for the vacancy. Candidates from these groups who wish to qualify for preferential consideration must fill the following self-identification form https://research.uottawa.ca/sites/research.uottawa.ca/-files/edi_questionnaire_ovpr_for_prizes_en_24-oct-2018-converted_fillable.pdf .The purpose of this measure is to improve the representation of the four designated groups in the allocation of Canada Research Chair positions.

Required Qualifications: A PhD or equivalent, outstanding independent research achievements in the CRC's identified area(s) and proof of interdisciplinary collaborations, an exceptional profile with respect to teaching and training of students at the graduate level, strong record of external research funding, excellent communication skills in either English or French. A passive knowledge of the other official language would be an asset.

Rank and salary: Regular tenure-track academic appointment in the relevant Faculty. This position is governed by a collective agreement between the University of Ottawa and the Association of Professors of the University of Ottawa.

Application Package: . A cover letter; . An up-to-date curriculum vitae (please include career interruptions such as parental or sick leaves that may have impacted your record of research. These will be taken into consideration in the selection process); . A research plan (2 to 3 pages); . A statement of teaching interests (1 to 2 pages); and . The names of three people who may be contacted by the University for letters of reference which will follow the Canada Research Chairs guidelines http://www.chairs-chaires.gc.ca/program-programme/referees-repondants-eng.aspx . Deadline:

June 14, 2019

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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

UPittsburgh AmphibianLabManagerTech

The Richards-Zawacki Lab (http://www.rzlab.pitt.edu/-) in the University of Pittsburgh Dietrich School of Arts & Sciences is seeking a Laboratory Technician/Manager that will manage the maintenance of laboratory equipment, purchase supplies, and supervise animal (amphibian) care and undergraduate lab assistants. Depending upon experience, the incumbent may also be responsible for generating and analyzing molecular data for ongoing projects on the topics of amphibian ecology, evolution, and conservation, and providing technical assistance to other personnel involved in these projects who are using similar techniques.

Management experience and excellent communications skills, as well as experience with basic molecular and microbiology techniques, are preferred. The incumbent will train new personnel who are recruited to the project and supervise the efforts of undergraduates. This includes regular meetings with personnel and supervision of notebook keeping. The incumbent will report to the primary investigator and work in collaboration with the primary investigator to manage laboratory activities.

The Dietrich School of Arts & Sciences is committed to building a culturally diverse staff.

Excellent interpersonal and relationship-building skills and the ability to work effectively with a wide range of individuals and constituencies in support of a diverse community.

Please see the full position posting for more information and to submit an application:

https://cfopitt.taleo.net/careersection/-pitt_staff_external/jobdetail.ftl?job=004271&tz=-GMT-04%3A00&tzname=America%2FNew_York For questions about the position, please contact Corinne Richards-Zawacki (clz17@pitt.edu)

Corinne L. Richards Zawacki, Ph.D. email: cori.zawacki@pitt.edu Associate Professor, Department

of Biological Sciences and Director, Pymatuning Laboratory of Ecology University of Pittsburgh

"At night I went out into the dark and saw a glimmering star and heard a frog and nature seemed to say, well do not these suffice?" - Ralph Waldo Emerson

"Zawacki, Corinne Lee" <cori.zawacki@pitt.edu>

UTexas Arlington HerpetologyCollectionManager

Herpetology Curatorial Manager

The Amphibian and Reptile Diversity Research Center (ARDRC) at the University of Texas at Arlington is searching for a Curatorial Manager for its herpetology collection. Responsibilities include: assist curators in the management, maintenance, and growth of the amphibian and reptile collection (more than 250,000 specimens); manage a team of curatorial assistants and student workers; participate in outreach and research. Please visit www.uta.edu/biology for an overview of the Biology Department and https://-www.uta.edu/biology/ardrc/index.php to learn more about the ARDRC.

For more details and to apply: https://-uta.peopleadmin.com/hr/postings/9084 Matthew K. Fujita Associate Professor Department of Biology University of Texas at Arlington Box 19850 Arlington, TX 76010 (817) 272-1464 http://www.fujitalab.com "Fujita, Matthew" <mkfujita@exchange.uta.edu>

VanderbiltU ResAssist HostMicrobeEvolution

Research Assistant II: Host-Microbe Ecology and Evolution

Position Summary: The Tate lab in the Department of Biological Sciences at Vanderbilt University is seeking a motivated and conscientious Research Assistant II to perform administrative tasks and experiments related to the ecology and evolution of infection and immunity. We use insect model systems and their natural parasites to study the evolution of immune systems and the impact of co-infection on within- and between-host disease dynamics. The primary responsibilities for this position include performing experiments, taking care of invertebrate organisms, and supporting day-to-day laboratory maintenance, inventory, and operations, including frequent communication with other lab members. The candidate should be capable of performing tasks and protocols independently after receiving training, and should be willing to troubleshoot failed procedures, including consultation of the primary literature. The candidate will be expected to attend laboratory meetings and be a scientifically engaged and collaborative member of the lab, including providing training and experimental support to other lab members. Vanderbilt University is a premier R1 research institution located in dynamic Nashville, Tennessee, USA, home to a world-renowned music scene, great restaurants, hiking, and other cultural attractions.

To see full description and application instructions: https://vanderuniv.taleo.net/careersection/-.vu_cs/jobdetail.ftl?job=00719&tz=GMT-05%3A00 Ann T. Tate, Ph.D. Assistant Professor of Biological Sciences Vanderbilt University

Veterinary StatisticalGenomicist

Job Title: Statistical Genomicist

Company Name: Embark Veterinary

Where: Boston, MA or Ithaca, NY

What: Full-time position

Love dogs? This is the place for you!

About us

Discover your dog more than fur deep with the most comprehensive DNA test on the market. Designed by world leaders in dog genetics, in partnership with Cornell University, the Embark DNA Test tells owners what breeds make up their pets, how to prevent future possible health problems, and what features and traits their pet might have. Help us end preventable disease in dogs and improve the lives of pets and their people through genomics.

Embark is the only dog DNA test using a research-grade DNA microarray, letting us give our customers the most accurate and comprehensive results on the market. More importantly, it allows us to do ongoing research into the genetics of dogs, which are a fantastic population for ge-

netic discovery due to selective breeding over time. Our research focuses on mapping new traits and diseases, improving personalized veterinary medicine, and developing new breeding programs to eliminate preventable diseases in pets.

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

The Role

We are looking to expand our science team and accepting applications for Scientists with extensive training and experience in Statistical Genetics and Genomics. Talented candidates at all levels of experience are encouraged to apply.

Our scientists are developing the next generation of breeding tools, novel genetic tests, and evolutionary research in dogs with the goal of accelerating canine genetic science and a long-term vision of ending preventable diseases in pets.

Embark's science team consists of leaders in the canine genomics research community and expert veterinary geneticists, computational biologists and population geneticists. The company is a research partner of the Cornell University College of Veterinary Medicine, with a science headquarters in Ithaca, NY and a company headquarters in Boston, MA. We are looking to hire top-notch scientists in both locations to expand our canine genetic testing product and accelerate our genetic discovery pipeline.

The Opportunity

- Design and execute genetic association studies. - Work collaboratively across teams to develop and accelerate Embark's canine genetic discovery platform. - Develop pipelines for processing and analyzing health and clinical data. - Build models to predict complex health and trait phenotypes from genetic and environment data.

Requirements

- Ph.D. or MS in Statistics, Genetics, or a related field. - Strong skills in applied statistical genetics and genomics. - Comfort with Linux/Unix environments and coding experience including python and SQL. Experience with AWS is a plus. - Excellent oral and written communication skills. - Add to a culture of teamwork and continuous learning/teaching. - A passion for pet health and desire to build products to improve the lives of pets and pet owners.

What We Offer

- Dog-friendly office - Perks tailored for dog lovers in-cluding subsidized dog-walking services and paw-ternity leave - Startup perks with big-company benefits - Competitive salaries, all-inclusive health care, and equity participation - A flexible vacation policy along with paid maternal and paternal leave - Fully-stocked office snack bar and regular office events - New iMacs and MacBook Pros, or laptops running Linux - Continuing education including attending conferences

Embark's proprietary database of phenotypic and genetic data from over a hundred thousand dogs is already the largest in the world and has led to exciting new genomic discoveries. We're looking for colleagues to build the engine driving a million-dog database to discover and prevent cancer, hip dysplasia, cardiac disease and inbreeding depression in dogs.

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

To apply for this job please visit: https://embarkvet.applytojob.com/apply/bp05nfEAYO/Statistical-Genomicist Thank you in advance and please let me know if there is any more information you need from our side.

Wishing you a great weekend!

Best, Evelin

< http://www.embarkvet.com/ > Evelin Calista HR MANAGER (617) 223-7377 < http://facebook.com/embarkvet > < http://www.instagram.com/embarkvet >

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WesternConnecticutStateU PartTime Systematics

Part-Time Faculty in Systematics

The Department of Biological and Environmental Sciences at Western Connecticut State University is seeking a scholar in systematic biology to instruct a Masters-level course in systematics during Spring 2020 (see

course description here: http://catalogs.wcsu.edu/-grad1819/sas/courses/biology/).

Students enrolled in the MS in Integrative Biological Diversity Program include diverse, non-traditional students who are seeking careers in conservation and resource management (http://catalogs.wcsu.edu/-grad1819/master-of-science-in-integrative-biological-diversity/). The ideal candidate will offer a course that can provide students hands-on experience and practical skills in contemporary tree-building methods and software, with an eye to how systematics may be used in conservation, policy, and management. The candidate will need to be able to instruct on evenings and/or weekends, and a hybrid instructional design (online + in-person) is possible. A PhD and evidence of scholarly activity in systematics or related field are required. We welcome applications from candidates interested in sharing their expertise with the department.

Candidates should send: a CV, and suggested list of topics to cover in the class to Theodora Pinou at PinouT@wcsu.edu by September 1, 2019. Western Connecticut State University is an Affirmative Action Equal Opportunity Educator/Employer.

Hannah Reynolds <reynoldsh@wcsu.edu>

WSU-Vancouver EvolutionAdjunctInstructor

Evolutionary Biology Adjunct Faculty

Biology Programs, College of Arts and Sciences, Vancouver Campus

Washington State University Vancouver's Biology Program is seeking applicants for Adjunct Faculty to teach an Evolutionary Biology course during the Fall 2019 semester (August 19 - December 13).

COURSE DETAILS: Evolutionary Biology (Biol 403). 3-credits. The survey of evidence for evolution and operation of evolutionary processes that influence adaptation, diversification and speciation in organisms. Prerequisites: Biol 301 (General Genetics). Lecture: Tuesday and Thursday 9:10 - 10:25 am. Expected enrollment: 70 - 80 students. Instructor will have access to existing course material.

COMPENSATION: $4,536 - $4,751 for a 3-credit lecture course; dependent on Master's or Ph.D. terminal degree, respectively.

QUALIFICATIONS: Candidates must possess a Master's degree in a related discipline. Preferred qualifications include Ph.D. terminal degree and experience teaching undergraduate courses at a college level. Successful candidates must demonstrate a commitment to working with diverse student and community populations.

APPLICATION PROCEDURE: Review of completed applications will begin immediately and continue until the position is filled.

Interested applicants should send by email 1) a cover letter discussing training and experience as related to the required and preferred qualifications, 2) curriculum vitae, 3) contact information for three references, and (4) evaluations of past teaching experience, if available to: msberger@wsu.edu

Informational inquiries can be directed to the Biology Program Leader, Michael Berger (msberger@wsu.edu).

Please visit http://admin.vancouver.wsu.edu/-marketing-and-communications/fact-sheet for more information about Washington State University Vancouver and http://cas.vancouver.wsu.edu/biology/ for more information about Biology at WSU Vancouver.

WASHINGTON STATE UNIVERSITY IS AN EQUAL OPPORTUNITY/AFFIRMATIVE ACTION EDUCATOR AND EMPLOYER. Members of ethnic minorities, women, special disabled veterans, veterans of the Vietnam-era, recently separated veterans, and other protected veterans, persons of disability and/or persons age 40 and over are encouraged to apply. WSU employs only U.S. citizens and lawfully authorized non-U.S. citizens. All new employees must show employment eligibility verification as required by the U.S. Citizenship and Immigration Services. Washington State University is committed to providing access and reasonable accommodation in its services, programs, activities, education and employment for individuals with disabilities. To request disability accommodation in the application process, contact Human Resource Services: 509-335-4521 (v), Washington State TDD Relay Service: Voice Callers: 1-800-833-6384; TDD Callers: 1-800-833-6388, 509-335-1259 (f), or hrs@wsu.edu.

stephanie.porter@wsu.edu

Other

Eswatini VolFieldAssistant SavannahBirds

The Social Savannah: studying cooperation and conflict in southern African birds

We are looking for field research assistants to work on our wild bird study in Mbuluzi Game Reserve, Eswatini (formerly Swaziland). This work is part of an ongoing project to monitor the reproductive and social behaviours of a number of bird species including speckled mousebirds, arrow-marked babblers, white-crested helmet shrikes and dark-capped bulbuls. Fieldwork involves catching and ringing individuals and taking biological samples (during the non-breeding season), and finding and monitoring nesting attempts (in the breeding season). Field assistants will also be responsible for tasks like data management and vegetation/arthropod surveys.

Field assistants will be stationed at the reserves research centre as part of a small collaborative research team from the Universities of Groningen and Wageningen in the Netherlands, and the University of eSwatini. The field base is in a remote but beautiful location and offers basic sanitary facilities, a research station, and clean but basic tented accommodation and food.

Most of the fieldwork is conducted by mountain bike or car V a valid driving licence is therefore needed and some experience driving on poor roads or dirt tracks would be a bonus (but not strictly required). Fieldwork at our study site is physically demanding, so applicants must be physically fit and able to cope in harsh conditions. Applicants are expected to work both independently and as part of a group, and experience of catching and observing wild birds would be a strong advantage. The position offers lots of opportunities to learn and practice important research and data collection skills and the chance to collaborate on projects covering a range of topics including parental care, endocrinology and sociality. There are also opportunities for field assistants to conduct their own small research projects as part of ongoing data collection.

The position will run from July to December 2019. A six month stay is preferable but we will consider all applicants than can stay for at least three months. The costs of accommodation and food will be covered for the duration of the position.

We are looking to fill this position quickly and will stop reviewing applications once a suitable candidate has been found, so we encourage potential candidates to get in touch ASAP. To apply, please send a cover letter explaining your suitability for the project, along with a CV, to the email address below. We look forward to hearing from you!

For further information or to submit an application, please contact:

Kat Bebbington University of Groningen, Netherlands k.bebbington@rug.nl

Kat Bebbington <katlbebbington@gmail.com>

EvolutionInUrbanEnvironments CallForSubmissions

***We invite contributions to a special feature on evolution in urban environments to be published in Evolutionary Applications in 2020. Instructions on how to be considered for this special feature are provided

below. This information is also available at: https://-urbanevolution-litc.com/evoapp_submission/ ***

Urban areas are among the fastest growing ecosystems on earth and the driver of local and global climate change. Despite this importance, little is known about the consequences of urbanization for evolutionary biology, and its application to human society and environmental sustainability. Consequently, the study of evolution in urban environments is among the fastest growing research areas in evolutionary biology, with important implications for fundamental questions in evolutionary biology and applied problems that relate to human health, conservation biology, environmental sustainability, and urban planning. To advance this research area, Evolutionary Applications will be hosting a Special Issue examining how urbanization affects the evolution of organisms living in or near cities, edited by Marc Johnson, Elizabeth Carlen, Lindsay Miles, and Kristin Winchell.

To be considered for the special issue, we invite Abstract submissions that propose original theoretical or empirical research, quantitative reviews/meta-analyses or perspective articles that offer a novel view on urban evolution. Contributions from diverse and cross-disciplinary fields are especially encouraged. We also encourage submissions from any country and research discipline. Papers should examine the effects of urbanization on evolution, or the applied consequences of urban evolution on urban planning and sustainability, conservation, genetics, human evolution, and the integration of ecological and applied research with an evolutionary perspective. Abstract submissions should be 250-400 words and can be submitted using this form: https://forms.gle/9BdwShrQz29MNh1j9. The deadline for abstract submissions is June 1st, 2019, and all decisions on invited papers will be communicated by July 1. Invited contributors should plan to submit manuscripts for peer review by February 1, 2020.

Please note that Evolutionary Applications is an Open Access journal, and the fee schedule for publications can be found on their site: https:-/onlinelibrary.wiley.com/page/journal/17524571/-homepage/article_publication_charges.htm . For questions, please contact one of the co-editors: Marc Johnson V marc.johnson@utoronto.ca Elizabeth Carlen V ecarlen@fordham.edu Lindsay Miles V lindsay.miles@utoronto.ca Kristin Winchell V kmwinchell@wustl.edu

"Winchell, Kristin" <kmwinchell@wustl.edu>

Genes CytonuclearInteractionsIssue

Please note that there will be a special issue on cytonuclear interactions in polyploid organisms in the journal Genes:

Manuscripts are due September 30th 2019

https://www.mdpi.com/journal/genes/special_issues/-polyploid_species? Polyploidy is widespread in plants and less frequent in animals but serves as an important speciation mechanism in both groups. Polyploidy is accompanied by drastic changes in genome organization including differential patterns of gene loss, gene silencing, genome-wide expression dominance, and epigenetic reprogramming. One underexplored dimension of polyploid evolution is cytonuclear interactions. Allopolyploid animals must ensure coordination between the effectively haploid and typically uniparentally inherited mitochondrial genome and the duplicated biparentally inherited nuclear genome. In allopolyploid plants, an additional cytoplasmic genome (the plastome) must interact with the duplicated nuclear genome. Whole genome duplication may lead to a stochiometric imbalance between these interacting genomes and perturb the assembly of enzyme complexes and the proper functioning of mitochondria and chloroplasts. Recent studies have shown compensatory mechanisms in young plant polyploids with organelle-targeting nuclear genes returning to a single copy following polyploidization. In animals, the mitochondrial genome is typically inherited maternally and numerous cases of hybrid breakdown and incompatibilities have been traced to the disruption of cytonuclear coordination in diploids. However, not much is known about how doubling the nuclear genome perturbs interactions with the mitochondrial genome in polyploid animals or plants. As polyploidy allows new interactions between highly divergent cytoplasmic and nuclear genomes, cytonuclear interactions may be more challenging in allopolyploids than in diploid hybrids.

This Special Issue aims to explore and contrast coordination and coevolution between cytoplasmic and nuclear genomes in both plant and animal polyploids.

Prof. France Dufresne Dr. Jennifer Tate Dr. Daniel Sloan?

France_Dufresne@uqar.ca

HarrySmithPrize Nominations

Nominations open for the 2019 Harry Smith Prize < https://www.molecularecologist.com/2019/04/-nominations-open-for-the-2019-harry-smith-prize/ >

The editorial board of the journal *Molecular Ecology *is seeking nominations for the Harry Smith Prize, which recognizes the best paper published in *Molecular Ecology*in the previous year by graduate students or early career scholars with no more than five years of postdoctoral or fellowship experience. The prize comes with a cash award of US$1000 and an announcement in the journal and in the Molecular Ecologist. The winner will also be asked to join a junior editorial board for the journal to offer advice on changing research needs and potentially serve as a guest editor. The winner of this annual prize is selected by the junior editorial board.

The prize is named after Professor Harry Smith FRS, who founded *Molecular Ecology* and served as both Chief and Managing Editor during the journal's critical early years. He continued as the journal's Managing Editor until 2008, and he went out of his way to encourage early career scholars. In addition to his editorial work, Harry was one of the world's foremost researchers in photomorphogenesis, where he determined how plants respond to shading, leading to concepts such as 'neighbour detection' and 'shade avoidance,' which are fundamental to understanding plant responses to crowding and competition. More broadly his research provided an early example of how molecular data could inform ecology, and in 2008 he was awarded the Molecular Ecology Prize that recognized both his scientific and editorial contributions to the field.

Please send a PDF of the paper you are nominating, with a short supporting statement (no more than 250 words; longer submissions will not be accepted) directly to Nick Fountain Jones (nfountainjones@gmail.com) by *Friday 31 May 2019*. Self-nominations are accepted.

Nick Fountain-Jones <nfountainjones@gmail.com>

LMU Smithsonian Internship ButterflyBehaviorSpeciation

We are seeking a research intern to work at the Smithsonian Tropical Research Institute (STRI) in Panama from July/August 2019 for six months. The internship will focus on behaviour and diversification in *Heliconius * butterflies.

The intern will work as part of a team involving collaboration between Ludwig-Maximilians-Universität, Munich (http://www.evol.bio.lmu.de/research/merrill/-index.html) and STRI (https://stri.si.edu/scientist/-owen-mcmillan). The intern will join a vibrant and highly international community of scientists studying the origins and maintenance of tropical diversity (see also: http://www.heliconius.org).

The project is based in Gamboa, Panama and the intern will be assisting a project investigating the role of female choice in the assortative mating behaviour between *Heliconius *species. The project involves breeding butterflies, managing crossing experiments and conducting behavioural assays. There will also be opportunities for the intern to develop his/her independent projects. Applicants must be able to work both as part of a team and independently and be committed to working full time in Panama for the duration of the project. A knowledge of Spanish and the ability to drive would be useful but are not essential. We especially encourage students with a biology background from Panama to apply.

A stipend of US$1000/month will be provided to cover accommodation and living costs in Panama; we will also cover the cost of airfare to Panama if necessary.

To apply, please send an up-to-date CV (including the names and contact details of two referees), and a cover letter explaining why you would be a good fit for this position. Please combine the CV and cover letter in one single pdf file with the file name in the format of YOURLASTNAME_STRI intern.pdf. Please send applications to Dr. Chi-Yun Kuo (kuochiyun@gmail.com); informal questions can be directed to Chi-Yun Kuo or Richard Merrill (merrill@bio.lmu.de). Please use the subject header: "PANAMA INTERN" before June 20, 2019. We will contact selected finalists for interviews after the deadline.

Chi-Yun Kuo, PhD Postdoctoral Associate Division of Evolutionary Biology, Faculty of Biology Ludwig-

Maximilians-Universität München Großhaderner Straße 2 82152 Planegg-Martinsried, Germany Personal website < http://www.chiyunkuo.com > Merrill lab website < https://richmerrill.wordpress.com >

Chi-Yun Kuo <kuochiyun@gmail.com>

MooreFoundationFunding SymbiosisInAquaticSystems

Dear colleagues,

The Gordon and Betty Moore Foundation's Symbiosis in Aquatic Systems Initiative <

https://moore.us10.list-manage.com/track/-click?u{645da1af2cebb8b03845b51&ide6c3c4f4&eÓf2aff4b7 > is soliciting pre-applications for investigator awards. Our goal with the awards is to provide scientists with the resources and flexibility to pursue innovative, risky research that has high potential for illuminating how aquatic symbioses involving microbes function, and how these interactions shape ecology and evolution in marine and freshwater habitats.

We invite applications from emerging and established aquatic symbiosis research leaders, as well as scientists and engineers who may not have worked extensively on the topic but who have essential perspectives, methods, and technologies to bring in. This particular opportunity is only open to individuals to apply. There is no limit to the number of applicants who may apply from an institution.

To be eligible for this competition, applicants must:

* Hold a tenured or tenure-track position (or equivalent) for a minimum of four years, with the first appointment no later than June 3, 2015; * Have served as principal investigator on one or more major, competitive research grants (for example, NSF, NASA, ERC, DFG, Wellcome Trust, Moore Foundation).

We anticipate different eligibility requirements for future funding opportunities and encourage prospective applicants to stay tuned for more information. If you would like to receive funding announcements from us, please add your contact information to our database using this link: Symbiosis in Aquatic Systems Initiative Announcements <

https://moore.us10.list-manage.com/track/-click?u{645da1af2cebb8b03845b51&idÕaa34e77b&eÓf2aff4b7 >

We recognize the value of diversity and encourage individuals from all identities and backgrounds to apply. The initiative expects successful candidates will represent a variety of scientific perspectives and disciplines to enhance the diversity of tools, ideas and approaches used to address outstanding questions in aquatic symbiosis. Applications are welcome from scientists based in the United States and internationally.

We anticipate supporting approximately 12 scientists for five years (2020-2025) who represent both early and established career stages and include both current and emerging leaders in their fields. Investigators will convene at an annual symposium to share research findings and build connections across symbiosis researchers. Awards will range from approximately $200K-$400K/year in direct costs.

The deadline for submitting a pre-application is June 3, 2019 at 23:59 PDT.

Submit pre-application <

https://moore.us10.list-manage.com/track/-click?u{645da1af2cebb8b03845b51&idÒ2a80e773&eÓf2aff4b7 >

To learn more about this funding opportunity, including FAQs and eligibility information and to apply, please follow this link: https://symbiosis.smapply.io <

https://moore.us10.list-manage.com/track/-click?u{645da1af2cebb8b03845b51&idE8ca66e7b&eÓf2aff4b7 >. We encourage you to share the link with others who also may be interested in applying.

Sincerely, Sara Bender, Alexandra Gonzlez, Adam Jones, Jon Kaye

Sara Bender <sara.bender@moore.org>

SouthAfrica VolFieldAssist SocialMoleRats

SouthAfrica.VolFieldResearchAssistant.SocialMoleRats

Cooperative breeding in Damaraland mole-rats (Fukomys damarensis).

We are looking for voluntary field research assistants to get involved with our research on the completely subterranean, highly social Damaraland mole-rat (Fukomys damarensis) in the Kalahari (South Africa). We are conducting a long-term capture-mark and recapture study, based at the Kalahari Research Centre, to investi-

gate the life-history and social behaviour of Damaraland mole-rats (http://kalahari-meerkats.com/kmp/research-publications/damaraland-molerats-group/). Entire groups of mole-rats will be captured and individually marked. Some individuals may be fitted with a collar to measure behavior. Morphological measurements and tissue samples will be obtained before the release of the animals. The field work is physically demanding and weather conditions are challenging (heat during the day, cold during the night). Field work may make trapping during the night necessary. The assistants will mostly be working in teams of two or three but will be embedded in a large research community. This position requires working in a small team in a remote location on free ranging animals. The trapping season will start in September and last for 3 months. Research assistant will require a valid driving license.

Accommodation is provided, and research assistants are paid a monthly allowance to cover their personal costs and food during the 3 months on site

We will review applications as they arrive. Please apply at latest the 30th of June 2019. Please include a cover letter explaining why you are interested in getting involved in this research project and a CV.

Please apply by email or contact for further information: Hanna Bensch, Linneaus University, hanna.bensch@lnu.se

Hanna Bensch <hanna.bensch@lnu.se>

SouthAfrica VolResAssist MoleRat HormonesBehaviour

We are looking for two volunteer research assistants to carry out exciting experiments with captive Damara-

land mole-rats, a cooperatively breeding subterranean rodent, at the Kuruman River Reserve in the South African Kalahari Desert.

