EvolDir

December 1, 2016

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.

—— / ——

Conferences

Aveiro ComputationalBiol Jun5-7

4th INTERNATIONAL CONFERENCE ON ALGORITHMS FOR COMPUTATIONAL BIOLOGY

AlCoB 2017 — Aveiro, Portugal — June 5-7, 2017 —

Organized by:

Center for Research & Development in Mathematics and Applications (CIDMA) Institute of Electronics and Informatics Engineering of Aveiro (IEETA) University of Aveiro

Research Group on Mathematical Linguistics (GRLMC) Rovira i Virgili University — http://grammars.grlmc.com/AlCoB2017/ — AIMS:

AlCoB aims at promoting and displaying excellent research using string and graph algorithms and combinatorial optimization to deal with problems in biological sequence analysis, genome rearrangement, evolutionary trees, and structure prediction.

Previous events were held in Tarragona, Mexico City, and Trujillo. — The conference will address several of the current challenges in computational biology by investigating algorithms aimed at:

1) assembling sequence reads into a complete genome, 2) identifying gene structures in the genome, 3) recognizing regulatory motifs, 4) aligning nucleotides and comparing genomes, 5) reconstructing regulatory networks of genes, and 6) inferring the evolutionary phylogeny of species. — Particular focus will be put on methodology and significant room will be reserved to young scholars at the beginning of their career.

VENUE:

AlCoB 2017 will take place in Aveiro, an industrial city with an important seaport on the Atlantic Ocean, and known as “the Portuguese Venice” due to its network of canals. The venue will be the Department of Mathematics of the University of Aveiro, Campus Universitário de Santiago, 3810-193 Aveiro.

SCOPE: — Topics of either theoretical or applied interest include, but are not limited to:

Exact sequence analysis Approximate sequence analysis Pairwise sequence alignment Multiple sequence alignment Sequence assembly Genome rearrangement Regulatory motif finding Phylogeny reconstruction Phylogeny comparison Structure prediction Compressive genomics Proteomics: molecular pathways, interaction networks Transcriptomics: splicing variants, isoform inference and quantification, differential analysis Next-generation sequencing: population genomics, metagenomics, metatranscriptomics Microbiome analysis Systems biology

— STRUCTURE: — AlCoB 2017 will consist of:

invited lectures invited tutorials peer-reviewed contributions posters — INVITED SPEAKERS:

tba — PROGRAMME COMMITTEE: (to be completed) — Can Alkan (Bilkent University, Ankara, TR) Stephen Altschul (National Institutes of Health, Bethesda, USA) Yurii Aulchenko (PolyOmica, Groningen, NL) Ken Chen (University of Texas MD Anderson Cancer Center, Houston, USA) Eytan Domany (Weizmann Institute of Science, Rehovot, IL) Dmitrij Frishman (Technical University of Munich, DE) Terry Furey (University of North Carolina, Chapel Hill, USA) Olivier Gascuel (Pasteur Institute, Paris, FR) Debashis Ghosh (University of Colorado, Denver, USA) Susumu Goto (Kyoto University, JP) Osamu Gotoh (Institute of Advanced Industrial Science and Technology, Tokyo, JP) Javier Herrero (University College London, UK) Karsten Hokamp (Trinity College Dublin, IE) Fereydoun Hormozdiari (University of California, Davis, USA) Kazutaka Katoh (Osaka University, JP) Lukasz Kurgan (Virginia Commonwealth University, Richmond, USA) Carlos Martín-Vide (Rovira i Virgili University, Tarragona, ES, chair) Zemin Ning (Wellcome Trust Sanger Institute, Hinxton, UK) William Stafford Noble (University of Washington, Seattle, USA) Cedric Notredame (Center for Genomic Regulation, Barcelona, ES) Christos Ouzounis (Centre for Research & Technology Hellas, Thessaloniki, GR) Manuel C. Peitsch (Philip Morris International, Bern, CH) Matteo Pellegrini (University of California, Los Angeles, USA) Graziano Pesole (University of Bari, IT) David Posada (University of Vigo, ES) Knut Reinert (Free University of Berlin, DE) Peter Robinson (The Jackson Laboratory, Farmington, USA) Julio Rozas (University of Barcelona, ES) David Sankoff (University of Ottawa, CA) Alejandro Schäffer (National Institutes of Health, Bethesda, USA) Xinghua Shi (University of North Carolina, Charlotte, USA) Nicholas D. Socci (Memorial Sloan Kettering Cancer Center, New York, USA) Alexandros Stamatakis (Heidelberg Institute for Theoretical Studies, DE) Granger Sutton (J. Craig Venter Institute, La Jolla, USA) Kristel Van Steen (University of Liège, BE) Arndt von Haeseler (Center for Integrative Bioinformatics Vienna, AT) Kai Wang (University of Southern California, Los Angeles, USA) Haim J. Wolfson (Tel Aviv University, IL) Ioannis Xenarios (Swiss Institute of Bioinformatics, Lausanne, CH) Shibu Yooseph (University of Central Florida, Orlando, USA) Mohammed J. Zaki (Rensselaer Polytechnic Institute, Troy, USA) Daniel Zerbino (European Bioinformatics Institute, Hinxton, UK) Weixiong Zhang (Washington University in St. Louis, USA)

— / —

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

---

:BatonRougeLA SocietyOfSystematicBiologists Jan7-10

Registration Open for Society of Systematic Biologists (SSB) Standalone Meeting January 7-10, 2017 Baton Rouge, LA

Following on the tremendous success of the 2015 Standalone Meeting in Ann Arbor, SSB is pleased to announce its next Standalone Meeting in Baton Rouge, LA, scheduled for January 7-10, 2017, and hosted by Louisiana State University. This meeting will feature a wide variety of workshops, lightning talks, as well as society-wide debates and discussions. The Society is committed to promoting the involvement of students and other early-career researchers by offering travel awards and a welcoming atmosphere. The meeting will offer many opportunities for meaningful interactions, with a maximum capacity of 300 attendees.

Meeting registration will cover attendance at all workshops, coffee breaks, talks, and debates, as well as an evening reception at the LSU Museum of Natural Science. NSF program directors will also be available to discuss the future of support for research in systematic biology.

Outstanding venues have been reserved for the meeting, including the newly renovated Hilton Capitol Center hotel and the beautiful Manship Theatre at the Shaw Center for the Arts, both in downtown Baton Rouge. These venues are in close proximity to a wide variety of excellent restaurants and cultural attractions.

Full details are available on the meeting webpage: https://ssb2017.github.io/ Follow @jembrown and @systbiol on Twitter for meeting updates, as they become available.

Confirmed workshops will offer training directly from the developers of popular software tools including Arbor, Bayou, BioGeoBears, Dendropy, RevBayes, Phrapl, and TreeScaper.

Confirmed debate and discussion leaders include:

Scott Edwards (Harvard University) Matt Hahn (Indiana University) Mark Holder (University of Kansas) Emily Jane McTavish (University of California, Merced) Gavin Naylor (College of Charleston) Rachel Schwartz (University of Rhode Island)

If you are interested in attending, you can register here:

https://www.regonline.com/registration/-checkin.aspx?MethodId=3D0&EventSessionId=-cf93b99f12c94b34a0ed4d8a5a433db0&EventId=1884549 Individuals registering early will be given preference for available spaces in workshops and lightning talk sessions. Registration prices will increase on Dec. 15.

Hotel rooms are available at a special group rate and can be booked here:

http://www.hilton.com/en/hi/groups/personalized/-B/BTRCPHF-SSB-20170105/index.jhtml SSB has recently expanded its membership options and members can register for the meeting at a reduced rate. Go here to become an SSB member:

http://www.oxfordjournals.org/our_journals/sysbio/-access_purchase/price_list.html "jembrown@lsu.edu" <jembrown@lsu.edu>

Calgary EvoDevo Aug19-23

The Pan-American Society for Evolutionary Developmental Biology 2nd Biennial Meeting August 19-23, 2017 University of Calgary Calgary, Alberta, Canada

The PanAm SEDB meeting organizers are pleased to announce the invited speakers for our next biennial meeting. (http://www.evodevopanam.org/-speakers2017.html)

Ehab Abouheif Craig Albertson Mariana Benitez Dominique Bergman Marianne Bronner Federico Brown Sean Carroll Cassandra Extavour Nadia Fröbisch Andreas Heyland Jukka Jernvall Tiana Kohlsdorf Elena Kramer Vincent Lynch Hillary Maddin Antónia Monteiro Annalise Paaby Michael Shapiro James Sharpe Stacey Smith Günter Wagner Tom Williams

Registration for the meeting will open online on January 1, 2017. The deadline for the early bird registration rates and abstract submission will be May 15, 2017. Please visit http://www.evodevopanam.org/ for news and updates as these dates approach. And be sure to follow us on Facebook (https://www.facebook.com/-EvoDevoPanAm) and on Twitter @EvoDevoPanAm!

-The EvoDevoPanAm Executive Board

— David R. Angelini Assistant Professor, Department of Biology, Colby College Secretary, Pan-American Society for Evolutionary Developmental Biology Director, Bugs In Our Backyard Project, http://-www.bugsinourbackyard.org/ 5734 Mayflower Hill, Waterville, ME 04901, USA - office phone: 207-859-5734 http://web.colby.edu/aphanotus/ Twitter: @Aphanotus @Jhaematoloma

david.r.angelini@gmail.com

Cambridge PopGenet Jan4-7

This is a final reminder that registration for the 50th Population Genetics Group (aka Pop Group) will close on the 30th November, and talk slots are nearly full. The meeting is in Cambridge, UK, January 4-7th 2017. Although named Population Genetics Group in the 1960s the meeting now covers most areas of evolutionary genetics and genomics. This meeting will be a celebration as it is the 50th in the series.

Plenary speakers are: Doris Bachtrog, Nancy Moran, Eske Willerslev and Howard Ochman

Registration includes a conference dinner in St John's College and is excellent value! As little as 180 for non-residential student, GenSoc member, or 390 for standard registration with accommodation. More details are on our web site: http://populationgeneticsgroup.org.uk "fmj1001@cam.ac.uk" <fmj1001@cam.ac.uk>

Chicago GLBIO PhylogeographyViruses May15-17

Announcing a special session on the "Phylogeography of Viruses" at the Great Lakes Bioinformatics Conference May 15-17 2017 in Chicago, Illinois, USA. https://www.iscb.org/glbio2017-special-sessions The submission deadline is January 23, 2017.

We are accepting abstracts or full-length papers. Accepted full-length papers will be considered for publication in a special issue of PLoS One.

Matthew.Scotch@asu.edu

ESEB FitnessLandscapes Aug20-25

Dear evolDir community,

we would like to draw your attention to the upcoming conference of the "European Society for Evolutionary Biology" (ESEB 2017) to be held at Groningen (Netherlands) from 20 to 25 August 2017 (for more details see http://www.eseb2017.nl/) and invite you all to submit an abstract to our symposium on "Fitness landscapes, big data and the predictability of evolution" (http://www.eseb2017.nl/sub/s14-fitness-landscapes-big-data-an/).

Please note that the deadline for abstract submission is January 10th. Abstracts can be submitted here: http://www.eseb2017.nl/call-for-abstracts/ [S14] Fitness landscapes, big data and the predictability of evolution

Evolutionary biology has become increasingly powerful in inferring past evolutionary processes from patterns in present-day genomes. However, forecasting evolution's future routes remains an exciting intellectual challenge with substantial implications for global health and species conservation. The concept of the fitness landscape has been central to recent studies of the predictability of evolution, and has inspired evolutionary biologists and mathematicians alike. Combining microbial experimental evolution with next-generation sequencing, efforts have now been made to rigorously test for the repeatability and dynamics of evolution. At the same time, theoretical studies try to provide the necessary navigational tools for exploring the terra incognita of molecular evolutionary biology. This symposium aims to identify the key issues and challenges – both methodological and theoretical - to advance our understanding of the predictability of evolution, particularly in the light of "big data". We anticipate that insights from our symposium will stimulate and direct future studies of the predictability of evolution. With next-generation sequencing on board, fitness landscapes are heading for new shores: It's now time to check whether "there be dragons"!

Organizers: Santiago Elena, Inês Fragata, Sebastian Matuszewski, Arjan de Visser

Invited speakers: Michael Lässig, Lilia Perfeito

Please feel free to contact sebastian.matuszewski[at]epfl.ch if you have any questions.

Looking forward to seeing you all in Groningen, Sebastian Matuszewski

"sebastian.matuszewski@epfl.ch"
<sebastian.matuszewski@epfl.ch>

Freising Germany PlantSelection

TheTUM Chair of Plant Breeding together with the German Plant Breeding Society(GPZ) will organize an international meeting on "Selection Theoryand Breeding Methodology" in March 2017. The primary aim will beto bring together researchers from the public and private sector whowould like to share their knowledge on plant and animal breeding methodologyand learn about the latest developments in the field.

InternationalConference on "Selection Theory and Breeding Methodology" Campusof the TUM School of Life Sciences Weihenstephan, Freising, Germany March23 - 24, 2017

Confirmedguest speakers: AlainCharcosset, INRA, Le Moulon Fredvan Eeuwijk, Wageningen University JeffEndelman, University of Wisconsin-Madison DanielGianola, University of Wisconsin-Madison MikeGoddard, University of Melbourne SusanneGroh, Pioneer Hi-Bred International NicolasHeslot, Limagrain BillHill, University of Edinburgh Jean-LucJannink, Cornell University ChristinaLehermeier, Technische Universität München IanMackay, NIAB, Cambridge AlbrechtMelchinger, Universität Hohenheim VanessaPrigge, SaKa Pflanzenzucht JochenReif, IPK Gatersleben HennerSimianer, Universität Göttingen PeerWilde, KWS Lochow JohnWoolliams, University of Edinburgh

Moreinformation and online registration: http://www.plantbreeding.wzw.tum.de/index.php?id" Contact: Chairof Plant Breeding TUMSchool of Life Sciences Weihenstephan TechnischeUniversität München UlrikeUtans-Schneitz, Ute Wiegand Liesel-Beckmann-Str.2 85354Freising, Germany Tel+49.8161.71.5226 plantbreeding.wzw@tum.de

UlrikeUtans-Schneitz <utansschneitz@tum.de>

Groningen ESEB2017 CallForAbstracts

Dear Colleagues,

we are happy to inform you that abstract submission is now open for the next congress of the European Society of Evolutionary Biology (ESEB). The congress will be held from August 20 - 25, 2017, in Groningen, The Netherlands

The list of symposia is available at: http://www.eseb2017.nl/scientific-programme/symposium-list/ Please note the following dates:

10 January 2017: Deadline for abstract submission

1 February 2017: Notification of acceptance and open pre-registration for accepted abstracts

15 February 2017: Open registration for the congress

For further details, please see: http://www.eseb2017.nl Best wishes, Leo Beukeboom, ESEB Congress Organizer

--

Prof. Dr. Leo W. Beukeboom Evolutionary Genetics Groningen Institute for Evolutionary Life Sciences (GELIFES) University of Groningen P.O Box 11103 9700 CC Groningen, The Netherlands Email l.w.beukeboom@rug.nl http://www.rug.nl/staff/l.w.beukeboom/ < http://www.rug.nl/staff/l.w.beukeboom/ >

ESEB <office@eseb.org>

Groningen ESEB IntegratingMicroMacroEvolutionSymp Aug2017

We are pleased to invite you all to submit abstracts for our symposium "Integrating micro- and macroevolution" planned for European Society for Evolutionary Biology meeting in Groningen, Netherlands 20-25th of August 2017.

[S29] Integration of micro- and macroevolution

Evolutionary biology studies the patterns and processes that shape biodiversity over long and short timescales. Traditionally microevolution focused on within-species dynamics in a short temporal perspective, while macroevolution deals with both within- and between species patterns and processes over longer periods of time. Although many macroevolutionary patterns still lack explanations that follow from microevolutionary theory and observations, exiting new developments now allow both micro- and macroevolutionary approaches to converge on understanding biological variation within the context of genomic organization, historical constraint, contingency as well as elucidating biotic and abiotic drivers of evolutionary change. The increasing genetic resolution provided by next-generation-sequencing technology impacts studies of both micro and macro-evolution; phylogenetic analyses are now increasingly based on many markers and include genome organization, and functional traits are commonly being linked to causal genetic determinants. It is now also possible to combine palaeontological and neontological data in the same analysis framework. In this symposium, we will explore insights from such new developments and their potential for determining the research agenda for evolutionary biology. Contributions shall address fundamental questions regarding the integration of macro- and microevolution, for instance how can macroevolutionary studies inform hypotheses of microevolutionary change and vice versa?

Organizers: Eric Schranz, Jostein Starrfelt, Kjetil Voje, Bas Zwaan

Invited speakers: Antonia Monteiro, Thomas Ezard

http://www.eseb2017.nl/sub/s29-integration-of-micro-and-macro/ Abstract submission is here, deadline is 10 January 2017. http://www.eseb2017.nl/call-for-abstracts/ best Jostein

Groningen ESEB InversionSymposium Aug2017

ESEB SYMPOSIUM ON INVERSIONS & SUPERGENES

Dear Colleagues:

We would like to invite you to attend and/or contribute to the ESEB symposium

"The Evolutionary Significance of Chromosomal Inversions" [S18]

which will take place at the 16th Congress of the European Society for Evolutionary Biology (ESEB), in Groningen, Netherlands, 20-25 August 2017.

INVITED SPEAKERS: Mark Kirkpatrick (Austin) Michael Fontaine (Groningen)

SYMPOSIUM DESCRIPTION: Chromosomal inversions represent common structural mutations that result in the reversal of gene order in the corresponding state, they have been associated with evolutionary processes that involve reduced recombination and gene flow such as speciation and sex chromosome evolution. Inversions might also play a pivotal role in adaptation. For example, inversions might act as adaptive "supergenes" by keeping together coadapted gene complexes or by protecting locally adapted alleles from maladaptive gene flow. Consistent with adaptive effects, several inversion polymorphisms exhibit strong, persistent frequency clines and have been associated with fitness-related traits. Despite almost 100 years of research on inversions since their discovery by Sturtevant in 1921, we are still far from fully understanding the mechanisms whereby inversion polymorphisms are maintained in natural populations and how selection acts on them. Recent advances in population genetic theory and genomics are now beginning to shed light on these fundamental questions. With this symposium we seek to foster a discussion between theorists and experimentalists about the causes and consequences of inversion evolution.

http://www.eseb2017.nl/sub/s18-the-evolutionary-significance-o/ Organizers: Martin Kapun and Thomas Flatt (University of Lausanne)

We invite submissions for oral and/or poster contributions; we are interested in both empirical and theoretical work addressing the evolutionary causes and consequences of chromosomal inversions.