The research the successful applicants will be taking part aims to experimentally investigate the hormonal and transcriptomic mechanisms underlying dominance and the transition from cooperation to conflict in social social vertebrates.

This position is particularly suited, but not exclusively, for people aiming to carry on their academic education. Successful applicants can expect to gain invaluable experience in animal handling procedures and in conducting and managing experiments. They will also gain database skills (MySQL) and will be provided with the opportunity to work on a personal analysis project. Costs of food and accommodation while at the project will be covered. A contribution towards travel costs will be made (300 Euros/Year) Applicants should be available for 6 to 12 months. They should be hardworking, enthusiastic, physically fit, and prepared for long hours in the laboratory. Successful applicants will be responsible to run experiments and will be involved in data collection, data editing and animal handling. Previous experience in the dissection and tissue collection of rodents (including brain) will be considered an asset.

If you are interested in this position send your CV and cover letter stating your availability to Philippe Vullioud (philippe.vullioud@gmail.com).

Shortlisted applicants will be invited for a Skype interview.

Deadline: 10th May 2019: (spontaneous applications beyond this date are welcome)

Philippe Vullioud <philippe.vullioud@gmail.com>

PostDocs

ArizonaStateU PopulationGenetics

Postdoctoral Position in Evolutionary/Population Genetics, Genomics, or Bioinformatics, Arizona State University (ASU)

The Pfeifer lab at Arizona State University invites applications for a postdoctoral position.

Research in the lab focuses on analyzing genomic variation to quantify evolutionaryprocesses, utilizing a combination of large-scale data analysis and modeling. Research topics are open to discussion and mutual interest though should fall within the general interests of the lab. Current research focuses on the study of population genetic processes in primates as well as of adaptation during rapid environmental change (more detailed information may be found on the lab website: http://-spfeiferlab.org/). The ideal candidate should hold a Ph.D. in evolutionary/population genetics, genomics, bioinformatics, statistics, or similar.

The lab offers a stimulating, interdisciplinary, and supportive work environment with excellent opportunities for collaborative efforts as well as independent accomplishments. The lab is based in the School of Life Sciences and is associated with both the Centers for Mechanisms of Evolution (biodesign.asu.edu/mechanisms-evolution) and Evolution and Medicine (evmed.asu.edu). The lab has strong intellectual ties - including weekly lab meetings, seminars, and journal clubs - with the local evolutionary/population genetics, primate genomics, and computational biology research community (ASUpopgen.org). Phoenix stays warm year-round with over 300 days of sunshine and offers many excellent restaurants, a vibrant art, music, and cultural scene, as well as beautiful nature preserves for any kind of outdoor activities.

Informal inquires as well as applications (including a short summary of research interests, CV, and contact information for two references) should be emailed to susanne.pfeifer@asu.edu. The evaluation of applications will begin immediately, and will continue until a suitable candidate has been found. The start date is flexible.

Susanne Pfeifer, tenure-track Assistant Professor, School of Life Sciences, Arizona State University

spfeife1@asu.edu

Berlin EvolGenomics EvoDevo SingleCell

My lab is recruiting a computationally oriented post-doc to analyse single-cell expression and chromatin datasets as part of a projected aimed at understanding regulatory sequence function and evolution in the sea urchin. https://tinyurl.com/yya99sny www.garfieldlab.org

Within this fairly broad domain, I'm open to (and encourage) the development of independent projects.

The position is an ERC funded position for three years at the TV-L 13 salary level. Applications are due June 1st (or ASAP!) with a decision expected shortly afterwards.

IRI Life Sciences is a collaboration between the Humboldt University, the MDC-BIMSB, and the Charité University Hospital. Located in the middle of Berlin, we offer a truly interdisciplinary working environment with access to the top notch facilities, seminars, and training courses of all three institutions. We're also walking distance from the Museum of Natural History in Berlin Mitte, opening the door to additional collaborations for motivated researchers.

If you are interested, please send a CV and a cover letter to dagarfield@garfieldlab.org. Questions prior to application are, of course, most welcome.

David Garfield, PhD

Research Group Leader IRI Life Sciences Humboldt-Universität zu Berlin Philippstr. 13 (Haus 18, Rm. 108) 10115 Berlin, Germany

Office: +49 (0)30 2093-92382 Fax: +49 (0)30 2093-47908 info:　www.garfieldlab.org　email:　david.garfield@hu-berlin.de

David Garfield <david.garfield@hu-berlin.de>

Berlin Metabarcoding Host-parasiteCoevolution

Postdoc:Berlin.Metabarcoding.Host-parasite.Coevolution.

We are currently recruiting a postdoc interested in applying for the "International IGB Fellowship Program in Freshwater Science" (1-year fellowship) for the next call (1 June 2019): https://www.igb-berlin.de/en/-fellowship-programme We are using DNA metabarcoding approaches to understand the interface between host-parasite co-evolution and major ecological processes. We focus on zooplankton (Daphnia)-parasite and phytoplankton-parasite model systems. This project will involve implementation of genomics approaches and analyses of existing metabarcoding data. The project will be carried out at the Leibniz Institute of Freshwater Ecology and Inland Fisheries (IGB) (https://www.igb-berlin.de/en) and the Berlin Center for Genomics in Biodiversity Research (BeGenDiv: http://begendiv.de/).

Applicants must have experience in community analysis of prokaryotes or eukaryotes using metabarcoding or metagenomic data, an interest in evolutionary and ecological questions, and must not currently reside in Germany. Preference will be given to candidates with a strong publication record. If an extension of this 1-year fellowship would be desirable by a candidate, we will actively support our candidate in a preparation of an application for an extension of funding, e.g. for Marie-Curie Fellowship, Humboldt Fellowship or DFG-Early-Career Position.

The successful applicant will then prepare, together with us, a 1-page fellowship application to be submitted by 1 June 2019 (please note that we were previously successful in supporting such IGB-Fellowship applications: Wolinska V three times; Monaghan V four times). Recipients are notified within 4-6 weeks of application and can start one month after notification. In keeping with the IGB's policy regarding gender equality, female applicants are particularly encouraged. Severely disabled applicants with equal qualification and aptitude are given preferential consideration.

If you have a strong CV and are interested in the research topic, please send an email (including a CV) with "IGB fellowship" in the subject line to both PIs by 17 May

2019: Prof. Justyna Wolinska (wolinska@igb-berlin.de) and Prof. Michael T. Monaghan (monaghan@igb-berlin.de).

Justyna Wolinska

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

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

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

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

CIBIO Porto DesertEcolGenomics

*** Postdoc in ecological genomics of desert adaptation ***

Post-doctoral position in animal ecological genomics is available at the CIBIO/InBio, Research Centre in Biodiversity and Genetic Resources, University of Porto, Portugal (https://cibio.up.pt/), to work with the BIODESERTS team (https://biodeserts.cibio.up.pt/). Successful applicant will coordinate laboratory work and bioinformatical analyses at CIBIO/InBio, in close collaboration and visits at University of Oulu (*https://bit.ly/2KV4epD*) and Free University of Berlin (*https://bit.ly/2ATA69P*). Candidate will have the opportunity to participation in field work in North Africa (*https://goo.gl/H1gptJ*) investigating unique desert rodents.

This project investigates the effect of past climatic changes on the genomic architecture of adaptation using Sahara desert specialist, jerboa *Jaculus jaculus*. Since the formation of the Sahara, during the Mid-Upper Pliocene, the region went through several climate changes. Those changes influenced habitat structure of recently described cryptic species within jerboa. Discovery of divergence in fur coloration and camouflage lead to the hypothesis that jerboa species specialized to explore divergent habitats. In this project we ask: what is the role of climate changes in shaping the genomic architecture of adaptations to extreme desert conditions, camouflage and habitat specialization?

Funding is available for up to 32 months with renewal after first year of satisfactory performance. Salary

level is according to the Portuguese state foundation (gross: 2130 /month, net: 1480-1560 /month, plus allowances/social security/insurance).

Qualifications. Candidate should have PhD in biology, or equivalent, with specialization in genomics/transcriptomics, experienced in analytical work (SNP calling, population demography and genomics, sequence mapping, gene expression analysis, network analytics). Knowledge in molecular laboratory work (methods: ddRAD sequencing including museum samples, transcriptome sequencing) is preferred.

Interested candidates should submit: 1) a letter of interest (maximum 1 page), 2) a CV (maximum 3 pages), and 3) a list of publications (indicating publications as first/corresponding author, and those with/without previous supervisors) and 4) PhD certificate to: *http://www.cibio.pt/?p=889*. Review of applications will begin immediately and continue until the position is filled. Inquires should be addressed to (Zbyszek Boratyṅski): *boratyns@cibio.up.pt*.

Zbyszek Boratyṅski <boratyns@gmail.com>

CIBIO Portugal 2 EvolutionaryBiology

Two post-doctoral positions are available at the CIBIO lab in Portugal (https://cibio.up.pt) for 15 months each on a project funded by FCT. *For full information, please see the advertisement of the postdoc position at*: Open Calls - CIBIO Concursos - under the References ICETA 2019-47 and ICETA 2019-48: https://www.cibio.pt/?cat   *Your application*

Deadline : 29.05.2019 Expected starting date: 01.10.2019 Contract length: 15 months Please sumbit your application letter with a statement of your research interests and qualifications for the position, CV, and contact details of at least two referees in Word or PDF. Only applications through this website will be taken into account.

Project abstract

DEEP: Deforestation and Evolutionary Ecology of Pathogens - Impacts of anthropogenic pressures on bird populations and infectious diseases in an insular context

Oceanic islands, by virtue of their simplicity, played a central role in the development of ecological and evolutionary theory. They constitute hotspots of both en-

demism, due to their isolation, and extinction, due to the increasing human impacts. To date, little is known on how anthropogenic changes influence the host-parasite interactions on islands and especially the distribution of parasites in endemic populations. Among the numerous anthropogenic pressures, agricultural expansion is one of the principal factors contributing to deforestation in tropical regions and in recent years, the cultivation of one crop, oil palm *Elaeis guineensis*, has been expanding at an annual rate of 9% worldwide. This rapid expansion has resulted in a significant loss of biodiversity across the tropics for various taxa: arthropods, birds, mammals and associated ecosystem services, but surprisingly very few studies investigated the effects of forest conversion to oil palm plantations on vectors and vector-borne diseases. This project will address this gap by using cutting-edge molecular technologies and a multi-disciplinary approach, bringing together epidemiology, vector ecology and immunoecology on an endemic-rich oceanic island, São Tomé in the Gulf of Guinea, Africa. The outcomes of the project will be of direct relevance not only for the conservation biology but also for the understanding of the dynamics of infectious diseases in a rapidly changing world - a subject of major implications for human health.

Contact for further information

Claire Loiseau: clair.loiseau@gmail.com

Claire Loiseau <clair.loiseau@gmail.com>

CIBIO Portugal CanineEvolution

Dear all,

I call your attention to this call from our research group:

International call for PhD holder Researchers within the *project WOOF *- Tracing the origins and evolutionary paths of the Iberian and the Maghreb Dog in the *area of Biological Sciences Sub research field: Zooarcheogenetics* (CIBIO, Portugal)

http://www.eracareers.pt/opportunities/-index.aspx?task=global&jobId4558 pdfs of this call are attached for further divulgation.

The application period is from 21/05/2019 to 11/06/2019

Thank you for your interest AEPires – *Ana Elisabete Pires* *Biologist*

http://orcid.org/0000-0002-1118-8569 https://-cibio.up.pt/people/details/piresae https://cibio.up.pt/-projects-1/page/579 (WOOF project)

vi Â'deo ImunoGenius http://-moodle.ordembiologos.pt/mod/page/view.php?id!7 < http://moodle.ordembiologos.pt/mod/page/-view.php?id!7 > *Post-Doctoral researcher*

Laboratorio de Arqueocii Âncias (LARC) / DGPC e CIBIO / InBIO ÃÂ euro " ArchGen and EnvArch groups,

Cali çada do Mirante i — Ajuda, 10A, 1300-418, Lisboa, Portugal

Assistant Professor

Faculdade de Medicina Veterinaria Universidade Lusofona de Humanidades e Tecnologias Campo Grande 376 1749-024 Lisboa

Ana Elisabete Pires <ana.elisabete.pires@gmail.com>

CIBIO Portugal HumanEvolution

The Human Evolutionary Genetics group at CIBIO is currently accepting applications to fill a 30 months contract for a PhD researcher under a work contract for a

non-fixed term to work on computational modeling aiming at the development of evolutionary and demographic models using genetic/linguistic data to infer the demographic history of the Khoe-Kwadi language dispersal, at CIBIO-ICETA- Research Centre in Biodiversity and Genetic Resources, Porto, Portugal.

Preferred candidates must possess a PhD a relevant discipline (e.g. population genetics, computational biology, quantitative linguistics, statistics, bioinformatics, evolutionary genetics), and

I. Solid background in computational / statistical skills II. Previous experience in the field of human evolutionary history and population genetics or linguistics

Please see more details using the link:

http://www.eracareers.pt/-opportunities/index.aspx?task=-showAnuncioOportunities&jobId4157&idc=1   The applications are formalized at the electronic address http://www.cibio.pt   with following documents in a digital form, in PDF format:

i) Curriculum vitae; ii) Motivational Letter; iii)Qualifications Certificate; iv) Other relevant documentation

*Deadline for application submission is May 29th, 2019.

Jorge Rocha, Principal Researcher

CIBIO - Research Centre in Biodiversity and Genetic Resources Campus Agrario de Vairao, Rua Padre Armando Quintas 4485-661 Vairao, Portugal

Magda Gayà <magdagaya@gmail.com>

CONABIO-UVermont Agrobiodiversity

The University of Vermont (UVM) invites applications for a consultancy in the Social Sciences on social aspects of Mexican agroecosystems, with funding equivalent to a postdoctoral fellowship ($1200 usd/month). The activities of the postdoctoral position will cover topics ranging from evolutionary ecology to rural sociology and the individual will collaborate with scientists and representatives from institutions from both Mexico and the United States. The main objective of the project is to design and implement fieldwork focused on understanding the values and practices of agrobiodiversity conservation in Mexico. Mexicos National Commission for the Knowl-

edge and Use of Biodiversity (CONABIO) will be UVM main collaborator to carry out this academic work.

Location: Mexico City and rural areas of Mexico

General activities:

a. Design and test household survey and semi-structured interview guide; b. Fieldwork in rural Mexico to conduct household surveys and semi- structured interviews; c. Data management; d. Qualitative and quantitative analysis; and e. Drafting and publishing scientific articles, technical reports, and grants

Candidate qualifications:

Minimum level of education: Doctorate Specialty areas: a. Rural sociology b. Anthropology c. Development sociology d. Etnobotany e. Economics f. Ecology

Required characteristics: a. Familiarity with issues affecting the livelihoods of smallholder farmers b. Spanish and English spoken and written at an academic level c. Experience with survey research d. Experience in analyzing qualitative data as well as bivariate and multivariate statistical methods using both primary and secondary datasets e. Strong communication and teamwork skills f. Ability to independently plan and implement fieldwork

Preferred characteristics:

a. Experience with digital technology to conduct fieldwork and manage data b. Scientific publications c. Experience working with interdisciplinary teams

Required documentation a. CV b. Letter of interest indicating how they meet qualifications c. Three letters of recommendation including contact information

Deadline for submitting materials: May 15, 2019

Email the application materials by email to: Dr. Daniel Tobin (Daniel.tobin@uvm.edu)

Alicia Mastretta <ticatla@gmail.com>

CSIRO Canberra WaspVenomEvolution

CSIRO's National Collections and Marine Infrastructure (NCMI) is seeking to appoint a CERC Postdoctoral Fellow in spider wasp venom evolution.

As the successful candidate you will work with a multidisciplinary team of researchers from CSIRO and the University of Queensland to develop and apply novel molecular and analytical methods for the study of the

spider wasp (Hymenoptera: Pompilidae) venom. This will include its genomic and chemical basis, effect on human receptors and evolution.

Open to all candidates

Location: CSIRO Black Mountain, Canberra, ACT, Australia Salary: AU$83,687-AU$94,679 plus up to 15.4% superannuation Tenure: Specified term of 3 years

CSIRO Early Research Career (CERC) Postdoctoral Fellowships provide opportunities to scientists and engineers who have completed their doctorate and have less than three years relevant postdoctoral work experience. These fellowships aim to develop the next generation of future leaders of the innovation system.

For more information and to apply go to: https://jobs.csiro.au/job/Canberra%2C-ACT-CSIRO-Postdoctoral-Fellowship-in-Spider-Wasp-Venoms/-557966800/ Juanita.Rodriguez@csiro.au

FieldMuseum Chicago PDF DataAnalyst

Dear Brian,

The Field Museum has two open positions which may be of interest to your readers. Were looking for:

1) Postdoctoral Research Scientist in Comparative Genomics and Phylogenomics (http://fieldmuseum.org/-about/careers/?hireology_job_id)5741)

2) Data Analyst to assist in genome analyses and collection-based research projects (http://-fieldmuseum.org/about/careers/?hireology_job_id)9629)

Please see detailed descriptions of both positions below and many thanks for your help. Please let me know if you have any further questions or need additional information.

Best wishes,

Felix

Postdoctoral Research Scientist, Comparative Genomics and PhylogenomicsChicago, IL

The Grainer Bioinformatics Center of the Science and Education Department at The Field Museum is recruiting a full-time Postdoctoral Research Associate to work on phylogenomic analyses of non-model organisms, with a focus on symbiotic fungi. We are looking for an individual with a strong interest and background in computational biology and/or bioinformatics. The position is for a term of 12 months, with the possibility for extension. Possible start date is June 1st, 2019 but is flexible.

The research entails studies on molecular evolution and diversification of non-model organisms. The successful applicant will be involved in various aspects of comparative genome analyses, including genome sequencing and analysis, phylogenomic applications, and species delimitation. Candidates should be able to demonstrate experience in phylogenetic analyses, generating and analyzing genomic datasets, competency with at least one scripting language (e.g., Perl, Python, R), and interest in applying new statistical approaches. Experience with phylogenetics and population genomics is a plus. Well-developed communication (verbal and written) and organizational skills are essential. The successful candidate will also demonstrate leadership ability to assist the PI with the direction and training of students.

The successful applicant is expected to publish at least one research paper as lead author within a year and collaborate as co-author on at least two additional research papers. Guidance will be provided following the Postdoctoral Mentoring Plan.

Please contact with questions Felix Grewe (www.felixgrewe.de, fgrewe@fieldmuseum.org)

All applicants need to include a statement of interest, CV with publication list, and contact information of 3 professional references to be considered.

Please apply at http://fieldmuseum.org/about/careers/-?hireology_job_id)5741.

Data AnalystChicago, IL

The Field Museum is recruiting a full-time Data Analyst to work on Big Data projects for the Grainger Bioinformatics Center (GBC) of the Science and Education Department. The center will be launched in June to support and enhance research in phylogenomics and biodiversity informatics. The Data Analyst conducts or assists in genome analyses or collection-based research projects and provides consultation on new and current GBC projects. In addition, the Data Analyst supports the bioinformatics Linux servers of the GBC. The position is for a term of 2 years, with the possibility for extension.

We are seeking an outstanding individual with a strong interest and background in data science and/or bioinformatics to join a diverse team of researchers working on interdisciplinary biological and ecological projects. Projects typically involve phylogenomic, biogeographic, or populations genomic research of non-model organisms.

Therefore, a background in Biology and experience in processing next-generation sequence data for comparative genomics or populations genomics is a plus. The Data Analyst will discuss their involvement in projects and report to the director of the GBC.

*Duties and Responsibilities *

- Analysis of big data sets, mostly next-generation sequence data. - Apply and adapt existing bioinformatics tools to analyze large, complex data sets. - Communicate highly technical results and methods clearly. - Interact cross-functionally with a wide variety of people and teams. - Linux server support with help of the Field Museums IT department, which includes but is not limited to software installation, user profile management, and problem-solving.

Qualifications

- M.Sc. in Data Science, Bioinformatics, Computer Science, Statistical Genetics or a related field at the time of start date. - Demonstrated experience in processing and analyzing big data sets, ideally data sets of biological nature. - 2-3 years programming experience (fluency in at least two common programming languages). - Strong experience working in a Unix environment.

— / —

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

HolarUC Iceland SticklebackEvolution

Post-doctoral position on long-term data analyses of ECO-EVO-DEVO dynamics in threespine stickleback of lake MÃÂ$\frac{1}{2}$vatn, Iceland

HÃÂ³lar University, Iceland, seeks a Post-doctoral fellow for a Grant of Excellence (RANNIS) project to study the dynamics of *Ecological (ECO), Evolutionary (EVO) and Developmental (DEVO) processes*

The phenotype is an important determinant of the dynamic interactions between ecological and evolutionary processes. We are looking for a highly motivated Postdoctoral candidate to study the interplay among ECO, EVO and DEVO including 1) the dual role of ecology in evolution (as driver of natural selection and phenotypic

plasticity), 2) the molecular mechanisms underlying phenotypic variation, and 3) the feedbacks between phenotypic change and ecosystem function (eco-evolutionary dynamics). The project uses threespine stickleback (*Gasterosteus aculeatus*) from lake MÃÂ$\frac{1}{2}$vatn, Iceland, as a model. The project is led by Prof. Bjarni K. KristjÃÂnsson (lead PI, HÃÂ³lar University College, Iceland) and Dr. Katja Räsänen (Swiss Federal Institute of Aquatic Sciences, Eawag, Switzerland). It is part of a large collaboration across HÃÂ³lar University (Prof. SkÃÂ_oli SkÃÂ_olason), Eawag (Dr. Blake Matthews), Univ. of Wisconsin-Madison, USA (Prof. Anthony R. Ives), Univ. of Iceland (Prof. ZophonÃÂ'as O. JÃÂ³nsson) and the MÃÂ$\frac{1}{2}$vatn research station (Dr. Ã rni Einarsson).

The postdoctoral fellow will *study spatial and temporal dynamics of selection in nature, integrating our long-term data on phenotypic variation with analyses of population genetic structure over space and time*. This project is an integral part of our integrative study that combines experiments (laboratory, mesocosm and field) and genomics tools (transcriptomics and genomics) with mathematical modelling. The postdoctoral fellow will have opportunities to develop the focus of their work, will be encouraged to further develop their research career, e.g. by opportunities in developing spin off projects, and through student supervision.

Location: The candidate will be based at the Dept. of Aquaculture and Fish Biology (DAFB - http://holar.is/en/department_of_aquaculture_and_fish_biology) at HÃÂ³lar University (HU, North Iceland). The candidate is also offered the opportunity to spend time at the institutes of the collaborators. HU is situated in the beautiful village of HÃÂ³lar (Skagafjördur), with offices and research laboratories in the nearby town SauÃÂºÃÂrkrÃÂ³kur. DAFB is an active research centre, where the postdoc is part of a dynamic international team of graduate students and faculty. The beautiful natural setting and central location in North of Iceland, allow both outdoor and cultural activities.

*Requirements: *The candidate must hold a PhD degree in Ecology, Evolution, Development or related disciplines. An ideal candidate should have a strong interest in *evolutionary ecology*, a solid background in molecular genetics and statistical analyses (ideally on long-term data sets), have a shown ability to publish her/his own findings, enjoy working in a dynamic group, and have experience from field work and working on large data sets. The candidate has to be able to work independently as well as a part of a team.

The working language is English. A valid driving license

is a requirement.

This is a 100% position for three years. Salary is in accordance with the current collective wage and salary agreement between the relevant union, and the Minister of Finance. Rights and obligations follow the Act 70/1996 on the Rights and Obligations of Civil Servants.

Applicants should send an application letter, labelled with their name and the code 'PD1', with a statement of research interests and relevant experience (max. 2 pages), *curriculum vitae* with a list of publications, copies of academic qualifications and the names and e-mail addresses of three referees, *as a single pdf* to ecoevodevo@holar.is. The positions are open until filled and suitable candidates will be interviewed on regular basis until the position is filled.

For further information contact Bjarni K. KristjÃÂnsson (Head of the Dept. of Aquaculture and Fish Biology, HÃÂ³lar Univ) (bjakk@holar.is) or Dr. Katja Räsänen (katja.rasanen@eawag.ch).

– Dr. Bjarni K. KristjÃÂnsson, PrÃÂ³fessor HÃÂ³laskÃÂ³li - HÃÂskÃÂ³linn ÃÂ HÃÂ³lum/ HÃÂ³lar University College HÃÂ³lar ÃÂ' Hjaltadal Iceland bjakk@holar.is Phone: +354 4556300 holar.is

Bjarni KristÃÂ³fer KristjÃÂnsson <bjakk@holar.is>

IUPUI IndianaU Genomics

Genomics Researcher Opportunity

Beta Hatch (www.betahatch.com), a leader in the mass production of quality insects as feed, is seeking an experienced genomics researcher and/or breeder with a background in entomology and/or evolutionary biology. As part of our R&D division, we are looking to produce an insect genetically specialized for mass production. The position is open to post-doctoral candidates and other qualified researchers.

Role The genomics postdoctoral or research scientist will report to the CSO and be involved in developing the Beta Hatch breeding program. Specific objectives include analysis of existing genomic data, using CRISPR to investigate key traits for commercialization, developing a long-term strategy for genomic resources at Beta Hatch, and establishing breeding and selection protocols in collaboration with researchers at the USDA. This position will be hosted for 2019-2021 at the laboratory of Dr. Christine Picard at Indiana University - Purdue University Indianapolis (IUPUI), with opportunity for a permanent full-time role as a senior researcher on the Beta Hatch R&D team based in Cashmere, WA.

Beyond technical skills, the researcher must be able to perform well in a fast-moving startup company and handle multiple priorities. Candidates must be self-motivated, become well-versed in the field and rapidly learn new techniques. Excellent communication skills are a requirement.

Primary responsibilities include: -Analysis of existing and future genomics data for Tenebrio molitor. -Use of RNAi and genomic manipulations to study insect development, physiology and reproduction. -Maintenance of insect colony used for study. -Development of specialized insect for commercialization.

Qualifications -PhD in genomics or related field, additional experience preferred. -Laboratory experience in genomics or entomology essential, with a preference for candidates who have experience in RNAi, CRISPR, and next-gen sequencing. -Background in population genetics. -Knowledge of insect physiology and development strongly preferred. -Proficiency in the analysis and presentation of genomic and transcriptomic data. -Excellent planning and organizational skills. -Excellent verbal, written and graphic communication skills. -Must be excited about bugs!

For more details, and confidential inquires please contact: Dr. Hans Kelstrup, Chief Science Officer hans@betahatch.com

– Hans Kelstrup, PhD CSO - Beta Hatch 206-488-6240

hans@betahatch.com

JagiellonianU Poland InsectSymbioses

Postdoctoral Researcher position: The evolutionary dynamics of insect symbioses

The new Symbiosis Evolution research group (www.symbioses.pl) at the Institute of Environmental Sciences of Jagiellonian University (www.eko.uj.edu.pl) in Krakow, Poland, is looking to hire a Postdoctoral Researcher. This is a full-time, 48-month position funded by the Polish National Science Centre (NCN) project "The evolutionary dynamics of the symbioses of Auchenorrhyncha", available from Summer 2019.

The project goal is to comprehensively describe the evo-

lutionary processes and patterns related to nutritional endosymbioses in a clade of sap-feeding hemipteran insects that includes cicadas, spittlebugs, leafhoppers, treehoppers, and planthoppers. In particular, the project will focus on the replacements of ancient heritable symbionts by other microorganisms that occurred in different Auchenorrhyncha clades. We will describe the incidence and nature of these symbiont replacements, the origins of the replacing microbes, their genomic evolutionary patterns, their biological roles, and the effects of the replacements on the ecology and evolution of hosts. We will achieve this through microbiome screens and reconstructions of the symbiont replacement patterns across the global auchenorrhynchan diversity, followed by phylogenomic, comparative genomic, and microscopy-based analyses of symbionts in host clades that have experienced the replacements.

The Postdoc will play the central role in this project and contribute to most aspects. Early on, they will participate in the planning and implementation of molecular and bioinformatic techniques for the microbiome survey across large numbers of samples, as well as the acquisition and management of insect specimens. Later, depending on expertise and interests, they may lead the reconstruction of the diversity and evolution of symbioses across Auchenorrhyncha clades and species, or focus on phylogenomic, comparative genomic, and functional analyses of symbiotic bacteria and fungi. They will also have an opportunity to contribute to the study of other aspects of insect symbioses.

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

The candidates must have a Ph.D. in Biological Sciences or a related field, or anticipate the completion of doctoral studies before the appointment starts. They should be able to demonstrate experience with molecular biology techniques and bioinformatic analyses of NGS data and be fluent in English. An ideal candidate will be able to demonstrate interest and scientific achievements related to the planned project, for example regarding the Auchenorrhyncha biology; the diversity, biology, and evolution of insect-microbe interactions; microbiome surveys; comparative microbial genomics, and phylogenomics. Familiarity with the Linux / Unix shell and scripting languages such as Python / Perl / R, and

interest in participating in international collaborations and research travel preferred.

The candidates are asked to submit a cover letter, a CV, and contact details of two references, to Dr. Piotr Lukasik (p.lukasik@gmail.com). The review of applications starts in mid-June. For further information and informal inquiries, please contact Dr. Piotr Lukasik.

References: Bennett G.M., Moran, N.A. (2015): Heritable symbiosis: The advantages and perils of an evolutionary rabbit hole. PNAS 112(33):10169-10176. https://www.pnas.org/content/112/33/10169 £ukasik P., Nazario K., Van Leuven J.T., Campbell M.A., Meyer M., Michalik A., Pessacq P., Simon C., Veloso C., McCutcheon J.P. (2018): Multiple origins of interdependent endosymbiotic complexes in a genus of cicadas. PNAS 115(2):E226-E235. https://www.pnas.org/content/-115/2/E226 Piotr Lukasik <p.lukasik@gmail.com>

JustusLiebigU ComparativeVenomics

Postdoc position in Comparative Venomics

In the interdisciplinary Animal Venomics group based at the Institute for Insect Biotechnology, Justus-Liebig-University Gießen, a fulltime postdoctoral researcher position is available as soon as possible for two years (Experience depending the salary band will be TV-H 13, 100%) within the German Science Foundation funded project:

Venom evolution in solitary and eusocial aculeate hymenopterans

Tasks - Working in the project that focuses on comparative venomics and toxin evolution of social and solitary bees and wasps. One aim is to understand better processes that drive toxin evolution in hymenopterans. Genomes will be analyzed to complementary proteomics and transcriptomics data to tackle this major aspect of mechanisms in venom evolution. - Proteomics is in parallel conducted via collaborations, depending on the results activity tests and assays are planned for some interesting toxin candidates. - If interested and suitable the possibility exists to help to establish proteomic methods.

Demanded skills and profile: - Diploma/Master degree in Biology or related natural sciences - PhD in Biology or related natural sciences

- Candidates should have a background in evolutionary biology, trait evolution and/or venomics - Proven background in transcriptomics and genomic work and analyses is necessary - Bioinformatics skills are important, experience in Perl or Python of advantage - Candidates should be highly motivated, self-organized but as well team players - Good communication and English skills are important. - Fieldwork experience and taxonomic knowledge of hymenopterans is a further asset - Laboratory experience in RNA extraction, library reconstruction and/or HMW DNA extraction and general knowledge in proteomic work (HPLC, and MassSpec) is an advantage.

We offer a unique opportunity to grow and participate in an integrative environment within the new Animal Venomics group creating workflows comprising genomics, transcriptomics, proteomics, and protein characterization with evolutionary and applied perspectives. The main PI in this project is Dr. Björn M. von Reumont.

Gießen is a vibrant student town at the river Lahn in the green heart of the State Hessen, very central in Germany. Other, old university cities like Marburg or Wetzlar are located within 20 km. The metropolis Frankfurt with its large international airport is roughly 50 km away and its center can be reached from Gießen within 40 minutes by regional trains.

Please send applications without photograph and without date of birth as single PDF file including a CV (with two references), certificates, motivation letter (â1 page) with additionally a short summary of previous work and applied methods (â 1 page), and one reference letter to: Bjoern.Von-Reumont@agrar.uni-giessen.de.

The JLU Gießen promotes equal opportunities and diversity in its employment relations. Women are expressly encouraged to apply and given priority in accordance with the Equal Opportunities Act. We expressly welcome applications from individuals with severe disabilities or people of equivalent status. Severely disabled applicants of equal merit and qualifications will be given priority.

Application deadline is the 07.06.2019

Dr. Björn M. von Reumont Research Associate LOEWE Center Translational Biodiversity Genomics University of Gießen & Fraunhofer IME Animal Venomics Winchesterstr 2 35394 Gießen Germany Tel +49 (0)641-99-39503

mob +49 (0) 151-61997924 www http://-www.reumont.net Björn Marcus von Reumont <bmvr@arcor.de>

KU Leuven EnvironmentalGenomics

The Department of Biology and The Genomics Core of the KU Leuven are currently looking for a postdoctoral fellow in Environmental genomics & bioinformatics to lead independent population genomic research and develop ESFRI-EMBRC bioinformatics services.

The successful candidate will join two international teams that study the molecular evolution of marine organisms and develop analytical tools for NGS data for research purposes, and transitions them to/towards marine scientists. The successful candidate will focus on independent scientific research in evolutionary genomics and the development of bioinformatic toolkits for external users. We also offer the possibility to develop our ongoing consultancy in marine genomics.

We are looking for a motivated and scientifically excellent candidate in environmental genomics/ bioinformatics with a problem-solving attitude to work in a collegial environment pervaded with intellectual rigor. Strong communication skills complemented with innovative and analytical thinking are important assets. Applicants must hold a PhD in a related field such as (Applied) Biology, Bioinformatics or Computational Biology. The individual we are looking for will have to be confrontable with common bioinformatics software and programming languages (Python, Perl, Java, R), and be highly motivated to solve biological problems. The successful applicant will also be adapting and implementing existing bioinformatics pipelines in an automated cloud-based analysis platform to make these algorithms available for marine biological and other fundamental biological questions. The candidate will also have an opportunity for the teaching and mentoring of students.

We look forward to receiving a motivation letter (max. 1 page), short CV (max. 3 pages), a scientific achievements track-record (max. 2 pages) including a list of your five most important publications, and three names of referees.

We offer an initial 18 Months contract (extendable with national or EU funds) a competitive salary and interactive work environment in collaboration with the European Marine Biological Resource Center (www.embrc.eu), a well-established marine research team (bio.kuleuven.be/eeb/lbeg) and the largest Genomics Service core (www.genomicscore.be) in Belgium. KU Leuven is a research-intensive, internationally ori-

ented university that has been elected Europe's most innovative university by Reuters and consistently ranks and features in Europe's top-15 universities within the Times Higher Education ranking. Leuven is a historic, dynamic and lively city located in the heart of Belgium, within 20 min from Brussels, the capital of the European Union, and less than 2 h from Paris, London and Amsterdam.

Working site: Leuven, Belgium Application deadline: The application must be sent as a single PDF by email to conny.coeckelberghs@kuleuven.be with as subject 'eGenomics/bioinformatics postdoc position' by midnight June 25th 2019.

For further information contact dr. Gregory Maes, phone +32 16 37 25 22, gregory.maes@ kuleuven.be and/or prof. Filip Volckaert, phone: +32 16 39 72, filip.volckaert@kuleuven.be.

Filip Volckaert <filip.volckaert@kuleuven.be>

Lisbon ModellingFish

Postdoc on Ecological Niche Modelling of Small Pelagic Fishes, Lisbon, Portugal

The Marine Ecology Group, at ISPA - Instituto Universitário (http://www.ispa.pt/), Lisbon is looking for a highly motivated postdoc to work on the SardiTemp project - The impact of Climate Change on the Ecology and Dynamics of Small Pelagic Fish" with the references LISBOA-01-0145-FEDER-032209 and PTDC/BIA-BMA/32209/2017, funded by Investment and Structural European Funds (FEEI) - through 'Programa Operacional Regional de Lisboa' and by National Funds through FCT, for up to June 2021. SardiTemp is a multidisciplinary project, where we will implement ecological, physical and biological variables to understand how species distribution will evolve facing climate change, by predicting species distribution and spawning areas according to IPCC predictions to 2100.

The candidate must hold a doctoral degree (mandatory) preferably in biological sciences, computation sciences or akin areas (optional) and must have previous experience in ecological niches modelling (preferentially in the marine environment) through mechanistic and/or correlative methods. The candidate must have a record of publications of merit in one of the areas aforementioned, in particular, on ecological niche modelling in marine environment and as a first author. The candi-

date must have advanced knowledge of programming in R and/Python. It is also valued experience in scientific outreach for different target audiences, in project management and in the submission of research projects to funding mechanisms.

DEADLINE for application: June 16th, 2019.

IMPORTANT NOTE:

For more details on the position and how to apply go to: http://www.eracareers.pt/opportunities/-index.aspx?task=global&jobId4408&fbclid=-IwAR2xFTJHbAzW3Jnt43ieCrUE5WUEMQNOH1QcpIVQ3oeKlhWz-zRgO-LRCxs If you have any doubts do not hesitate to contact me gsilva@ispa.pt For more information about the project http://sarditemp.com/ Thank you very much.

Gonçalo Silva

Researcher MARE - Marine and Environmental Sciences Centre ISPA - Instituto Universitário, Departamento de Biociências R. Jardim do Tabaco, 34, 1149-041 Lisboa, Portugal Tel.: +351 218811700; Fax.: +351 218860954 E-mail: gsilva@ispa.pt

Gonçalo Jorge Franco Silva <gsilva@ispa.pt>

MichiganStateU SalmonPopulationGenomics

Postdoctoral opportunity in conservation biology and population genomics The Meek Lab at Michigan State University is looking for a highly motivated postdoctoral scholar to study population and conservation genomics in Chinook salmon. The Meek lab uses field studies and next-generation sequencing to address fundamental ecological questions that are directly relevant to the conservation and management of threatened species. We study biodiversity at the level of genotype up to phenotype. The focus of this position will be to serve as the lead on a newly funded study aimed at improving our ability to protect life history trait diversity in Chinook salmon. We will use high-throughput sequencing to genotype thousands of historical juvenile Chinook salmon samples, and then combine this information with environmental data to evaluate the relationship between environmental conditions, genetic diversity, and life history traits.

Please look at our website (meeklab.com) to get a more complete picture of the work we do. The post-doc will

have the opportunity to work on one or several of the ongoing projects in the lab, based on interest and fit. There is also potential for developing new projects, based on the candidates interests. We are a very interactive lab and are looking for an excellent scientist, who cares about conservation, and is a good collaborator. The Meek lab strives to be a safe space and support diversity in STEM.

The initial hire is for one year with an additional year of funding contingent upon satisfactory progress. The position will be based in the Department of Integrative Biology at Michigan State University. Start date is negotiable and position is open until filled.

Qualifications Applicants should have a PhD in ecology, evolution, genetics, bioinformatics, or related fields. We are looking for a creative and talented scientist with a good publication record and excellent organizational and communication skills. We are especially interested in candidates with a strong bioinformatics background and previous experience with next-generation sequencing data analysis. Experience working in the Unix environment is essential and familiarity with one or several programming languages is highly desirable.

How to apply Interested candidates should apply through the MSU Applicant Page at http://-www.careers.msu.edu/cw/en-us/job/501447/research-associatefixed-term .Please feel free to email (mhmeek@msu.edu) before applying to ask questions (but do not submit your application material to Dr. Meek, that must be done online). Required application material: 1) Brief cover letter describing research interests and motivation 2) CV 3) Names and email addresses for 3 references 4) 2-3 published papers or manuscripts in preparation

Mariah Meek, PhD Assistant Professor Department of Integrative Biology Michigan State University East Lansing, MI meeklab.com

"Meek, Mariah" <mhmeek@msu.edu>

Montpellier ButterflyEvolutionaryGenomics

2-year Postdoc on the genomics of supergene evolution in butterflies - CNRS Montpellier, France

A 2-year post-doctoral fellowship is available at the CNRS Centre for Evolutionary and Functional Ecology (CEFE) in Montpellier, France, to work on the evolutionary genomics and demography of inversion polymorphism in tropical butterflies with Dr Mathieu Joron and colleagues (http://joron.cefe.cnrs.fr).

Full ad: http://bit.ly/2Jz565A Closing date: 20 June 2019

Supergenes are genetic architectures underlying the coordinated variation of many characters within populations. Supergenes are often associated with chromosomal rearrangements and with specific genomic signatures of natural selection. Our lab focuses on a complex of distinct chromosomal types characterized by distinct combinations of inversions, and associated with wing-pattern mimicry polymorphism, in the tropical butterfly Heliconius numata. The project aims at understanding the consequences of supergene formation by dissecting the traits and population parameters affected by chromosomal polymorphism. The position is open to contribute to understanding how inversions have established and spread through populations across the range, how inversion polymorphism involves deleterious mutations, changes in mating systems, and shifts in population connectivity, which may profoundly change ecological and evolutionary trajectories of polymorphic populations.

The postdoctoral researcher will be in charge of population genomic approaches. She or he will investigate signatures of selection, genomic association of fitness traits, as well as population demography and differentiation across the range. Datasets such as 120 resequenced genomes, multiple independent genome assemblies, transcriptomes and annotations are available, and will be expanded during the project. The project allows for much flexibility in the direction taken, for instance by combining population genomics with field or morphometric data, depending on the postdocs interests and ideas.

The postdoc will join a lively consortium of teams whose research combines experimental/trait-based approaches and population genomics (CEFE Montpellier), bioinformatics (Claire Lemaitre, INRIA Rennes), and evolutionary theory (Violaine Llaurens, MNHN Paris). The postdoc will interact with team members working on the ecology of inversion polymorphism, the modelling of balancing selection, or the functional dissection of wing-patterning. Our partner institution INRIA Genscale is a major bioinformatics institute in Rennes, so the postdoc will enjoy direct support from a bioinformatics team.

Candidates should have a PhD or equivalent in evolutionary sciences, advanced knowledge of population genetic theory, a keen interest in understanding biodiversity. Candidates should have experience with genomic datasets, population genomics and/or demographic infer-

ences using genomic data. Experience with heterozygous genomes, inversion polymorphisms, and/or the mapping of complex phenotypes will be appreciated.

Starting date is flexible but should ideally be in the autumn 2019. Net salary: between 25 k/year and 35 k/year depending on experience, including social benefits and public health insurance.

The CEFE is the largest ecology lab in France and is a major institute for evolutionary ecology and genetics. Within CEFE, our team comprises 12 researchers whose research combines genetics and evolutionary ecology to address a diversity of topics on adaptation and natural variation. Our group focuses on butterfly wing patterns as a model to decipher how diversity is shaped by natural selection and other processes at the phenotypic and genomic level. Montpellier is a major hotspot for evolutionary and environmental research worldwide and has a vibrant research community with several hundred researchers in this domain, and highly praised graduate programmes. The University of Montpellier ranked 1st in the 2018 Shanghai ranking in Ecology. Montpellier lies near the Mediterranean region in the South of France and enjoys pleasant weather, fantastic nature and great cultural and city life..

Applications should be done through the CNRS portal. See http://bit.ly/2Jz565A. Applicants should upload a letter of application with details on their motivation and achievements and including proposed research directions, a full CV, the names and contact details of two references, and their date of availability. Closing date : 20th June. Interviews : early July.

Informal enquiries are encouraged. Please contact Mathieu Joron, mathieu.joron@cefe.cnrs.fr. Website: http://joron.cefe.cnrs.fr JORON Mathieu <Mathieu.JORON@cefe.cnrs.fr>

NaganoU Japan 2 EelPopulationDynamics

Job Opportunities: Postdoctoral Researchers (temporary job) Nagano University - Nagano, Japan

Nagano University is planning to seek two trained researchers to work with a team on a study about the population dynamics and fisheries management of Japanese eel (Project Head: Professor Hiroshi Hakoyama). The project is supported by the Fisheries Agency of Japan, and is going to last for at least several years. The outcome of the project is expected to contribute to discussions at FAO, IUCN and CITES and policy design and implementation on the management of Japanese eel. Lab technicians (several people) are going to help the postdoctoral researchers.

Duties & Responsibilities: (1) Postdoctoral Researcher #1 (Data Scientist/Bioinformatician, population genetics, SNPs (MIG-seq and/or RAD), effective population size, pairwise sequentially Markovian coalescent, PSMC) The researcher's primary responsibilities include: developing the research design to get information about SNPs (MIG-seq and/or RAD) and estimating the yearly effective population size of Japanese eel; estimating demographic history by the PSMC method; developing statistical and mathematical methods for population genetics; and writing papers with co-workers.

(2) Postdoctoral Researcher #2 (Statistician, frequentist, time-series analysis, fisheries management, mathematical modeling) The researcher's primary responsibilities include: analyzing multivariate time-series of fisheries and environmental data of Japanese eel in frequentist approaches (not Bayesian); developing statistical and mathematical methods for fisheries management; and writing papers with co-workers. The spatiotemporal data include missing values.

Moreover, all postdoctoral researchers should cooperate with each other, participate in team discussions, assist the members of the team and the lab in all respects, and accept other duties as assigned.

Minimum education: Ph.D. in a related field

Applications: When applying for this position, please send a CV/cover letter and letters of recommendation from the research supervisor or the department head to Hiroshi Hakoyama, hiroshi-hakoyama@nagano.ac.jp by e-mail with the title 'Nagano_2019'.

Deadline to apply: Ongoing (Open until filled)

Location: 1088 Komaki, Ueda, Nagano 386-0031, Japan

Employment period: from 2019/07/01 (if possible, as soon as possible) to 2020/03/31. The employment period may be extended based on performance and availability of funding.

Regular work hours: 8:30-17:30 (Break time 12:00-13:00), Monday-Friday

Salary: 470,000 yen a month (including tax)

Employee benefit: various social insurance equipping (inquiry e-mail address: soumu@nagano.ac.jp)

Contact: Hiroshi Hakoyama <hiroshi-hakoyama@nagano.ac.jp> (https://hako.space)

We already employed a postdoctoral Researcher who also contribute our team (Pop-up Argos tag, experimental researcher, fieldworker: The researcher's primary responsibilities include: conducting field experiments to track silver eels using pop-up Argos tags (e.g., Wildlife Computer) at several locations in Japan, Indonesia, and Philippines; conducting laboratory experiments using yellow eels for developing the new pop-up Argos tag cooperating with Little Leonardo Co).

Thank you.

Akiko Hayashi

<akiko-hayashi@nagano.ac.jp>

NewYorkU EvolutionaryGenetics

Postdoctoral position in Matt Rockman's Lab in New York

Join us at NYU to work on fundamental questions in evolutionary genetics. We're studying the characteristics, causes, and consequences of segregating recessive variation in natural populations. The study organism is an obligately-outcrossing worm closely related to C. elegans, chosen because populations harbor intermediate levels of recessive deleterious variation, convenient for experimental and genomic analyses.

The postdoctoral researcher would have opportunities to analyze datasets we have generated from laboratory evolution experiments and broad latitude to develop new datasets or conduct new experiments.

This position is ideal for someone with experience or interests in statistical genetics, quantitative genetics, population genetics, comparative genomics, or experimental evolution. The position can fit anywhere on the computational-experimental spectrum according to the researcher's goals and background.

The Rockman Lab studies evolutionary genetics, with a focus on the relationship between developmental mechanisms and population-level phenotypic variation and evolution. NYU is home to a number of evolution and comparative genomics research groups, and the New York area is increasingly a center for evolutionary genetics. New York is one of the most diverse and diversity-embracing cities in the world and so is a great place to live and work. It's also a reasonable place to live thanks to subsidized postdoc housing.

Please send informal inquiries to Matt at mrock-man@nyu.edu, or submit a formal application at http://apply.interfolio.com/63560. The start date is very flexible but we will start interviewing candidates by mid-June.

mrockman@nyu.edu

NHM UOslo EvolutionaryBiolOrnithology

For the following Postdoctoral fellowship (Jobbnorge ID: 169624), please apply at https://www.jobbnorge.no/en/available-jobs/job/169624/postdoctoral-fellowship-in-evolutionary-biology-ornithology The deadline for applications is 19.05.2019.

Job description A position as Postdoctoral Research Fellow in Evolutionary Biology/Ornithology is available at the Natural History Museum, University of Oslo. The position is placed in the ?Sex and Evolution Research Group? (SERG). The appointment is a fulltime position and is made for a period of four years with 25 % duty work devoted to teaching, supervision, collection management (curatorial work in the ornithological collection of NHM), outreach activities and administration. The postdoctoral fellow is expected to acquire basic pedagogical competency in the course of the fellowship period within the duty component of 25 %. The main purpose of the fellowship is to qualify researchers for work in higher academic positions within their disciplines.Starting date no later than 01.10.2019.

More about the position The position is placed in the Sex and Evolution Research Group (SERG). The research group currently consists of two professors, two researchers and two PhD-students, as well as master students. The research themes are concentrated on the importance of sex, sex roles and sexual conflict in shaping evolutionary processes such as speciation, hybridization, diversification and adaptation. These processes are studied at different levels of organization, like genes, genomes, gametes, individuals, populations and species. Most projects use birds as their study systems. The research group has access to large museum collections in ornithology, including a unique collection of formalin-preserved sperm cells from more than 500 species, and a DNA bank with more than 50 000 bird tissue samples. Field work for comparative studies is often carried out abroad and in collaboration with other institutions and research groups.

We invite a highly motivated researcher to work on and develop a project entitled ?Macroevolution of avian spermatozoa? in close collaboration with the scientific staff in the SERG group. The project will consist of three main parts, (1) a descriptive analysis of the major patterns of sperm phenotype differentiation across the passerine phylogeny, (2) analyses of evolutionary rates of sperm variation among and within lineages, and (3) investigation of the genomic mechanisms underlying sperm trait evolution. The approach will be largely phylogenetically controlled comparative analyses combined with in-depth phylogenomics of selected taxa. There will also be a need for additional field work to sample important taxa currently lacking in our sperm database.

Qualification requirements The candidate must have a PhD in ecology, evolution or avian systematics. We seek a highly competent and motivated early career evolutionary biologist, with skills in comparative analyses and evolutionary modelling and experience with bioinformatic tools for handling large genomic data sets. Experience with ornithological field work and good knowledge in bird systematics is required, while experience with work on spermatozoa, including microscopy and morphometry, and other natural history collection work, will be considered advantageous. A good command of written and spoken English is required.

We offer - Salary NOK 515 200 ? 597 400 per annum depending on qualifications in position as Postdoctoral Research Fellow (position code 1352) - Challenging research questions and a friendly working environment - Full funding of the project research-related activities, including field work, lab work and presentation of results at international conferences - Membership in the Norwegian Public Service Pension Fund - Attractive welfare benefits

How to apply The application must include: - Application letter (statement of motivation, background and research interests) - CV (summarizing education, positions, pedagogical experience, museum experience, administrative experience, popular science experience and other qualifying activity) - Copies of educational certificates and transcript of records - A complete list of publications and up to 5 academic works (in pdf format) that the applicant wishes to be considered by the evaluation committee - Names and contact details of 2-3 references (name, relation to candidate, e-mail and telephone number). The references will be contacted if necessary. Letters of recommendation are therefore not required for the initial application.

The application with attachments must be delivered in our electronic recruiting system. Please remember that all documents should be in English or a Scandinavian language.

Evaluation of the applicants

— / —

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

NIAB Cambridge Bioinformatics

Post-Doctoral Research Associate in Bioinformatics & Quantitative Genetics (3 years fixed term)

We are looking for an enthusiastic and talented bioinformatician/quantitative geneticist to work on the genetics of wheat yellow rust resistance at NIAB in Cambridge, UK. The post is funded by a BBSRC-LINK grant to investigate the best way to combine complementary adult plant disease resistance loci to obtain durable resistance. Working with seven commercial breeding companies, the project will characterise (a) the in-field effectiveness of combinations of disease resistance loci in multi-site trials, (b) the location and timing of action of resistance within the plant at the microscopic level and (c) the underlying genetics of resistance using differential RNA expression analysis. The successful candidate will mostly be responsible for the quantitative genetic analysis of the field trial data, particularly the detection of genetic interactions, and the bioinformatics analysis of the differential expression data. With the majority of the UK commercial wheat breeding companies involved, the project offers an excellent opportunity to work on translational research at the academic-commercial interface.

The essential requirements for this role are:

§Relevant BSc;

§PhD in quantitative genetics, bioinformatics, plant genetics or similar with evidence of specialisation in data analysis;

§Evidence of training in statistics and basic bioinformatics

§Experience of genetic data analysis and bioinformatics analysis;

§Good knowledge of a statistical package, preferable R or GenStat

§Programming skills e.g. Python

§Ability to work independently, once given adequate training

§Ability to work in a team

§Presentation skills both written and verbal

The desirable requirements for this role are:

§RNA seq/differential expression analysis

§Advanced genetic mapping skills

§Advanced Quantitative Genetics or bioinformatics training

§Experience of curation and analysis of large data sets

§Good knowledge of experimental design

§Interest in plant breeding, plant pathology or crop science

§Glasshouse/field data collection or laboratory genetics experience

§Positive attitude to challenges, views problems when they arise with creativity

§Enthusiasm for developing new ideas

§Driving Licence

The post will require travel within the UK and internationally.

NIAB is the UK's fastest growing crop science organisation, with rapidly expanding research capabilities in plant genetics, agronomy, farming systems and data science, the largest national field trials capability, and strong research links with industry, government and academia. The NIAB Genetics and Breeding team, based at Cambridge, carries out leading-edge crop genetics research, with direct translation to plant breeding programmes in the UK and elsewhere.