The deadline for abstract submission is 10 January 2017.

http://www.eseb2017.nl/call-for-abstracts/ We are very much looking forward to seeing you in Groningen!

Martin and Thomas.

— Thomas Flatt Department of Ecology and Evolution University of Lausanne UNIL Sorge, Biophore CH-1015 Lausanne Switzerland

E-mail: Thomas.Flatt@unil.ch Office: +41 21 692 4203 Fax: +41 21 692 4165 Web: http://www.unil.ch/dee/page94630_en.html Mechanisms of Life History Evolution: http://ukcatalogue.oup.com/product/9780199568765.do thomas.flatt@unil.ch

Groningen ESEB TransitionsInEvolution Aug20-25

Conference: Groningen.ESEB2017_Major_transitions_in_evolution.Aug2
25

Dear evoldir members,

We would like to announce the symposium [S8] Major transitions in evolution at the upcoming ESEB 2017 conference and would like to invite abstract submissions.

This symposium focuses on major evolutionary transitions to eusociality and multicellularity.

Complex life has evolved through a series of evolutionary transitions in individuality. During these transitions, existing individuals merged to become parts of a new higher-level individual, which consists of specialised subunits that divide labour. Recent years have seen major advances in the field that were enabled by experiments examining the origin of chemical replicators capable of Darwinian evolution, the evolution of simple multicellular organisms from single-celled ancestors in test tubes, solitary organisms attaining a group-living lifestyle, the origin and evolution of digital organisms in silico, and work examining how symbioses can lead to the origin of new organisms. Moreover, some of the exciting discoveries made in this field sparked intensive debate among philosophers on how organisms should be defined.

Drawing on this diverse work, our symposium will highlight recent developments in this rapidly progressing area. By bringing together empirical, theoretical, and philosophical contributions, this symposium will not only facilitate discussions among scientists that otherwise would not meet, but will also help identify priorities for future research.

* Invited speakers:

Richard Michod (University of Arizona)

http://michodlab.arizona.edu Silvia de Monte (Ecole Normale Supérieure Paris)

http://www.biologie.ens.fr/eceem/demonte.html Ellen Clarke (Oxford) http://ellenclarke.net * Organisers:

Abel Bernadou (University of Regensburg)

http://www.uni-regensburg.de/biologie-vorklinische-medizin/evolutionsbiologie/team/dr-abel-bernadou/-index.html Christian Kost (University of Osnabrück)

http://www.ice.mpg.de/ext/index.php?id=-experimental-evolution Boris Kramer (University of Groningen)

https://www.researchgate.net/profile/Boris_Kramer Karen Meusemann (University of Freiburg)

http://www.bio1.uni-freiburg.de/oeko/evo-eco/eco-lab-members/karen-meusemann William Ratcliff (Georgia Tech)

http://www.ratclifflab.biology.gatech.edu * Deadline for submission for abstracts for contributed talks and posters is 10th January 2017. More information can be found at http://www.eseb2017.nl/call-for-abstracts/-abstract-guidelines-/ . We look forward to receiving your submissions and to seeing you at the conference and our symposium.

Christian Kost <christiankost@gmail.com>

Hannover Germany EcoEvoDynamcis Oct9-13

Conference: Flexibility matters: Interplay between trait diversity and ecological dynamics using aquatic communities as model systems

The conference will address trait-based ecology with a focus on biomass-trait feedbacks and eco-evolutionary dynamics typically arising from trophic interactions. We aim to bridge between theoretically guided empirical field and laboratory studies and data-informed development of theory and modelling. The meeting will provide opportunities to exchange ideas and results with members of the DFG funded Priority Program DynaTrait and guests through a series of contributed and invited talks, poster sessions and small working groups. The meeting focuses on aquatic systems, but other systems are welcome as well if results are sufficiently generalizable. For more information and list of speakers see http://web.evolbio.mpg.de/dynatrait/-Site_2/DynaTrait_Meeting_2017.html . The meeting will take place 9th-13th October 2017 in Hannover, Germany. If you are interested in joining us, please contact Alice Boit (alice@boit.net) .

Organizers and Contact Ursula Gaedke (University Potsdam) & Lutz Becks (MPI Evolutionary Biology)

Lutz Becks <lbecks@evolbio.mpg.de>

Harpenden UK InsectGenomics May16

Dear all,

I'd like to let the community know that the registration has opened for the /Insect Genomics Special Interest Group meeting/ of the /Royal Entomological Society/.

The development of the new sequencing technologies has placed the field of genomics at the heart of biological research. Many genomes have already been published and many more are being generated. This abundance of genomic data is proving to be fundamental to a wide range of research areas including functional genomics, the evolution of diversity and insect management.The purpose of this meeting is to discuss the latest developments in the field of genomics and how they are being applied in entomology. We will bring together researchers with different backgrounds to promote the exchange of ideas and explore collaborations that can further advance insect science.

We welcome presentations from researchers at all stages of their careers working on insect genomics and the development of bioinformatics tools, as well as from those applying these methods to study questions ranging from insect ecology and evolution to management and control.

We are really excited to have Nicola Nadeau (University of Sheffield), Chris Bass (Unversity of Exeter) and Luke Alphey (The Pirbright Institute) as invited speakers.

It will take place on the 16th of May 2017 at Rothamsted Research, Harpenden, UK. The registration fee is 15 to cover for lunch, tea/coffee and a wine/refreshment reception during the poster session.

The deadline for abstract submission is the 16th of

March 2017 and deadline for registration is the 2nd of May 2017.

For further details and registration form visit:

http://www.royensoc.co.uk/content/insect-genomics-special-interest-group-meeting-16th-may-2017 or send us an e-mail.

Ramiro Morales-Hojas - ramiro.morales-hojas@rothamsted.ac.uk

Martin Williamson - martin.williamson@rothamsted.ac.uk

Dr. Ramiro Morales-Hojas Molecular Ecologist / Entomologist Rothamsted Insect Survey Agroecology Department

e-mail: ramiro.morales-hojas@rothamsted.ac.uk; r.moraleshojas@gmail.com web-site: https://sites.google.com/site/ramiromoraleshojas/ web-site: http://www.rothamsted.ac.uk/insect-survey r.moraleshojas@gmail.com

Lisbon InvasivePlants Sep4-8

Please, find below the first announcement for the *14th International Conference on Ecology and Management of Alien Plant Invasions*, which will be held in *Lisbon *between the *4th and 8th of September, 2017.*

The aim of the EMAPI 2017 is to promote the opportunity to share findings and experiences research, management, and policy with professionals from around the world. Following the decision of the EMAPI Core Group in Hawaii during the last EMAPI meeting, the 14th Ecology and Management of Alien Plant Invasions World Congress will be held in Lisbon, from 4th to 8th September 2017.

The Congress aims to become a benchmark event, by gathering a large number of scientists, managers and policy makers from around the world, who will interact and explore ways to face global and regional challenges presented by alien plant invasions, for the benefit of the present and future generations.

A mid-conference field trip will offer first-hand experience with Portuguese coastal plant invasions, while also allowing extensive opportunities for networking. For this international meeting, we are expecting to bring together ˜ 300 active researchers, managers and policy makers. A special discount registration will be available to students.

Organizer: Center for Ecology, Evolution and Environmental Changes (cE3c), University of Lisbon

Contact: Cristina Maguas < http://ce3c.ciencias.ulisboa.pt/member/cristina-maria-filipe-maacuteguas-silva-hanson > / Catarina Costa < http://ce3c.ciencias.ulisboa.pt/member/catarina-antunes-da-costa >

University of Lisbon, Botany Department

Email: emapi2017@fc.ul.pt

http://ce3c.ciencias.ulisboa.pt/outreach/press&events/ver.php?id=698 Daniel Montesinos <danimontesinos@gmail.com>

LundU SwedishOikos2017 Feb7-9 RegistrationOpen

Registration has now opened for the 2017 Oikos meeting in Lund! Abstract submission is open until Monday December 12th, registration is open until January 16th.

Register here: http://oikos2017.event.lu.se/registration The Swedish Oikos Congress 2017 will take place 7ˆth -9ˆth February 2017 in Lund. Venue for the meeting will be Paleastra, in the heart of the city. A conference dinner will be held on the evening of February 8ˆth , and there will be pre-congress workshops on Monday February 6th. The meeting is open to all ecologists and evolutionary biologists regardless of subdiscipline, and we hope to have a wide breadth of talks and plenaries!

– Dr. Jessica K. Abbott Senior University Lecturer Department of Biology Section for Evolutionary Ecology Lund University Solvegatan 37 223 62 Lund, Sweden Phone: 046 222 9304 Website: http://jessicakabbott.com “It is those who know little, and not those who know much, who so positively assert that this or that problem will never be solved by science.” - Charles Darwin, Descent of Man

MaxPlanckInst Ploen EvolutionaryBiol Apr19-21

We are happy to announce that the German Zoological Society (DZG) will hold its

22nd Graduate Meeting in Evolutionary Biology

from 19th to 21st of April 2017 at the Max Planck Institute for Evolutionary Biology in Ploen, Germany (meeting will be in English!).

The 2017 theme of the graduate meeting will be "Antagonistic Coevolution", but the meeting is open to all graduate/PhD students and early postdocs in evolutionary biology.

Please visit the meeting website for more information and registration:

http://web.evolbio.mpg.de/coevolve The main goal of the meeting is to foster interactions among early career evolutionary biologists and provide opportunities for presenting your work in a semi-official environment. The program includes time slots for both oral and poster presentations.

Keynote speakers: Kayla King (Oxford University) Sylvain Gandon (CEFE Montpellier)

Local organizers: Tobias Lenz Lutz Becks

Deadline for registration is January 15th 2017.

MaxPlanckInst Plon GeneticsOfMigration Apr4-7

GENETICS OF MIGRATION

Tuesday 4th April - Friday 7th April 2017

Venue: Max Planck Institute of Evolutionary Biology, Plön, Germany

REGISTRATION DEADLINE DECEMBER 1ST

We are pleased to announce that a symposium on the Genetics of Migration will be held at the Max Planck Institute of Evolutionary Biology (Plön, Germany) in spring 2017 (April 4th-7th).

The aim of the symposium is to bring together a multidisciplinary group of scientists working on the ecology, genomics, epigenetics, evolutionary theory and biostatistics of animal migration. The development of next generation sequencing technology and improvements in tracking the movement of migratory species is certain to advance this field of science in the coming years so now is an excellent time to synthesize what we currently understand about the genetic basis of migration as well as highlight future avenues of research. The symposium will be based on a series of talks, posters, workshops and discussions and will encompass a wide range of migratory taxa including birds, fish and insects.

Keynote speakers:

Jochen Wolf - Ludwig Maximilian University of Munich Claudia Bank - Gulbenkian Institute Guojie Zhang - Beijing Genomics Institute/University of Copenhagen Melinda Baerwald - University of California, Davis Nancy Chen - University of California, Davis Christine Merlin - Texas A&M University

There are 50 spots available for the symposium.

Please register before DECEMBER 1ST at https://genmig.wordpress.com/ Any queries please email the organising committee (Miriam Liedvogel, Kira Delmore, Christopher Jones) at mailto:genmig@evolbio.mpg.de

Christopher Jones <christopher.jones@rothamsted.ac.uk>

Melbourne GalaxyAustralasia Feb3-9

Galaxy Australasian Meeting (GAMe 2017) 3-9 February 2017 Melbourne, Victoria, Australia http://www.embl-abr.org.au/game2017/ 30 Nov: Oral presentation abstracts due 31 Dec: Early registration ends

The Galaxy Australasia Meeting will bring together biomedical researchers, bioinformaticians, infrastructure providers, and data producers from across Australia and Asia.

GAMe 2017 spans a week and includes a two day conference, one day of training for researchers, and four days of training for Galaxy administrators.

The two day conference starts 4th February with a BIO day - for Galaxy users (biologists and bioinformaticians) - followed by an INFO day on 5th February, focussing on technical aspects of Galaxy - for bioinformaticians, tool and software developers, and research infrastructure providers. Both days feature keynotes, accepted and sponsored talks, poster and sponsor sessions, birds'-of-'a'-feather gatherings, and lots of opportunities for networking. The conference is preceded by a Researcher Training Day on 3 February for analysis-focussed biologists and biomedical researchers with limited experience of Galaxy. A four day intensive Galaxy Admin Training session for those installing and maintaining Galaxy servers follows the conference.

Early registration ends 31 December. Register now. Space is limited.

About Galaxy: Galaxy is an open web based platform for biomedical data integration and analysis. It is deployed at large and small organizations around the world and used in a broad range of biomedical research domains, and across the tree of life. Galaxy enables life science researchers to perform their own data analysis without having to learn command line interfaces or Linux package management. Galaxy transparently records all analysis steps and eases workflow reuse and sharing.

– http://galaxyproject.org/ http://getgalaxy.org/ http://usegalaxy.org/ https://wiki.galaxyproject.org/ Dave Clements <clements@galaxyproject.org>

Mosocow ICIM Aug18-23 OldSpecimensNewTechnology

Dear all

Contributions are welcome to a symposium we are organising within the International Congress on Invertebrate Morphology, in Moscow, 18-23 August 2017.

The symposium "Morphological Lazarisation: when new technology brings life to historical specimens" will bring together researchers that use old specimens, reexamined with new technology or just new perspectives. (Examples include 3D scanning/ tomography, electron microscopy, DNA barcoding, UV light and fluorescence, etc.) This is a celebration of the enduring usefulness of museum collections, and how material collected long ago can find new unanticipated purposes.

We would love to have you join us!

earlybird registration (EUR 250) - 1 Feb registration and abstract deadline - 30 April conference website - http://www.icim4.com in the abstract submission form, please mark it as a contribution to session D1

See you in Moscow,

Julia Sigwart & Lauren Sumner-Rooney j.sigwart@qub.ac.uk

– Dr Julia Sigwart Queen's University Belfast, Marine Laboratory http://www.qub.ac.uk/qml/People/Sigwart sabbatical address (2015-2018): University of California, Berkeley, Museum of Paleontology

"j.sigwart@qub.ac.uk"

Norman LiveBearingFish May24-26

Join us for the 7th Meeting of Poeciliid Biologists at the University of Oklahoma in Norman May 24 - 26 2017 (http://poeciliid2017.com/).

Each and everybody interested in any aspects of the biology of livebearing fishes should attend. Poeciliids are used as model species for many different questions including (and not limited to), evolution, ecology, genomics, genetics, cancer research, morphology, life-history evolution, systematics, taxonomy, and behavior. This meeting is totally open to every aspect of livebearing fishes - and even if you are interested in livebearing organisms per se, this will be a good meeting for you.

For any questions relative to the conference please use the following e-mail address: poeciliid@ou.edu.

See you in Norman!

Dr. Ingo Schlupp Presidential Professor of Biology

"Schlupp, Ingo B." <schlupp@ou.edu>

Paris BiologyofSymbiosis Mar15-17

The Institute of Biology Paris-Seine (IBPS, Universite Pierre et Marie Curie, Paris) is organizing its annual international symposium on the biology of symbiosis.

During the three days of the conference, 18 French, European and North-American scientists will present their work in four main sessions:

Symbiosis in our environment and within several species (gorilla, chimp, worm...)

Symbiotic interactions during the immune response in infectious diseases (malaria, dengue virus...)

Evolution, modelling and biology of symbiosis

The importance of the microbiota in human health (metabolic diseases, neurologic troubles, obesity...)

Speakers :

Antoine Danchin - ICAN, Paris, France — Nicole Dubilier - MPI Bremen, Germany Colomban de Vargas - Roscoff Station, France Eric Bapteste - IBPS, Paris, France Howard Ochman - Texas University, Austin, USA Marc-Andre Selosse - MNHN, Paris, France Bruno Lemare - EPFL, Lausanne, Switzerland Georges Dimopoulos - Johns Hopkins University, Baltimore, USA Louis Lambrechts - Pasteur Institute, Paris, France Philippe Sansonetti - Pasteur Institute, Paris, France Jan Sapp - York University, Toronto, Canada Marco Vignuzzi - Pasteur Institute, Paris, France Jeroen Raes - Catholic University of Leuven, Belgium Nancy Moran - Texas University, Austin, USA Jens Nielsen - Gothenburg University, Sweden Karine Clement - ICAN, Paris, France Sven Pettersson - Karolinska Institute, Stockholm, Sweden Nanyang Tech. University, Singapore Michel Neunlist - Nantes University, France

Venue:

March 15-17, 2017

Amphitheater Durand, Esclangon building, Jussieu Campus, 4 place Jussieu, 75005, Paris

Registration open here on November 15th: https://-symbiosis.sciencesconf.org

Symposium announcement page: http://-www.ibps.upmc.fr/en/news-events/events/ibps-symposium-symbiosis

Contact: ibps.comm@upmc.fr

Smithsonian BGI BioGenomics Feb21-23

BioGenomics2017

TheSmithsonian Institute for Biodiversity Genomics and BGI invite you to the Inaugural Global Biodiversity Genomics Conference in Washington, D.C. February 21-23, 2017 at the Smithsonians National Museum of Natural History and the JW Marriott.

TheKeynote Address will feature Dr. E. O. Wilson, Professor Emeritus, Harvard University

EdwardO. Wilson is regarded as one of the worlds preeminent biologists and naturalists. During his long career, Dr. Wilson has applied his scientific perspective and experience to illuminate the human circumstance, including human origins, human nature, and human interactions. He is the author of more than twenty books, including The Creation and the Pulitzer Prize-winning The Ants and Naturalist. Wilson has been a pioneer in spearheading efforts to preserve and protect the biodiversity of this planet. His most recent book, Half-Earth, concludes his trilogy begun by The Social Conquest of Earth and The Meaning of Human Existence.

ConfirmedPlenary and Featured Speakers include:

MayBerenbaum, University of Illinois at Urbana-Champaign AndrewClark, Cornell University ThomasGilbert, Natural History Museum of Denmark HarrisLewin, University of California Davis NancyMoran, University of Texas at Austin GeneRobinson, Institute for Genomic Biology OliverRyder, San Diego Zoo PamelaSoltis, University of Florida RobertWayne, The University of California, Los Angeles

Theconference will bring together thought leaders and research and academic scientists and IT professionals. The conference will feature interactions and synergies among biodiversity researchers, technologists, software developers, and research computing professionals discussing topics related with technological and analytical advances and their application in Diversity, Environmental, Ecological, and Conservation Genomics.

Sessionswill include invited speakers as well as selected talks and posters from applicants, including students.

Registrationdeadlines for talks and posters is November 15, 2016.

Attendancewill be limited to 450 people.

Registrationinformation visit: http://-biogenomics2017.org/ TuesdayFeb 21 will be the first official conference day including an evening event in the Rotunda of the National Museum of Natural History.

WednesdayFeb 22 and Thursday Feb 23 will be held at the Conference facilities at the JW Marriott near the NMNH, and poster reception will be the evening of the 22nd. The conference will conclude Thursday late afternoon.

MondayFeb 20 will consist of pre-conference meetings and student workshops.

Pleasedirect questions to Warren Johnson at:contactbiogenomics@si.ed

JohnsonWE@si.edu

StowersInst KansasCity EvolutionGeneRegulation Jul13-16

Registration is now open for an ASBMB Special Symposium on gene expression and evolution. The symposium brings together groups interested in mechanistic and evolutionary aspects of gene regulation. A preliminary program is posted and additional talks and posters will be selected from submitted abstracts.

http://www.asbmb.org/SpecialSymposia/2017/-geneexpression/registration/ http://www.asbmb.org/-SpecialSymposia/2017/geneexpression/program/ http://www.asbmb.org/SpecialSymposia/2017/-geneexpression/abstracts/ EVOLUTION AND CORE PROCESSES IN GENE EXPRESSION

July 13 - 16, 2017, Kansas City, MO Organized by: Julia Zeitlinger, Stowers Inst., David Arnosti, Michigan State Univ., Justin Fay, Washington Univ. in St. Louis

MEETING DESCRIPTION Evolutionary processes operate at all levels of gene expression, and increasingly detailed mechanistic understanding has provided rich hunting grounds for pathways and processes which underlie evolutionary variation, providing the molecular explanation for the beaks of Darwin's finches, for example. Most studies that have tracked down detailed molecular changes linked to the evolution of morphological variation have highlighted the importance of cis-Â'âvariation, as well as changes to sequence-Â'â€specific transcription factors. Such changes are expected to have less pleiotropic effects than alterations in the core transcriptional machinery, however new evidence points to high levels of complexity in what was initially assumed to be conserved core transcription machinery, suggesting that variation in these components are likely to play similar roles in evolutionary variation. Similarly, genetic variation in core machinery for protein translation has been shown to be associated with a variety of human diseases, providing a glimpse of the likely variation that underlies population-Â'âdifferences relevant to studies of "personalized genomics" in humans.

fayjustin@gmail.com

UOklahoma EvolutionPoeciliidFish May24-26

Registration is now open for the 7th Meeting of Poeciliid Biologists at the University of Oklahoma in Norman May 24 - 26 2017 (http://poeciliid2017.com/).

Each and everybody interested in any aspects of the biology of livebearing fishes should attend. Poeciliids are used as model species for many different questions including (and not limited to), evolution, ecology, genomics, genetics, cancer research, morphology, life-history evolution, systematics, taxonomy, and behavior. This meeting is totally open to every aspect of livebearing fishes - and even if you are interested in livebearing organisms per se, this will be a good meeting for you.

For any questions relative to the conference please use the following e-mail address: poeciliid@ou.edu.

See you in Norman!

Dr. Ingo Schlupp Presidential Professor of Biology http://poeciliid2017.com/ "Schlupp, Ingo B." <schlupp@ou.edu>

UUtah Species Mar23-25

Call for Abstracts - extended deadline

Species in the Age of Discordance

University of Utah Department of Philosophy Annual Conference Series

March 23rd 25th 2017 Salt Lake City, Utah

The *University of Utah* *Department of Philosophy* cordially invites submissions of abstracts or prospecti (up to 1000 words) for paper and poster presentations at our upcoming conference "Species in the Age of Discordance". Submissions should be prepared for blind review and uploaded at https://easychair.org/-conferences/?conf=3D3Dsitaod2017. Please be sure to indicate whether your submission is for a paper or a poster. The submission deadline is Nov. 15 Dec 1st, 2016.

Biological lineages move through time, space, and each other. As they do, they diversify, diverge, and grade away from and into one another. One result of this is genealogical discordance, i.e., the lineages of a biological entity may have different histories. We see this on numerous levels, from microbial networks, to holobionts, to population-level lineages.

The focus of this project is whether and how genealogical and other sorts of biological discordance impact our views on species. Other kinds of relevant discordance might include geographic discordance due to habitat fragmentation and human mediated dispersal of species in new environments, discordant government policies which affect populations that straddle or migrate across international borders, and discordant use of language or theoretical terms between researchers in different disciplines.

To promote a cross-disciplinary examination of this question, investigators from a variety of fields will participate in a series of interdisciplinary meetings. This includes researchers working on phylogenetics, microbiology, symbiosis, population genetics, taxonomy, philosophy, and history.

The Utah meeting is the first of three meetings on this topic. Follow up sessions are tentatively planned for the 2017 Evolution Meeting (Portland, OR) and the 2017 ISHPSSB Meeting (Sao Paulo, Brazil). The Utah meeting will be a mix of invited and refereed papers and posters.

For a list of invited speakers, please visit our conference webpage: http://philosophy.utah.edu/-conferences_workshops/species.php For questions, please contact *Dan Molter* <dan.molter@utah.edu> or *Matt Haber* <matt.haber@utah.edu>.

Dan Molter <speciesdan@gmail.com>

WashingtonDC Biogenomics Feb21-23

Dear Students,

The first Global Biodiversity Genomics Conference will be held in Washington, D.C. February 21-23, 2017 at the Smithsonian's National Museum of Natural History. This conference will discuss exciting topics in the field of conservation, ecological, environmental, and diversity genomics with a Plenary Address by E.O. Wilson. To learn more see: (http://biogenomics2017.org).

Are you interested in attending Biogenomics 2017 and getting a free waiver? Read below:

DEADLINE NEAR:

For a limited time, GIGA (Global Invertebrate Genome Alliance) will be offering a small number of full registration waivers courtesy of the American Genetics Association (value of $500) to qualified students who are currently working on or have recently finished a GIGA-related Big Data genomics or transcriptome project. *Students should still register to the conference website for a headcount.*

Then, to apply for the waiver, please send a project description to the GIGA steering committee (find on the GIGA webpage - or mail to Keith Crandall - kcrandall@gwu.edu ; Gonzalo Giribet - ggiribet@g.harvard.edu ; Steven Haddock - haddock@mbari.org ; or Jose Lopez - joslo@nova.edu). The committee will evaluate each summary based on merit and need.

The description should aim to be concise, no more than 1000 words that fully describes the project details - organism, questions, goals, genomics methods, hurdles etc.

Please include the name of your major advisor, your full contact information, university and the current source of funding to attend the conference.

The deadline for receipt of the abstract is Nov 28, 2016. Please send the project description as a Word file to one of the members above , and use the Subject header: "*GIGA Waiver Application for the 2017 Global Biodiversity Genomics Conference: Student's last name".*

– Heather Bracken-Grissom, PhD Assistant Professor Dept. of Biological Sciences Florida International University-Biscayne Bay Campus 3000 NE 151 Street, MSB-353 North Miami, Florida 33181, USA 305 919-4190 (Phone) 305 919-4030 (Fax)

CRUSTOMICS: Crustacean Genomics and Systematics Lab *http://www.brackengrissomlab.com/
heather.brackengrissom@fiu.edu
<Valerie.Hall@fiu.edu> www.fiu.edu/ ˜ marine
heather.bracken@gmail.com

GradStudentPositions

AMNH NewYork ComparativeBiology

American Museum of Natural History Richard Gilder Graduate School Comparative Biology Ph.D. Program and Graduate Fellowships Program

The AMNH RGGS Ph.D. Program in Comparative Biology is training the next generation of biologists through an integrative approach that focuses on the history, evolutionary relationships, and interactions among species. It utilizes the Museum's strength and experience in research and training to educate a new generation of scientists and industry leaders. The AMNH provides exceptional support facilities for student research, with collections of more than 33 million specimens and artifacts. Training and research opportunities exist across a wide array of disciplines in comparative biology, incorporating research in systematic and evolutionary biology, paleontology, conservation biology, comparative genomics, computational biology, Earth history, anthropology, and biological and cultural diversity. Global fieldwork, with AMNH faculty, student-led or in partnership with others, provides exceptional research opportunities for students. RGGS students may take advantage of RGGS course cross-enrollment agreements with partner universities Columbia and the City University of New York. Armed with a Gilder School education, graduates will not only understand the history and diversity of life on Earth, but may contribute to advances in human health, biodiversity conservation, and other related biological research fields as well.

This is an accelerated program, designed for students to complete their degrees in four years. Students will earn a minimum of 62 credits through a combination of coursework, teaching assistantships, and individual dissertation research. The Richard Gilder Graduate School will typically provide full financial support to students matriculating in the Comparative Biology Ph.D. Program.

We also offer Graduate Fellowships for students interested in earning a Ph.D. at one of our partner institutions (Columbia University, CUNY, NYU, Stony Brook and Cornell University), when they are advised by an AMNH curator.

The AMNH Graduate Student Fellowship Program is an educational partnership with selected universities, dedicated to the training of Ph.D. candidates in those scientific disciplines practiced at the Museum. Our current collaborations are with Columbia University, City University of New York (CUNY), Cornell University, Stony Brook University, and New York University (NYU). The host university in which the student enrolls exercises educational jurisdiction over the students and formally awards the degree. In these partnership programs, at least one Museum curator must serve as a graduate advisor, co-major professor or major professor, and adjunct university faculty member. Each student benefits by having the staff and facilities of both the university and the Museum to support his/her training and research. To be eligible for the AMNH Graduate Fellowship, students must apply to both the host University's Ph.D. program and to the AMNH Graduate Student Fellowships Program. Students already matriculated in a Ph.D. program are not eligible to apply; only new, first-time Ph.D. applicants will be considered.

SUMMARY OF APPLICATION REQUIREMENTS FOR FALL 2016 APPLICANTS Bachelor of Arts or Bachelor of Science or equivalent degree, from an accredited institution Official transcripts from all undergraduate/graduate institutions attended GRE (general) results (taken within the past five years–Institution Code 2471 or 1760) Three letters of support Statement of Academic Purpose (Essay 1: past research experience [length of up to 500 words] and Essay 2: proposed research interests [length of up to 500 words]) Interview (Final candidates will be interviewed) AMNH Faculty sponsor Application fee of $50 (Comp Bio Only) Proficiency in English (TOEFL [100 or higher] or IELTS scores [total 7.0 or higher] are required for non-native English speakers, taken within the past 2 years)

Deadline: December 15, 2016

For more info, please visit: http://www.amnh.org/our-research/richard-gilder-graduate-school/academics-and-research/fellowship-and-grant-opportunities/doctoral-and-graduate-student-fellowships Anna Manuel <amanuel@amnh.org>

AuburnU EvolutionaryPhysiology

The Hood lab at Auburn University is looking to recruit 2 grad students (Ph.D. preferred) for fall 2017 to evaluate the role that mitochondria play in variation in reproductive fitness and longevity of animals. Students may work on our wild-derived house mouse model or alternate species. You can learn more about the lab at http://www.thehoodlaboratory.com/ . The project is supported by a 5-year NSF CAREER award to Hood. Our lab works closely with an established expert on mitochondrial function, Dr. Andreas Kavazis in the Dept. of Kinesiology at Auburn and a lab with an emerging interest in mitonuclear interaction and sexual selection, Dr. Geoff Hill, Dept. of Biological Sciences. Please review the papers listed below (available at http://www.thehoodlaboratory.com/-publications) and the abstracts of our funded projects (http://www.thehoodlaboratory.com/funding) to learn more about future directions of our lab.

Interested applicants should send an email to Dr. Wendy Hood at wrhood@auburn.edu. In the email, please include a description of prior research experience, your training in evolutionary biology, physiology, and cell biology. If available, please also include an unofficial copy of your undergraduate and graduate institution transcripts (if post- masters), GPA and GRE scores, an example of your scientific writing, and the email address for 1-2 references. Please contact Dr. Hood ASAP if you would like to be considered for invitation to our graduate student recruitment day in January.

You can learn more about Biological Sciences at Auburn and our grad program at http://www.auburn.edu/-cosam/departments/biology/grad/index.htm Key papers:

Zhang, Y and WR Hood. 2016. Current versus future reproduction and longevity: a re- evaluation of predictions and mechanisms. Journal of Experimental Biology 219: 3177- 3189.

Mowry, AV, AN Kavazis, AE Sirman, WK Potts, WR Hood. 2016. Reproduction Does Not Adversely Affect Liver Mitochondrial Respiratory Function but Results in Lipid Peroxidation and Increased Antioxidants in House Mice. PLoS ONE 11(8): e0160883.

“wrh0001@auburn.edu” <wrh0001@auburn.edu>

BinghamtonU InsectSpeciation

Graduate positions in ecological speciation and the evolution of life history timing in the Powell lab at Binghamton University

I am currently seeking one or two PhD students to join my lab (www.powellevolab.com) in the fall semester of 2017. Our work is broadly focused on understanding how ecological processes, physiological systems, genetic variation, and genome structure interact during the origin of species and adaptation to novel niches and changes environments. We are particularly interested in understanding the origin and maintenance of diversity in specialist insect communities. Graduate students in my lab will have opportunities to address these questions from a range of approaches, from field work and physiological assays to transcriptomics and population genomics, and I am specifically looking for students that are interested in engaging in integrative work for their dissertations.

Current work in the lab is centered on two classic study systems: Rhagoletis fruit flies and goldenrod gall flies. Students will have opportunities to develop independent dissertation projects that contribute to the long term research goals of the lab, including contributions to a recently funded NSF Dimensions of Biodiversity project on the coevolution of life history timing among Rhagoletis flies and their parasitoid wasps and the use of this system as a model for evolutionary responses of communities to altered phenology under climate change.

Students will be supported on teaching assistantship lines through the Department of Biological Sciences (https://www.binghamton.edu/biology/), and be enrolled (tuition waived) in the EEB (Ecology, Evolution, and Behavior) track of our doctoral program. The EEB group at Binghamton is comprised of several active research groups with considerable overlap in fundamental research interests with our lab. This includes labs focused on coevolution, quantitative genetics and complex traits, ecological speciation in plants, genomic variation in natural populations, insect-plant interactions, and evolutionary responses to anthropogenic change. The department is also home to a unique interdisciplinary Evolution Studies Program, headed by David Sloan Wilson. All of this makes our department a particularly rich intellectual environment for students working at the intersection of evolution, ecology, and genetics.

Binghamton University is the top-ranked institution in the SUNY system and is consistently rated as one of the premier public universities in the Northeast. Our campus is located in the Southern Tier of New York, between the Catskills and Finger Lakes, about a 3 hour drive from NYC. The region features abundant opportunities for outdoor recreation and an extremely reasonable cost of living. Our setting on the Allegheny Plateau isn?t just aesthetically pleasant, it also happens to be an excellent geographic location for our study systems. Many of our insects' host plants are locally abundant in the upland deciduous forests and old fields in the region, and populations of the most of the members of the Rhagoletis pomonella species complex as well as both host races of gall flies can be found right on campus in BU's Nature Preserve (https://www.binghamton.edu/-nature-preserve/).

Formal applications will have to be made to the Graduate School: (http://www.binghamton.edu/grad-school/admissions/apply/index.html), but I strongly encourage interested students to contact me first. Please send me an email at powellt@binghamton.edu, including a letter outlining your qualifications, your specific interest in this position, your broader biological interests, and your reasons for wanting to pursue a PhD as well as a CV including your educational background, GPA, GRE scores, publications (if any), and any relevant experience. The official deadline for application to the Graduate School (including letters of recommendation) is January 15. However, interested students will have to begin the conversation with me well in advance of the application deadline. Please email me before Friday December 2 for consideration.

Tom Powell

Assistant Prof. Department of Biological Sciences Binghamton University Binghamton, NY 13902 607-777-4439

"powellt@binghamton.edu" <powellt@binghamton.edu>

Budapest BirdEvolutionaryBehaviour

Life history consequences of nest site selection in birds PhD studentship based in Hungary & the UK, 2017-2020 Supervisors: Dr A Kosztolányi (Univ Vet Med Budapest, Hungary), Prof Z Barta (Univ Debrecen, Hungary) and Prof T Székely (Univ Bath, UK)

Choosing nest sites is a major life history decision, since the location of nest influences both the risk of predation and the thermal properties of eggs, nest and the incubating parent. This PhD project will focus on shorebirds that nest on the ground. Our previous research has showed that some plovers nest in the open whereas others nest under small bushes. However, it is not known why these consistent individual differences (i.e. animal personalities) exist, how they relate to other personality traits (e.g. boldness, neophobia) and whether the costs and benefits of the different nesting strategies vary under different climatic conditions where the plovers breed.

The PhD student will investigate the interaction between consistency in nest site selection and climate, and the life-history consequences of this interaction. The student will test (i) how consistent are the individuals in their nest site selection under hotter and milder climates, (ii) whether the nesting personality correlates with other personality traits (e.g. bolder individuals nests in open area), and (iii) how nest site selection influences reproductive success and survival.