Starting salary is in the range of pounds 30,042 to pounds 39,640 per annum depending on qualifications, skills and experience. Further details and an application form are available at: http://www.niab.com/vacancies/-index/ or from the HR Office, NIAB, Huntingdon Road, Cambridge CB3 0LE, Tel No. 01223 342282, Email: jobs@niab.com, quoting Ref No. T/354. Closing date for applications: 16 June 2019 Interviews to be held week of 1st July 2019

Keith Gardner | Programme Leader in Quantitative Genetics NIAB | Huntingdon Road | Cambridge CB3 0LE Office (dd) +44 (0) 1223 342484| Mob +44 (0) 7765 508940 Email keith.gardner@niab.com | Web niab.com

Keith Gardner <Keith.Gardner@niab.com>

NTNU Trondheim EvolQuantGenetics

NTNUTrondheim.EvolutionaryQuantitativeGenetics

Post-doc position in Evolutionary quantitative genetics, NTNU, Trondheim Norway

We have a fully-funded 3 year Post-doc position in evolutionary biology available at the Centre for Biodiversity Dynamics, NTNU (Trondheim, Norway). The Centre for Biodiversity Dynamics is a leading cross-disciplinary Centre of Excellence from the Norwegian Research Council, with primary interests in evolutionary biology, population ecology and community dynamics. It works at the interface between biology and mathematical sciences and strives to apply cutting-edge theoretical and statistical frameworks to field data to resolve key questions in the context of both fundamental and applied sciences. Further information is available at http://www.ntnu.edu/cbd About the position

The post-doc position is part of a project financed by the Norwegian Research Council on evolvability. In brief, evolvability is the ability of organisms to respond to selection. On short time-scales, evolvability depends on the amount of additive genetic variance. Yet, evolvability, variation in evolvability and the factors responsible for this variation are poorly understood. To improve our understanding of evolvability, we will synthesize the empirical knowledge on additive genetic variance and identify key factors affecting this property of living organism by performing quantitative reviews and meta-analyses of published results on evolvability. More specifically, we will investigate questions such as: Does variation in life history strategy affect evolvability? Does environmental fluctuation increase evolvability? Ultimately, we will build a large open-access data base on evolvability. Using newly developed statistical methods to analyze line-cross data, we will also investigate the importance of epistatic interactions in quantitative traits. The post-doc will work with Professor C. Pélabon at NTNU, Professor T.F. Hansen (University of Oslo), and senior researcher G.H. Bolstad (NINA, Trondheim). Part of the work during the first years of the post-doc will be located in Oslo.

Job description

The main tasks of the post-doc will be to gather information from the literature with the rest of the team

and analyze these data to test specific hypotheses about the factors affecting evolvability. The post-doc is thus expected to lead part of the project and develop his/her own research questions within the general framework of the project. We thus seek candidates highly motivated for theoretical work and data analysis with a broad understanding of the evolutionary theory.

Qualification requirements

We seek candidates who have a strong academic record and interests in evolutionary theory and quantitative genetics. The candidate must have a PhD degree in biology preferably related to evolutionary biology or quantitative genetics, but candidates with a background in statistics may be also considered for the position.

Other desired qualifications:

Good competences in statistical genetics.

Strong interest for the theory.

Willingness to learn and extend new forms of statistical and/or mathematical analyses.

Good theoretical knowledge of relevant topics in evolutionary biology and quantitative genetics such as the multivariate Lande equation, epistasis, genetic architecture.

Some experience of meta-analytical work and work with large data-base would be an advantage.

Good skills in written and oral English.

The candidate should present excellent ability for teamwork, but should be also able to work independently.

We are seeking innovative candidates that are able to generate their own research questions within the framework of the project.

We offer

Exciting and stimulating tasks in a strong international academic environment

An open and inclusive work environment < https://innsida.ntnu.no/wiki/-/wiki/Norsk/-Inkluderende+arbeidsliv > with dedicated colleagues

Favourable terms in the Norwegian Public Service Pension Fund < https://www.spk.no/en/ > employee benefits < https://innsida.ntnu.no/wiki/-/wiki/Norsk/-Ansattegoder+og+fordeler >

Salary and conditions

Postdoctoral candidates are remunerated in code 1352, and are normally remunerated at gross from NOK 515 200 per annum before tax. From the salary, 2% is deducted as a contribution to the Norwegian Public Service Pension Fund. The period of employment is for 3 years.

Appointment takes place on the terms that apply to State employees at any time, and after the appointment you must assume that there may be changes in the area of work.

General information

We encourage qualified candidates to apply, regardless of their gender,

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Paris BacterialEvolutionaryEpidemiology

Postdoc position in bacterial evolutionary epidemiology in Paris (France)

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

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

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

The position start in September 2019 and is for two years. Salary depends on experience (see table below).

To apply:

If you are interested in this position, please send a CV, a 1-page description of your research interests and motivation, and the contact details of potential references (all in one single pdf) to François Blanquart (francois.blanquart@college-de-france.fr) no later than May 31st 2019.

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

François Blanquart

Net monthly salary as a function of experience:

<2y after PhD: — — — — 2,166.42 euros

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

âÂÂ¥7y after PhD: 3,247.97 euros

Further information:

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

Seattle Microbiome

Beta Hatch, a leader in the mass production of quality insects as feed, is seeking an experienced microbiologist with a background in microbiome research. As part of our R&D division, we are looking to harness the power of the insect gut to breakdown harmful toxins in agricultural waste by-products, using host-mediated selection. The position is open to post-doctoral candidates and other qualified researchers.

Company Beta Hatch is pioneering a new industry in agriculture: Insects as animal feed. Since 2015, the company has been growing insect protein to feed aquaculture and poultry at Washingtons first insect farm. Nutrient balanced fertilizer is a by-product of our process. We are industrializing insects to transform organic by-products, combining our expertise in entomology and mechanical engineering to scale production, automate, and control costs. Our goal is to disrupt the $400B animal feed industry and provide more sustainable nutrients for our food systems. For more information on Beta Hatch go to www.betahatch.com Role The microbiology postdoc-

toral or PhD-level research scientist will report directly to the CSO and be central to developing new probiotic products for Beta Hatch insects. Specific objectives include analysis of existing microbiome data, development of protocols for microbiome cultivation, tracking the evolution of microbiome communities, experimentation with microbial transfers between individuals and developing a long-term strategy for probiotics in insects. This position will be based at Beta Hatch facilities in SeaTac, WA (2019-2020) and Cashmere, WA (2020).

Beyond technical skills, the researcher must be able to perform well in a fast-moving startup company and handle multiple priorities. Candidates must be self-motivated, become well-versed in the field and rapidly learn new techniques. Excellent communication skills are a requirement.

Primary responsibilities include: - Analysis of existing and future gut microbiome data - Development of protocols for cultivating and transferring gut microbiomes from donor to receipt insect hosts - Maintenance of specialized insect colonies used for study - Development of stable probiotics for commercialization

Qualifications - PhD in microbiology, genomics or related field, additional experience preferred. - Research experience on microbiomes is essential, with a preference for candidates who have experience working with insects. - Ability to maintain a sterile working environment in a non-traditional lab setting. - Expertise in software(s) used for microbiome analysis and presentation. - Excellent planning and organizational skills. - Excellent verbal, written and graphic communication skills. - Must be excited about evolution and bugs!

For more details, and confidential inquires please contact: Dr. Hans Kelstrup, Chief Science Officer hans@betahatch.com

– Hans Kelstrup, PhD CSO - Beta Hatch 206-488-6240

hans@betahatch.com

SGN Frankfurt CarnivoreConservation

The Senckenberg Gesellschaft fÃÂ$\frac{1}{4}$r Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. SGN conducts natural history research with almost 800 employees and research institutions in six federal states. Within SGN, the Senckenberg Biodiversity and Climate Research Cen-

tre (SBiK-F) explores the interactions between biodiversity, climate, and society.

Senckenberg BiK-F invites applications for a

PostDoc position (m/f/d)

Human-carnivore coexistence across borders

(full time)

The transfer of evidence-based information to society is essential for human-carnivore coexistence, because knowledge is a key factor in conservation debates.

In the context of the project "Transfer of evidence-based and co-produced Knowledge for Human-Wolf Coexistence ' KnowWolf", funded by the Leibniz Association, we plan to tackle three challenges in science communication to society: i) media literacy, ii) science literacy and iii) emotional barriers. The aim of the postdoctoral position is to overcome these barriers by developing models of social-ecological sustainability that will be implemented in a modular tablet application as an innovative, immersive and adaptive interface between science and society, focused on human-wolf coexistence.

In collaboration with a diverse team of scientists and communication experts of the KnowWolf project, the candidate will actively contribute to the design, the development and the implementation of the Digital Transfer Tool (DTT), by i) designing social surveys targeting the broad public, ii) developing choice experiments related to wolf management and iii) developing models of social-ecological suitability in different human-wolf coexistence contexts. With data collected during the project, the candidate will examine questions related to public perceptions and emotions towards wolves in different contexts of coexistence, identify potential drivers of human-wolf coexistence, and evaluate the importance of knowledge transfer focused on the wolf topic.

Your tasks:

§Contribute to KnowWolf project management: strategic planning, meetings, promotion, implementation, reporting

§Collaborate with the KnowWolf team to design choice experiments related to wolf management

§Develop adaptive social-ecological models of suitability for human-wolf coexistence in different contexts (i.e. within and outside Europe)

§Cooperate with a Digital Agency to implement the social-ecological models, choice experiments and games in the DTT

§Analyse results of the social surveys across contexts of coexistence and evaluate the performance of the knowledge transfer in relation to the adaptive information content

§Publish research results in international journals in cooperation with the project team

Your profile:

§A PhD degree in ecology, conservation science, interdisciplinary environmental science, environmental management, sustainability, social ecology, or another relevant field

§Management skills with ability to coordinate a team of collaborators with diverse backgrounds, and ability to work independently as well as in an interdisciplinary environment

§Statistical skills (experience with designing statistical models in R) are required.

§Experience in developing or applying social-ecological models, population models, choice experiments is advantageous

§Interest in knowledge transfer to broad public on the topic of carnivore conservation and human-wildlife conflicts

§Familiarity with Shiny R, JavaScript or equivalent tools for designing web applications of statistical analyses is a plus

§Excellent publication record

§Excellent English and good German language skills

What is awaiting you?

§An interesting task in a dynamic team of researchers in an international research group

§The possibility to build and extend your network with scientists at an international level and to attend national and international conferences

§Flexible working hours ' annual special payment ' company pension scheme ' Senckenberg ID card for free entry in museums in Frankfurt

Salary and benefits are according to a full time public service position in Germany (TV-H E 13, 100 %). The position is a 2-year fixed-term post (with a possible extension of another year), starting as soon as possible.

This project takes place in the group of Prof. Dr. Thomas MÃÂ$\frac{1}{4}$ller (thomas.mueller@senckenberg.de).

The Senckenberg Biodiversity and Climate Research Centre supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of work is in Frankfurt am Main at the Senckenberg

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ShandongFirstMedicalU Virusevolution

Two International Postdoc positions available from the Shi's Lab

Professor Weifeng Shi is the director of the Key Laboratory of Etiology and Epidemiology of Emerging Infectious Diseases in universities of Shandong province affiliated at the Shandong First Medical University (Shandong Academy of Medical Sciences) and is supported by the Taishan Scholar project of Shandong province. His research interests include: 1. Emerging and Re-emerging infectious diseases; 2. Infection and Immunology mechanisms of Human enteroviruses; 3. The China virome project (CVP) and novel pathogen discovery. Professor Shi has published >100 publications in peer reviewed journals and the details can be found: http://scholar.google.com/citations?user=-HHdszD0AAAAJ&hl=en. Professor Shi has a laboratory with the construction area >800 square meters, including biosafety-2-level (BSL2) laboratory of 300 square meters, which is equipped with modern instruments for molecular biology, cell biology, and animal experiments. He also has ~300 computation cores and >120Tb hard disk for dry lab. Now two postdoc positions are available from the Shi's Lab. The successful candidates will be working on virus evolution-related projects.

A. Recruitment Requirements 1. Applicants should have obtained a doctor's degree from well-known universities or scientific research institutes. 2. Applicants should have a strong background of evolutionary biology or data mining of NGS data. 3. Applicants should be aged 40 years or younger (born after January 1st, 1979). 4. Applicants should be fluent in both spoken English and written English.

B. Benefits and Policy Support Salary is no less than 300,000 RMB before tax (~44,000 US\$) and up to 400,000 RMB before tax (~58,600 US\$) per year. The contract will be 2 years with a possible extension to 4 years.

C. Contact infor For queries or sending CV, please contact Professor Shi: shiwf@ioz.ac.cn.

Weifeng Shi

shiwf@ioz.ac.cn

StateUSaoPaulo BacterialGenomics

Postdoctoral Research Fellow position available at the State University of São Paulo, Brazil, at the Institute of Biosciences (IBRC), Dept. of Biochemistry and Microbiology, campus of Rio Claro. The position is part of the project "Xanthomonas citri subsp. citri citrus canker in São Paulo. Molecular epidemiology and biocontrol potential of bacteriophage and their depolymerases", which has financial support from FAPESP and the BBSRC/UK. It is intended for a motivated PhD in Genetics of Bacteria with experience in genomics, knowledge of molecular biology, cell biology, basics on plant genetics is welcome. The selected PhD will conduct epidemiological and evolutionary studies of the plant pathogen Xanthomonas citri, the isolation and analyses of bacteriophage that have Xanthomonas citri as a host, general cloning, and assemble of protein expression systems for the production of viral enzymes to be assessed as agents for the control of citrus canker; finally, PhD is expected to help with experiments of citrus plant transformation and challenge with Xanthomonas citri. Successful applicant will be working in a multi-disciplinary environment coordinated by Henrique Ferreira (Associate Professor at IBRC), and Mark Enright (Professor at Manchester Metropolitan University, UK). The candidate for the position is expected to have good communication skills (English), and no more than 2 years post-PhD. Preference will be given to individuals who have first author publication(s) in first-rate journals and show previous expertise considering the topics above-mentioned. The ideal candidate will be able to work independently to develop and drive his/her research project, as well as to work in a team-based environment. Please send your CV, an introduction (one-page) letter describing your skills and why you are applying for the position, and contact information for 2 referees all electronically to Henrique Ferreira (henrique.ferreira@unesp.br). The selected candidate will receive a Post-doctoral fellowship from FAPESP, and he/she may be eligible to a moving/installation support. For more information check http://www.fapesp.br/en/postdoc Applications will be received from the 6th of May, 2019 until the 14th of June, 2019.?

Mark Enright <M.Enright@mmu.ac.uk>

StockholmU 2 EvolutionaryGenomics

Two positions are currently available in the European Research Council (ERC) funded project SuperGenE at Stockholm University, Sweden.

Full Ads: 1. Postdoctoral fellow in Evolutionary Genomics: https://tinyurl.com/yygoqqln 2. Researcher in Evolutionary Genomics: https://tinyurl.com/y3t8fs6g Deadline to apply: June 7th, 2019

Project description The positions are associated with the European Research Council (ERC) funded project SuperGenE: Supergene evolution in a classic plant system - genomic studies of distyly.

The aim of this project is to investigate the genomic architecture underlying the balanced floral polymorphism termed distyly in wild Linum species. Specifically, the project aims to investigate the genomic region (termed supergene) that governs distyly and test whether this supergene exhibits evolutionary genetic similarities to sex chromosomes. For this purpose, we are conducting evolutionary genetic analyses of cutting-edge genomic data to comprehensively investigate the tempo and mode of recombination suppression, the impact of natural selection, and regulatory evolution at the supergene in several distylous species. Within the project we are generating several new high-quality de novo genome assemblies for wild Linum species, as well as large population genomics and expression data sets.

The positions will be based in the Slotte lab (https://tanjaslottelab.se), a part of the Dept. of Ecology, Environment and Plant Science, Stockholm University (http://su.se/deep/english/). The working atmosphere is international with English as the working language, and the position offers plenty of opportunities for scientific exchange with both genomicists, evolutionary biologists and ecologists.

Qualification requirements A relevant PhD degree and training in evolutionary genetics or population genomics is required. For the postdoctoral position the PhD degree must have been completed no more than three years before the deadline (see full ad for details). Candidates who do not meet this requirement should instead apply for the researcher position.

Main responsibilities The positions involve research

in the ERC project SuperGenE, primarily evolutionary genetic analyses of genomic data and gene expression data. Some lab work and plant work (e.g. sampling of natural populations in the Mediterranean region) may also be included.

Assessment criteria In the appointment process, special attention will be given to research skills, in particular pertaining to experience of analyses of large-scale genomic data. Excellent proficiency in English (the working language of the group) is required. The postdoctoral fellow needs to be able to work well in a collaborative environment, as well as independently. Finally, initiative, analytical skills and drive are personal characteristics that are desirable. See full ad for detailed assessment criteria for each position.

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

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

Contact Further information about the position can be obtained from Dr. Tanja Slotte, tanja.slotte@su.se.

Application Full ad and application at: 1. Postdoctor in Evolutionary Genomics: https://tinyurl.com/yygoqqln 2. Researcher in Evolutionary Genomics: https://tinyurl.com/y3t8fs6g Tanja Slotte PhD, Associate Professor SciLifeLab Fellow

Department of Ecology, Environment and Plant Sciences (DEEP) Stockholm University 106 91 Stockholm

E-mail: tanja.slotte@su.se

Tanja Slotte <Tanja.Slotte@scilifelab.se>

UArizona EvolutionaryModeling

A Two-Year Post-Doctoral Research Associate Position in Eco-Evolutionary Modeling and Statistical Inference at the University of Arizona

A post-doctoral fellowship is available to work on an NSF /Dimensions of Biodiversity/-funded project to develop statistical inference tools for eco-evolutionary dynamics, and apply these tools to analyze the eco-evolutionary drivers of toxic algal blooms. The postdoc will work under the supervision of Dr. Regis Ferriere to (1) develop general methods for inferring eco-

evolutionary feedbacks using eco-evolutionary dynamics models and statistical methods such as particle MCMC and Approximate Bayesian Computation, (2) develop eco-evolutionary models specifically targetting the empirical system (blooms of the toxic haptophyte alga /Prymnesium parvum/ in Eastern U.S. lakes), (3) apply the newly developed models and statistical inference tools using ecological time series, ¥omics data and phylogenies from natural lakes and laboratory mesocosm experiments. The work will be done in close collaboration with Principal Investigator Dr. Jennifer Wisecaver (Purdue University) and Collaborator Dr. William Driscoll (Penn State University at Harrisburg).

Applicants should have a PhD in Biological sciences, Statistics, Applied Mathematics, or a related quantitative field. The successful candidate will have a background and/or strong interest in computational ecology, statistical inference, data assimilation and modeling in a Bayesian framework, dynamical system modeling, and/or computer science (e.g., writing MCMC samplers). Experience working with large ecological and/or genomic datasets or databases, strong writing skills and associated publications in peer-reviewed literature, communication skills, and mentoring and collaboration skills are also strongly valued.

The position is funded for two years, beginning as soon as August of 2019. The position will be based in the Department of Ecology and Evolutionary Biology at the University of Arizona, and associated with the Ecosystem Genomics InitiativeXa nexus for coalescing University of Arizona strengths in environmental science, ecology, genome-enabled science, and bio-computational research to address the grand challenge of scaling biology from genes to ecosystems. The University of Arizona-based, NSF-supported cyberinfrastructure CyVerse will provide exceptional computational means and support. The position also involves opportunities for traveling to collaborators institutions, nationally (Purdue and Penn State) and internationally (Paris, France), and attending major international conferences (e.g. Ecological Society of America annual meeting).

The University of Arizona is a committed Equal Opportunity/Affirmative Action Institution. Women, minorities, veterans and individuals with disabilities are encouraged to apply. Situated an hour and a half from Mexico in the Sonoran desert and Sky Island region of southeastern Arizona, Tucson has an exceptionally low cost of living along with a wide range of opportunities for outdoor recreation and biological and cultural richness. One example is the recent designation of Tucson as a UNESCO World City of Gastronomy. Complete applications must include (1) a cover letter, (2) curriculum vita, and (3) names and contact information for three references, and should be submitted through the UACareers portal at http://uacareers.com/postings/-38194. Review of applications will begin June 3, 2019, and continue until the position is filled.

ferriere@biologie.ens.fr

UBayreuth EvolutionaryBiology

PostDoc/Senior Scientist (fixed term) (Akademischer Rat/Akademische Rätin auf Zeit) (m/f/d)

Research Position in Evolutionary Animal Ecology, University of Bayreuth

The University of Bayreuth, Germany, is a research-oriented university with internationally competitive, interdisciplinary focal areas in ecology & environmental science. The Department of Evolutionary Animal Ecology headed by Prof. Dr. Sandra Steiger studies various aspects within the fields of Behavioral-, Chemical-, and Evolutionary Ecology (www.eae.uni-bayreuth.de). Our research focuses on the ecology and evolution of communication, family life (including parental care) and host-parasite interaction.

The department invites applications for a

PostDoc/Senior Scientist (fixed term) (Akademische Rat/ Akademische Rätin auf Zeit) (m/f/d)

The contract shall start on October 1st, 2019. The position will initially be restricted to 3 years. Extension to further 3 years is possible. The salary will be determined in accordance with national guidelines for civil service at paygrade A13 (100%).

We are seeking a highly motivated, team-oriented candidate with a strong background in the research area of the department. Preference will be given to applicants working with terrestrial arthropods and a proven record in the use of molecular techniques (RNAseq, RNAi, etc.). However, we also encourage researches with a more theoretical approach to apply. The position comes with a teaching requirement of 5 hours per week during the semester and the candidate is expected to supervise undergraduate as well as graduate students. Teaching of undergraduate students must be performed in German, consequently the willingness to learn German is required. Furthermore, we expect the successful candidate to apply for third party funding.

The formal requirements for application are a PhD in biology and a good research record as demonstrated

by publications in international journals. A previous Postdoc experience would be desirable.

We offer an inspiring and stimulating research environment with state-of-the-art laboratories and techniques. The possibility for "habilitation" is given.

How to apply:

Please send your application electronically (in one pdf file) containing:

 Curriculum vitae including publication record

* Cover letter detailing research interests and experience
* Name and email address of a least to people to provide reference

Deadline for application is June 1st, 2019. However, the position will remain open until a suitable candidate is found. The University of Bayreuth advocates gender equality. Woman are therefore strongly encouraged to apply. Equally qualified handicapped applicants will be given preference. Please note that travel costs and other expenses for an application interview will not be covered.

Please send your application by email as a single pdf file to: sandra.steiger@uni-bayreuth.de

PD Dr. Johannes Stokl

Lehrstuhl fur Evolutionäre Tierokologie Universität Bayreuth Gebäude NW 1 Universitätsstr. 30 95447 Bayreuth

Tel. +49 921 55 2742 Fax. +49 921 55 2743 www.eae.uni-bayreuth.de "Stokl, Johannes" <Johannes.Stoekl@uni-bayreuth.de>

UBritishColumbia 2 PlantEvolution

The Davies lab at the University of British Columbia is advertising two funded postdoctoral positions

A phylogenetic framework for the macroecology of plant disease

Applications are invited for a fully funded one-year postdoctoral position, starting September 2019 with possibility of extension, on the development of a phylogenetic framework for the macroecology of plant diseases that merges theory with phylogenetic, spatial and trait-based approaches.

Project Description

Emerging infectious diseases (EIDs) represent one of the single biggest threats to humans, wildlife, and domesticated plants and animals. Traditional approaches for modelling infectious disease dynamics have assumed a single-host single-pathogen framework, but many pathogens infect multiple host species, and hosts are infected by multiple pathogen species. This position aims to develop new theoretical and statistical models to examine multi-host multi-pathogen disease dynamics in plants, and validate them using large databases on the plant pests and pathogens of wild and agricultural species.

The successful candidate will be expected to work with a disperse team of collaborators, participate in working groups, assist in supervision of graduate students, and contribute to the lively research community at UBC.

Requirements

Key requirements include a strong conceptual and quantitative background in phylogenetic methods and/or spatial ecology, proficiency in programming (preferably in R), and an excellent understanding of community ecology and/or disease biology. Candidates with a proven track record in analyzing large datasets and statistical modelling will be given preference.

The changing intensity of plant pests and pathogens with climate warming

Applications are invited for a fully funded one-year postdoctoral position, starting September 2019 with possibility of extension, on modelling the changing intensity of plant pests and pathogens with climate warming using data from herbaria and new, field-based sequencing platforms.

Project Description

Species are responding to a warming climate in multiple ways. Animals are migrating or reproducing sooner. Plants are shifting their phenology, leafing out and flowering earlier in the growing season, or moving their geographic distributions pole-wards or upwards in elevation. There has been increasing concern that such shifts might result in spatial or phenological asynchronies between tightly coupled species, for example, flowers and their insect pollinators. To date, asynchrony in antagonistic interactions, such as between hosts and pathogens, has received less attention; nonetheless, climate change is predicted to facilitate the emergence of pests and pathogens in new regions. This postdoctoral position will use the vast historical record housed in herbarium collections to document shifting pest and disease pressures through time, and track contemporary pathogen spread using new field-based sequencing tools, such as the Nanopore Minion sequencer, that can generate data in near real time.

The successful candidate will be expected to assist in the development of statistical and molecular methods, help in the supervision of graduate students, and contribute to the lively research community at UBC.

Requirements

Key requirements include an excellent understanding of community ecology and/or disease biology, a strong conceptual and quantitative background, proficiency in programming (preferably in R). Candidates with experience in analyzing next generation sequence data, and/or working with herbarium specimens will be given preference.

Location

The position will be in the Davies lab (https://-phyloecology.wordpress.com/) within the Biodiversity Research Centre at the University of British Columbia (https://biodiversity.ubc.ca/), with strong ties to the Departments of Botany, and Forest and Conservation Sciences.

Application

Please send a current CV, a letter of interest and the name and emails of two references to Jonathan Davies, UBC (j.davies@ubc.ca). Informal enquires welcome. Review of applications *will begin 15 May* and continue until the position is filled.

"Davies, Jonathan" <j.davies@ubc.ca>

UBritishColumbia GrapeAdaptation

Postdoctoral Fellow in Winegrape Research

The Temporal Ecology Lab is looking for a bright, motivated and collaborative researcher to join the lab and develop new winegrape models using Stan (mc-stan.org). The project combines decades of historical records with modern Bayesian modeling to address the challenge of shifting climate regimes on the wine industry, with implications for crops across the globe. The fellow will join an interdisciplinary team of researchers based across Canada, the United States and Europe.

The position would be based at the University of British Columbia in the Forest and Conservation Sciences Department. Applicants must be willing to travel to the Okanagan winegrowing region (in southern British Columbia) and France for field work and to meet with collaborators. Travel costs are covered by the lab (in advance of travel as needed).