The ideal candidate has a strong interest in evolutionary biology, behavioural ecology and field biology, and willing to work in remote areas in Madagascar, Cape Verde or Mexico. He/she need to have solid background in data analyses preferably in R, and statistical modelling. We are seeking candidates willing to raise their own funding. Note that for students from eligible countries the Stipendium Hungaricum offers a scholarship programme (www.stipendiumhungaricum.hu). A condition of the application is a Master degree (or equivalent) in biology, zoology or similar subject.

Interested candidates should contact the lead supervisor, Dr András Kosztolányi (Kosztolanyi.Andras@univet.hu). Applications that include a CV (max 3 pages) and a max 2 page cover letter with personal motivation and the name and contact details of two references should be sent to Dr Kosztolányi. Deadline of application: 1 January 2017.

References

AlRashidi, M., A. Kosztolányi, M. Shobrak, C. Küpper & T. Székely. 2011. Parental cooperation in an extreme hot environment: natural behaviour and experimental evidence. Animal Behaviour 82: 235-243.

Barta, Z., T. Székely, A. Liker & F. Harrison 2014. Social role specialization promotes cooperation between parents. The American Naturalist 183: 747-761.

Reme, V., R. P. Freckleton, J. Tökölyi, A. Liker & T. Székely. 2015. The evolution of parental cooperation in birds. Proceedings of National Academy of Sciences, US 112: 13603-13608.

Vincze, O., T. Székely & A. Kosztolányi. 2013. Local environment but not genetic differentiation influences biparental care in ten plover populations. PLOS ONE 8: p.e60998.

Vincze, O., A. Kosztolányi, Z. Barta & T. Székely. 2016. Parental cooperation in a changing climate: fluctuating environments predict shifts in care division. Global Ecology and Biogeography (in press).

andras.kosztolanyi@gmail.com

Cambridge ButterflyBehaviourEvolution

Cambridge_Butterfly_behaviour_evolution

Two PhD projects on butterfly brain and behavioural evolution are currently available in my research group in the Dept. of Zoology, University of Cambridge:

i) Sensory adaptations in mimetic butterflies Processing sensory information from the environment is a vital aspect of any behavioural response. Micro-habitat partitioning between mimicry rings in Neotropical butterflies provides a case study in adaptation to different sensory environments. Species belonging to the same mimicry ring show convergence in micro-habitat preference, whilst distinct mimicry rings diverge in microhabitat preference, exposing closely related species to contrasting sensory environments. Microhabitat preference influences a range of behaviours, including foraging and intra-specific communication. This dual pattern of convergence and divergence provides a range of opportunities for comparative analyses. This project will use Ithomiine butterflies as a study system to ask how species adapt to novel sensory environments: For example, what is more important for sensory adaptation, changes in perception or sensory processing? How does selection for sensory specialisation shape peripheral and neuronal structures? Does the convergent colonisation of the same micro-habitat produce the same evolutionary solutions? And how are sex-specific behaviours shaped by variation in brain structure? The approach taken can be tailored to the particular interests of the student. Opportunities exist to investigate: i) molecular evolution of sensory receptors, ii) interspecific variation in brain architecture, iii) comparative physiology of sensory adaptations.

ii) The evolution of social caterpillars Gregarious behaviour has evolved many times in a wide range of animals. The prevalence of gregarious behaviour poses many interesting evolutionary questions; How is the conflict between competition and cooperation balanced? What are the advantages and what are the costs? But it also poses many mechanistic questions; how do animals sense each other? How do they track each other's behaviour? This project aims to tackle these questions using Heliconiini, a diverse tribe of Neotropical butterflies, as a study system. Gregarious larval behaviour has evolved convergent in multiple independent lineages, and in some cases closely related species differ dramatically in egg laying and larval behaviour. The primary goal of the project is to understand the genetic and behavioural mechanisms that underpin gregarious behaviour, and to investigate the selection pressures shaping behavioural variation across species. The approach taken can be tailored to the particular interests of the student. Opportunities exist to investigate: i) the behavioural mechanisms behind gregarious behaviour, what sensory cues do they use? ii) Ecological correlates of gregarious behaviour; why do they do it? What effects does it have on other aspects of their behaviour? iii) Comparative genomics of convergent gregarious behaviour; how do changes in gene function and regulation produce behavioural variation?

FUNDING These projects are one listed in competition for funding from doctoral training grants and scholarships. Further details can be found from: i) the departmental prospectus: http://www.zoo.cam.ac.uk/-grads/prospec ii) the University's student funding portal: http://www.student-funding.cam.ac.uk Key deadlines for funding applications are: i) BBSRC DTP PhD studentships - application deadline 1st December 2016 ii) NERC DTP PhD studentships - application deadline 4th January 2017

iv) The Cambridge Trust - application deadline for International applicants: 7th December 2016, and for Home/ EU applicants: 4th January 2017 iii) Gates Cambridge scholarships - application deadline for US applicants: 12th October 2016, and for Overseas/EU (non-UK) applicants: 7th December 2016

Interested applicants should contact Dr. Stephen Montgomery (shm37@cam.ac.uk) with a CV and brief summary of research interests.

Stephen Montgomery <shm37@cam.ac.uk>

CardiffU 4 EvolBiol

NERC GW4+ Doctoral Training Program - PhD in Biosciences at Cardiff University:

Is food availability and choice a limiting factor for declining UK Hawfinch populations?

To apply go to: http://courses.cardiff.ac.uk/funding/-R2590.html Project description: Hawfinches in the UK have declined over the past 40 years and the breeding range has contracted to a few well-wooded locations in western Britain. Changes in food availability are suspected as one cause. For example, hawfinches were once pests in traditional stone fruit orchards, but such orchards have largely disappeared. They are dispersed foragers, specialising on the seeds of trees which are patchy in time and space, and roost communally, which may allow them to exchange information about the status and location of food resources. They can move hundreds of kilometres between seasons in relation to variation in food availability, and have recentlybeen found to move over a scale of several kilometres during the breeding season.

This PhD aims to investigate whether food resources are a limiting factor for hawfinch populations in the UK, and whether landscape-scale habitat manipulations could be used as a conservation tool. It will characterise the current diet of Hawfinches, map the distribution of potential food resources and investigate the interplay between food resources and climate. The current diet in the UK will be investigated using molecular techniques (Next Generation Sequencing of faecal DNA)to identify both plant and invertebrate components. This will be based on faecal samples collected by the Hawfinch-Study Network coordinated by RSPB, when they were widespread, and also from contemporary faecal samples from continental Europe where populations are stable. These results will be used to identify what the key food resources are and how this changes through the year.

The dispersed nature of different food sources means that this species forages over large areas across patchy landscapes. Understanding how food sources are distributed, and foraging behaviour, will be essential. RSPB is currently trialling the use of GPS tags to investigate short term local foraging patterns. The student will createa tree species map of the study area based on classification of remote sensing LiDAR and reflectance data to investigate the distribution and abundance of key tree species that have been shown to be exploited by Hawfinches from the diet analysis. The combination of identification of key food resources, resource distribution and behavioural foraging data can be used to identify options for improving forest management to benefit hawfinches.

Finally, the student will examine whether landscape and climate correlates of population change could relate to changes in abundance or fruiting of key food resources identified. Spatially explicit estimates of change in abundance between time periods is available from BTO bird distribution atlases covering both the breeding season and winter.

Training: The student will obtain the broad rangeof training experience needed for modern conservation work, integrating both lab (molecular diagnostics, bioinformatics, tree species mapping) and field skills (survey work, bird handling, faecal sampling, remote sensing), thereby developing skills to fill gaps in the UK's research capacity.

Associated Partners: Thestudent will collaborate with partners at the Royal Society for the Protection of Birds (RSPB) and the Centre for Ecology and Hydrology (CEH), where opportunities to build new links will be encouraged, as well as engage with the development of skills relevant to practical conservation using cutting edge technologies (e.g. LIDAR).

Main supervisor: Dr Pablo Orozco-terWengel

Co-supervisor(s): Mr Paul Bellamy (RSPB Centre for-Conservation Science),Prof William O. C. Symondson (Cardiff University), Dr France Gerard (Centre for Ecology and Hydrology),Dr Ian P. Vaughan (Cardiff University)

Project enquiries Email: orozco-terwengelpa@cardiff.ac.uk or symondson@cardiff.ac.uk Host institution: Cardiff University

CASE Partner: RSPB Centre for Conservation Science Closing Date: 6/01/2017

Duration: 3.5 years

Starting Date: September 2017

Funding Amount: UK/EU tuition fees plus stipend (14,296 per annum for 2016/17, updated each year).

Level of Study: Postgraduate Research

Eligibility:

Residency: The NERC GW4+ DTP welcomes applications from both UK and EU applicants.

[DEL: All EU applicants must have been ordinarily resident in the EU for at least 3 years prior to the start of their proposed programme of study. Due to funding regulations there are fewer studentships available for EU students who have not been resident in the UK for at least 3 years prior to the start of this course. By using a mixture of NERC and Cardiff University funding all studentships will be fully funded. :DEL]

— / —

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

CardiffU LocalAdaptation

BBSRC SWbio Doctoral Training Program - PhD in Biosciences at Cardiff University:

Unravelling local adaptation in the genome of British sheep

To apply go to: http://courses.cardiff.ac.uk/funding/R2865.html Project description: Understanding how species adapt to the environment they live in is a major goal in evolutionary biology. This is of particular value in light of climate change, where extant species will have to adapt to warmer and potentially harsher conditions relatively fast. However, identifying the genomic regions involved in local adaptation has been a challenging problem because the tools to survey species' genomes have only become available in the last two decades, e.g. SNP arrays and whole genome sequencing. The aim of this project is to analyse British sheep occurring in contrasting environments (mountain vs. lowland) using the OvineSNP50 arrays (~51,000 SNPs) to identify genetic variation linked to local adaptation in the UK's heterogeneous agricultural landscape. Additionally, the SNP arrays data will be analysed in combination with whole genome data for a population of Iranian wild mouflon (the sheep's ancestor) and other sheep breeds in order to identify genomic signatures of selection specific to the domestication event.

The PhD student will be based 80% at Cardiff University, where the research group specialises in identifying signatures of selection using next generation sequencing in livestock and wildlife, and 20% at Bristol University, a world leader in the development of statistical approaches to study demographic history using genetic data. For this project the PhD student will be trained in sample preparation for SNP chip analysis and bioinformatics analyses (e.g. data quality filtering, demographic analyses, and identifying signatures of selection). This experimental design will allow the PhD student to compare populations of British mountain vs. lowland sheep, in the equivalent of a replicated experiment, to identify specific signatures of local adaptation to the environment where these populations live in, while controlling for confounding factors such as the demographic history (to be simulated with approximate Bayesian computation) and the selection signature left by the domestication process (to be accounted for by comparing domestic sheep against Iranian wild mouflon).

Training: The student will obtain the broad range of training experience needed for genomic analysis integrating wet lab (i.e. molecular genetics) and bioinformatics (e.g. population modeling and selection scans), thereby developing skills to fill a gap in the UK's research capacity.

Collaborators: The student will collaborate with partners at the Parco Tecnologico Padano (Italy) who will contribute to SNP array analysis and training.

Main supervisor: Dr Pablo Orozco-terWengel Co-supervisor(s): Prof. Mark Beaumont (Bristol University), Prof. Mike Bruford (Cardiff University)

Project enquiries Email: orozco-terwengelpa@cardiff.ac.uk

Host institution: Cardiff University

Closing Date: 5/12/2016

Duration: 4.0 years

Funding Amount: UK/EU tuition fees plus stipend (pounds 14,296 per annum for 2016/17, updated each year).

Level of Study: Postgraduate Research

Start Date: September 2017

Eligibility: The Doctoral Training Partnership welcomes applications from both UK and EU applicants; however, as a consequence of the EU referendum result, final award decisions will depend on the outcomes of the UK/EU negotiations. If the Research Council (BBSRC in this instance) withdraws funding for EU students, all EU applicants will be ineligible for entry into the SWBio BBSRC DTP. All EU applicants must have been ordinarily resident in the EU for at least 3 years prior to the start of their proposed programme of study. Due to funding regulations there are fewer studentships available for EU students who have not been resident in the UK for at least 3 years prior to the start of this course. By using a mixture of BBSRC and Cardiff University funding all studentships will be fully funded.

Academic criteria: Applicants for a studentship must have obtained, or be about to obtain, a First or Upper Second Class UK Honours degree, or the equivalent qualifications gained outside the UK, in an appropriate area of science or technology. Applicants with a Lower Second Class degree will be considered if they also have a Master's degree or have significant relevant non-academic experience.

In addition, due to the strong mathematical component of the taught course in the first year and the quantitative emphasis in our projects, a minimum of a grade B in A-level Maths or an equivalent qualification or experience is required.

If English is not your first language you will need to have achieved at least 6.5 in IELTS (and no less than 6.5 in any section) by the start of the programme. Please refer to the relevant institution for further

— / —

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

---

CotedIvoire TrematodePopulationGenetics

The Swiss Tropical and Public Health Institute (Swiss TPH) is a public institution with the mandate to contribute to the improvement of the health of populations internationally and nationally through excellence in research, services, and teaching and training. We are looking for a highly motivated student for a

PhD Thesis on Trematode Population Genetics in Côte d'Ivoire

The student will investigate the transmission dynamics of all Fasciola and Schistosoma species occurring in humans and animals in Côte d'Ivoire. The thesis will primarily be based in Basel but includes field trips. The student is expected to develop/optimize methods for DNA extraction, storage and analysis from single parasite eggs in animal and human stool and urine, establish optimal population genetic markers for Fasciola and Schistosoma species, and analyze parasite population structure and transmission dynamics in Côte d'Ivoire using population genetic approaches.

Absolutely required are: - hands-on experience with basic molecular techniques (DNA extraction, PCR, sequencing), - hands-on experience with population genetics and phylogeography, - very good written command of English, - high level of self-reliance and stress tolerance, - willingness to work under difficult conditions.

The ideal candidate further combines the following qualifications: - master's thesis on a related topic, - good oral command of French and German, - desire to collaborate with others both locally and internationally, - track record of scientific publications.

We offer a challenging Swiss National Science Foundation-funded 3-year PhD position in the Human and Animal Health Unit, a very diverse group with long-running links to our partners in Côte d'Ivoire. The PhD student will collaborate with other scientists at Swiss TPH and in Africa. A tentative starting date is January 1st, 2017. For further inquiries please contact oliver.balmer@unibas.ch. Please submit your application (letter of max. two pages, CV and two references) as a single pdf file to oliver.balmer@unibas.ch.

–

Dr. Oliver Balmer Project leader Tel. +41 (0)61 284 8748 oliver.balmer@unibas.ch

Swiss Tropical and Public Health Institute Socinstrasse 57, 4051 Basel, Switzerland www.swisstph.ch
"oliver.balmer@unibas.ch" <oliver.balmer@unibas.ch>

DurhamU PlantEvolutionaryGenetics

PhD project: The evolution of inbreeding depression in wild flax and implications for crop development. Project based at Durham University, UK.

Funding details: Durham/Newcastle/Liverpool BBSRC Doctoral Training Partnership, 4 years starting from Oct 2017, competitive selection process, full funding for UK resident applicants, university fees only for EEA applicants

Supervisory team: Dr Adrian Brennan, Prof Rus Hoelzel (Durham), Dr Kirsten Wolff (Newcastle)

Application: CV and covering letter to a.c.brennan@durham.ac.uk before 5th Jan 2017

Summary: Avoidance of inbreeding depression is understood to be a major force driving the evolution and maintenance of sexual outcrossing reproductive systems. Surprisingly little is known about reproductive system and fitness in wild flax, a potentially valuable source of genetic variation for crop improvement. We will use new genotyping by sequencing technologies to obtain an unprecedented genome-wide perspective on inbreeding and its evolution, allowing the identification of relevant genes and molecular mechanisms. These insights could then be applied to genetic improvement of flax to sustainably enhance agricultural production as well as improve our understanding of this fundamental aspect of evolution.

More information: See https://www.dur.ac.uk/-biosciences/postgrad/current_phd/brennanbbsrc16/ Contact Dr Adrian Brennan at the email address provided above with any other questions.

"BRENNAN, ADRIAN C." <a.c.brennan@durham.ac.uk>

ETHZurich Eawag ImmuneDefenseEvolution

A PhD student position is available in the group of aquatic ecology at ETH Zurich (Swiss Federal Institute of Technology Zurich) / Eawag (Swiss Federal Institute of Aquatic Research), Switzerland

to study natural selection on immune function at gene expression level. Parasites present a serious threat for natural populations of free-living species. Immune defence is generally considered as an important trait in determining organisms' fitness as it eliminates harmful parasites. Therefore, understanding the evolution of immune defence is one of the key topics in predicting dynamics of host-parasite interactions. However, knowledge on the type and strength of selection on immune defence traits is very limited. The goals of the project are to assess (1) the type and strength of natural selection on the expression of several immune defence genes/pathways, (2) variation in selection imposed by infection risk, (3) trade-offs related to immune activity, and (4) local adaptation of hosts to parasites in the wild. The study system is a freshwater snail Lymnaea stagnalis, and the work utilises the recently sequenced transcriptome of this species. The work will be conducted in c ollaboration with the Prof. Coen Adema (University of New Mexico) and the Genetic Diversity Centre at ETH (http://www.gdc.ethz.ch/).

General information about the research group can be found at http://www.ae.ethz.ch/ We invite highly motivated students with a good background in transcriptomics and evolutionary ecology to apply for the position. A MSc or equivalent degree is required. Earlier experience with the study system is not required. The project is funded by Swiss National Science Foundation for 3 years.

Earliest starting date: February 1, 2017

Qualified persons are invited to apply by email. Please attach a single PDF file including a letter of motivation, CV, and names plus contact information of two references to otto.seppaelae@env.ethz.ch. Subject line should read "PHD-Position 2016". Evaluation of applications starts November 7, 2016. Top candidates will be interviewed.

Dr. Otto Seppälä

"Otto.Seppaelae@eawag.ch"

GeorgiaSouthernU PlantEvolution

M.S. Position, Plant Evolution and Systematics, Georgia Southern University

The Schenk lab at Georgia Southern University invites applicants for a Masters Degree in plant systematics and evolution, starting Fall semester, 2017. Our lab group is interested in how botanical diversity has been shaped by the interactions among morphological, ecological, and species diversification. We apply statistical phylogenetic approaches that quantify and incorporate molecular, morphological, and ecological variation to plant systems in order to understand the evolutionary processes of how and why species diversify.

An ideal candidate will have interest in using plant systems to better understand the evolutionary processes of diversification by applying statistical phylogenetic approaches. Competitive students that meet all requirements will be supported with either a teaching or research assistantship.

Interested students should contact Dr. John Schenk (jschenk@georgiasouthern.edu) prior to submitting an application (the earlier the better).

For more information, visit the Schenk lab website (https://sites.google.com/a/georgiasouthern.edu/-schenk) and the Department of Biology's website (http://cosm.georgiasouthern.edu/biology). More information about the Biology graduate program can be found at the departmental web page (http://-

cosm.georgiasouthern.edu/biology/graduate-program-2/).

Additional questions about the GSU graduate program can be directed to the Graduate Student Program Director: Dr. Checo Colon-Gaud (jccolon-gaud@georgiasouthern.edu). For full consideration, the application deadline is March 1st, 2017.

John J. Schenk, Ph.D.

Assistant Professor of Plant Biology Georgia Southern University Herbarium (GAS), Curator Department of Biology 4324 Old Register Road Georgia Southern University Statesboro, GA 30460-8042

Office: 2260 Biology Building Office phone: (912) 478-0848

Lab website: sites.google.com/a/georgiasouthern.edu/schenk

Herbarium website: sites.google.com/a/georgiasouthern.edu/gasherbarium

jschenk <jschenk@georgiasouthern.edu>

GuangxiU EvolBiol

InternationalGraduate Program 2017 with multiple MSc and PhD positions available at the College of Forestry of Guangxi University, Nanning, China

ThePlant Ecophysiology and Evolution Group, Conservation Biology Group and Forest Dynamics Research Laboratory at Guangxi University (Nanning, China) are seeking highly motivated and productive International MSc and PhD students to engage in 3-4 year projects, starting in 2017, in the following research fields:

(1)Plant Ecophysiology -A:Plant Physiological Ecology including water relations -B:Functional Plant Anatomy -C:Photosynthesis and Photoprotection -D:Functional traits and community assembly of subtropical forests Projectsare supervised by Prof. Kun-Fang Cao (kunfang.cao@gxu.edu.cn or caokf@xtbg.ac.cn) and Associate Prof. Shidan Zhu (zhushidan@gxu.edu.cn) . Moreinformation here: http://www.plant-ecophysiology-evolution.com/-person/cao-kunfang/ http://www.plant-ecophysiology-evolution.com/person/shi-dan-zhu/ (2) Biodiversity Genomics -A:Plant Genomics and Evolutionary Diversification -B:Molecular Systematics and Plant Taxonomy -C:Historical Plant Biogeography and Biome Assembly Projectsare supervised by Associate Prof. Joeri S. Strijk (jsstrijk@gxu.edu.cn). Moreinformation here: http:/-/www.plant-ecophysiology-evolution.com/person/-joeri-sergej-strijk/ http://www.asianfagaceae.com/ (3) Genetics -A:Ecological Genomics. -B:Conservation Genetics. Projectsare supervised by Associate Prof. Alison Wee (alisonwks@gmail.com). Moreinformation here: http://www.plant-ecophysiology-evolution.com/-person/alison-kim-shan-wee/ (4) Seed Ecophysiology -A:Seed Ecology and Physiology Projectsare supervised by Associate Prof. Uromi Goodale (uromi.goodale@outlook.com). Moreinformation here: http://www.plant-ecophysiology-evolution.com/-person/uromi-manage-goodale/ (5)Ecophysiology and Coevolution -A:Plant Ecophysiology of Mangroves. -B:Phylogenetics and Coevolution in Gymnosperms. Projectsare supervised by Dr. Jiang Guofeng (gfjiang@gxu.edu.cn). Moreinformation here: http://www.plant-ecophysiology-evolution.com/-person/jiang-guofeng/ (6)Ecology -A:Animal Behaviour. -B:Breeding and Nesting Ecology. -C:Ecotoxicology. -D:Social and Economic Influences on Conservation Species Interaction Networks. -E:Urban Ecology. Projectsare supervised by Faculty members of the Conservation Biology Group (Prof. Eben Goodale (eben.goodale@outlook.com), Dr. Aiwu Jiang, Dr. Christos Mammides, Dr. Myung-bok Lee, Dr. Ari Martinez). Moreinformation here: http://animal-ecology-guangxi.com/ (7)Tropical Forest Botany and Ecology

-A:Biodiversity Monitoring Forest Plots in Guangxi Province. -B:Distribution and composition of the Philippine Island Flora: phylogenetics, ecological features, plant functional and reproductive traits.

Projectsare supervised by Prof James V. LaFrankie of the Forest Dynamics Research Laboratory

https://www.researchgate.net/profile/-James_Lafrankie3 TheInternational Graduate Program at the College of Forestry offers fully funded MSc and PhD Fellowships for 4-year projects, with complete waivers for tuition fees and housing fees. Housing is provided in the International Student dormitories of the campus in Nanning. The first year will consist of orientation and study of Chinese language through courses in combination with introductory courses taught by faculty members of the three research groups. The other three years will be filled with fieldwork, professional courses and the research project.

Projectapplications are now invited for starting dates of projects in September 2017. The application deadline is March 31, 2017. Fellowships come with an ample monthly allowance for the full duration of the project. Applicants with a proven track record of successful publication in peer-reviewed journals will have an advantage.

Opportunitiesfor the development of individual research projects as well as collaborative work, exist within our lab and with external groups. Candidates will be integrated in growing and multidisciplinary teams of Chinese and foreign researchers, providing a creative and stimulating research environment, and will work as part of teams studying the evolution, ecology, distribution, conservation and/or ecophysiology

— / —

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

ImperialC London 12 Evolution

The Quantitative and Modelling Skills in Ecology and Evolution (QMEE) CDT is pleased to announce 8 NERC-funded PhD studentships plus 4 institutional PhDs starting in October 2017.

The QMEE CDT will train a cohort of researchers in Ecology and Evolution with the quantitative and modelling skills to solve real-world problems by connecting theory, data, and practice. To view example projects, instructions on how to apply and information on eligibility please visit our website.

The deadline for applications is 19th January 2017.

For any questions, please contact Ibi Wallbank, Departmental Manager, at qmee.cdt@imperial.ac.uk

Please help disseminate this opportunity to anyone you think may be interested.

QMEE CDT <qmee.cdt@imperial.ac.uk>

ImperialCollegeLondon Adaptations

Two phd projects (theoretical and empirical):

Offering two PhD studentships, one with a more theoretical focus and one with an empirical research focus, on trans-generational effects. The current speed at which environmental conditions change is unprecedented, endangering vulnerable populations and species. A novel idea for how organisms can sustainably respond to rapid environmental changes are environmentally induced adaptations that are heritable. Such trans- generational, potentially epigenetic effects can, with high precision mediate evolutionary rescue of populations that experience rapidly changing environments. These advantages put TAGs at the forefront of mechanisms leading to adaptations to global change. These projects will use a wild population of passerines, and experiments in captivity, to disentangle phenotypic plasticity induced during development from epigenetic TAGs, to better understand the epigenetic mechanism, and evolution of TAGs. We will use molecular analysis (telomeres, methylation), physiology and behavioural observations to test the hypotheses. The theoretical project will use population modelling and individual-based simulations infer evolutionary consequences of TAGs.

For both projects, you should have solid foundation in quantitative biology. Experience in advanced statistical methods using R is an advantage for both projects. The empirical project requires a student willing to conduct fieldwork in the UK during the breeding season of each year. A bird ringing license (BTO) is not required, but a big advantage. Students applying for the theoretical project should be highly quantitative and have at least some programming experience.

The Silwood Park Campus is a vibrant graduate campus one hour by train from London City with more than 120 graduate students from countries all over the world. https://www.imperial.ac.uk/visit/campuses/silwood-park/prospective- students/life-at-silwood/ Silwood's academics are world-class scientists, and we offer a range of graduate courses to improve hard and soft skills. https://www.imperial.ac.uk/visit/campuses/silwood- park/research/

To apply, please send your CV, a motivation letter detailing your relevant expertise, and contact information for two references to: Julia.schroeder@imperial.ac.uk

Eligibility: To be eligible for a full award a student must have: - Settled status in the UK, meaning they have no restrictions on how long they can stay, - Been ordinarily resident' in the UK for 3 years prior to the start of the studentship. - This means they must have been normally residing in the UK (apart from temporary or occasional absences) - Not been residing in the UK wholly or mainly for the purpose of full-time education. (This does not apply to UK or EU nationals).

For FAQs and to apply please visit: http://www.imperial.ac.uk/grantham/education/science-and-solutions-for-a-changing-planet-dtp/studentship-opportunities/ julia.schroeder@imperial.ac.uk

IST Austria EvolBiol

Dear Colleague,

The Institute of Science and Technology Austria (IST Austria) is looking for highly qualified candidates to apply for our ISTScholar PhD program. We offer fully-funded PhD positions in the natural and mathematical sciences in a world-class research environment on the outskirts of Vienna. The research topics that might interest students in your department include:

Biology

- Barton Mathematical Models of Evolution
- Benkova Hormonal Cross-Talk in Plants
- Cremer Behavioral and Evolutionary Ecology
- Danzl Nanoscale Photonics for Biology
- Friml Developmental and Cell Biology of Plants
- Guet Systems and Synthetic Biology of Genetic Networks
- Heisenberg Cell and Developmental Biology
- Janovjak Synthetic Physiology
- Kicheva Tissue Growth and Developmental Pattern Formation
- Loose Self-Organization of the Cell
- Sazanov Structural Biology of Membrane Protein Complexes
- Siegert Neuroimmunology in Health and Disease
- Siekhaus Invasive Migration of Immune Cells
- Sixt Morphodynamics of Immune Cells
- Tkaèik Biophysics and Neuroscience
- Vicoso Sex-Chromosome Biology and Evolution

Neuroscience

- Csicsvari Systems Neuroscience
- Danzl Nanoscale Photonics for Biology
- Hippenmeyer Genetic Dissection of Cerebral Cortex Development
- Jonas Synaptic Communication in Hippocampal Microcircuits
- Jösch Neuroethology
- Novarino Genetic and Molecular Basis of Neurodevelopmental Disorders
- Shigemoto Molecular Neuroscience
- Siegert Neuroimmunology in Health and Disease
- Tkaèik Biophysics and Neuroscience

Our PhD program is characterized by innovative training with a special focus on interdisciplinarity, close mentoring by outstanding faculty within small research groups, and access to first-rate facilities. Students spend the first year completing coursework and rotations before choosing a thesis group and passing the qualifying exam. Our PhD graduates have gone on to top positions in academia and industry all over the world.

Students with a bachelor's or master's degree in a relevant field are encouraged to apply. We offer internationally competitive salaries co-funded by an EU Marie Sklodowska-Curie grant, full health benefits, and subsidized on-campus housing in the first year.

For more information about the ISTScholar PhD program and application process, as well as faculty profiles, please visit our website at http://phd.ist.ac.at, or come to our Student Open Day on November 25th (register at: http://ist.ac.at/studentopenday).

The deadline for PhD applications is January 8th 2017 for a start date in September 2017.

Yours sincerely,

Hania Köver, Ph.D. Head of the Graduate School Office

Institute of Science and Technology Austria

gradschool@ist.ac.at

IST Austria Gradschool_Student Open Day 2016_banner_medium < http://ist.ac.at/studentopenday >

Nov 25, 2016 (Friday)

Lab Tours | Meet the Profs | Campus Tours | Internships | PhD Program | Think & Drink Talk

Register here for the Student Open Day: http://ist.ac.at/studentopenday gradschool@ist.ac.at

Kansas DrosophilaEvolGenetics

KUDrosophila Biology Graduate Student Recruitment for Fall 2017

Drosophilaresearch labs in the departments of Molecular Biosciences (MB) and Ecology and Evolutionary Biology (EEB) at the University of Kansas seek talented applicants for graduate admission to begin study in the Fall of 2017. Our strengths include evolutionary and quantitative genetics, behavior and development with labs working on specific projects including genetic conflict, mating behavior, the genetics of complex traits, the evolution of immunity and limb development.

Pleasevisit: http://kuflygroup.weebly.com for more details.

Facultymembers:

JustinBlumenstiel (genetic conflict, EEB, can take students through MB) JenniferGleason (evolution and genetics of courtship behavior, EEB, can take students through MB) StuartMacdonald (genetics of complex traits, MB) RobUnckless (evolution of immunity and genetic conflict, MB, can take students through EEB) JamieWalters (sex chromosome evolution and reproductive proteomics in lepidoptera, EEB) RobWard (tissue growth and morphogenesis, MB)

Applicantsto the EEB program (https://eeb.ku.edu/-prospective-students) are admitted directly to work with a specific advisor while applicants to the MB program (https://molecularbiosciences.ku.edu/-graduate-program-faqs) complete a rotation cycle before choosing a laboratory. Interested candidates should peruse the MB faculty website (https://-molecularbiosciences.ku.edu/faculty) and the EEB faculty website (https://eeb.ku.edu/faculty) and contact the department or specific faculty members for more information.

Applicationmaterials can be found at:

MolecularBiosciences - http://-molecularbiosciences.ku.edu/admissions Ecologyand Evolutionary Biology - https://eeb.ku.edu/how-apply Deadlinesfor Fall 2017 admission:

MolecularBiosciences - December 15, 2016 Ecologyand Evolutionary Biology - December 1, 2016

EEBand MB are both diverse departments ranging from ecosystem ecology to biophysics with significant interaction within and between groups.

AboutKU:

TheUniversity of Kansas is located in Lawrence, KS, less than an hour from Kansas City. Lawrence, Kansas is a terrific place to live, with a vibrant downtown, fantastic restaurants, lively arts scene, and beautiful rural scenery. The KU campus is an exciting, beautiful, invigorating environment with highly active research faculty.

EEOStatement:

TheUniversity of Kansas prohibits discrimination on the basis of race, color, ethnicity, religion, sex, national origin, age, ancestry, disability status as a veteran, sexual orientation, marital status, parental status, gender identity, gender expression, and genetic information in the university's programs and activities. Retaliation is also prohibited by university policy. The following persons have been designated to handle inquiries regarding the nondiscrimination policies and are the Title IX coordinators for their respective campuses: Executive Director of the Office of Institutional Opportunity & Access, IOA@ku.edu, 1246 West Campus Road, Room 153A, Lawrence, KS 66045, 785-864-6414, 711 TTY (for the Lawrence, Edwards, Parsons, Yoder, and Topeka campuses); Director, Equal Opportunity Office, Mail Stop 7004, 4330 Shawnee Mission Parkway, Fairway, KS 66205, 913-588-8011, 711 TTY (for the Wichita, Salina, and Kansas City, Kansas medical center campuses).

unckless@ku.edu

KansasStateU MicrobialEvolution

The Platt lab at Kansas State University is recruiting PhD or MS graduate students interested in the evolution and population dynamics of bacterial pathogens. Our current research projects focus on the evolution and ecology of cooperative pathogenesis, the impact of quorum sensing and plasmid dynamics on bacterial competition, and interspecific interactions occurring within rhizosphere microbiomes. We integrate theoretical and quantitative ecology and evolution with microbial genetics using the plant pathogen Agrobacterium tumefaciens. Funds are available for partial support of a Graduate Research Assistant working on an NSF-funded grant to develop a high-throughput platform to identify interactions within microbiomes. Please visit www.platt-lab.com for more information about our work and current projects.

Our lab is in KSU's Division of Biology (http://-

www.k-state.edu/biology/), which houses the Ecological Genomics Institute (http://www.k-state.edu/biology/interdisciplinary/egi.html) and the Konza Prairie Biological Station (http://www.k-state.edu/biology/interdisciplinary/konza.html). For information about graduate studies at KSU's Division of Biology please visit: http://www.k-state.edu/biology/grad/index.html. We offer competitive research assistantships and fellowships that cover stipend, tuition, and medical insurance. Kansas State University is in Manhattan, Kansas in the Flint Hills region of Kansas. The town offers excellent schools, parks, and a college town atmosphere. The surrounding area features many outdoor opportunities including the nearby Tuttle Creek State Park and Konza Prairie, a tallgrass prairie reserve and LTER site.

If interested please contact Tom Platt (tgplatt@ksu.edu) with a brief statement of your research interests and experiences and your CV.

"tgplatt@ksu.edu" <tgplatt@ksu.edu>

KansasStateU PlantEvolution

Ph.D. Student Position in Land Plant Evolution

Kansas State University

The Schrick lab in the Division of Biology at Kansas State University is seeking candidates to fill a Ph.D. student position in the area of Evolutionary Biology to begin in the Fall Semester of 2017. We are studying the molecular events leading to the appearance of the land plants from charophycean green algae ~450 million years ago. Colonization of terrestrial environments by plants required critical changes in the epidermis to protect against desiccation and solar radiation. One potential project focuses on homeodomain regulatory proteins and flavonoid biosynthesis genes that were required for elaboration of the epidermis. This research utilizes the emerging genomics model system Penium margaritaceum as well as functional studies in Arabidopsis, and has implications for uncovering mechanisms underlying adaptation to climate change. Work in the Schrick lab is interdisciplinary and collaborative, and involves interactions with the Ecological Genomics Institute, Bioinformatics Center, Integrated Genomics Facility, the Biotechnology/Proteomics Core Lab, as well as the Kansas Lipidomics Research Center at Kansas State University.

For more information see http://www.k-state.edu/schricklab/Schrick_Lab/Welcome.html. A link to the Division of Biology at Kansas State University can be found at http://www.k-state.edu/biology/. Learn more about the Ecological Genomics Institute at http://ecogen.k-state.edu/. Qualified applicants should submit an email message (with "Ph.D. position" in the subject line) containing a cover letter, academic transcript from relevant undergraduate degree, GRE scores, and CV, including contact information for three academic references, to kschrick@ksu.edu by December 1, 2016.