The ideal researcher will be both able to lead current projects, develop their own projects, and support ongoing work in the lab. Current lab research covers a broad range of topics'climate change impacts via phenology on forests and winegrapes, community assembly via the temporal niche'using a variety of methods from field empirical data, to meta-analyses and analytical coexistence models. More details on the lab's research can be found at www.temporalecology.org . A successful applicant would have/be: - — — — Either a Ph.D. in evolution, ecology, agriculture or related fields with a strong interest in statistical modeling or a Ph.D. in computer science, statistics, physical sciences or related fields with a strong interest in agriculture and/or ecology/evolution. - — — — Strong quantitative and computational skills. - — — — Experienced with R or Python (or similar skills), ideally with proficiency in LaTeX, git and Stan (applicants without experience in these languages must be excited to learn them quickly). - — — — Comfortable working with diverse file structures and large datasets (e.g., climate data in formats such as NetCDF). - — — — Excellent writing skills and good publication record. - — — — Experience relevant to mentoring undergraduate and graduate students - — — — Excellent record of being a good lab and community member.

To apply email the following in PDF format (preferably one file) to E. M. Wolkovich at e.wolkovich@ubc.ca (informal inquiries welcome): - — — — Cover letter (see 'successful applicant' list above and detail relevant skills and experience) - — — — Curriculum vitae - — — — Brief Description of research interests (maximum of two pages) - — — — Two examples of published papers (one in prep acceptable). - — — — Names and contact information of 3 references.

Application review will begin 15 May and continue until the position is filled.

– Elizabeth M Wolkovich Forest and Conservation Sciences University of British Columbia 2424 Main Mall Vancouver, BC V6T 1Z4 Office: 604-827-5246 www.temporalecology.org   Elizabeth M Wolkovich <wolkovic@mail.ubc.ca>

UCaliforniaLosAngeles UrbanConservationGenomics

The UCLA La Kretz Center for California Conservation Science (http://www.environment.ucla.edu/-

lakretz/) and the UCLA Sustainable LA Grand Challenge (https://grandchallenges.ucla.edu/sustainable-la/) invite applications for a joint Postdoctoral Fellowship in Molecular Urban Ecology and Bioinformatics. The work is embedded in an ongoing project on the impact of urbanization on a suite of 22 plant, invertebrate and vertebrate species spanning the Urban/Wildland interface of the Los Angeles basin. Our overarching goal is to determine such issues as the contribution of protected lands to the conservation of genetic diversity, the ability of species to traverse the urban landscape, and genetic resilience to future climate change.

We are looking for a highly motivated individual with experience in the collection and/or downstream analysis of comparative genomics data to participate in an innovative research initiative and interface with the conservation and management agencies that direct and lead California conservation. The project has large scale data collection and analysis components, and an individual who excels in one, or ideally both areas could be a valuable addition to our group.

The ideal candidate should have a PhD and relevant research experience in the collection, curation and analysis of genome-scale data, ideally across multiple taxonomic groups. Although the primary goals and direction of the project are already established, we hope that the candidate will also bring their own unique direction to the project. The candidate would work collaboratively with Dr. Joscha Beninde (https://www.ioes.ucla.edu/person/joscha-beninde/), an urban landscape geneticist already working on the project.

The Fellowship is for two years, subject to review after the first year. Our preferred start date is summer, 2019. The position has an annual salary of approximately $49,000 plus full benefits as well as funds for molecular lab work.

Interested candidates should submit 1) cover letter, 2) current CV, 3) maximum 2-page description of their research accomplishments and how they would contribute to this multispecies project in urban landscape genomics, 4) copies of two research publications that highlight your abilities in molecular ecology/informatics , and 5) names and contact details of two or three referees, including your Ph.D advisor, all as a single PDF file.

Deadline for completed applications is July 1, 2019.

E-mail questions and application materials to Brad Shaffer (Director of the La Kretz Center) at brad.shaffer@ucla.edu or Joscha Beninde (postdoc in this project) at beninde@ucla.edu.

Brad Shaffer brad.shaffer@ucla.edu Phone: (310) 825-3836

H. Bradley Shaffer Distinguished Professor Department of Ecology and Evolutionary Biology www.eeb.ucla.edu/Faculty/Shaffer/ Director UCLA La Kretz Center for California Conservation Science Institute of the Environment and Sustainability University of California, Los Angeles https://www.ioes.ucla.edu/lakretz/ hb-shaffe@g.ucla.edu

UCIrvine MicroEvoEco

Postdoc in the Microbial Evolutionary Ecology Lab at UCI

I am seeking to hire a highly-motivated *Postdoctoral Researcher *to investigate how interactions between species and their environment shape how microbial communities respond to environmental changes. In our lab we combine diverse approaches such as experimental evolution on synthetic communities, whole genome sequencing, single-cell biology and mathematical modelling to formulate hypotheses that can be tested with experiments. More information about our research can be found in https://faculty.sites.uci.edu/verdugolab/ The successful candidate will have a substantial degree of independence and will have

opportunities to pursue their own research interests in *microbial evolutionary ecology*.

The successful candidate will have a PhD. in the following or related fields: microbial ecology, evolutionary genetics, genomics, molecular microbiology, computational biology. Expertise in microbial experimental evolution, high-throughput sequencing and/or quantitative skills are highly desired.

The position is available as of summer 2019. The successful candidate will join the Department of Ecology and Evolutionary Biology and the Center for Evolutionary Genetics at UCI. The department is part of the Network of Experimental Research on Evolution (NERE) and the UCI Microbiome Initiative, providing exciting networking opportunities.

Interested candidates please send me a letter of inquiry indicating your previous research experience and your motivations to join the lab, as well as a CV including publication list and the contact information for three references to Dr Alejandra Rodriguez Verdugo (alejanr1@uci.edu) with the subject line 'MicroEvoEco; Postdoc position'. Review of applications will begin May 15th, 2019 and continue until the position is filled.

Alejandra Rodriguez Verdugo <alejanr1@uci.edu>

UCopenhagen AncientPlantGenomics

Postdoctoral position in ancient plant genomics in ERC-funded project TIMBER

The SAXO Institute, Faculty of Humanities, University of Copenhagen (UCPH), Denmark, in collaboration with GeoGenetics, invites applications for a 1-year post-doctoral position in ancient plant genomics to be filled by 1st September 2019 or as soon as possible thereafter.

The position is for 12 months.

The project The project 'TIMBER' Northern Europe's timber resource - chronology, origin and exploitation, led by Aoife Daly, has received funding from the European Research Council (ERC) under the European Union's Horizon 2020 research and innovation programme (grant agreement No. 677152). In this project, timber in Northern Europe is being studied, to attain a precise chronology for trade of timber over a long time period (c. 1100 to 1700). Using material and textual evidence to identify the source of timber (provenance) the aim is to map the trade in this construction material and to show the regional and temporal fluctuations in timber exploitation and availability. Using a multi-disciplinary approach (archaeological analysis, archival research and a range of archaeological sciences) on a variety of specific case studies, the team is working together to analyse the sources and destinations of traded timber through time.

Job content The postdoc will perform analyses on archaeological oak timber using ancient DNA (aDNA) techniques with a view to identifying the timber's region of origin. The genomic research should complement the dendrochronological provenance analysis to locate historical sources of wood and better understand trade routes within the Baltic region. The main focus will be to develop an aDNA approach to study historical wood samples, using it to identify the origin of the wood. Specific archaeological case studies are the focus of the project, and these have been preserved in a variety of conditions, both in their in situ environments and after excavation.

Qualification requirements In order to be considered for the position, applicants must have research qualifications at least corresponding to what can be achieved as part of a successfully completed PhD within a relevant field.

Candidates that have experience in working with aDNA and/or population genomics are highly encouraged to apply. The project will consist of both laboratory work and bioinformatics, but support is available for each, through collaboration with the GeoGenetics Centre (also within the University of Copenhagen). The Centre has specialized DNA-free laboratories dedicated to performing aDNA work, and is consequently a world leader in the discipline.

The postdoc will work closely with the other postdoc appointees in the team and with the PI at the SAXO Institute; so that the information gathered in the entire project disciplines will be incorporated into a wider analysis referring to the main project research questions.

The appointee will be part of a cross-disciplinary team with emphasis on researching evidence for the trade of timber in the past.

Application procedure at https://jobportal.ku.dk/-videnskabelige-stillinger/?show=9594 Aoife Maeliosa Daly <aoife.daly@hum.ku.dk>

UCopenhagen EvolutionaryEcol

Postdoc in ecology and evolution

A 2 years postdoctoral fellowship in ecology and evolution is available at the Center for Macroecology, Evolution and Climate, Department of Biology, University of Copenhagen.

Overall description of the project: Climate change poses a major threat to biodiversity, potentially outpacing the ability of species to adapt.Yet the scientific community still struggles to anticipate the responses of biodiversity to climate change.Integrating pioneering data and methods across macroecology, evolutionary genomics and paleoclimatology we propose to elucidate the demographic history of bird species during the last million years of climate change.These species inhabit different biomes (from the tropics to the poles) and represent a variety of life strategies and ecological traits.We will reconstruct the demographic history under past climate change of a variety of populations across 320 bird species using PSMC methods, and identify the role of life strategies and species to explain different demographic responses across species.We will also provide relevant baselines for avian population dynamics under

climate change.Revealing past demography will largely improve our ability to anticipate potential responses or species to ongoing climate warming.

The position is part of a recently funded DFF2 project "DEMOCHANGE", lead by David Nogués-Bravo, University of Copenhagen, and Guojie Zhang, University of Copenhagen.This position will be in the group of Prof.Guojie Zhang in Department of Ecology and Evolution at Department of Biology, University of Copenhagen and both Zhang and Nogues-Bravo will be the co-supervisors.

The position is open from September 2019 and is time limited for two years with the possibility of extension for another two years.

Tasks to carry out: Coordination of sample collections and sequencing, population genomic analysis for inferior paleo-demography, alignment of temporal trends in demography and paleoclimatic conditions, estimates of different responses to climate change and model how species trace modulate those responses across space, time and phylogeny.

Qualifications: We are looking for highly motivated individuals with a PhD from ecology and evolutionary, population genomics, macroevolution, phylogenetics / phylogenomics, or similar fields.Candidates with below experiences will be highly preferred.

Skills / expertise: Computational modeling, population genomics analysis, phylogenomic / macroevolutionary methods (ie, how ecological traits control demographic responses to climate change after controlling by evolutionary patterns represented in phylogenies), large data sets management and data curation, strong coding abilities, project coordination, curatorial or collection of research-based expertise in birds.

Software / programming languages: R.

For consideration, applications must: -Have published in international peer-reviewed journals -Highly independent and have experience in project coordination -Have good communication skills

The working language is English, thus excellent English speaking, reading and writing skill are required.For further information about the position, please contact Prof.Guojie Zhang (guojie.zhang@bio.ku.dk) or David Nogues-Bravo (dnogues@bio.ku.dk).

Further information on the Department is linked to http://www.science.ku.dk/english/about-the-faculty/organisation .

The University wishes our staff to reflect on the diversity of society and thus the applications come from all qualified candidates regardless of personal background.

Terms of employment The position is covered by the Memorandum on Job Structure for Academic Staff. Terms of appointment and payment accord to the agreement between the Ministry of Finance and the Danish Confederation of Professional Associations on Academics in the State.

The starting salary is currently up to DKK 430,569 including annual supplement (+ pension up to DKK 76,627).Negotiation for salary supplement is possible.

The application, in English, must be submitted electronically by clicking APPLY NOW below.

Please include - Curriculum Know - Diplomas (Master and PhD degree or equivalent) - Research plan - description of current and future research plans - Complete publication list - Separate reprints of 3 particularly relevant papers

The deadline for applications is Friday 31 May 2019, 23:59 GMT +2.

After the expiry of the deadline for applications, the authorized recruitment manager selects applicants for assessment on the advice of the interview committee. You can read about the recruitment process at http://employment.ku.dk/faculty/recruitment-process/ .

Prof. Guojie ZhangVillum Investigator Section for Ecology & Evolution Department of Biology University of Copenhagen

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UEastAnglia ClimateAdaptation

Senior Research Associate (postdoc) position open

Understanding the impact of climate change on reproductive fitness and biology in any organism is key to estimate species survival. Externally fertilising ectotherm organisms such as fish are particularly vulnerable to changes in temperature and other environmental factors as all life stages - from gametes to adults - are exposed to these changes. In this NERC funded project, we aim to understand the role of genetic and non-genetic mechanisms in reproduction and fertilisation in responding to environmental changes. We will combine experimental

manipulations and assays with next-generation sequencing (RNA and DNA sequencing) to estimate the impact of changes in environmental conditions across generations using the zebrafish.

The successful candidate will be a full member of the PIs group (see our lab homepage for more information: https://simoneimmler.com/) and will actively participate in the diverse group and departmental activities including lab meetings, departmental seminars and journal clubs. The School of Biological Sciences (BIO) at UEA offers a vibrant research environment with a large number of research groups working on questions related to this project. The Norwich Research Park V home of BIO V hosts a number of world-leading research institutions including the Earlham Institute with its cutting-edge sequencing technology platforms.

Candidates must hold a PhD (or equivalent experience) in evolutionary biology, ecology or genetics and have an excellent understanding of experimental design and solid experience in the molecular lab with RNA/DNA extractions.

The full time post is for a fixed term of 36 months and is due to commence on 31 August 2019.

Please email me with any questions: s.immler@uea.ac.uk

To apply follow this link: https://myview.uea.ac.uk/-webrecruitment/pages/vacancy.jsf?vacancyRef=-RA1628 "Simone Immler (BIO - Staff)" <S.Immler@uea.ac.uk>

UExeter InsectEvolution

Postdoctoral Research Fellow in Insect Evolution to Xenobiotics

Starting salary will be up to 37,345 on Grade F, depending on qualifications and experience.

The University of Exeter wishes to recruit a Postdoctoral Research Fellow to participate in a high profile ERC funded project entitled 'Understanding and exploiting the P450 insect resistome' and then subsequently a BB-SRC project entitled 'The adaptive potential of clonality in aphid crop pests'. This post is available for four years from July 2019. The post-holder will be based in the Bass lab and be part of a thriving group comprising several PhD students, post-doctoral research fellows and technicians.

Both projects focus on different aspects of the evolu-

tion of insect resistance to natural and synthetic toxins. We will use a range of genomic, transcriptomic and epigenetic approaches to understand the (epi)genetic mechanisms that allow clonally reproducing insects to adapt to sudden environmental change (such as that imposed by pesticides) in the absence of sexual reproduction.

The successful applicant will employ a range of bioinformatic and molecular approaches to investigate this topic. Their primary role will be to generate and analyse next generation sequence data, including resequenced insect genomes, transcriptomes and whole genome bisulfite sequencing (WGBS) data. The fellow may also conduct, or contribute to, follow-on work to functionally validate the role of candidate resistance genes.

Over the duration of the project, the postdoc will be encouraged to develop their own avenues of research with a view to establishing themselves as an independent investigator. The project includes substantial funds for sequencing, research consumables, and to facilitate attendance at national and international conferences/workshops.

About you

Applicants will possess a relevant PhD or equivalent qualification/experience in a related field of study. Experience working with genomic data and bioinformatics skills are essential. Experience with standard molecular biology methods and post-genomic functional approaches would be advantageous.

What we can offer you

* Freedom (and the support) to pursue your intellectual interests and to work creatively across disciplines to produce internationally exciting research; * Support teams that understand the University wide research and teaching goals and partner with our academics accordingly * An Innovation, Impact and Business directorate that works closely with our academics providing specialist support for external engagement and development * Our Exeter Academic initiative supporting high performing academics to achieve their potential and develop their career

§A multitude of staff benefits including sector leading benefits around maternity, adoption and shared parental leave < http://www.exeter.ac.uk/staff/employment/-parents/ > (up to 26 weeks full pay), Paternity leave (up to 6 weeks full pay), and a new Fertility Treatment Policy

* A beautiful campus set in the heart of stunning Cornwall

For further information please contact Professor Chris

Bass, e-mail c.bass@ex.ac.uk.

To apply go to: https://jobs.exeter.ac.uk/-hrpr_webrecruitment/wrd/run/-ETREC107GF.open?VACANCY_ID66021Og93&WVID817591jNg&LANG= USA Professor Chris Bass Chair in Applied Entomology and ERC fellow Biosciences, College of Life and Environmental Sciences, University of Exeter, Penryn Campus, Treliever Road, Penryn TR10 9FE UK Phone: 01326259084 Email: c.bass@exeter.ac.uk

"Bass, Chris" <C.Bass@exeter.ac.uk>

UExeter InsectPathogenInteractions

We wish to recruit a full time Postdoctoral Research Fellow to participate in research on host-pathogen interactions/insect antiviral immunity working with Dr Ben Longdon. This Wellcome Trust and Royal Society funded post is available for 2 years starting in 2019 (latest possible start beginning of 2020).The successful applicant will responsible for the day-to-day management of the project and will collaborate in designing and implementing an array of molecular biology experiments using up to 50 species of Drosophilidae and a natural RNAvirus called Drosophila C Virus. The project will examine why viruses can infect some hosts and not others by examining the cellular and immune factors underlying these differences in susceptibility. We plan to examine the ability of the DCV-1A suppressor of RNAi to prevent processing of dsRNA into siRNAs by Dicer-2 in different host species. We will then look to see how the suppressor functions across the host phylogeny. Some background to the project can be found here https://journals.plos.org/plospathogens/-article?id=.1371/journal.ppat.1004728 and here http:/-/genesdev.cshlp.org/content/20/21/2985.long Applicants will be able to independently plan,run and collect data from molecular biology experiments. The post will be based at the University of Exeter, but will collaborate with and spend significant amounts of time in the lab of Prof Ronald Van Rij (Radboud Institute for Molecular Life Sciences, Nijmegen, the Netherlands) and also collaborate with Dr Darren Obbard (University of Edinburgh, UK).

The post will include carrying out molecular and biochemistry assays to examine antiviral RNAi immunity in different species of Drosophila. Experience with molecular procedures (RNA work including: RNA extractions, qRT-PCR, siRNA isolation and denaturing gel electrophoresis/native PAGE, RNAi assays) is essential. Experience in working with insects/Drosophila, viruses and R is desirable. The successful applicant will be able to present information on research progress and outcomes, communicate complex information, orally, in writing and electronically.

Please highlight in your cover letter why you would like to work on this project, and how your skill set/experience is relevant to the planned project (see overview and papers above).

Whilst the ideal candidate would have experience in both molecular and evolutionary biology, our main goal is to find someone with a background in molecular biology who can bring their expertise into a more evolutionary lab group. However, this is flexible, so if you think you might be a great fit for this position but are concerned about meeting all criteria please get in touch before applying.

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

Apply here https://jobs.exeter.ac.uk/-hrpr_webrecruitment/wrd/run/-ETREC107GF.open?VACANCY_ID03973OyFC&WVID817591jNg&LANG USA – Ben Longdon University of Exeter Penryn Campus Cornwall TR10 9FE +44 (0) 1326 259460 https://benlongdon.com/ "Longdon, Ben" <B.Longdon2@exeter.ac.uk>

UInnsbruck PDF PhD AquaticEvolution

University Assistant - Postdoc (Code BIO-10561)

University Assistant ' Postdoc (40 hours per week), University of Innsbruck, Research Department for Limnology, Mondsee, Austria, starting on 1st September 2019, duration 3 years.

In this position, you will carry out independent research in the field of aquatic evolutionary ecology by developing a project at the interface of ecology and evolution. The initial idea for the project comes from you, and you develop it in collaboration with Prof. Seppälä and other research groups at the Research Department for Limnology. Collaboration with the research groups at other departments is also encouraged. Possible research fields include, but are not limited to, species interactions, responses to environmental change, evolutionary

genetics, and ecosystem functioning. In an ideal case, your project combines different fields.

Qualifications:

- PhD in Aquatic Ecology/Evolutionary Ecology, Research experience in Evolutionary Ecology

- Desired: Earlier Postdoc experience, Experience in supervision of graduate students, Publications in high-ranking journals, Acquisition of third-party funds, and work experience abroad

- Social skills and ability to work in a team, as well as flexibility, are essential

- For this position we would need a CV, a Motivation letter and a brief (max. 2 pages) description of the research idea (i.e. study question, taken approach, groups that could be involved)

Job profile: The description associated with this job duties and requirements can be found at www.uibk.ac.at/-karriere, Code BIO-10561. We are looking forward to receiving your online application by 14th June 2019. For questions or more information concerning research, please contact Prof. Seppälä: otto.seppaelae@eawag.ch Travel costs cannot be reimbursed.

Salary: The minimum gross salary for this position amounts to €3.804,00 per month (14 times). Furthermore, the university has numerous attractive offers.

University Assistant ' PhD Position (Code BIO-10559)

University Assistant ' PhD Position (20 hours per week, with the submission of the dissertation agreement the working hours will be 30 hours per week), University of Innsbruck, Research Department for Limnology, Mondsee, Austria, starting on 1st September 2019, duration 4 years.

In this position, you will conduct experimental research on the evolutionary ecology of the responses of freshwater snails to changing environmental conditions under climate change. The main goal of the project is to learn to understand the relative importance of different genetic and non-genetic factors in determining snails' responses to high temperature in a quantitative genetic framework. Additionally, the fitness consequences of snails' responses will be described to predict their evolutionary change. Details of the project will be planned together with Prof. Seppälä. Available resources include, for example, tens of inbred Lymnaea stagnalis lines as well as transcriptomic tools.

Qualifications:

- Master in Biology

- Experience in laboratory work

- Experience in carrying out experimental research

- Statistical knowledge in the evaluation of experiments

- Communicative personality

- Social skills and ability to work in a team, as well as flexibility, are essential

- Please attach a written idea to your dissertation project (max. 5 pages)

Job profile: The description associated with this job duties and requirements can be found at www.uibk.ac.at/-karriere, Code BIO-10559. We are looking forward to receiving your online application by 13th June 2019. For questions or more information concerning research, please contact Prof. Seppälä: otto.seppaelae@eawag.ch Travel costs cannot be reimbursed.

Salary: The minimum gross salary for this position amounts to €1.432,00 per month (14 times). Furthermore, the university has numerous attractive offers.

Kind regards, [cid:image003.jpg@01D45CBA.C883A490] Universität Innsbruck Forschungsinstitut für Limnologie, Mondsee Sonja Burggraf Institutssekretariat Mondseestraße 9, A-5310 Mondsee Telefon +43 512 507-50201 Fax +43 512 507-50299 E-Mail sonja.burggraf@uibk.ac.at, office-ilim@uibk.ac.at Bürozeiten: Dienstag ' Freitag 8:00-16:00

"Burggraf, Sonja" <Sonja.Burggraf@uibk.ac.at>

UKentucky
EvolutionaryTheorySocialGenomics

Postdoctoral position available in Mathematical/Computational Evolution and Ecology at the University of Kentucky.

The Van Cleve lab in the Department of Biology (http://vancleve.theoretical.bio) at the University of Kentucky is seeking one Postdoctoral Scholar broadly interested in using mathematical and computational tools to study evolutionary and population genomics, evolutionary ecology, and social behavior. Support for the positions comes from a recent NSF CAREER award (https://nsf.gov/awardsearch/-showAward?AWD_ID=46260); the specific project is flexible and will broadly relate to understanding how processes at the genetic scale, such as recombination, interact and coevolve with processes at the individual and social group scales. There will be opportunity to

develop new theoretical models and new computational methods or tools.

The successful candidate will have a Ph.D., expertise in mathematical or computational modeling, experience with scientific computing, interests in evolution and ecology, and a record of publication that reflects the ability to conduct original and independent research. Familiarity with C++/Python/Julia is a plus.

The start date is flexible, though a prospective start date sometime in summer 2019 is preferred. The position is renewed each year with review and is funded for a maximum of three years. Salary is $50,000, and benefits are included.

Interested applicants should submit via e-mail (jvancleve@uky.edu): 1. a 1-2 page statement describing their research interests 2. a CV including contact information (e-mail and phone) for three references.

Review of applications will begin immediately and will continue until the position is filled. For additional information regarding the position, please contact Jeremy Van Cleve (jvancleve@uky.edu).

The University of Kentucky is the home of a diverse set of research groups that use laboratory, field, computational, and mathematical tools to study questions in population and evolutionary genetics and genomics, ecological genetics, phylogenetics, evolutionary ecology, physiological ecology, conservation biology, behavioral ecology, plant ecology, and other fields in evolution and ecology. These research groups are housed in a number of departments on campus including the Departments of Biology and Mathematics in the College of Arts and Sciences and the Departments of Entomology, Plant and Soil Sciences, Plant Pathology, and Forestry & Natural Resources in the College of Agriculture, Food and Environment.

The University of Kentucky is located in Lexington, KY, known for the many bucolic horse farms that surround the city, thoroughbred racing at Keeneland, equestrian events at Kentucky Horse Park. Lexington and the surrounding area is home to many bourbon distilleries and microbreweries and numerous outdoor activities including hiking and world-class climbing at the nearby Red River Gorge. The cost of living in Lexington is modest and many UK students, faculty, and staff live close to the University and commute by walking or biking.

The University of Kentucky is an Equal Opportunity Employer and encourages applications from veterans, individuals with disabilities, women, African Americans, and all minorities.

– Jeremy Van Cleve

Assistant Professor Department of Biology University of Kentucky E-mail: jvancleve@uky.edu Webpage: http:/-/vancleve.theoretical.bio Phone: (859) 218-3020

Jeremy Van Cleve <jvancleve@uky.edu>

ULausanne CassavaGenetics

Postdoctoral position VGenetics and epigenetics of cassava and its responsiveness to inoculation with mycorrhizal fungi (Uni. Lausanne, Switzerland)

Job Description: We are looking for a highly motivated postdoctoral researcher to study the role of genetics and epigenetics in cassava responsiveness to the mycorrhizal symbiosis. Our research indicates that different cassava varieties respond very differently to the mycorrhizal symbiosis and we would like to investigate this in greater depth.

It is intended that the results of this project will be combined with research in the field where our work is leading to real solutions to increase production of food in areas of the world where starvation is a major problem. More information about our work can be found at http://people.unil.ch/iansanders/ The project is part of a wider collaboration between the University of Lausanne, Prof. Alia Rodriguez at the National University of Colombia and our partners in Kenya and Tanzania.

Your skills and qualifications: Candidates must be highly motivated, have a PhD (or expect to have very soon), and have knowledge in one or more of the following fields: genetics; plant molecular biology; epigenetics; quantitative genetics, gene silencing. Sound knowledge of bioinformatics would be an advantage and an interest in solving problems in an analytical way. The successful candidate should also have good interpersonal skills and an ability to work well in a multicultural team.

Job information: The position is available as soon as possible and is initially for 1 year (100% contract), renewable for 1 more year (or longer, depending on the availability of external funding). Preference will be given to someone who very recently obtained, or will very soon obtain, a PhD.

Most of the researchers time will be dedicated to research, but a contribution to teaching is expected, including the possibility of supervising master students. Formally, the contract stipulates : 70% Personal research, 25% Participation to teaching activities, 5% group-related tasks such as data management.

Applications: To apply you must upload a CV and motivation letter in English, including the names of 2-3 referees, to the University of Lausanne job portal at: https://bit.ly/2Yy64CA Applications must be received not later than 30th June 2019. Informal enquiries may be made by email to ian.sanders@unil.ch

Ian Sanders <ian.sanders@unil.ch>

chickadeecognition.com Facebook lab page: https://www.facebook.com/chickadeecognition/ Twitter: https://twitter.com/CognitiveEcol vpravosu@unr.edu

UppsalaU AncientDNA

Postdoctoral fellowship in ancient DNA and population genomics

Project description: The process of domestication has fascinated biologists since the early days of the evolutionary theory. Domestication represents observable evolutionary change in a relatively short time span making it an ideal subject to study these processes. Recent technological advances in archaeogenomics allow to study such evolutionary changes through time by obtaining genomic data from populations across time and space. The project will conduct temporal sampling of sheep populations in Central Asia in order to understand how neutral and selective processes changed these populations over time.

Qualifications: A doctoral degree in a relevant field is required at the starting date. The ideal candidate is highly motivated with a thorough education and strong interest in archaeo-/palaeogenomics, evolutionary and population genetics. Experience in working in a molecular biology research lab is required, previous experience in working in an ancient DNA lab is a big plus. Experience with handling Next Generation Sequencing data, population genomic data analysis and scripting/programming is also advantageous. Candidates must have excellent written and oral communication skills in English.

How to apply: Please email your application to Torsten Günther (torsten 'dot' guenther 'at' ebc 'dot' uu 'dot' se). The email should use the subject line "CTS Postdoc application" and all documents should be attached as a SINGLE PDF file. The application should include a letter of intent describing your research interests and your suitability for the position. The application should also include a CV with a publication list and other relevant achievements. Please provide contact details for at least two references.

The position: Staring date is September 1st or according to agreement (but no later than December 2019). This position is funded by a tax-free two year stipend (23,000 SEK per month) awarded by Carl Tryggers Foundation. The regulations of the foundation require

UNevada Reno ChickadeeEvolution

Postdoc position is available at the University of Nevada Reno in the lab of Vladimir Pravosudov to work on the NSF funded project on social networks and cognition in wild mountain chickadees using our established RFID-based system in the Sierra Nevada mountains. Start date is flexible. The position could be up to 5 years conditional on satisfactory performance. The ideal candidate should be capable and willing to work in some of the harshest winter mountain conditions, to use skis and snowshoes to hike several miles while ascending 1,000 feet in deep snow in various weather conditions, to use snowmobiles and ATVs with snow-tracks in extremely challenging mountain conditions and sometimes to shovel snow to arrange save passage of these snow vehicles. Field work will be conducted throughout the entire year at our long-term study area in Sagehen Experimental Forest in northern Sierra Nevada (near Truckee, CA), which is ca. 40 miles from Reno. The ideal candidate should have field experience working with small passerine birds (mistnetting, collecting blood samples), be fluent in R (both managing large data sets and stats) and preferably in either Perl or Python programming. Any familiarity with analyzing social networks is a plus. Per UNR rules, a postdoc must be within 5 years of finishing PhD, so I am looking for candidates who either just got their PhD or within 1-3 years after PhD. If interested, please contact vpravosu@unr.edu. In your email, please address: (1) your experience with field work and with small birds, (2) your field experience in winter conditions, (3) your fluency in R, (4) your experience with Perl or Python, and (5) your experience with analyzing social networks. Applications can be submitted at https://nshe.wd1.myworkdayjobs.com/UNR-external/job/University-of-Nevada-Reno—Main-Campus/Postdoctoral-Fellow–Biology_R0115248-1
Dr. Vladimir Pravosudov UNR Foundation Professor Department of Biology University of Nevada Reno Office phone: 775-784-1271 Lab website:

that the candidate is an incoming postdoc (i.e. the PhD degree should not be from Uppsala University).

Please contact Torsten Gi $\frac{1}{4}$nther (torsten 'dot' guenther 'at' ebc 'dot' uu 'dot' se) for informal inquiries. Reviewing applications will begin on May 1st 2019 and continue until a suitable candidate is found. The final candidate will have to be approved by the foundation.

More information: https://gunther-lab.org/-postdoctoral-fellowship-in-ancient-dna-and-population-genomics/ Torsten Gi $\frac{1}{4}$nther Group Leader/Forskare Human Evolution Program Department of Organismal Biology Uppsala University Norbyvi Âgen 18C 752 36 Uppsala, Sweden https://gunther-lab.org/ 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 Torsten Gi $\frac{1}{4}$nther <torsten.guenther@ebc.uu.se>

UppsalaU EvolutionaryGenomics

Dear colleagues,

A 2-year postdoc position is available in my group to work on evolutionary genomics of birds. More information here: https://www.uu.se/en/about-uu/join-us/-details/?positionId'2959 Please forward this ad to anyone who might be interested. Application deadline is June 20.

Thanks and cheers, Alex

– Dr. Alexander Suh Dept. of Evolutionary Biology (EBC) Uppsala University Norbyvägen 18D SE-752 36 Uppsala, Sweden Alexander.Suh@ebc.uu.se https://twitter.com/alexander_suh (Twitter) http://-/genomicrocosm.wordpress.com (Blog) http://-www.ieg.uu.se/evolutionary-biology/suh/ (Lab website)

När du har kontakt med oss på Uppsala universitet med e-post så 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 Alexander Suh <alexander.suh@ebc.uu.se>

Usheffield SpeciationGenomics

Postdoc with Roger Butlin and Kerstin Johannesson, working on genomics of speciation in Littorina.

At the Marine Science department there is a long tradition in working with marine snails of the genus Littorina as models for studies of local adaptation, hybrid zones and speciation. This study focuses on ecotype formation and the subsequent evolution of barriers to gene exchange in L. saxatilis. This species forms multiple ecotypes but we concentrate on contrasting adaptations to crab predation and wave action that occur in many parts of its North Atlantic distribution, particularly comparing Spanish and Swedish contact zones. We have extensive phenotypic and genomic data sets (targeted capture sequencing, whole genome re-sequencing and SNPs). This postdoc project will contribute to bioinformatic processing of data and analyses aimed at detecting selection and its phenotypic correlates, including contributions to reproductive isolation. One focus will be on the phenotypic effects of inversions and the factors influencing clinal variation in both inversion frequencies and phenotypes. An L. saxatilis reference genome and a genetic map is available. This postdoc may also contribute to efforts to improve these resources.

The candidate will join an international team working on the evolutionary biology of Littorina based in the Department of Marine Science, both at Tjärno Marine Laboratory and in Gothenburg, and at the University of Sheffield.

The candidate is expected to lead and perform the bioinformatic and population genomic analyses of multiple data types using standard software and custom scripts and to present the results of the analyses in manuscript(s) and at conferences, and communicate the findings at various dissemination activities. The candidate is also expected to take part in other research-related activities at the department, and within the research group in particular.

Informal enquiries welcome, contact Roger on r.k.butlin@shef.ac.uk

Deadline for applications 2 June. Please apply via this link:

https://www.gu.se/english/about_the_university/-job-opportunities/vacancies-details/?idD05 – Roger Butlin

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

Guest Professor Marine Sciences University of Gothenburg

r.k.butlin@shef.ac.uk

Roger Butlin <r.k.butlin@sheffield.ac.uk>

are welcome.

–Jeff Dudycha

*****

Jeffry L. Dudycha Professor Dept. of Biological Sciences University of South Carolina Columbia, SC 29208 dudycha [at] biol.sc.edu www.tangledbank.org

USouthCarolina ExpressionPlasticityDaphnia

Post-doc: Expression plasticity in Daphnia

The Dudycha lab at the University of South Carolina is recruiting a post-doctoral research associate to join an NSF-funded project addressing the mutational origins of phenotypic plasticity. As a whole, the project aims to use Daphnia as a model system to understand how expression plasticity and phenotypic plasticity evolve. The post-doc will use next-gen sequencing to test hypotheses about how spontaneous mutation alters transcriptomes and their responses to environmental variation, potentially developing approaches to evaluate allele-specificity and connections to organismal phenotypes.

Qualifications: The selected candidate must have a Ph.D. in a relevant field completed prior to beginning the position, including experience in the statistical design and analysis of biological data. The ideal candidate would have experience analyzing RNAseq datasets, and some experience quantifying phenotypes with live organisms (not necessarily Daphnia). In addition, candidates should be comfortable working in a diverse collaborative environment, have excellent quantitative skills, strong written and verbal communication skills, along with an intellectual interest in the project.

The Dudycha lab has broad evolutionary interests: current projects range from evolutionary genomics of photosynthesis, to evolutionary ecology of vision, to ongoing work on life history, resource acquisition, and phenotypic plasticity. For more information, see the lab website at www.tangledbank.org

Interested individuals should contact Dr. Jeff Dudycha via email (dudycha [at] biol.sc.edu), attaching a single .pdf file that includes 1) a cover letter describing your qualifications for the position and research experience, 2) a C.V., 3) contact information for three references, and 4) a brief statement of your research interests and how they dovetail with our project. Informal inquiries

UVienna EcolEvolGenomics

UVienna.EcolEvolGenomics

A 6-year post-doctoral position is available at Department of Botany & Biodiversity Research, Faculty of Life Sciences, University of Vienna, to work on the ecological & evolutionary genomics of plant adaptation, speciation and species radiation with Christian Lexer and colleagues (https://evolgenomics.univie.ac.at/). We are looking for a person with experience in the use of current DNA / RNA sequencing approaches to address fundamental questions in population genetics, evolutionary biology and / or biogeography in plants. This includes a keen interest in integrative approaches towards understanding the origin, maintenance, and functioning of biological diversity.

University of Vienna offers an attractive and dynamic research location in a city with exceptional quality of life and in a country with excellent research infrastructure and funding provision.

Extent of Employment: 40 hours/week. Salary grading in accordance with relevant work experience.

Job Description: Participation in research projects in the group, including co-supervision / mentoring of PhD and MSc students V International publication and presentation activities V Contribution to high-quality external (third-party) research grant applications V Freedom to develop high-quality external (third-party) research grant applications as main applicant V Opportunity to participate in teaching topics of shared interest.

Profile: Doctoral degree in biology or equivalent field / Focus on molecular evolutionary biology or biogeography of plants - Experience in population genetics, evolutionary genomics, and/or evolutionary systems biology, especially the use of current DNA / RNA sequencing approaches and associated analytical tools - Excellent written and oral communication skills in English - Computer literacy, including experience with Unix / Linux based analysis software and R - Ability to work in teams

- Experience in teaching. Duration of the contract: 6 years.

To apply: Your application must include the following documents: motivation letter (<1 page)- Scientific CV - List of publications V Brief draft of research interests V Contact details of three references. Please see full job description and submit your application via the website of the Job Center at the University of Vienna (http:/-/jobcenter.univie.ac.at; email: jobcenter@univie.ac.at) no later than 16.06.2019, mentioning job reference no.

9678.

For more information please contact: Christian Lexer, christian.lexer@univie.ac.at

Christian Lexer Professor of Systematic and Evolutionary Botany Department of Botany and Biodiversity Research University of Vienna, Faculty of Life Sciences Rennweg 14, A-1030 Vienna, Austria Email: christian.lexer@univie.ac.at Tel: +41 (0)1 4277 541 40 https://evolgenomics.univie.ac.at/

WorkshopsCourses

Barcelona GeometricMorphometricsPhylogeny,Sep9-13

Dear colleagues,

Transmitting Science course "Geometric Morphometrics and Phylogeny" has open registration.

Dates: September 9th-13th, 2019, Barcelona.

Instructor: Dr. Chris Klingenberg (University of Manchester, United Kingdom)

Place: Capellades, Barcelona (Spain).

Registration and more info:

https://www.transmittingscience.org/courses/-geometric-morphometrics/geo metric-morphometrics-phylogeny/

PROGRAM: 1. Phylogeny, trees and phylogenetic reasoning. 2. Brief review of geometric morphometrics (Procrustes fit, PCA, etc.). 3. Mapping traits onto phylogenies: squared-change parsimony. 4. Practice: making/editing Nexus files, mapping morphometric data onto the tree (Mesquite, MorphoJ). 5. Phylogenetic signal, morphometric traits and estimating phylogeny. 6. Comparative methods: independent contrasts. 7. Application in morphometrics: evolutionary allometry and size correct ion. 8. Practice: comparative methods (MorphoJ). 9. Application of comparative methods: morphological integration. 10. Multi-level analyses of integration: inferring evolutionary mechanisms. 11. Application of comparative methods: partial least squares (ecomorphology, etc.). 12. Practice: comparative methods (cont.). 13. Morphometrics, phylogenies and qualitative characters. 14. Disparity and diversification. 15. Presentations of group work.

Please feel free to distribute this information between your colleagues if you consider it appropriate.

With best regards

Sole

Soledad De Esteban-Trivigno, PhD

Scientific Director

Transmitting Science

www.transmittingscience.org

Barcelona PhylogeneticAnalysis Oct14-18

Dear Colleagues,

Registration is open for the sixth edition of the course PHYLOGENETIC ANALYSIS USING R, October 14 th-18 th , 2019.

INSTRUCTORS: Dr. Emmanuel Paradis (Institut de Recherche pour le Développement, France) and Dr. Klaus Schliep (University of Massachusetts, USA).

More information: https://-www.transmittingscience.org/courses/evolution/-phylogenetic-analysis-using-r/ This course is for biologists dealing with the analysis of multiple molecular sequences at several levels: Populations, species, clades, communities. These biologists address questions relative to the evolutionary relationships among these sequences, as well as the evolutionary forces structuring biodiversity at different scales. The objectives are: (i) to learn the theoretical bases phylogenetic analysis, (ii) to know how to choose a strategy of molecular data analysis at the inter or intraspecific levels, (iii) to be able to initiate a phylogenetic analysis starting from the files of molecular sequences until the interpretation of the results and the graphics. The software used for this course will be centered on the R language for statistics. This will include the use of specialized packages particularly ape, phangorn, and adegenet.

PLACE: Capellades, Barcelona (Spain).

Organized by: Transmitting Science and the Research School in Biosystematics (ForBio).

Other Transmitting Science courses: https://-www.transmittingscience.org/courses/ With best regards

Sole

Soledad De Esteban-Trivigno, PhD Scientific Director Transmitting Science www.transmittingscience.org

Soledad De Esteban Trivigno <soledad.esteban@transmittingscience.org>

Berlin BioinformaticsWithBashAndPython Oct14-18

Course: Bioinformatics with Bash and Python

Where: Free University of Berlin (Germany)

When: 14-18 October 2019

Instructor: Dr. Martin Jones (founder, Python for biologists)

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.

PROGRAM

Monday 14th V Classes from 09:30 to 17:30

Session 1 V connecting to the server and basic Linux commands

Session 2 V assembling Linux commands into pipelines

Tuesday 15th V Classes from 09:30 to 17:30

Session 3 V introduction to bash scripting and variables

Session 4 V flow control in bash, aliases and paths

Wednesday 16th V Classes from 09:30 to 17:30

Session 5 V introduction to Python, text and files

Session 6 V lists and loops in Python

Thursday 17th V Classes from 09:30 to 17:30

Session 7 V conditions in Python

Session 8 V writing functions in Python

Friday 18th V Classes from 09:30 to 17:30

Session 9 V paired data and dicts in Python

Session 10

The afternoon of Friday 18th is reserved for finishing off the next-gen workflow exercise, working on your own datasets, or leaving early for travel.

For more information, please visit the course website: https://www.physalia-courses.org/courses-workshops/course1/ Here is the full list of our courses and Workshops: https://www.physalia-courses.org/courses-workshops

Should you have any questions, please feel free to contact us: info@physalia-courses.org

Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org http://www.physalia-courses.org/ Twitter: @physacourses mobile: +49 17645230846 https://groups.google.com/forum/-#!forum/physalia-courses "info@physalia-courses.org" <info@physalia-courses.org>

Berlin eDNAMetabarcoding Jul8-12

Dear all,

there are still a few places available on our 5-day course "Introduction to Environmental DNA research and analysis": [https://www.physalia-courses.org/-courses-workshops/course40/](https://www.physalia-courses.org/courses-workshops/course40/)

Where: Free University (FU) Berlin (Germany)

When: 8-12 July 2019

Registration deadline: 10th June 2019

Instructors:

1)Mathew Seymour (Bangor University, UK)

2) Luke E. Holman (University of Southampton, UK)

Overview: Here we offer an introduction into eDNA based science with key emphasis on how to design, implement and analyze 1) species specific (targeted) eDNA using qPCR and 2) community based analyses using metabarcoding and high throughput sequencing.

After completing the workshop, students should be in a position to (1) Design their own eDNA study based on their research needs (2) understand the principles of qPCR, including in-silico primer development and experimental setup (3) analyse high throughput sequencing eDNA metabarcoding data (4) Perform preliminary analyses of both qPCR and metabarcoding data and (5) Create publication quality figures.

Curriculum:

Monday

-Introductions and course overview

-Environmental DNA research and experimental design

-PRACTICAL:Getting started with UNIX

Tuesday

-Single species detection using qPCR

-qPCR primer selection and primer design

PRACTICAL: in silico qPCR primer design and selection

Wednesday

-Introducing eDNA metabarcoding, monitoring biological communities using high throughput sequencing (HTS).

-Metabarcoding primer selection, overview of different primers and targets.

-Overview of the lab work to construct Illumina libraries, concepts in sequencing.

PRACTICAL: Getting started with R, HTS data input and quality control.

Thursday

-Bioinformatic pipelines, operational taxonomic units (OTUs) clustering vs denoising

-Taxonomic assignment, sequence databases

PRACTICAL: Sequences to tables, clustering and denoising eDNA data to make biologically meaningful groups.

Friday

-Ecological analyses

-Ordination methods for eDNA metabarcoding data

-Linear and generalized linear models introduction

PRACTICAL: Preliminary statistical analysis of qPCR data and OTU tables using ordination and lm/glm in R, Generating plots in R.

Here is the full list of our courses and Workshops: [https://www.physalia-courses.org/courses-workshops/](https://www.physalia-courses.org/-courses-workshops/)

All the best,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org   http://www.physalia-courses.org/ Twitter: @physacourses mobile: +49 17645230846   https://groups.google.com/forum/-#!forum/physalia-courses "info@physalia-courses.org" <info@physalia-courses.org>

Berlin LandscapeGenomics Nov25-29

Dear all,

we will run the 3rd edition of our LANDSCAPE GENOMICS course in Berlin, from the 25th to the 29th of November 2019, at the Freie Universität (FU) Berlin.

INSTRUCTORS :

1) Dr. Stèphane Joost (Lab of Geographic Information Systems (LASIG), EPFL, Lausanne, Switzerland)

2) Oliver Selmoni, MSc (Lab of Geographic Information Systems (LASIG), EPFL, Lausanne, Switzerland)

Course overview

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, we 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. We will give an overview of the different statistical approaches to study local adaptation, and the participants 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. Fi-

nally, the course will consider the crucial aspects and good habits to account for when planning a landscape genomics experiment (e.g. sampling design).

Targeted Audience & Assumed Background

This course is aimed at all biologists, ecologists, geneticists, veterinarians that want to implement the landscape genomics approach in their own studies of evolutionary biology and conservation. Even though the course is not intended for a specialized audience, basic knowledge in evolutionary biology and population genetics would help. Students will learn how to use GIS, but basic computer skills are desirable (e.g. in the R environment). A basic understanding of statistics is also necessary.

Teaching Format

The course is organized in ten learning sessions. During the first two sessions, the course will provide a contextualization of the research field. Then, students will be guided through a landscape genomics experiment with sessions that couple brief theoretical introductions with practical work.

Please visit our website to have more information about the course content: https://www.physalia-courses.org/-courses-workshops/course17/   Here is the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

Please feel free to contact us if you need any further information.

Thanks!

Carlo

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Berlin Paleogenomics Jun17-21 LastCall

Dear all,

We have the last 5 places left on our aDNA Paleogenomics course!

When: 17th -21st of June 2019.

Where: Free University of Berlin (Germany).

Application deadline is: May 18th, 2019.

Instructors:

Dr. Claudio Ottoni (Sapienza University of Rome (Italy))

Dr. Amine Namouchi (University of Oslo (Norway))

Overview

This course will introduce biologists to the main bioinformatic tools for the analysis of Next Generation Sequencing (NGS) data from ancient samples. Through a series of theoretical and practical hands-on sessions, the main goal of this course is to provide a clear understanding of the most common bioinformatic methods adopted in a wide range of paleogenomics projects (from metagenomic screening of ancient samples, to NGS reads mapping and phylogenetic tree reconstruction). Particular attention will be given to quality control, DNA damage assessment and variants calling. A basic introduction to NGS platforms and the main file formats used in most common bioinformatics pipelines will be provided. Each day will consist of a mix of introductory lectures on the theoretical background of the programs that will be used, followed by hands-on exercises using command line tools performed by the participants under guided supervision.

Target Audience & ASSUMED BACKGROUND

The course is aimed primarily at researchers (MSc and PhD students, postdoctoral fellows, engineers) interested in learning the different steps from NGS raw data analysis to phylogenetic tree reconstruction in archaeological samples. The hands-on sessions are targeted to beginners and more advanced users alike. The practical sessions will cover the most common pipelines adopted in paleogenomics, and can be applied to a wide range of projects, from metagenomics to genome resequencing. Attendees should have a background in biology and some familiarity with genomic data.

STRUCTURE

The course material will be delivered over 5 days, in 10 half-day sessions. These lessons will build off of one another, and feature a mix of lecture and in-class exercises.

For more information about the course program, please visit our website: (https://www.physalia-courses.org/-courses-workshops/course27/)

Here is the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

All the best, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org   http://www.physalia-courses.org/ Twitter: @physacourses mobile: +49 15771084054   https://groups.google.com/forum/-#!forum/physalia-courses info@physalia-courses.org

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Berlin Selection Oct28-Nov1

Course: GENOME-WIDE SIGNATURES OF SELECTION AND ASSOCIATION STUDIES

Where: Free University of Berlin

When: 28 October -1 November 2019

General Topic: Genome-wide analysis of selection signatures and genotype-phenotype associations

INSTRUCTORS:

Dr. Pablo Orozco-terWengel (Cardiff University, Wales (UK))

(https://scholar.google.co.uk/citations?user=-urqxLJgAAAAJ&hl=en)

Dr. Filippo Biscarini (CNR, ITA)

(https://www.researchgate.net/profile/-Filippo_Biscarini)

Overview

This course will introduce students, researchers and professionals into the field of using genomics data to identify meaningful genomic regions. The course comprises two approaches: one based only on genomic information, which will use populations genetics techniques to detect signatures of selection (both natural and artificial); the other approach will combine genomic and phenotypic data to identify genetic associations for specific phenotypes (i.e. GWAS, genome-wide association studies).

Format

The course is structured in modules over five days. Each day will include an introductory lecture with class discussion of key concepts. The remainder of each day will consist of practical hands-on sessions. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete individual exercises. After and during each exercise, interpretation of results will be discussed as a group.

TARGETED AUDIENCE & ASSUMED BACKGROUND

The course is aimed at advanced students, researchers and professionals interested in learning how to make use of genomic information to study how selection has shaped the genome and how the genome influences measurable phenotypes. It will include information useful for both beginners and more advanced users. We will start by introducing general concepts of population genetics, which will take up most of the first half of the course; the second half of the course will be centered mainly on GWAS and related aspects.

Attendees should have a background in biology, specifically genetics. There will be a mix of lectures and hands-on practical exercises using R and the Linux command line, and bespoke software. Some basic understanding of R programming and the Linux environment will be advantageous. Attendees should have also some familiarity with genomic data such as those arising from NGS experiments, including genotyping-by-sequencing (GBS), and commercial genotyping platforms.

Please visit our website to have more information about the course content: (https://www.physalia-courses.org/courses-workshops/course36/curriculum-36/)

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>

Berlin SexChromosomes Sep20-22

Dear colleagues,

we hereby announce an international workshop, funded by the German Science Foundation (DFG) and supported by the Leibniz-Institute of Freshwater Ecology and Inland Fisheries (IGB), on sex chromosome evolution, to be held in Berlin, Germany, 20-22 Sept. 2019:

"Paradigm shift in sex chromosome evolution: Conceptual and empirical challenges from studies in vertebrates". Preliminary website: http://bit.ly/-IGBworkshopSep2019 Talks and discussions will be on Friday 20 and Saturday 21.

We encourage especially early career researchers to apply for participation; no attendance fees are required (but please organize transfer and stay by yourself)

We can offer up to 6 slots for talks by interested participants (max. 15 min talks + 5 min discussion); additional applicants can present posters.

If interested, please, send an email to: matthias.stoeck@igb-berlin.de Or: lukas.kratochvil@natur.cuni.cz

with information on career stage, few sentences on motivation and an abstract IF you would like to present a poster or a talk (till June 30 at the latest).

Confirmed invited speakers include: Mónica Bullejos Martín, Universidad de Jaén, Spain Blanche Capel, Duke University, USA Ben Evans, McMaster University, Canada Tony Gamble, Marquette University, USA Yann Guiguen, INRA, Rennes, France Amaury Herpin, INRA, Rennes, France Karel Janko, Czech Academy of Sciences, LibÄchov, Czech Republic Daniel L. Jeffries, University of Lausanne, Switzerland Martina Johnson Pokorná, Charles University, Prague, Czech Republic Werner Kloas, IGB, Germany Ikuo Miura, Hiroshima University, Japan Catherine Peichel, University of Bern, Switzerland Nicolas Perrin, University of Lausanne, Switzerland Michail Rovatsos, Charles University, Czech Republic Manfred Schartl, University of Würzburg, Germany (and Texas A&M University, USA) Vladimir Trifonov, Russian Academy of Sciences, Novosibirsk, Russia Nicole Valenzuela, Iowa State University, USA

We are grateful for distributing this announcement through relevant websites or sending it to interested colleagues.

Best, Matthias Stöck and Lukáŵ Kratochvíl

Matthias Stöck Leibniz-Institute of Freshwater Ecology and Inland Fisheries - IGB (Forschungsverbund Berlin) Müggelseedamm 301, D-12587 Berlin, Germany http://www.igb-berlin.de/ Tel.: ++49 (0) 30 64 181 629 Email: matthias.stoeck@igb-berlin.de Websites: http://matthiasstoeck.com http://matthiasstoeck.com/-publications/ Lukáŵ Kratochvíl Department of Ecology Charles University in Prague Faculty of Science ViniÄná 7, 128 43 Praha 2 www.natur.cuni.cz/enTel.: +420 221 95 1745 E-mail: lukas.kratochvil@natur.cuni.cz

Matthias Stoeck <matthias.stoeck@igb-berlin.de>

Crete IntroModelingR Oct14-18

Dear evoldir members,

Transmitting Science is offering the course 'INTRODUCTION TO GENERALIZED LINEAR MODELING AND MIXED MODELS USING R'.