Kathrin Schrick Associate Professor Molecular, Cellular and Developmental Biology (MCDB) Biochemistry and Molecular Biophysics Graduate Group (BMBGG) Division of Biology 116 Ackert Hall Kansas State University Manhattan, KS 66506-4901 Tel (office) (Ack 303): +1-785-532-6360 Tel (lab) (Ack 321): +1-785-532-7322 Fax: +1-785-532-6653 Email: kschrick@ksu.edu http://www.k-state.edu/schricklab Kathrin Schrick <kschrick@ksu.edu>

KingAbdullahU CoralAdaptations

Dear EvolDir listers,

We are looking for a MS student to join our group at the Red Sea Research Center of the King Abdullah University of Science and Technology (KAUST) next fall.

The proposed project focuses on studying evolutionary adaptations underlying the coral-dinoflagellate symbiosis. As part of this project the candidate will use spatial transcriptomics data from our model organism *Aiptasia* to identify putative candidate genes involved in symbiosis maintenance and to trace their evolutionary origins and adaptations using phylogenomic approaches.

We are seeking highly motivated, self-dependent applicants with an interest in molecular biology and/or genomics. Desired qualifications are experience in molecular biology, bioinformatic analyses and/or immunohistochemistry. The candidates will be working in an international research environment and are expected to be proficient in spoken and written English.

The King Abdullah University of Science and Technology (KAUST) is located directly on the Red Sea on more than 36 square kilometers encompassing state-of-the-art research facilities as well as housing and recreational facilities for the campus community. More information is available at www.kaust.edu.sa. The MS student package includes: a generous annual stipend, remission of tuition, housing, relocation, yearly repatriation travel, and medical insurance. Interested candidates should send a short motivation letter and up-to-date CV to manuel.aranda@kaust.edu.sa.

Best,

Manuel Aranda

Manuel Aranda Lastra Assistant Professor Red Sea Science and Engineering Research Center 4700 King Abdullah University of Science and Technology (KAUST) Building 2, 2216 Thuwal 23955-6900, Kingdom of Saudi Arabia Mobile: +966 544700661 Office: +966 2808 2979

<manuel.aranda@kaust.edu.sa>

LavalU GymnospermPopGenetics

One MSc position is available for a motivated student interested in the study of population genetics of endemic gymnosperms The MSc program will be pursued at the Biology Department of Laval University (https://www.bio.ulaval.ca/accueil/) and part of the BESS program (CREATE, https://www.mcgill.ca/bess/bess). The project is in collaboration with colleagues of the Smithsonian Tropical Research Institute.

Project description:

Population genomics of endangered Zamia species:

Recent estimates suggest that 65% of all cycads are endangered (Fragniere et al. 2015, J. Biog.). Among Neotropical countries, Panama has a high endemism with 65% of endemic Zamia species (a total of 17 described for the isthmus, Taylor et al. 2012). Human development and poaching activities due to the ornamental value of the Isthmian Zamias are threatening the habitats where these plants naturally occur. As part of a long-term program to study the diversity of Panamanian zamias and their symbionts (nitrogen-fixing bacteria and fungi) we are looking for a motivated MSc student to study the species Zamia pseudoparasitica. This species, endemic to Central Panama, is the only strictly epiphytic gymnosperm and the genetic diversity is unknown. The project consists in collecting, culturing and genotyping populations of Zamia pseudoparasitica in the country. Additionally, the student will be contributing to the current efforts to assess endophyte diversity, the functional genomics of the association and their chemical diversity. Assessing multiple, sequenced genomic regions of diverged populations of Z. pseudoparasitica will aid in understanding the genetic diversity and channel efforts to pursue genetic and demographic rescue of less diverse populations in Panama.

The successful candidate must have strong field skills, adaptabil ity; a background in bioinformatics is preferred. Also, it is desirable a strong background in biology and willingness to learn French. We are looking for an in dividual who is highly self-motivated and can work independently. Field and most lab work will be conducted in Panama, at STRI, while the student must take a fe w courses (in French) at Laval University. Additionally, the student will be wor king at the Institute of Integrative Biology and systems of Laval University (ht tp://www.ibis.ulaval.ca/).

To be considered, please send a single PDF file merged from the f ollowing parts: CV including publication list, academic transcripts, a statement of research interests not exceeding two pages, and the name of two academic ref erences to juan-carlos.villarreal-aguilar@bio.ulaval.ca. The statement should i nclude the student's initiative to obtain a fellowship for tuition. Applicatio ns will be considered until December 15, 2016, or until the position is filled, whichever comes first. The position is available from the winter or summer of 20 17.

Juan Carlos Villarreal Aguilar <juan-carlos.villarreal-aguilar@bio.ulaval.ca>

McGillU Biodiversity Jan15

The NSERC-CREATE on Biodiversity, Ecosystem Services and Sustainability is recruting PhD and MSc students interested in, but not restricted to, biodiversity, ecology, evolution, conservation, environmental management, and human-environment interactions. The BESS Program provides a multidisciplinary and immersive training experience to help prepare the next generation of environmental scientists to work with industry, environmental consulting firms, governments, NGOs, and universities. BESS training provides students with skills in environmental monitoring, biodiversity surveying, ecological impact assessment, mitigation strategies, the design of restoration projects, statistical analysis, adaptive forest and agricultural management, and mathematical modeling for predictive and prescriptive planning.

The Program has a strong multidisciplinary component and a diverse group of researchers and collaborators Quebec universities, Canadian companies working in

Panama, and several Panamanian institutions, particularly the Smithsonian Tropical Research Institute who administer and supervise complementary courses, an internship rotation, and thesis research. BESS also provides students with an immersive experience through courses and internships in Panama, and elsewhere in the Neotropics.

BESS provides funding to students in the form of stipends and travel allowances. There are no citizenship restrictions. Stipends are given on an individual basis and depending on budget availability, but will not surpass $14,000 CAD per year. Students who are holders of a major fellowship (NSERC, NSF, Fullbright, etc.) will receive a $5000 CAD per year top-up. In addition, all students are eligible for up to $1500 CAD per year to travel to internships, conferences, courses and/or fieldwork.

Applicants must first contact a potential supervisor in one of the three partnering universities (McGill, Laval and UQAM). Students must then apply to the supervisor's department. All students must meet the admission criteria of Graduate and Postdoctoral Studies at the university and the entrance requirements of the specific department.

Candidates applying to BESS will be considered by the Program Delivery Committee, who will take into account the following criteria:

Academic background Relevance and viability of proposed research Accordance and suitability with BESS goals

*Priority will be given to students working with a BESS lead reasearcher.

DEADLINE: JANUARY 15TH, 2017. FOR INFORMATION ON HOW TO APPLY VISIT: https://-www.mcgill.ca/bess/apply

Felipe Pérez-Jvostov BESS Postdoctoral Fellow and Program Coordinator http://www.mcgill.ca/bess/bess Stewart Biology Building N3/12B 1205 Avenue du Docteur-Penfield, Montréal, QC.

BESS- NSERC CREATE <bess.redpath@mcgill.ca>

Melbourne GeneticAdaptation

The Hodgins lab is currently seeking outstanding PhD candidates interested in studying plant ecological genomics (www.hodginslab.com). Our laboratory studies the genetic basis for adaptation in plants. We are particularly interested in using introduced species as a model for studying rapid adaptation. We also study adaptation to climate in forest trees and plant domestication. To address evolutionary questions relating to these topics, we use a combination of genomics, ecological fieldwork and experimental approaches.

The project can commence any time during 2016/17 and will be developed in collaboration with the student (but see potential project descriptions). Teaching is not required for the duration of the PhD (3.5 years in Australia). Research funding as well as attendance in one conference per year is guaranteed.

Successful candidates will be fully funded for 3.5 years with an annual tax-free stipend of approximately $26,000 AUD, which includes tuition and medical cover. Fully funded PhD stipends are available for either international students or domestic students.

Melbourne is diverse and thriving city with a desirable climate. It is one of the most livable cities in the world and is a cultural and recreational hub.

Monash is a member of the Group of Eight, a coalition of top Australian universities recognized for their excellence in teaching and research.

The School of Biological Sciences is a dynamic unit with strengths in both ecology and genetics and the nexus between these disciplines.

Please send your CV, a transcript, a brief statement of your research interests and the contact details of two referees to kathryn.hodgins@monash.edu.

Potential project descriptions Replaying the evolutionary tape: the genetics of parallel adaptation Repeated adaptations to similar selective environments certainly occur.

The recurrent evolution of pesticide resistance, as well as parallel geographic patterns of flowering time invasive plants stand out as classic case studies. Given the involvement of chance and the myriad of possible ways a species could evolve, why are the phenotypic outcomes often so consistent? Is adaptive evolution of phenotypes to similar environments always highly repeatable, or is our attention diverted to a biased selection of examples? Even if similar phenotypes evolve independently in different geographic regions, are they as alike as they appear: could different genetic mechanisms be responsible in some cases?

This project aims to gain insight into the repeatability of local adaptation, and the genetic constraints that may underlie this, using a set of replicated range expansions along major climatic gradients. The annual plants

Cakile maritima and Cakile edentula (both 2n) evolved along parallel gradients of great climatic range (over ~30o of latitude) on either side of the North Atlantic in a narrow coastal habitat. They have since undergone human-assisted introductions and subsequent range expansions in multiple regions (e.g. western North America, Australia, New Zealand, Japan, South America). Thus, we can compare local adaptation during range expansions differing in evolutionary timescales (millennia for post-glacial spread in native ranges vs. decades in their exotic ranges) in the same species as well as between species. Moreover, each invasion arises from unique combinations of source and recipient climates. Adaptation is potentially ongoing, since they are still expanding their exotic geographic ranges. These species afford us an exciting opportunity to examine fundamental evolutionary hypotheses about the genetic basis of adaptation outside the laboratory, in ecologically realistic experimental conditions.

Reconstructing the genetics of rapid adaptation using historic DNA Invasive species are increasingly commonplace as human activities accidentally or intentionally move species or their propagules from place to place. When species are first introduced to a new location they must often contend with new abiotic environments, different species, and a lack of mates. How do introduced species manage to overcome these barriers to their survival and reproduction? In some cases species may be genetically predisposed to thrive in their new environment, or possess high levels of plasticity. In other cases newly introduced populations may have to adapt genetically to their local environments. Although invasive species have substantial economic and environmental consequences, they represent success stories for how organisms can deal with novel environments. These species offer an exciting avenue to address fundamental evolutionary questions, as each introduction can be analogous to a natural experiment where adaptation to local environments can begin anew. The species Ambrosia artemisiifolia is a highly successful invasive species showing strong evidence for rapid local adaptation of flowering time in the introduced

— / —

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

---

Melbourne MonashU ExperimentalEvolution

Experimental evolution of microbes

A fully funded PhD position is available in the research group of Dr. Michael McDonald to undertake research at the interface of evolutionary genetics and microbial ecology. The project will involve the handling and passaging of yeast and bacteria, whole genome sequencing, cutting edge molecular genetic techniques and DNA sequence data analysis. Specifics of the research project will be discussed upon application.

The ideal candidate for this scholarship will have some basic microbiology or molecular biology skills and experience with computer programming or statistical analysis. A strong background in evolutionary biology is of an advantage, but not strictly necessary.

The studentship covers all university fees and includes an annual

stipend of AUD$26,300. The Monash University PhD program has been adapted to the multiple potential career outcomes of the 21^st century PhD graduate, including extensive training and support.

Applicants must have a BSc(Hons) or MSc degree in a relevant discipline. Both local and international students are encouraged to apply.

Monash University is located in Melbourne- a city consistently ranked as the most livable city in the world. Monash is one of Australia's prestigious group of eight research institutions- this is your chance to work in a collegial, research intensive environment with access to excellent facilities.

To apply for the position, please send a cover letter stating your

Research interests, a Curriculum Vitae, a copy of your academic transcript, and the names of two referees.

Enquires and applications should be sent to Dr. Michael McDonald at

mike.mcdonald@monash.edu

for more information see:

http://www.mcdonald-lab.com/ Mike McDonald <mike.mcdonald@monash.edu>

MemorialU CapelinAdaptation

The PhD student will integrate information generated from geneticists and evolutionary biologist on stock structure and local adaptation with local ecological knowledge. It could be an asset for any evolutionary biologists that might be interested in working with indigenous people or in a northern context in the future.

Ph.D. Opportunities Integrating scientific and local ecological knowledge towards improving capelin stock management

In partnership with Duke University, the Centre for Fisheries Ecosystems Research (CFER) at Memorial University is seeking candidates to undertake a multidisciplinary PhD project aimed at incorporating scientific and local ecological knowledge and the findings of an observer network towards improving policies and management practices for the sustainability of capelin fisheries and conservation. This PhD project is part of a larger research project entitled “Integrating genomics, phenotypes and local ecological knowledge towards improving capelin stock management in Canadian Atlantic and Arctic waters”. Despite capelin’s economic, social and ecological value in Canada, its populations remain largely unknown, particularly in northern regions. We will rigorously document genetic population structures, local adaptations, biological characteristics and population dynamics for capelin in the boreal, subarctic and Arctic regions of eastern Canada, and will document the connectivity between capelin stocks in Canadian and Greenland waters. To achieve these goals, we will fully integrate the most recent developments in population genomics (objective 1) with phenotypes and life history information (objective 2), and local ecological knowledge (LEK) and observer networks (objective 3).

Under the co-supervision of Drs. Grant Murray (Duke University) and Marie Clément (Memorial University), the successful candidate will be responsible for developing objective 3 (LEK and observer network) in Labrador and the Quebec Lower North Shore . The successful candidate will be working in close collaboration with Drs. Louis Bernatchez (Université Laval) and Pascal Sirois (Université du Quebec à Chicoutimi), whose research groups are responsible for the genetic and phenotypic components of this project as well as with indigenous communities, fishers, industry, non-profit organizations, and the provincial and federal governments as well as.

LOCATION: The candidate will be stationed at Memorial University, at either the CFER of the Marine Institute in St. John’s, NL, or at the Labrador Institute in Happy Valley-Goose Bay, NL, depending on preference. Field work will be conducted in Labrador and the Quebec Lower North Shore.

QUALIFICATION: The position is open to all candidates holding an M.Sc. degree in biology but a strong background in evolutionary biology will be a significant asset, as will experience in conducting semi-structured interviews, using ArcGIS, and working in a northern context or with indigenous communities.

STIPENDS: $20,000/ year for 3 years. Funding, including travelling for conducting research has been secured. Students are encouraged to apply for applicable scholarships.

ANTICIPATED START DATE: January 2017 or April 2017 To apply, email a cover letter describing your research interests, your curriculum vitae and the names of three references to marie.clement@mi.mun.ca or grant.murray@duke.edu

Marie Clément, Ph.D. Research Scientist Centre for Fisheries Ecosystems Research Fisheries and Marine Institute in partnership with the Labrador Institute Memorial University of Newfoundland P.O. Box 490, Stn. B, 219 Hamilton River Road Residence Building Happy Valley - Goose Bay, NL A0P 1E0 Telephone: (709) 896-6215 / Fax: (709) 896-2970 e-mail: marie.clement@mi.mun.ca

Marie Clement <Marie.Clement@mi.mun.ca>

NewZealand FishDiseaseGenomics

PhD Scholarship: Disease genomics of two New Zealand finfish species

We are seeking a highly motivated PhD student to be part of a group to investigate the disease genomics of the New Zealand snapper (Chrysophrys auratus) and trevally (Pseudocaranx georgianus).

Supervisors Dr. Maren Wellenreuther, Plant and Food Research (PFR), Nelson, New Zealand Dr. Steve Bird, Waikato University, New Zealand

Aquaculture is the fastest growing food-production sector and New Zealand has the potential to develop a range of locally grown finfish species to meet this increasing demand. New genomics-based selective breeding programs are needed to help develop recently domesticated fish species into premium products. Plant and Food Research (http://www.plantandfood.co.nz) is known worldwide for its innovative breeding and genomics research, and it is leading the development of New Zealand seafood genomics.

This PhD project will involve working alongside a group of experienced researchers to study the genomes of the New Zealand snapper and trevally to identify and characterize immune genes, screen for genome-wide disease markers using a pedigree from domesticated populations, evaluate the bacterial disease metacommunities and conduct gene expression analyses using transcriptomics and qPCR. This will involve using high-throughput sequencing approaches, coupled with automated and error-reduced phenotyping. The overall goal is to characterize the immune systems of both fish species to better understand disease resistance in domesticated populations, facilitating a rapid and efficient selective breeding programme.

PhD Project Aims 1. Use whole genome assemblies and transcriptomes to identify immune genes and pathways, 2. Use genomic information to improve detection of novel disease QTLs, 3. Assess stress and disease resistance of hatchery individuals, and understand their bacterial disease communities.

This PhD project will provide an excellent opportunity to learn the latest interdisciplinary technologies and apply them to fish genomics. The PhD student will gain experience working in academic, government and private sector institutions. They will be a member of a highly active and collaborative group of researchers, and help develop new technological approaches and applied-genomic tools.

The successful candidate will be a highly motivated researcher, with a strong background and interest in genomics and molecular biology. Experience with a coding and/or scripting languages is a bonus. This position will be based primarily in Nelson (http://www.nelsonnz.com) and comes with a three-year scholarship that provides a stipend and university (domestic-level) fees. This project is supported by the MBIE grant 'Enhancing production of New Zealand's seafood sector using accelerated breeding techniques'.

Applicants should send a CV, a statement of their research interests and a cover letter to Maren Wellenreuther (Maren.Wellenreuther@plantandfood.co.nz) and Steve Bird (sbird@waikato.ac.nz). Candidate selection will begin mid-December but applications will be considered until the position is filled. The ideal starting date is 1 April 2017. International students with strong credentials are welcome and encouraged to apply. For more information about studying at Waikato University and the entry requirements for the PhD program please see http://www.waikato.ac.nz/study/postgraduate-studies/higher-degrees/ . Maren Wellenreuther Senior Scientist

< http://www.plantandfood.co.nz/ >

T: +64 3 989 7658 F: +64 3 546 7049 E: maren.wellenreuther@plantandfood.co.nz www.plantandfood.co.nz The New Zealand Institute for Plant & Food Research Limited

Postal Address: Plant & Food Research Box 5114, Port Nelson, Nelson, 7043, New Zealand Physical Address: Plant & Food Research Seafood Research Unit, 293 Akersten St, Port Nelson, Nelson, 7010, New Zealand

Maren.Wellenreuther@plantandfood.co.nz

NewZealand FishGenomics

PhD Scholarship: Genomics of New Zealand trevally

We are seeking a highly motivated PhD student to be part of a group to develop a genomics-informed selective breeding programme for New Zealand trevally (Pseudocaranx georgianus).