Instructor: Dr. Dan Warren (Senckenberg Biodiversity and Climate Research Center, Germany) Dates: October 14th-18th, 2019 Location: Crete, Greece

COURSE OVERVIEW: This course will teach some basic skills to help students get the most out of the R statistical programming language and provide an accessible *introduction to generalized linear models, generalized additive models, and mixed models*. We will cover the *basic R skills* necessary to conduct most of the common analyses in the sciences, and then will focus on giving students a working understanding of *ANOVA, GLM, GAM, and GLMM*. The course is intended to give students a conceptual understanding of these methods, not just a set of recipes to follow.

By the end of this course, participants will understand: How to perform basic actions in R, like reading, writing, and manipulating data. How to design workflows for efficient and reproducible scientific computing. How to make attractive and informative colour graphics from R. The importance of likelihood in statistics. How regression works and what it means. How to choose the appropriate link function and why it is important. How to model fixed vs. random effects. How to construct, validate, and visualize complex models (GLM, GAM, GLMM).

*The course is intended primarily for participants who have some experience in R and wish to develop their

skills.*

PROGRAM: Monday, October 14th, 2019. - Introduction to R and RStudio - Basic R programming - Writing and reading scripts - What to do when things go wrong - Workflows for efficient and reproducible science

Tuesday, October 15th, 2019. - Plotting data and models - Viridis: making colour plots accessible to everyone - Likelihood - ANOVA - AIC and deviance

Wednesday, October 16th, 2019. - Simple linear regression - Multiple regression - Variance inflation factors - GLM V extending linear regression to different types of data - Model diagnostics for complex models

Thursday, October 17th, 2019. - Mixed models and applied mixed model exercises - Simulation

Friday, October 18th, 2019. - Generalized additive models (GAM and GAMM) - Wrap-up

For more information and registration: http://bit.ly/introduction-to-generalized-linear-modelling-and-mixed-models-using-R . Contact: courses.crete@transmittingscience.org

All the best, Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.org haris.saslis@transmittingscience.org

Haris Saslis <haris.saslis@gmail.com>

Crete PythonMachineLearning Oct07-11

Dear evoldir members,

Transmitting Science is offering the course 'PYTHON MACHINE LEARNING IN BIOLOGY'.

Instructor: Nichole Bennett (The University of Texas at Austin, USA) Dates: October 7th-11th, 2019 Location: Crete, Greece

COURSE OVERVIEW:

The field of biological sciences is becoming increasingly information-intensive and data-rich. For example, the growing availability of DNA sequence data or clinical measurements from humans promises a better understanding of the important questions in biology. However, the complexity and high-dimensionality of these biological data make it difficult to pull out mechanisms from the data. Machine Learning techniques promise to be useful tools for resolving such questions in biology be-

cause they provide a mathematical framework to analyze complex and vast biological data. In turn, the unique computational and mathematical challenges posed by biological data may ultimately advance the field of machine learning as well. This course will cover basics of the Python programming language as well as the pandas and sklearn Python libraries for data wrangling and machine learning. The course is intended to give participants a conceptual overview of machine learning algorithms and an intuition for the mathematics underlying them, equipping participants to be able to choose and implement appropriate models for biological datasets.

PROGRAM:

Monday, October 7th, 2019. Python Foundations Morning: Python Basics, Handling Data in Pandas, Basic Pandas Data Cleaning Afternoon: Exploratory Data Analysis in Pandas, Data Visualization in Python.

Tuesday, October 8th, 2019. Supervised Machine Learning: Classification Morning: KNN, Introduction to sklearn workflow. Afternoon: Train/Test Split, and Bias-Variance Tradeoff, Model Evaluation.

Wednesday, October 9th, 2019. Supervised Machine Learning: Classification Morning: Decision Trees and Random Forest Afternoon: Support Vector Machines

Thursday, October 10th, 2019. Unsupervised Machine Learning Morning: Clustering Methods (K Means Clustering) Afternoon: Advanced Clustering Methods Hierarchical Clustering, DBSCAN

Friday, October 11th, 2019. Special Topics Participants will have the option to learn a particular model or receive an introduction to Neural Networks theory and applications.

For more information and registration: http://bit.ly/python-machine-learning-in-biology Contact: courses.crete@transmittingscience.org

All the best, Haris Saslis, PhD Course Coordinator Transmitting Science www.transmittingscience.org haris.saslis@transmittingscience.org

Haris Saslis <haris.saslis@gmail.com>

Cyprus MetageneticsBiodiversity Oct2-8

Workshop: Analysis of metagenetic data for macroecology

Where: University of Cyprus, Nicosia, Cyprus

When: 2nd-8th October 2019

Fees: FREE for all participants

Apply now! Application deadline extension: 7th of June

www.metagenecol.eu   Workshop overview:

New sequencing methods are rapidly changing the analysis of biodiversity. Metagenetics of community, ingested or environmental samples generates high-resolution data on composition, diversity and evolutionary history in a fraction of the time of traditional methods. However, using the great flood of DNA data for macroecology requires new bioinformatics and statistical skills. This course will teach procedures for the bioinformatic processing of major types of genetic data for species composition and phylogeny. Statistical analysis of the resulting biodiversity data will then be explored for community analysis and patterns of diversity distribution. The course is unique in that it takes students from the basics of bioinformatics and data handling to advanced topics in the use of large-scale DNA data in evolutionary and ecological analysis. The course will comprise 5 days of guided practicals using real-world data, supplemented by short talks and thematic lectures. There will be open time for discussions around issues in metagenetics, with the particular aim of discussing participant queries and ideas.

Instructors:

The instructors are prominent evolutionary biologists and ecologists, who have developed many of the protocols and methodologies used in the analysis of metagenetic data for macroecology: Prof. Alfried P. Vogler (Imperial College London and the Natural History Museum,UK), Dr. Carola Gómez-Rodríguez (University of Santiago de Compostela, Spain) and Dr. Thomas J. Creedy (Natural History Museum, UK). The local workshop organizers are Dr. Anna Papadopoulou and Dr. Vasilis Promponas (University of Cyprus).

Workshop details:

There will be no fees for participants as the work-

shop is organized within the framework of the iBio-Gen project under the Horizon 2020 Twinning funding scheme (www.ibiogen.eu). Free coffee breaks and lunch during weekdays, as well as a free excursion on the weekend, will be offered to all participants. However, travel and accommodation costs should be covered by the participants themselves.

The course is aimed at graduate students and early-career researchers interested in applying novel DNA-based methods to macroecological questions. The course focuses on bioinformatic and analytical methods, and participants are expected to have a working knowledge of R for linear parametric statistics and basic community data analysis. Some prior experience with the linux command line is also preferred, although pre-course online study materials will be available to all attendees to ensure a common starting point. An understanding of phylogenetics would be useful to get the most of out of some sessions. For applications, please send a Curriculum Vitae and a short motivation letter to ibiogen.project@gmail.com by the 7th of June 2019.

More details can be found on the website:

www.metagenecol.eu   Anna   Papadopoulou
<a.papadopoulou05@alumni.imperial.ac.uk>

Glasgow AdvancedPython Jun10-14

PART-FUNDED SCHOLARSHIPS - Intro and Advanced Python for biologists

PR informatics through their funding scheme have 3 places on both their Intro and Advanced Python for biologists courses subsidized at almost 1/2 price to pounds 275 from pounds 525.00

June 10th ' 14th 2019 INTRODUCTION TO PYTHON FOR BIOLOGISTS (IPYB06) Glasgow, Scotland, Dr. Martin Jones http://www.prinformatics.com/course/-introduction-to-python-for-biologists-ipyb06/   and

June 17th ' 21st 2019 ADVANCED PYTHON FOR BIOLOGISTS (APYB03) Glasgow, Scotland, Dr. Martin Jones www.prinformatics.com/course/advanced-python-biologists-apyb03/   This courses will take place from June 10th ' 14th in

Applications   should   be   sent   to
oliverhooker@prinformatics.com
<oliverhooker@prstatistics.com>   and   contain   the
following.

1. Full name 2. Institute name 3. PhD subject title or Post doc research questions 4. Do you hold a funded position 5. 150 words why this course would be relevant to your research or how it would help.

Application deadline is Thursday 23rd May and decisions will be made by Friday 24th.

– Oliver Hooker PhD.

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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6 Hope Park Crescent Edinburgh EH8 9NA

+44 (0) 7966500340

Oliver Hooker <oliverhooker@prinformatics.com>

Glasgow AnalysingAdaptationUsingR Jul15-19

Analysing Environmental Adaptation Using Landscape Genomics in R (EDAP01)

https://www.prstatistics.com/course/adaptive-landscape-genomics-in-r-edap01/ This course will be delivered by Matt Fitzpatrack and Dr Aki Laruson form the 15th - 19th July in Glasgow City Centre.

Course Overview:

Local adaptation to climate and other environmental drivers increasingly is being studied at the molecular level using high-throughput sequencing methods, with applications spanning both model and non-model organisms. At the same time, statistical tools for modeling and mapping patterns of biodiversity have seen increasing application, including to the challenge of understanding the drivers of spatial variation in adaptive genomic variation and mapping these patterns under current and future climate. This 5-day course will provide the skill set necessary to analyze sequence data for signatures of natural selection and to apply spatial

modeling techniques to these patterns to quantify and map population-level genetic variation using two spatial modelling algorithms V Generalized Dissimilarity Modelling (GDM) and Gradient Forest (GF).

The course will include introductory lectures, instruction on using the Linux command line for manipulation of genomic data, guided computer coding in R, and exercises for the participants, with an emphasis on visualization and reproducible workflows. Portions of each day will be allotted for students to work through their own datasets with the instructors.

Course Programme Sunday 14th

Meet at the accommodation at approx. 17:00 onwards

Monday 15th V Classes from 09:00 to 17:00

Day 1 V Background and introduction

1) Introduction to approach

2) Data types (spatial, environmental, and genomic)

3) Considerations (quality control, SNP calling, filtering)

Tuesday 16th V Classes from 09:00 to 17:00

Day 2 V Natural Selection I

4) Introduction to the genomics of natural selection

5) Review of population genomic approaches to inferring selection

6) Implementing FST- and differentiation-outlier tests and interpreting results

Wednesday 17th V Classes from 09:00 to 17:00

Day 3 V Natural selection II

7) Principles of inferring selection from environmental association analyses

8) Review of landscape genomics approaches to inferring selection

9) Preparing SNP data from VCF and environmental data from rasters

10) Implementing multiple association methods (e.g., LFMM, RDA, etc.) and interpreting results

Thursday 18th V Classes from 09:00 to 17:00

Day 4 V Spatial Modeling I

11) Introduction to GDM and GF

12) Review of genetic and environmental data preparation

13) Interpreting model results

14) Model fitting / testing / validation / variable selec-

tion

Friday 19th V Classes from 09:00 to 16:30

Day 5 V Spatial Modeling II

15) Predictions & Applications of GDM / GF

16) Transforming environmental grids

17) Visualizing spatial variation in genetic composition

18) Calculating genetic differences between locations / times

19) Projecting patterns under climate change

Email oliverhooker@prstatistics.com

Check out our sister sites,

www.PRstatistics.com (Ecology and Life Sciences)

www.PRstatistics.com/consultancy (Statistical and bioinformatics consultancy in all fields)

www.PRinformatics.com (Bioinformatics and data science)

www.PSstatistics.com (Behaviour and cognition)

1. June 10th V 14th 2019

STABLE ISOTOPE MIXING MODELS USING SIAR, SIBER AND MIXSIAR (SIMM04)

Glasgow, Scotland, Dr. Andrew Parnell, Dr. Andrew Jackson

www.prstatistics.com/course/stable-isotope-mixing-models-using-r-simm04/   2.   June 10th V 14th 2019

INTRODUCTION TO PYTHON FOR BIOLOGISTS (IPYB06)

Glasgow, Scotland, Dr. Martin Jones

http://www.prinformatics.com/course/introduction-to-python-for-biologists-ipyb06/   3. June 17th V 21st 2019

ADVANCED PYTHON FOR BIOLOGISTS (APYB03)

Glasgow, Scotland, Dr. Martin Jones

www.prinformatics.com/course/advanced-python-biologists-apyb03/   4. June 24th V 28th 2019

MICROBIOME DATA ANALYSIS USING QIIME2 (MBQM01)

Glasgow, Scotland, Dr. Yoshiki Vazquez Baeza, Dr. Antonio Gonzalez Pena

https://www.prinformatics.com/course/microbiome-data-analysis-using-qiime2-mbqm01/   5. July 1st V 5th 2019

BIOACOUSTICS FOR ECOLOGISTS: HARDWARE,

SURVEY DESIGN AND DATA ANALYSIS (BIAC01)

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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

Gothenburg PhylogeneticAnalysis Aug22-25

Dear colleagues,

Registration is opened for the course PHYLOGENETIC ANALYSIS: FOUNDATIONS AND METHODS -1st edition'.Dates: August 22nd-25th, 2019.This course is organized and sponsored by the Willi Hennig Society, and only cost 100 .Instructors: Dr. Mark Siddall (American Museum of Natural History, USA), Dr. Sebastian Kvist (Royal Ontario Museum, Canada), Dr. Ward Wheeler (American Museum of Natural History, USA), Dr. James S. Farris (Gothenburg Botanical Garden, Sweden), Dr. Pablo A. Goloboff (Fundacin Miguel Lillo CONICET, Argentina), Dr. Kevin Nixon (Cornell University, USA)Place: Gothenburg Botanical Garden (Sweden)Registration and more information: https://www.transmittingscience.org/evolution/phylogenetic-analysis-foundations-and-methods (historical, operational, and probabilistic). Dr Kevin Nixon.Tree-searches (both standard and hard datasets). Dr Pablo Goloboff.Linnaeus, the codes and taxonomy. Dr Sebastian Kvist.Sequence alignment. Dr Ward Wheeler.Dr. Sebastian Kvist.Character weighting (with a little bit on ML models in morphology). Dr Pablo Goloboff.Measures of support. Dr Mark Siddall.Beyond the making of trees: correlated homoplasy, selection, and co-speciation. Dr Mark Siddall Dr Sebastian Kvist.Please feel free to distribute this information between your colleagues if you consider it appropriate.With best regards,SoleSoledad De Esteban-Trivigno, PhDScientific Director-Transmitting Sciencewww.transmittingscience.org soledad.esteban@transmittingscience.org

Italy PhylogenomicsPopGenomics Aug27-Sep1

Dears, we are pleased to announce the summer course:

"Bridging Phylogeny and Population genetics: Inferring divergence and selection at both interspecies and intraspecies level"

When: 27 August-1 September 2019.

Where:The Campus at Fondazione Edmund Mach in San Michele all'Adige (Trento, Italy between mountains and vineyards, http://www.fmach.it/eng), and the (world oldest) Botanical Garden of University of Padua (http://www.ortobotanicopd.it/en).

What: Phylogeny studies inter-specific variations and typically describes the macroveolutionary changes of organisms over long time scales; population genetics instead typically focuses on the intra-species variability and describes microevolutionary changes occurred during the relatively recent history of a population. The two disciplines are characterised by different tools and methods, and too often phylogeneticists do not understand what population geneticists do, and vice versa. With this course we aim at stimulating a dialogue and a constructive discussion between students and teachers with phylogenetics, population genetics, but also ecological backgrounds, in such a way that we can appreciate the complementary nature of these disciplines. All students should be united by the will to understand better each other's methodological processes. The aim is to form students that are capable of understanding both approaches and filling the gap between the two disciplines. We will do this by providing the theoretical and practical bases of both phylogenetics and population genetics. The course will cover some important applications such as genome scaled detection of positive selection using PAML, site frequency spectrum analysis using Sweepfinder, inference of divergence time using BEAST, inference of population past demography using Fastsimcoal. Every day we will alternate topics on PHYLOgenetics, POPulation genetics, and a MIXture of them.

Teachers: Lino Ometto (evolutionary zoologist, University of Pavia) Emiliano Trucchi (population geneticist, Marche Polytechnic University and University of Oslo) Omar Rota-Stabelli (molecular phylogeneticist, Fondazione Edmund Mach) Francesca Cagnacci (Movement Ecologist, Fondazione Edmund Mach) Daniele Silvestro (molecular phylogeneticist, University of Gothenburg) Erlend Nilsen (population ecologist, NINA- Norway)

Participation: This course is aimed at PhD students, but participation of post-docs, researchers, managers and motivated MSc is also encouraged. There will be room for a maximum of 25 participants, with priority given to students from the IRSAE network and the SIBE society.

Fees and costs: The course is supported by the International Research School in Applied Ecology (IRSAE www.irsae.no), and co-organized by Fondazione Edmund Mach, NINA, and the Italian Society for Evolutionary Biology. Fees and costs vary according to affiliations. IRSAE participants: Fees, board and lodging are covered by the IRSAE network; they may also obtain reimbursement for travel costs through IRSAE and their institution. SIBE members pay no fees. Otherwise, students: 130€; Researchers/Seniors: 250€. In all cases food (lunch+dinner) plus lodging in the campus can be booked at 80 €/day. Alternative lodging possibilities are available in the area.

5 ECTS credits will be assigned, after positive grades in a final exam.

Format: This 5 days course consists of a meet and greet evening + three full days with technical seminars and practical labs + one day of excursion to nearby hut with symposium and lectures + a trip to Padua (2h bus drive, organised by the school) with final lectures. For those interested is possible to extend the staying in Padova to attend the congress of the Italian Society for Evolutionary Biology https://sibe2019.sibe-iseb.it/; the first day of the congress is free for students; to attend full meeting registration is required.

Registration: Please send an Email (with subject: PhyloPopSchool2019), containing a brief description of your PhD project and a description of the relevance of the course to your research, along with your CV, to Omar Rota Stabelli (omar.rota@fmach.it), cced to Henriette Gelink (henriette.gelink@inn.no). Deadline: 25th June, 2019. Notification of acceptance: 28th June, 2019. More and upcoming info/material on: http://irsae.no/-courses-conferences-and-workshops/upcoming-courses Program:

Tue 27th August Pm: Arrival & Meet and Greed pm: MIX Why merging phylogeneticists and population geneticists? (all teachers)

Wed 28th August am: PHYLO Introduction to Phylogeny for population geneticists + Hands-on (Rota-Stabelli) pm: POP Introduction to Population genetics for phylogeneticists +

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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>

LavalU Quebec SpeciationGenomics Sep2-6

Dear all,

Physalia-courses in collaboration with Laval University (Québec, Canada) is organizing two courses (1 - Speciation Genomics; 2- Introduction to GWAS) in Canada this September.

The first one is on Speciation Genomics!

Where: Institut de Biologie Intégrative et des Systèmes (IBIS), Université Laval Québec (Québec) , Canada

When: 2-6 September

Instructors: 1 - Dr. Mark Ravinet (University of Oslo; Norway) 2- Dr. Joana I. Meier (University of Cambridge, UK).

Overview: This course will provide a thorough introduction to the growing field of speciation genomics. The course aims to take students from the initial steps required for handling raw sequencing data to demographic modelling and inference of genome-wide signatures of selection and introgression. Through a combination of lectures covering key theoretical and conceptual topics, alongside hands-on exercises, participants will learn the most important computational approaches used in speciation genomics. This will include a heavy emphasis on data visualization and intepretation. After completing of the course, the participants should be able to begin using NGS data to shed light on the genomic aspects of speciation in their study system of choice.

For more information, please visit our website: (https://www.physalia-courses.org/courses-workshops/-course37/)

Here is the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

Please feel free to contact us if you need any further information.

Thanks!

Carlo

LodzU Poland MolecularPhylogenies Jul15-18

Dear all,

we are happy to inform you that Physalia-courses in collaboration with the University of Lodz (Poland) is organizing a course on "DNA-sequence data and phylogenies in biodiversity" which will take place in Poland from the 15th to the 18th of July.

Instructor: Dr. Diego Fontaneto (National Research Council, Institute of Ecosystem Study (ITALY))

Overview: This course will introduce scientists interested in biodiversity to the use of DNA-sequence data to address questions that cannot be addressed by using only morphological and ecological data in their studies. After a short introduction on how to obtain DNA sequences and reliable molecular phylogenies, the focus of the questions that could be addressed will be on taxonomy, community ecology, and comparative methods.

For more information, please visit our website: https://www.physalia-courses.org/courses-workshops/-course28/ Here is the full list of our courses and Workshops: (https://www.physalia-courses.org/-courses-workshops/)

Please feel free to contact us if you need any further information.

Thanks!

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>

Modica BioinformaticsForNGS Jul22-26 EarlyBirds

Dear all,

the early-birds option is now available for the course "Bioinformatics for Next-Generation Sequencing" with the deadline set on the 30th of May. More info at https://www.hybleatraining.com/course/-bioinformatics-for-next-generation-sequencing/ Where: Modica, Sicily, Italy What: Bioinformatics for Next-Generation Sequencing When: 22-26 July 2019

OUTLINE: Next-Generation Sequencing (NGS) has become an essential tool in genetic and genomic analysis. It is increasingly important for experimental scientists to gain the bioinformatics skills required to assess and analyze the large volumes of sequencing data produced by next-generation sequencers.

Advantages and disadvantages of current sequencing technologies and their implications on data analysis will be discovered.

This course will provide an introduction to the technology, analysis workflows, tools, and resources for Next-Generation Sequencing data analysis. The content will provide insights into how biological knowledge can be derived from genomics experiments and explain different approaches to analyzing such data.

THEMES: -NGS ABCs -R-python workflow -data visualization -from code to interpretation

CALENDAR: Day 1 - Linux for Bioinformatics:

-Introduction to the command line and important commands -Combining commands by piping and redirection -Introduction to R and Python -Introduction to bioinformatics file formats and databases -Usage of important bioinformatics toolkits

Day 2 - Introduction to NGS data analysis:

-Raw sequence files (FASTQ format) -Preprocessing of raw reads: quality control V adapter clipping V quality trimming -Introduction to read mapping -Read mapping (Bowtie V BWA V STAR)

Day 3 - Introduction to NGS data analysis :

-Mapping output (SAM/BAM format) -Usage of NGS toolkit (samtools V BEDtools V Picard tools) -Mapping Statistics -Visualization of mapped read

Day 4 - Variant Calling V RNASeq Data Analysis:

-DNA variant calling methods and tools -Variant Call File Format -Filtering and annotation of genetic variants -Split-read mapping -Tuxedo suite -Statistics behind DESeq2 V EdgeR -Quantify exons/genes/transcripts - Predict differential splicing -Differential gene expression using DESeq2 / EdgeR -Differential isoform expression using cuffdiff -Create graphics using R

Day 5 - ChIP-Seq V Metagenomics:

-ChIP-Seq: -Experimental design -Mapping software -Peak calling -Analysis of enriched area -Viewing ChIP-Seq data in genome browsers -Metagenomics: -Overview of existing methods for metagenomics data analysis -Run QC: run assessment -Read QC: metrics for read quality evaluation -Preprocessing of raw data -Mapping reads to a reference database -Examination of the community composition (taxonomic and functional) -Evaluation of the community saturation and diversity

INSTRUCTOR: Giorgio Giurato, Ph.D. University of Salerno, Italy, Senior Bioinformatician Genomix4life - Co-founder

For more info regarding the course, please visit: https:/-/www.hybleatraining.com/course/bioinformatics-for-next-generation-sequencing/ or get in touch with us at: info@hybleatraining.com

Best regards, Pierluigi - - - HYBLEA TRAINING Co-founders: Pierluigi Colangeli, PhD Silvia Lechthaler, PhD

pierluigi colangeli <pierluigi.colangeli@gmail.com>

Modica ImageJforBiologists Oct22-24

Where: Modica, Sicily, Italy What: ImageJ for Biologists When: 22-24 October 2019

LINK: https://www.hybleatraining.com/course/imagej-for-biologists/ OUTLINE: Counting and measuring particles like cells and individuals from a population is a time-consuming process which is a necessary step in several research fields. Automatization can increase accuracy and reduce the time spent on such a process. The open-source software ImageJ is a powerful tool for image, images stacks, time-lapse and video analysis. This course will serve as an introduction to image analysis workflows, spanning from basic particle counting (e.g. algae cells counts, measurements of plant anatomical

sections, etc) to custom macro design. After the course, the student will be able to integrate image analysis in his experimental routine.

THEMES: -Image analysis basics -Particle analysis -Data import in R -Data visualization with ggplot -Random forest classification

CALENDAR: Day 1 - Intro to ImageJ:

Image acquisition tips and tricks Import images in ImageJ Introduction to the available commands Particle analysis Morphological descriptors

Day 2 - ImageJ customization:

Macro language and design Available plugins Intro to video analysis Intro to particle tracking

Day 3 - From ImageJ to R:

Intro to R software Data visualization with ggplot Plot animation with gganimate Machine learning tools (random forest classification)

NOTES: A notebook is required. The installation of ImageJ and R is suggested.

INSTRUCTORS: Pierluigi Colangeli, Ph.D. Silvia Lechthaler, Ph.D. Co-founders of Hyblea Training

REGISTRATION DEADLINE: 30 SEPT 2019 EARLY-BIRDS DEADLINE: 1 AUG 2019

For more info regarding the course, please visit: https://www.hybleatraining.com/course/imagej-for-biologists/ or get in touch with us at: info@hybleatraining.com

Best regards, Pierluigi - - - HYBLEA TRAINING Co-founders: Pierluigi Colangeli, PhD Silvia Lechthaler, PhD

pierluigi colangeli <pierluigi.colangeli@gmail.com>

Modica VideoAnalysisInvertebrates-Movement Jun24-28 Deadline

Dear all,

The deadline to the course: "Video Analysis of Invertebrates' Movement" is approaching (5 June 2019). Please find more info at https://www.hybleatraining.com/course/video-analysis-of-invertebrates-movement/ Where: Modica, Sicily, Italy What: Video analysis of invertebrates movement When: 24-28 June 2019

OUTLINE: In this course, you will learn how to analyse the movement and behavior of invertebrates from videos. The aim is to offer you a new, open-source, analytical tool to study causes and consequences of movement in small organisms, ranging from insect to zooplankton. The course will cover all the salient aspects of video analysis, starting with basic and advanced video filming techniques (data acquisition), experimental design, and analytical pipelines for testing movement and behavior under different environmental conditions, and at population and community level. Original data will be collected and analysed, plus an original dataset (https://www.doi.org/10.4228/ZALF.DK.92) will be explored during the course.

THEMES: - filming techniques and video setup - experimental design - data extraction with R and ImageJ (BEMOVI package) - data cleaning and visualization - statistical methods of movement analysis

PROGRAM:

Day 1 - Movement ecology and behavior:

Observing behavior in small organisms Filming techniques Introduction to R, ImageJ & ffmpeg Introduction to video file formats and databases Movement and morphology descriptors

Day 2 - Data acquisition:

Experimental design Filming techniques (bright light, dark fieldK) Find best signal-to-noise ratio Trigger dramatic responses

Day 3 - Introduction to BEMOVI:

Video files batch conversion Contrast, exposure, gamma, saturation Folder structure and data input/output The BEMOVI pipeline Error filtering V trajectory clean-up

Day 4 - Data visualization:

Static vs. dynamic graphics Basic and advanced trajectories visualization Base R and ggplot Graph animation (gganimate) GIF output for data presentation

Day 5 - From code to interpretation:

Statistics for movement data Movement parameters (speed, turning anglesK) HMM models (state-space models) Fit a distribution

AUDIENCE: Biologists, zoologists, behavioral and movement ecologists, ecotoxicologists. Researchers that want to implement the study of behavior and movement in their experiments. Ideally, the attendee should have basic knowledge of R and ImageJ, however, the inexperienced users will be able to run the pipeline successfully. PLEASE, BRING YOUR LAPTOP.

INSTRUCTOR: Pierluigi Colangeli, PhD Hyblea Training co-founder

For more info regarding the course, please visit: https://www.hybleatraining.com/course/video-analysis-of-invertebrates-movement/ or get in touch with us at: info@hybleatraining.com

Best regards,

Pierluigi - - - HYBLEA TRAINING Co-founders: Pierluigi Colangeli, PhD Silvia Lechthaler, PhD

pierluigi colangeli <pierluigi.colangeli@gmail.com>

Montana PopulationGenomics Sep2-6

Genomics Data Analysis Course and Workshop: "ConGen-2019"

Theme: Applications of Next Gen Sequencing Data to Understand Population Structure, Adaptive Evolution, and Environmental Influences on Genomic Variation.

Instructors include: Fred Allendorf, Eric Anderson, Chris Funk, Brian Hand, Marty Kardos, Brenna Forester, Tabatha Graves, Joanna Kelley, Gordon Luikart, Mike Miller, Rena Schweizer, Robin Waples, and more TBA.

When: September 2-6, 2019

Where: Flathead Lake Biological Station, Polson, Montana

For details on ConGen-2019: see http://www.umt.edu/sell/cps/congen2019/ Travel support: The first 25 students or postdocs accepted to participate will receive a $400-$600 travel support scholarship

ConGen 2013 dinner by the lake ConGen 2018 view from Biostation

Course Objective: To provide training in conceptual and practical aspects of data analysis for understanding the population and evolutionary genomics of natural and managed populations. Emphasis will be on next generation sequence data analysis (RADs, whole genome sequence analyses, RNAseq) and interpretation of output from recent novel statistical approaches and software programs. The course include discussions among early career researchers (student participants) and >12 leaders in population genomics (instructors) to help develop our next generation of conservation and evolutionary geneticists.

Who should apply: Advanced Undergrads, M.S. &

Ph.D. students, post-docs, faculty, agency researchers, and population biologists that have taken at least one semester university-level course in population genetics and a course in population ecology. Participation will be limited to ~30 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own NGS data to analyze.

Past courses: see Andrews & Luikart 2014, http://onlinelibrary.wiley.com/doi/10.1111/mec.12686/abstract . and

Benestan et al. 2016: http://onlinelibrary.wiley.com/doi/10.1111/mec.13647/full; Cost: Early Bird (before June 15th): $US 1,650 - which includes all lodging, meals, many coffee breaks, transportation (to/from airport), a short field or lake/boat trip, worksheets, dummy data sets, PowerPoint slides, audio-visual recordings of lectures. USD $1,790 if payment after June 12th.

gordon.luikart@mso.umt.edu

ProvidenceRI AnalysisOfIntegratedTraits Jun26

** REGISTRATION DEADLINE approaching soon: May 15, 2019**

Short Course at Evolution 2019: Phylogenetic comparative analysis of integrated anatomical traits

* Where: Providence, RI * When: June 26, 2019 (Wednesday), 9 am-12 pm * Program: https://scate.phenoscape.org/2019-workshop-cfp.html
* Free Registration: https://goo.gl/forms/802KN6cd6cQOI01Q2 COURSE OVERVIEW: Ontologies encode information about a domain of knowledge, such as how anatomical structures are related, which is crucial information for modeling character evolution. Phenoscape, in its current Semantic Comparative Analyses for Trait Evolution (SCATE; http://scate.phenoscape.org) project, is developing tools that use the computable knowledge in ontologies to improve phenotypic character modeling and inform analyses of trait evolution. To train evolutionary biologists and developers of comparative analysis tools to adopt these new capabilities, the SCATE team will be holding a short course on using ontologies in comparative analyses of integrated anatomical traits, in conjunction with iEvoBio and the Evolution Meetings, on June 26, 2019 in Providence, Rhode Island.

Attendees will learn how to use R packages such as RPhenoscape (http://rphenoscape.phenoscape.org) to access a knowledgebase of ontology-linked phenotypes (kb.phenoscape.org), build character matrices that take anatomical dependencies into account, and use these to construct stochastic character maps on a phylogeny. The course will also include a practical introduction to community ontologies for biodiversity domain knowledge (anatomy, taxonomy, phenotypic attribute).

Graduate students, postdocs, faculty, and software developers with interests in comparative analyses, morphology, and phylogenetics are encouraged to apply.

Free registration: Applications accepted until May 15th or capacity is reached. Register by filling out the form at https://goo.gl/forms/802KN6cd6cQOI01Q2 Wasila.Dahdul@usd.edu

SouthAfrica MosquitoTickIdentification Oct13-19

Mosquito identification course What to expect This course will follow a holistic approach, addressing general aspects of mosquito biology and ecology, leading onto the main focus of morphological mosquito identification, and field collecting methods, providing an introduction to mosquito survey methodology as well as practical exposure to several techniques in a unique wildlife/livestock/human interface.

Facilitators The course will be led by Prof. APG de Almeida, an internationally recognised mosquito taxonomist with a special interest in Afrotropical mosquitoes

Participants The course is open to all local or international biologists, veterinary technologists and veterinarians.

Dates Participants should arrive at Hoedspruit airport or Hans Hoheisen (Orpen, Kruger National Park) on Sunday the 13th of October and will depart on Saturday the 19th of October.

Tick identification course: What to expect The Ivan Horak tick identification course will provide participants an insight into the identification, biology, ecology and collection of the medically/veterinary important tick species. During the course, 42 species (38 Ixodidae, 4 Argasidae), considered to be major vectors of disease, will be covered in detail. Additionally, a fieldwork component in a unique wildlife/livestock/human interface

will cover current collection methodologies that can be used for the planning and execution of tick surveillance projects

Facilitators The course will be led by three internationally recognised tick experts, Dr. Maxime Madder, Prof. Luis Neves and Dr. Hein Stoltsz.

Participants The course is open to all local or international biologists, veterinary technologists and veterinarians.

Dates The duration of the course is five days to be held in the latter half of October 2019. Fixed dates will at the latest be communicated by end May 2019.

Venues The courses will be held at the laboratories of Hans Hoheisen Wildlife Research Station (HHWRS) with fieldwork in the surrounding wildlife/livestock/human interface areas.

Transport Participants will be responsible to arrange their own transport to the venue or to Hoedspruit Airport where transfer to the venue will be provided.

Course fee R 9500.00 (ZAR) per course. Fees include airport transfer, fieldwork transport (mini-bus), accommodation, and meals for the duration of the course

Application procedure Please send an email to lokisnyman@gmail.com expressing your interest in the course, your title and full names, your institution details, your research/employment field of interest and if you have funding available to attend the course. The application submission deadline is Friday 27 September, 2019.

Alternatively, follow the following links and complete the form

Mosquito Identification Course < https://forms.gle/-o7hYsYeWBWEvroBL8 > Ivan Horak Tick Identification Course

Regards *Louwtjie Snyman (PhD)* Post-doctoral fellow Vector and Vector-Borne Diseases Research Programme Department of Veterinary Tropical Diseases Faculty of Veterinary Sciences University of Pretoria Paraclinical Building Room 2-50

Cell: +2782 344 4389 Email: lokisnyman@gmail.com *Physical Address*: Room 2-50, Paraclinical building, Soutpan road, Onderstepoort, 0110

Louwtjie Snyman <lokisnyman@gmail.com>

SummerInstStatGenetics EarlyBirdDeadline ExtendedJun10

The early bird deadline for the 24th Summer Institute in Statistical Genetics has been extended to June 10, but some modules are nearing capacity.

Register at www.biostat.washington.edu/suminst/sisg to learn about current methods for interpreting modern genetic and genomic data, in the beautiful summertime Pacific Northwest.

Hope to see you here,

Bruce bsweir@uw.edu

Bruce S Weir <bsweir@uw.edu>

UCalifornia Davis NGSAnalysis Jul1-13

Hello everyone,

We're excited to announce our 10th consecutive workshop on analyzing sequencing data, ANGUS 2019!

Please see http://ivory.idyll.org/dibsi/ANGUS.html, or below, for all the details

July 1 - July 13, 2019 University of California, Davis, USA

This workshop is organized and hosted by Dr. C. Titus Brown and Dr. Karen Word. Please contact us at dibsi.training@gmail.com.

This intensive two week summer course introduces attendees with a strong biology background to the practice of analyzing big shotgun sequencing data sets (Illumina, PacBio, and Nanopore). We introduce students to computational thinking and large-scale data analysis on UNIX platforms, and cover genome and transcriptome analysis. We also cover computational topics including R scripting, software installation with bioconda, cloud computing, and building efficient and automated workflows. We use hands-on tutorials, live coding, group notes, and in-class exercises to support an effective learning experience.

Lead instructors for 2019:

* Mike Lee - https://twitter.com/astrobiomike * Rocio Martinez-Nunez - https://twitter.com/rociotmartinez * Sateesh Peri - https://twitter.com/perisateesh * Taylor Reiter - https://twitter.com/ReiterTaylor * Chissa Rivaldi - https://twitter.com/Powerofcheez * Marian Schmidt - https://twitter.com/micro_marian **Confirmed lecturers for 2019:**

* Meg Staton, https://ag.tennessee.edu/EPP/-Pages/Dr.MegStaton.aspx * Erich Schwarz, https://scholar.google.com/citations?hl=en&user=-VllBDvcAAAAJ&view_op=list_works&sortby=pubdate Registration is now open until June 1! https://-/registration.genomecenter.ucdavis.edu/events/-2019_angus/register/ Please also see the Frequently Asked Questions for 2019 at https://hackmd.io/s/-BkjZDqNNV **No prior programming experience is required**, although bravery in the face of the unknown is necessary! A year or more of graduate school in a biological science is strongly suggested. Faculty, postdocs, and research staff are more than welcome, as are researchers from industry.

The 2019 schedule is up! http://ivory.idyll.org/dibsi/-SCHEDULE.html We plan to run multiple independent classrooms of 20-30 participants each. Each classroom will have 2 lead instructors and 3-4 TAs and helpers. In 2019, we will provide both introductory and intermediate tracks to accomodate all levels of learners.

We strive to provide a welcoming and inclusive environment, and work hard to accommodate learner needs. This course supports and encourages diversity by creating an environment in which people can communicate effectively and share their unique talents. This diversity of talents enriches the course by fuelling creativity, innovation, and success!

What will I learn if I attend?

Our goal for these two weeks is to get students to the point where they are ready to begin analyzing their own data on a computer cluster, and are more comfortable with help forums and other online resources to be able to continue advancing their own skills.

Students will gain practical experience in:

- bash shell and R scripting - Cloud computing/Jetstream - Installing and running many bioinformatics tools (e.g.BLAST, bwa, samtools) - Querying mappings and evaluating assemblies - Running workflows in the cloud and evaluating their results - Estimating computational resources

Materials from previous courses are available at http://-angus.readthedocs.org/ under a Creative Commons/full use+reuse license.

You can read a blog post about the 2015 course here: http://ivory.idyll.org/blog/2015-small-batch.html The course fee will be $950 for this workshop. On-campus housing for the two weeks of the ANGUS course is $1005; housing includes breakfast and dinner, but not lunch.

What do people say about this workshop?

Quotes from previous attendees:

'I would climb a mountain and share this awesome program with the rest of the world.'

'We had great teachers and helpers. They made me feel comfortable in making mistakes and learn from them.'

'You don't have to be a programmer to use or do computational science, and that is awesome¡'

— / —

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

UCopenhagen
AncientDNAHumanHistory Aug5-9

Course Description: Ancient DNA has revolutionized the field of archaeology over the past few years by providing unprecedented insights into past population movements, admixture events with other hominins - like Neanderthals - and adaptation to particular environments. This revolution is tightly linked with the introduction of high-throughput DNA sequencing technologies and the rise of 'big data'. This intensive one-week course will provide students with a broad introduction to the varied uses of ancient DNA in archaeology and hands-on experience working with high-throughput sequencing datasets. The course is composed of a series of lectures, covering a wide range of topics and hands-on computing practicals, and is primarily aimed at students in biology, archaeology, linguistics, and related fields who would like to learn more about ancient DNA applications in the post-genome era.

Where: University of Copenhagen

When: August 5th-9th, 2019

ECTS credits: 5.0

Formal requirements: Applicants should have a first degree in archaeology, biology, linguistics or a related field.

Teaching and learning methods: Lectures, computing practicals, and seminars based around paper discussions.

Please refer to external course website and schedule: www.archaeomics.ku.dk Contact people: Hannes Schroeder <hschroeder@snm.ku.dk> Fernando Racimo <fracimo@bio.ku.dk>

Fernando Racimo <fernandoracimo@gmail.com>

UEastAnglia NorwichUK
SLiMEvolutionaryModeling Sep9-13

Hi all.

First of all, as background: SLiM is a software package for creating evolutionary models/simulations that are individual-based and genetically explicit. It is scriptable, flexible, fast, and includes an interactive graphical modeling environment. You can read more about it on its home page (https://messerlab.org/slim/).

September 9-13, 2019, a five-day workshop will be offered at UEA, the University of East Anglia (Norwich, UK). It will be hosted by Simone Immler, of UEA. It will be free, and open to participants outside of the university. HOWEVER, registration is required, a limited number of seats are available, and priority will be given to registrants affiliated with UEA. To apply, please send an email to both of us (S.Immler@uea.ac.uk, bhaller@mac.com) with the info below. The deadline for applying is the end of the day on 1 August.

For this workshop, your application email should include: (1) your name, (2) your university or institutional affiliation, (3) a link to a research website or similar academic page, if you have one, (4) a 1-2 sentence description of your level of experience with SLiM and any other forward genetic simulation software, if any, (5) a 1-2 sentence summary of why you want to attend the workshop (i.e., the connection to your research), and (6) 1-2 sentences about any specific topics within SLiM that you hope to learn about in the workshop. Note that you will be responsible for your own lodging and your own transportation. Please do not apply to the workshop unless you are sufficiently serious that you will actually attend, if accepted. Note that acceptance will likely be first-come-first-served (apart from the priority for those from the hosting institution), so early application is advised.

The plan is to try to cover all the major topics in the SLiM manual, starting with lots of introductory material

to get beginners up to speed with SLiM and its associated scripting language Eidos, and hopefully ending up at advanced topics like non-Wright-Fisher models, tree-sequence recording, continuous-space models, and nucleotide-based models. We won't cover everything in the manual - that would be overwhelming! - but we'll try to cover all the big topics. There will also be time for attendees to work on their own models with help from me, and we may also have time to explore some optional side topics that are of particular interest to those attending each workshop. The workshops will be taught principally using SLiMgui on macOS. For this workshop, ATTENDEES MUST BRING THEIR OWN MAC LAPTOP. (A Mac is required to run SLiMgui, which is necessary for teaching purposes.)

I'm hoping to continue doing workshops in future; if you would like to invite me to give a workshop at your institution, please send me an email (off-list).

Cheers,

Benjamin C. Haller Messer Lab Cornell University

bhaller@mac.com

UK MicrobiomeDataAnalysisUs-ingQIIME2
Jun24-28

Microbiome Data Analysis Using QIIME2 (MBQM01)

https://www.prinformatics.com/course/microbiome-data-analysis-using-qiime2-mbqm01/ This course will be delivered by Dr. Yoshiki Vazquez Baeza and Dr. Antonio Gonzalez Pena from the 24th - 28th June in Glasgow City Centre.

Course Overview: This course will provide a theoretical, analytical and practical introduction to QIIME 2 (canonically pronounced ¥chime two), which stands for Quantitative Insights into Microbial Ecology 2, and Qiita (canonically pronounced ¥cheetah), a multiomics and multi-study online tool. QIIME 2 and Qiita are open source software packages for comparison and analysis of microbial communities, primarily based on high-throughput amplicon sequencing data (such as SSU rRNA) generated on a variety of platforms, but also supporting analysis of other types of data (such as shotgun metagenomic, metabolomics or proteomics). The main Qiita deployment (http://qiita.microbio.me/) allows users to manage and analyze large studies, their metadata and the multiple data types generated from the

same samples. Additionally, it allows users to combine their samples with other published and public studies available in the system. QIIME 2 is a stand-alone environment for the analysis of individual microbiome data sets that can be used on your laptop, university computational resources, and cloud computing resources.

Course objectives: By the end of the course, participants will be able to: 1) Understand the most recent QIIME2 and Qiita features for microbial community analysis 2) Select the best workflow and parameters to perform the different steps for microbial community analysis 3) Understand and apply on their own datasets different phylogenetic and non-phylogenetic metrics to compare microbial diversity samples 4) Upload and analyze their own datasets using Qiita and compare their studies with other public studies

Course Programme Monday 24th V Classes from 09:30 to 17:30 Module 1: Introduction to the microbiome. Module 2 (optional): Refresher of the command line interface and UNIX-like systems. Module 3: Bioinformatics challenges in the microbiome. Module 4: Introduction and search for public studies via Qiita.

Tuesday 25th V Classes from 09:30 to 17:30 Module 1: Connecting to workshop server and CLI Refresher. Module 2: QIIME 2 concepts (artifacts, visualizations, methods, plugins, interfaces, etc). Module 3: Sample, sequence, and phylogeny processing. Module 4: Importing and exporting data in QIIME 2.

Wednesday 26th V Classes from 09:30 to 17.30 Module 1: Diversity analyses (alpha diversity). Module 2: Diversity analyses (beta diversity). Module 3: Taxonomic classification for target gene data.

Thursday 27th V Classes from 09:30 to 17:30 Module 1: Differential abundance testing. Module 2: Meta-analyses using Qiita. Module 3: Creating a study in Qiita. Module 4: Searching for sequences and environments using redbiom.

Friday 28th V Classes from 09:30 to 16:00 Module 1: Compare the commands and tools we reviewed in the workshop with recent papers. Module 2: Review other Qiime2 plugins available and tools: PICRUSt, 'ili, time series analysis, etc. Module 3: The Python API for QIIME2. Module 4: Open science considerations before and after publication.

email oliverhooker@prinformatics.com

Check out our sister sites! www.PRstatistics.com (Ecology and Life Sciences) www.PRinformatics.com (Bioinformatics and data science) www.PSstatistics.com (Behaviour and cognition)

1. June 10th V 14th 2019

STABLE ISOTOPE MIXING MODELS USING SIAR, SIBER AND MIXSIAR (SIMM04)

Glasgow, Scotland, Dr. Andrew Parnell, Dr. Andrew Jackson

www.prstatistics.com/course/stable-isotope-mixing-models-using-r-simm04/ 2. June 10th V 14th 2019

INTRODUCTION TO PYTHON FOR BIOLOGISTS (IPYB06)

Glasgow, Scotland, Dr. Martin Jones

http://www.prinformatics.com/course/introduction-to-python-for-biologists-ipyb06/ 3. June 17th V 21st 2019

ANALYSING GENETIC ADAPTATION USING LANDSCAPE GENOMICS IN R (ANGA01)

Glasgow, Dr. Matt Fitzpatrick

https://www.prstatistics.com/course/analysing-genetic-adaptation-using-landscape-genomics-in-r-agad01/ 4. June 17th V 21st 2019

ADVANCED PYTHON FOR BIOLOGISTS (APYB03)

Glasgow, Scotland, Dr. Martin Jones

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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

ULeeds HPCCloudComput

Next Generation Biologists: Essential Computing Skills for Molecular Biology (http://nextgenbiologists.org) is a BBSRC-STARs programme-funded project to introduce and train researchers in the skills and best practices in scientific computing and bioinformatics. The format of the materials and the nature of the delivery is based on the successful "Software Carpentry" (http://software-carpentry.org/) blended-learning model, where students learn by developing skills through hands-on, live coding and peer programming sessions led by experienced Software Carpentry instructors and supported by a small team of helpers.

This is the announcement of the seventh overall and the first "advanced" workshop in the series. The workshop will take place at the University of Leeds on the 17-18th June.

AUDIENCE The workshops are aimed at researchers who are comfortable with command line.

ORGANISERS AND INSTRUCTORS The main organisers of the workshops are Dr Mary J. O'Connell (@Evol_Molly), Dr Martin Callaghan (both at the University of Leeds) and Dr Jarek Bryk (@jarekbryk at the University of Huddersfield). The project is a joint initiative of the University of Leeds and the University of Huddersfield. The instructors include Martin Callaghan, Jarek Bryk and Dr Alastair Droop (also from the University of Leeds).

PRELIMINARY PROGRAMME

MONDAY: HPC in a day (spuninng-up-for-the-occasion of a cloud-based HPC cluster)

TUESDAY: Cloud in a day (setting up your own RStudio server in the cloud, look at Machine Learning tools, tour of the Google Genomics/AWS Genomics/Azure Genomics platforms)

DATE 17-18th June 2019 (Mon-Tue).

VENUE University of Leeds, UK.

COSTS The workshops are free of charge for all BBSRC-funded researchers, as well as staff and students from the Universities of Leeds and Huddersfield. For all other participants a course fee of 100 will apply that will need to be paid before the workshop begins. Travel and accommodation costs are *not* covered by the organisers.

HOW TO APPLY To apply for a place on the workshop, prepare a 200 words' summary of your curriculum vitae and a 200 word statement detailing why this course if of particular importance to your research. Submit your information via the registration form at https://forms.gle/jd5sym9nz8W7NjnK7 by Monday 3rd June. The selection committee will notify successful applicants by the end of the 4th of June. The workshops are limited to 25 participants, who are expected to bring their own computers on the workshop.

More details about the project and the workshop are available on our website at http://nextgenbiologists.org. We are also on Twitter at @nextgenbiol (the ^{o}l± is important :-).

See you on the workshop! The organisers

Jarek Bryk <J.Bryk@hud.ac.uk>

UmeaU UmeaSweden SLiMEvolutionaryModeling Aug12-16

Hi all.

First of all, as background: SLiM is a software package for creating evolutionary models/simulations that are individual-based and genetically explicit. It is scriptable, flexible, fast, and includes an interactive graphical modeling environment. You can read more about it on its home page (https://messerlab.org/slim/).

August 12-16, 2019, a five-day SLiM workshop will be offered at Umea University (Umea, Sweden). It will be hosted by Ake Brannstrom and Xiao-Ru Wang, both of Umea University. It will be free, and open to participants outside of the university. HOWEVER, registration is required, a limited number of seats are available, and priority will be given to registrants affiliated with Umea. To apply, please send an email to all three of us (ake.brannstrom@umu.se, xiao-ru.wang@umu.se, bhaller@mac.com) with the info below. The deadline for applying is the end of the day on 1 July.

For this workshop, your application email should include: (1) your name, (2) your university or institutional affiliation, (3) a link to a research website or similar academic page, if you have one, (4) a 1-2 sentence description of your level of experience with SLiM and any other forward genetic simulation software, if any, (5) a 1-2 sentence summary of why you want to attend the workshop (i.e., the connection to your research), and (6) 1-2 sentences about any specific topics within SLiM that you hope to learn about in the workshop. Note that you will be responsible for your own lodging and your own transportation. Please do not apply to the workshop unless you are sufficiently serious that you will actually attend, if accepted. Note that acceptance will likely be first-come-first-served (apart from the priority for those from the hosting institution), so early application is advised.

The plan is to try to cover all the major topics in the SLiM manual, starting with lots of introductory material to get beginners up to speed with SLiM and its associated scripting language Eidos, and hopefully ending up at advanced topics like non-Wright-Fisher models, tree-sequence recording, continuous-space models, and nucleotide-based models. We won't cover everything in the manual - that would be overwhelming! - but we'll try to cover all the big topics. There will also be time for attendees to work on their own models with help from me, and we may also have time to explore some optional side topics that are of particular interest to those attending each workshop. The workshops will be taught principally using SLiMgui on macOS. For this workshop, we will have a classroom arranged with Macs at each seat. (A Mac is required to run SLiMgui, which is necessary for teaching purposes.)

I'm hoping to continue doing workshops in future; if you would like to invite me to give a workshop at your institution, please send me an email (off-list).

Cheers,

Benjamin C. Haller Messer Lab Cornell University

bhaller@mac.com

UStAndrews EvolutionaryGenetics Jun5-7

Fantastic Forces is a workshop for postgraduates to get introduced to the cutting edge of evolutionary genetics research. By bringing together researchers from across the spectrum of evolutionary biology research, this workshop aims at promoting an environment for reflection and discussion about how different tools can be used cooperatively to answer complex questions.

Our workshop will comprise three themed days, each consisting of a series of talks in the morning followed by tutorials in the afternoon. Fantastic Forces will be held on *June 5th - 7th 2019 at the University of St Andrews*, Arts Building.

With a terrific list of expert speakers, Fantastic Forces is an excellent opportunity for students to meet with experts in the field, learn valuable data analysis skills, and discuss research ideas and career prospects.https://twitter.com/ForcesWorkshop/stathttps//t For more details on the programme, how to register and how to travel to St Andrews, check our website https://fantastic4cesworkshop.wordpress.com/ and follow us on Twitter: https://twitter.com/ForcesWorkshop/status/1124340333880512512 Attendance is free, and a few travel awards will also be available. There are only 20 attendee slots, so apply soon! And please forward this to any students who might be interested.

Best wishes, Carolina Barata

On behalf of the organising committee

Alberto Carmagnini, Queen Mary University of London

Bernardo Gutierrez, University of Oxford

Carolina Barata, University of St Andrews

Jessica King, University of Edinburgh

Carolina Barata <cdcbrb@st-andrews.ac.uk>

YaleU SustainingBiodiversityInfrastructure Jun12-14

Application Deadline: This Friday, May 17th

What: Ecological Society of America Training: Sustaining Biological Infrastructure, Strategies for Success

When: June 12-14, 2019

Where: Yale University, New Haven, CT

Description: Take your lab, field station, collection, or research center to the next level of success with our 3 day intensive training.

What will you learn? View our video here: https://esa.org/sbi/about/video/ -Create a plan to make your project more financially sustainable; -Learn how to secure funding from private foundations; -Hone your skills in strategic planning, finances, and communication; and -Network with colleagues who face similar challenges.

Contact: Emily Mastrianni, ESA Science Programs Specialist, 202-833-8773 ext. 221, Emily@esa.org

Emily Mastrianni <emily@esa.org>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.