Supervisors Dr. Maren Wellenreuther, Plant and Food Research (PFR), Nelson, New Zealand Dr. Peter Ritchie, Victoria University of Wellington (VUW), New Zealand

Aquaculture is the fastest growing food-production sector and New Zealand has the potential to develop a range of locally grown finfish species to meet the increasing demand. New genomics-based selective breeding programs are needed to help develop recently domesticated fish species into premium products. Plant and Food Research (http://www.plantandfood.co.nz) is known worldwide for its innovative breeding and genomics research, and it is leading the development of New Zealand seafood genomics.

This PhD project will involve work with a group of researchers to assemble the trevally genome, screen for genome-wide markers using a pedigree from a domesticated population, and conduct QTL mapping and gene expression analyses. The research will involve using high-throughput sequenced approaches, coupled with automated and error-reduced phenotyping. The overall goal is to enable rapid and efficient selective breeding of complex polygenic traits.

PhD Project Aims 1. Develop genomic and phenomic tools for selectively breeding trevally, 2. Use genomic information to improve conventional breeding approaches and apply multitrait MAS/GS selection to improve trait gains, 3. Assess fitness of hatchery individuals.

This PhD project will provide an excellent opportunity to learn the latest interdisciplinary technologies and apply them to fish genomics. The PhD student will gain experience working in academic, government and private sector institutions. They will be a member of a highly active and collaborative group of researchers, and help develop new technological approaches and applied-genomic tools.

The successful candidate will be a highly motivated researcher, with a strong background and interest in genomics and molecular evolution. Experience with a coding and/or scripting languages is a bonus. This position will be based primarily in Nelson (http://www.nelsonnz.com) and comes with a three-year scholarship that provides a stipend and university (domestic-level) fees. This project is supported by the MBIE grant 'Enhancing production of New Zealand's seafood sector using accelerated breeding techniques'.

Applicants should send a CV, a statement of their research interests and a cover letter to Maren Wellenreuther (Maren.Wellenreuther@plantandfood.co.nz) and Peter Ritchie (Peter.Ritchie@vuw.ac.nz). Candidate selection will begin mid-December but applications will be considered until the position is filled. The ideal starting date is 1 April 2017. International students with strong credentials are welcome and encouraged to apply. For more information about studying at VUW and the entry requirements for the PhD program please see http://www.victoria.ac.nz/study/programmes-courses/postgraduates/phds-doctorates Maren Wellenreuther Senior Scientist

< http://www.plantandfood.co.nz/ >

T: +64 3 989 7658 F: +64 3 546 7049 E: maren.wellenreuther@plantandfood.co.nz www.plantandfood.co.nz The New Zealand Institute for Plant & Food Research Limited

Postal Address: Plant & Food Research Box 5114, Port Nelson, Nelson, 7043, New Zealand Physical Address: Plant & Food Research Seafood Research Unit, 293 Akersten St, Port Nelson, Nelson, 7010, New Zealand

Maren.Wellenreuther@plantandfood.co.nz

NicolausCopernicusU Poland 2 PlantEvolBiol

Ph.D. opportunity in plant evolutionary biology Nicolaus Copernicus University, Torun, Poland

The Chair of Ecology and Environment Protection (http://www.keib.umk.pl/?lang=en) is recruiting two PhD students interested in studying evolution of morphological traits in plants at various time scales. The goal of this project is to contribute towards an understanding of how genetic architecture (the structure of genotype to phenotype mapping) affects the evolution of quantitative traits. According to quantitative genetics theory, the evolution of phenotypic traits depends on the strength of selection and the amount of genetic variation. However, part of this variation maybe constrained by correlations with other traits that are under conflicting selective regimes. In consequence, the ability to respond to selection (evolvability) may be limited, even if a trait has high heritability. However, the extent to which genetic architecture limits phenotypic evolution remains an open question. Likewise, it is unknown whether it affects evolution at the short time scale and is easily overcome by selection, or if the genetic architecture is an important long-term determinant of the direction of evolution. In this project we aim to answer these questions using two plant species from the family Apiaceae, Daucus carota and Ferula communis, as a model system. This project will be carried out in collaboration with Prof. Thomas Hansen (University of Oslo) and dr Krzysztof Bartoszek (Uppsala University).

PhD 1 Major tasks: - generate RADseq population data for Ferula communis and Daucus carota - delimit independently evolving lineages in Ferula communis and Daucus carota species complexes - determine G-matrices for fruit and seedling traits based on molecular data for several populations - estimate various measures of evolvability for Ferula and Daucus system

PhD 2 Major tasks: - phylogenetic analysis of various taxa from the family Apiaceae based on RADseq data - establish a database of phenotypic traits (seedlings, fruits, inflorescences and flowers), life history strategies and geographic distributions for species from the family Apiaceae - estimate the rate of morphological trait evolution using phylogenetic comparative methods - help in developing the R package mvSLOUCH dedicated to analysis of multivariate Ornstein-Uhlenbeck models on phylogeny

The ideal candidate will have a background in molecular biology/population genetics/phylogenetics, as well as experience working with Linux and modern programming languages such as R. Previous experience in generating and analysis of next-generation sequencing data will be considered positively. A condition of the application is a Master degree (or equivalent) in biology or similar subjects.

The stipend for both positions is 3 000 PLN net monthly (app. 700 EURO) for three years. The living cost in Torun is low. For example, a room in a student house (inc. Wi-Fi, kitchen, heating, hot water) is app. 100 EURO monthly, loaf of bread 0.5 EURO, beer 0.5-0.7 EURO, beer in pub 1-2 EURO, dinner in restaurant 5-8 EURO.

Nicolaus Copernicus University is located close to the medieval center of Torun (http://www.visittorun.pl/) which is listed among UNESCO World Cultural and Natural Heritage sites. Torun is a dynamic academic city and provides many opportunities for intellectual and cultural stimulation. The Vistula river runs through town and is ideal for the naturalists as many natural protected areas are located in its valley.

If you are interested, please send a CV, a short statement of your research interests (max. one page) and the contact details of at least one academic referee to Marcin Piwczynski (piwczyn@umk.pl). Feel free to contact him by email for further information. Review of applicants will start in the first week of January 2017. The positions will stay open until filled.

Marcin Piwczynski Chair of Ecology and Biogeography, Faculty of Biology and Environment Protection, Nicolaus Copernicus University Lwowska 1, 87-100 Torun POLAND

“Marcin.Piwczynski@umk.pl”
<Marcin.Piwczynski@umk.pl>

NortheasternU EvolutionaryGenetics

Graduate position: Evolutionary genetics and statistical genomics

The Lotterhos Lab at Northeastern University is recruiting a PhD student starting Fall 2017. The student will work on a research project integrating evolutionary theory with statistical methods for analyzing genomic data. Therefore, the candidate should have a strong interest in modeling, simulations, statistics, and coding. A high level of organization will be necessary for conducting this type of research.

Interested candidates can learn more about our research at:

https://sites.google.com/site/katielotterhos/home
With your inquiry, please include a cover letter, CV, unofficial transcript, and unofficial copy of your GRE scores.

k.lotterhos@gmail.com

PortlandStateU PlantEvolution

Graduate position: Landscape genetics of plants

Plant species present unique opportunities and challenges for landscape genetic analyses, as the behavior of their associated biotic and abiotic dispersal vectors as well as the distribution of suitable habitat may affect patterns of genetic variation.Understanding how landscape features may facilitate or limit the dispersal of plants is particularly critical as climate change affects the distribution of suitable habitats.We are looking to recruit graduate students (Ms or PhD) interested in plant ecological genomics. We have already established wet-lab and bioinformatics pipelines for conducting chloroplast genome capture and SNP/haplotype analyses. Students will be encouraged to develop their own projects in the context of understanding the processes and consequences of plant dispersal.Experience with laboratory assays and data analyses for genetic markers, GIS analyses, bioinformatics, and field ecological methods would be beneficial but not necessary.If interested, please send a letter of introduction to Cruzan@pdx.edu that includes a brief statement of your background and academic record (including GPA and GRE scores if available).Please include an essay outlining your research interests and a recent copy of your CV.

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

Mitch Cruzan Professor of Biology Portland State University PO Box 751 Portland, OR 97207 USA Web: http://web.pdx.edu/ ˜ cruzan/ cruzan <cruzan@pdx.edu>

PurdueU 2 GeneticAdaptation

Graduate positions are available in lab of Mark Christie at Purdue University. Up to two PhD positions are available for highly-motivated candidates interested in rapid genetic adaptation, conservation, and population genetics. For more information on research in the Christie lab please visit: https://www.bio.purdue.edu/lab/christie/ Potential projects include: 1. Examining the rapid adaptation of introduced fishes into the Great Lakes, 2. Identifying the genetic and evolutionary consequences of domestication, captive breeding, and supplementation of wild populations, and 3. Using existing and novel approaches to determine patterns of dispersal within a metapopulation context. These are the current research themes in the Christie laboratory, with research often focusing on fishes, but graduate students are free to explore independent lines of inquiry in any system. Previous research experience with molecular techniques, computational work, statistics, bioinformatics, and assisting with the design and implementation of experiments will be highly regarded.

If you are interested in joining the lab, please contact me directly at markchristie@purdue.edu with a resume/CV and a brief description of your research interests and experience. Formal applications are due by December 7th.

Mark Christie <redpath.christie@gmail.com>

Queensland 2 FruitFlyGenomics

Project 1: Genetics and Genomics of Qfly Sexual Performance Closing Date: Expressions of interest close at midnight on Friday 20 January 2017

A PhD opportunity is available on a project investigating the genetics and genomics of sexual performance in the Queensland fruit fly (Qfly; Bactrocera tryoni). This project is part of a significant collaboration between Drs John Oakeshott and Ronald Lee at Australia's Commonwealth Scientific and Industrial Research Organisation (CSIRO) and Prof Phil Taylor at Macquarie University's Department of Biological Sciences (http://bio.mq.edu.au/).

Sexual performance is key to Darwinian fitness. In some insect systems the key elements of sexual performance (e.g. pheromonal communication, courtship rituals) exhibit strong genetic influences. However, the genetic factors governing sexual performance in Qfly are yet to be discovered. The emergence of powerful âtechnologies has vastly advanced the scope and depth of mating system research, and the recent development and deployment of such tools for Qflies enables unprecedented opportunities for investigation of traits underpinning sexual performance in this species.

The approaches and methods will be highly multidisciplinary. The PhD candidate will combine bioassays to measure reproductive behaviours with state-of-the-art genomic, proteomic and metabolomic technologies to understand the genetic basis and molecular mechanisms underpinning male mating success. Traits of potential interest include pheromone synthesis and composition, calling behaviour, reproductive effort and sperm transfer. Strains from a wide variety of locations and with different histories of domestication (which inevitably impose different selection pressures on reproductive behaviour) are already available for study.

In addition to being of fundamental interest, knowledge gained in this PhD project will contribute to environmentally sustainable pest management through the Sterile Insect Technique (SIT). In SIT millions of mass-reared sterile male flies are released to mate with wild females and induce reproductive failure through the transfer of sterile sperm and induction of sexual inhibition. For SIT programs to succeed, the released male flies must be sexually competitive. Knowledge gained in this PhD will later assist in the development of field-competitive strains for use in in SIT control programs.

The project will be based mainly at the Commonwealth Scientific and Industrial Research Organisation (CSIRO) in Canberra but with significant involvement also from Macquarie University in Sydney. The two laboratories provide an ideal environment for this research; both have invested heavily in the infrastructure necessary for Qfly research and have deep experience in Q-fly biology, molecular and quantitative genetics and the various â' technologies that will underpin this research. Numerous PhD students and Research Fellows are already working in the two laboratories on diverse aspects of Qfly biology, genetics and genomics, providing an exciting learning environment and an opportunity to contribute meaningfully to an environmentally sustainable new technology for controlling a major horticultural pest.

The value and tenure of the scholarship is: - $30,849 pa (2016 rate, subject to annual indexation, tax free) for

3 years. This includes a stipend of $25,849 pa plus a scholarship âup' of $5,000 pa.

- For International candidates, scholarships will also cover all tuition fees.

To be eligible for a scholarship, applicants are expected to have a record of excellent academic performance and preferably, additional relevant research experience and/or peer-reviewed research activity, awards and/or prizes in line with the University's scholarship rating guidelines. Refer to the Rating Scholarship Applicants section for more information about these guidelines.

Students on scholarships are not obliged to contribute to teaching, but may do so to supplement their income if desired. In addition to substantial financial resources to draw on for research, several generous schemes are available to fund travel to visit overseas laboratories or to attend overseas conferences.

Interested applicants should email a letter of interest, academic transcripts, curriculum vitae and the names and contact information of three referees to Dr John Oakeshott (john.oakeshott@csiro.au).

Closing Date: Expressions of interest close at midnight on Friday 20 January 2017

Project 2: Nutrigenomics in Qfly

Closing Date: Expressions of interest close at midnight on Friday 13 January 2017 A PhD opportunity is available on a project investigating metabolic adaptations using the Queensland fruit fly (Bactrocera tryoni; Tephritidae) (â-fly') as a model system. The project is part of a significant collaboration between Drs John Oakeshott and Ronald Lee at

— / —

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

---

RiceU EvolutionaryBiol

Graduate Coordinator | BioSciences at Rice University | marya@rice.edu |

W131 George R. Brown Hall - MS 140 | 713-348-4230 (phone) / 713-348-4790 (fax)

The Graduate Program in Ecology and Evolutionary Biology in the Department of BioSciences at Rice University invites applications for admission into our PhD program. The department is home to a vibrant community of faculty, postdoctoral, graduate, and undergraduate scholars in ecology and evolution. Our program has particular strengths in population and community ecology, behavioral ecology, conservation biology, evolutionary ecology, speciation, and evolutionary genetics and genomics.

We are located in Houston, Texas, an exciting, diverse, and affordable city with world-class opportunities for dining, arts, and entertainment and access to diverse terrestrial and aquatic environments. Rice is located beside one of the country's largest medical research centers, providing additional opportunities in bioinformatics, genomics, and translational research.

Completed applications should be received by December 31 to ensure full consideration. There is no application fee for US citizens and permanent residents. Prospective applicants are encouraged to contact potential faculty advisors before applying. Complete information about the graduate program, including application instructions, may be found at https://biosciences.rice.edu Mary Aycock <marya@rice.edu>

SamNobleMuseum UOklahoma NeotropicalOrnithology

Please visit this announcement at: https://mjmillerlab.github.io/blog/recruit I am recruiting 1-2 PhD students to join my lab in the Ornithology Department of the Sam Noble Museum at University of Oklahoma for the Fall 2017. Students should be willing to take a creative leadership role in the comparative genomics of secondary contact and speciation in Neotropical birds. These positions would involve considerable time in the field on expeditions in Latin America to collect birds, supported by the Sam Noble Oklahoma Museum Department of Ornithology.

The ideal student will have previous Latin American ornithological field experience, as well as the ability to understand and speak Spanish. Students from Latin America are particularly encouraged to apply. These projects will consist of developing genomic datasets from massively-parallel sequencing efforts (i.e. next gene sequencing) at the University of Oklahoma. Strong computational skills in UNIX, R and Python are a real plus. However, all potential students with strong field, lab, and museum ornithological skills are encouraged to contact me.

Students can undertake projects in two areas where we have existing datasets: either in the comparative genomics of secondary contact of lowlands birds (see Secondary Contact Project) or in the genomics of species isolation of Lampornis hummingbirds (see Lampornis Genomics Project), or the student can develop her/his own project. We have active funding for field research in Bolivia and Peru as well, so projects in this area could be developed.

Students in our lab are enrolled in either the Biology or closely allied Ecology and Evolutionary Biology PhD program, but maintain offices and a lab home in the Ornithology Department at the Sam Noble Oklahoma Museum of Natural History. The Ornithology Department consists of a fast-growing ornithological collection, state-of-the-art molecular genomics labs (capable of doing all NGS preparations including ddRAD-Seq, hybrid capture, and whole genome sequencing), multiple bioinformatics Linux workstations (as well as access to the OU Supercomputer), and an impressive ornithological research library.

OU Biology/EEB has a strong focus on "geographical ecology", and our group participates in the Geographical Ecology working group, which is organized by Mike Kaspari (tropical community ecology), and includes the following faculty: Katie Marske (phylogeography) Katie Marshall (physiological ecology), Dan Allen (stream and riparian ecology) and Cam Siler (herpetology and systematics). Collectively, our group provides a rich environment for students to interact with these and other talented faculty and students in the Geographical Ecology working group and throughout the Biology department.

We are also allied with the Oklahoma Biological Survey, which has considerable strengths in ornithology. This includes Jeff Kelly's lab, Eli Bridge's group, and Jeremy Ross's lab. Collectively, this makes OU among the best universities for ornithology in the country.

Funding for graduate students is currently available in the form of 10-month teaching assistantships with reasonable stipends, full tuition waivers and excellent health care coverage. In addition, students can expect to be funded during the summer by the OU Sutton Avian Research Scholarships, Adams Scholarships, and Curatorial Assistantships in Ornithology at the Sam Noble Museum. Our lab has existing funds for field expeditions and specimen collection, and there are several funding sources on campus and elsewhere for the development of next-generation genomic datasets. Norman is an amazing college town, and the cost of living is quite reasonable for graduate students.

Interested students should contact me (mjmiller@ou.edu) with a brief summary of your research interests and relevant experiences and attach a CV. All prospective students must also apply through the OU Biology Graduate Program by mid December. Candidates from groups underrepresented in STEM are encouraged to apply. Se habla español aqui!

Matthew J. Miller Assistant Curator of Ornithology Sam Noble Oklahoma Museum of Natural History & Assistant Professor, Department of Biology University of Oklahoma mjmiller@ou.edu https://mjmillerlab.github.io
"Miller, Matthew J." <mjmiller@ou.edu>

SanDiegoStateU EvolutionaryBiol

Ph.D. Program in Evolutionary Biology San Diego State University.

The Joint Doctoral Program in Evolutionary Biology at San Diego State University is currently seeking graduate students to join our program. This is a joint program with the University of California Riverside. At SDSU and UCR, students may study a broad range of topics in evolutionary biology including systematics, paleontology, molecular evolution, population biology, and organismal/biodiversity biology.

Detailed information on the program, admission requirements and procedures, and the participating faculty can be found at: http://www.sci.sdsu.edu/eb/jdeb.html . The application deadline is December 14 2016.

For more information about please contact Dr. Elizabeth Waters, Program Coordinator, at: ewaters@mail.sdsu.edu.

Elizabeth R. Waters, PhD Professor of Biology San Diego State University San Diego, CA 92182 617-594-7036

Elizabeth Waters <ewaters@mail.sdsu.edu>

Spain EvolutionaryGenomics

INPhINIT-La Caixa PhD position on ecological genomics

We are seeking highly motivated PhD candidates to apply for an *INPhINIT-La Caixa* < https://obrasociallacaixa.org/en/educacion-becas/-becas-de-posgrado/inphinit/programme-description > fellowship (3-year contract, gross salary 34 800 /year) to develop the PhD project "*Integrating genomic and ecological data to infer community-level responses to past and ongoing global change*" (see details below). The PhD will be developed under the supervision of Dr. Joaquín Ortego < https://sites.google.com/site/-joaquinortegolozano/ > at Estación Biológica de Doñana (EBD-CSIC, Seville, Spain), a reference center for ecological and evolutionary research.

Research project description: Understanding how different organisms interact with landscape heterogeneity and environmental fluctuations is central to infer their future responses to global change. Most studies have addressed these questions focusing on a single or a few taxa, a fact that has strongly limited our ability to predict how entire-communities/ecosystems will be impacted by different sources of human-induced environmental alterations. This takes more relevance if we consider that assemblages of co-distributed species (i.e. sharing a common geographic space) are often composed by taxa with very contrasting life-history traits (e.g. dispersal capacity, phenology, climatic tolerances, etc.) and, thus, they are expected to respond to ongoing global change in very different ways. This research project will focus on the study of several co-distributed or partially co-distributed grasshopper species occupying different climatic niches (montane *versus* alpine species) and showing remarkable differences in dispersal capacity (flightless taxa *versus* good dispersers), degree of ecological specialization (habitat specialists *versus* generalists) and distribution ranges (widely distributed taxa *versus* narrow endemics). The project will be developed in the Pyrenees Mountains, an area which offers a superb template to address the above described questions due to its step environmental gradients, rough topography, and considerable impacts of past and ongoing climate change on the demographic and evolutionary history of the rich biota from the region.

Job position description: The PhD project will be highly multidisciplinary, requiring the integration of field sampling campaigns, molecular lab work, and several analytical approaches. The main tasks will include: 1) Intensive field-work campaigns (1-2 months/year) in the Pyrenees Mountains to get samples and ecological/distributional data; 2) Molecular lab work to prepare genomic libraries for high-throughput sequencing (using double-digest RadSeq); 3) Obtaining phenotypic information from collected specimens using linear and geometric morphometric analyses; 4) Ecological and climatic niche modeling of the studied species and lineages; 5) Bioinformatic treatment of genomic data; 6) Integration of genomic, phenotypic and ecological data to infer past and future responses of the studied taxa to landscape heterogeneity and environmental changes. The PhD student will also have access to the large entomological wet collection available in our lab (>10000 ethanol-preserved specimens). Previous experience with molecular lab work, bioinformatics, genetic data treatment, and/or geographic information systems are welcome but not necessary, as all the skills required to develop the PhD project will be acquired at our lab. At the end of the PhD the student will have an extraordinary multidisciplinary training on the state-of-the-art of a suite of analytical techniques and methodological approaches, placing him/her at the forefront of research on evolutionary biogeography and conservation genomics.

Applications must be submitted online through this website:

https://obrasociallacaixa.org/en/educacion-becas/-becas-de-posgrado/inphinit/programme-description The candidates must fulfill the requirements of the call (please pay attention to the residency eligibility requirements):

https://obrasociallacaixa.org/en/educacion-becas/-becas-de-posgrado/inphinit/call-for-application Deadline for applications is 02/02/2017 (starting September/October de 2017)

Do not hesitate to contact me (joaquin.ortego@csic.es) if you have any questions about the PhD project or the fellowship.

– Joaquín Ortego Department of Integrative Ecology Estación Biológica de Doñana Avda. Américo Vespucio s/n 41092 Sevilla, Spain

— / —

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

StonyBrookU EvolutionaryBiol

The Graduate Program in Ecology and Evolution in the Department of Ecology and Evolution at Stony Brook University is recruiting doctoral and master's level graduate students for Fall 2016. The program trains students in Ecology, Evolution and Biometry.

The following faculty are seeking graduate students this year:

DEPARTMENTAL FACULTY Resit Akcakaya - Population and conservation ecology http://life.bio.sunysb.edu/ee/akcakayalab/ Stephen B. Baines - Ecosystem Ecology and Biogeochemistry http://life.bio.sunysb.edu/ee/baineslab/ Liliana M. Dávalos - Phylogenetics, Molecular Evolution, and Biogeography http://lmdavalos.net/lab/The_Lab.html Jessica Gurevitch - Plant Population and Invasion Ecology http://gurevitchlab.weebly.com/ Brenna Henn - Human Evolutionary Genomics https://ecoevo.stonybrook.edu/hennlab/ Jesse D. Hollister - Plant Evolutionary Genomics and Epigenetics https://genomeevolution.wordpress.com/ Heather Lynch - quantitative ecology and conservation biology https://lynchlab.com/ Dianna K. Padilla - Invertebrate Aquatic Ecology and Conservation Biology http://life.bio.sunysb.edu/ee/padillalab/ Joshua Rest - Evolutionary genomics http://life.bio.sunysb.edu/ee/restlab/Home.html Robert Thacker- Systematics, phylogenetics, and ecology http://thackerlab.weebly.com/ John True - Evolutionary Developmental Biology http://life.bio.sunysb.edu/ee/truelab/True_Lab.html Kishna M. Veeramah - Primate Comparative Genomics http://life.bio.sunysb.edu/ee/veeramahlab/ PROGRAM FACULTY IN OTHER DEPARTMENTS Nolwenn Dheilly - Evolution of Host-Parasite Interactions http://you.stonybrook.edu/dheilly/ Andreas Koenig http://www.stonybrook.edu/commcms/anthropology/faculty/akoenig.html Sasha Levy - Microbial Evolution http://laufercenter.stonybrook.edu/group/sasha/people.html David Matus - Evolution of Cell Invasion http://www.stonybrook.edu/commcms/biochem/research/faculty/matus.html# Janet Nye - Quantitative Fisheries Ecology https://you.stonybrook.edu/jnye/ Alistair Rogers - Plant Physiology and Climate Change www.bn.gov/TEST Shawn Serbin - Plant Physiology and Remote Sensing www.bn.gov/TEST Leslie Thorne - Ecology and Behavior of Marine Birds and Mammals http://you.stonybrook.edu/thornelab/ Patricia Wright - Tropical Conservation and Primatology http://www.patwrightlab.net/pat-wright.html For more information regarding the Graduate Program in Ecology and Evolution

See http://www.stonybrook.edu/ecoevo/index.html for general information. For specific information on the PhD and MA programs see http://www.stonybrook.edu/commcms/ecoevo/program/index.html and http://www.stonybrook.edu/commcms/ecoevo/program/maprogram.html The deadline for receipt of all application materials for the PhD program is Dec 1 2016 although earlier submission is encouraged to ensure full consideration for available fellowships. The deadline for receipt of all application materials for the master's program is April 15, 2017. The Graduate School's Center for Inclusive Education is offering application fee waivers if a student has met with SBU representatives at a recruitment event and provided SBU with their contact information. For assistance, with this or other aspects of the application process, e-mail our Graduate Program Coordinator, Melissa Cohen melissa.j.cohen@stonybrook.edu.

– Liliana M. Davalos

Office phone: 631 632 1554

http://lmdavalos.net/lab/The_Lab.html

— / —

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

StonyBrookU NY EvolutionaryGenomics

The Veeramah Lab in the Department of Ecology and Evolution at Stony Brook (http://life.bio.sunysb.edu/ee/veeramahlab/index.html) is looking to recruit two PhD Students to begin in Fall 2017. The primary focus of the lab is examining genetic diversity in human and non-human primates. The lab currently has ongoing projects examining primate evolution through genomic scale data, as well as a variety of paleogenomic projects involving European human and non-human populations. The exact research project topics for potential students are flexible, but those individuals looking to perform research within the general research themes of the lab will be preferred. Applicants must hold a university degree.

Please note that while interested applicants are encouraged to contact Krishna Veeramah before applying, students wishing to join the lab must ultimately apply to the Stony Brook Ecology and Evolution Graduate Program. All relevant information for this program can be found at the website (http://www.stonybrook.edu/commcms/ecoevo/-program/index.html) and a link to the application can be found at https://www.grad.stonybrook.edu/ ProspectiveStudents/app_info.shtml. Please note that the deadline for receipt of all Ph.D. application materials is December 1st, 2016. Earlier submissions are encouraged, particularly for those wishing to be considered for Campus wide Graduate Council Fellowships and W. Burghardt Turner Fellowships.

Prospective students are encouraged to address specific questions to the Ecology and Evolution Graduate Program Coordinator (melissa.j.cohen@stonybrook.edu) or to Krishna Veeramah (krishna.veeramah@stonybrook.edu).

“krishna.veeramah@stonybrook.edu”
<krishna.veeramah@stonybrook.edu>

TexasAMU MosquitoEvolutionaryGenomics

APhD position to study the genomics of disease transmitting mosquitoes is available in the laboratory of Michel Slotman in the Department of Entomology at Texas A&M University. The Slotman lab focuses on evolutionary and behavioral genomics and genetics of Anopheles and Aedes mosquitoes. Research topics of the lab include the genetic basis of host seeking behavior, genomic analyses of behavioral resistance against vector control, and the genomics of speciation.

Thespecific research questions will be defined in consultation with the successful applicant, but will fall within the research areas explored by the lab (see here for description < http://slotmanlab.tamu.edu/Home.html >).

Candidatesshould have some background in evolutionary biology and/or entomology with an interest in some or all of the following fields: genomics/genetics, bioinformatics, vector biology and behavior. Candidates with a MSc degree in a related field are preferred. Start date is August 2017.

VectorBiology < http://vectorbiology.tamu.edu/ > is a major and expanding research strength of the Department of Entomology < http://entomology.tamu.edu/ > at Texas A&M University. Its excellent resources and large faculty provide an outstanding graduate experience. Michel is also a faculty in the interdisciplinary Ecology and Evolutionary Biology < http://-vectorbiology.tamu.edu/ > degree program which unites a large cadre of like-minded faculty, post-docs and students.

Interestedapplicants should send a C.V., a brief statement about research interests, (unofficial) transcripts, GRE scores and contact information for three references to maslotman@tamu.edu

maslotman@tamu.edu

TexasTechU MicrobialEvolution

Graduate Student Research Assistantships in Microbial Evolution at Texas Tech

We have two openings for graduate students to join the laboratory of Dr. A.M.V. Brown in the Department of Biological Sciences at Texas Tech University. Dr. Brown’s lab (see http://www.amvbrown.com) investigates how bacteria and other microbes interact with hosts in beneficial or harmful ways, asking how ecological and evolutionary constraints limit or facilitate species invasions, disease outbreaks, or biomass production. We use metagenomics, transcriptomics, bioinformatics, and other techniques. Systems include agricultural and medically related organisms. Students will begin in the summer or fall of 2017, in a Master’s or PhD program. We seek applicants who are (1) committed to achieving scholarly excellence, (2) ambitious and passionate about deep questions in biology, (3) conscientious learners and communicators wishing to be involved in dynamic and diverse research.

Dr. Brown’s lab will provide cutting-edge training in important areas of biological research, and together with the graduate program in the Department of Biological Sciences (http://www.depts.ttu.edu/biology), will provide possible funding for summer Research Assistant salary and students must also be willing to act as a Teaching Assistant if available. Applicants will also be encouraged to seek other funding support as part of their training. Texas Tech is a large university, growing in research strength and status, located close to important centers for agriculture, medicine, and genomics. We welcome applicants of all backgrounds, without discrimination on the basis of an applicant's race, ethnicity, color, religion, sex, sexual orientation, gender identity, national origin, age, disability, genetic information or status as a protected veteran. To apply, first notify Dr. Brown of your interest as soon as possible at amanda.mv.brown@ttu.edu. After initial contact, you may be asked to provide: a resume or CV, a short statement describing your skills, knowledge, and goals, contact information for 2-3 academic references, and GPA and/or GRE and/or TOEFL scores, as appropriate. You will then also need to fulfill application requirements for graduate studies (see http://www.depts.ttu.edu/-gradschool/Programs/GraduatePrograms.php).

Dr. Amanda M.V. Brown Assistant Professor Department of Biological Sciences, Texas Tech University Biological Sciences MS3131, Lubbock, TX 79409 Work Ph: 806-834-0984

Amanda Brown <amanda.mv.brown@ttu.edu>

TexasTechU PlantSexChromEvolution

PhD Graduate Student Positions in Plant Ecological Genetics

Olson Lab, Texas Tech University

The Olson lab at Texas Tech University is recruiting PhD Graduate students interested in the field of plant ecological genetics to start in spring, summer or fall of of 2017. Funds are available for partial support on a Graduate Research Associate on an NSF-funded grant to study the ecological and genetic factors influencing the dynamic movement of sex determination regions and sex chromosome evolution within the Salicaceae (poplars and willows). The overall project focuses on mapping sex determination regions from representatives Populus and Salix species, understanding the genetic basis of gender dimorphism in defense and pollinator attraction chemistry, and the assessment of population genetic patterns across the sex determination and pseudo-autosomal regions of the sex chromosomes. Graduate students working on this project will have the opportunity to choose from a variety of projects including, but not limited to, mapping the locations of previously unknown sex determination regions, development of phylogenies for important plant groups, and studying the ecology and evolution of sexual dimorphism in plant defensive and pollinator attraction compounds. Moreover, the grant provides for a unique multi-institutional and international training environment, with potential funding to visit labs at the University of West Virginia, the University of Wisconsin, Cornell University, and Sichuan University and Nanjing Forestry University in China for cross-disciplinary training.

In general, the Olson lab studies a variety of questions including the evolution of breeding systems, sex chromosome evolution, the evolution of gender dimorphism in plants, and local adaptation to latitude in relation to climate change. We use a variety of experimental techniques including common garden studies, field ecology, transmission genetics, genomics and bioinformatics. For the past decade we have studied these processes in forest trees and expect that this will continue to be the main taxonomic focus of our research.

The Olson lab is part of a dynamic Ecology and Evolutionary Biology group at Texas Tech. Courses and focused training in ecology, bioinformatics, and genomics are available from a highly interactive faculty. Texas Tech boasts excellent laboratory and research resources as well as easy access to some of the most beautiful and remote regions of the lower 48 United States.

Please contact Matt Olson directly at matt.olson@ttu.edu for more information regarding opportunities and application information.

"Olson, Matt" <matt.olson@ttu.edu>

TulaneU EvolutionaryBiol

Graduate Fellowships at Tulane University

The Department of Ecology and Evolutionary Biology at Tulane University seeks applications from students who are pursuing a Ph.D. in Ecology and Evolutionary Biology. The department has fellowships from the Louisiana Board of Regents. We strongly encourage applicants from groups who are under-represented in STEM. Areas of study in our department include tropical biology, evolutionary biology and river/coastal ecology. Applicants should be in contact with specific faculty members well before the application deadline. A complete list of faculty and their research interests can be found here:http:/-/www2.tulane.edu/sse/eebio/faculty-and-staff/faculty/ The program deadline is January 15, and application details can be found here: http://www2.tulane.edu/-sse/eebio/academics/graduate/apply.cfm For questions about the Ph.D. program, email our graduate student coordinator, Dr. Jordan Karubian, atjk@tulane.edu.

Tulane University is a member of the prestigious Association of American Universities, a select group of the 62 leading research universities in the United States and Canada with 'preeminent programs of graduate and professional education and scholarly research.' Tulane is located in the historic Gulf Coast city of New Orleans, which is known for its culture, food and music.

Elizabeth Derryberry, Ph.D. Assistant Professor Ken and Ruth Arnold Early Career Professor in Earth & Ecological Science Department of Ecology & Evolutionary Biology Tulane University New Orleans, LA 70118 504-862-8285 (office) 504-862-8706 (fax) elizabethderryberry.tulane.edu

ederrybe@tulane.edu

UAdelaide HumanAncientDNA

Graduateposition: PhDs Position in Human Population/Quantitative/Statistical Genetics using ancient DNA

Location:Australian Centre for Ancient DNA (ACAD), University of Adelaide, South Australia

Wehave three (3) PhD positions for highly motivated students to join our dynamic research team in one of the world's leading ancient DNA centres. Candidates must have a 1st Class Honours or Masters degree, an excellent undergraduate academic record and meet the English Language Proficiency (ELP) requirement. The call is open to international and domestic students with a background in bioinformatics, programming or population/quantitative/statistical genetics. In addition, a passion for human history and archaeology is desirable along with demonstrable analytical skills. The projects will suit hard-working and self-motivated candidates equipped with good skills in critical and independent thinking. Training will focus on the analysis of Next-Generation Sequencing data with a special emphasis on the utilisation and expansion of population and quantitative genetic methods for paleogenomic data. Successful candidates will also have the opportunity to assist in the development and application of cutting-edge reference genome approaches for humans and other organisms. Training opportunities to advance wet-laboratory techniques can be offered in parallel.

Greatcomputational skills are required and a successful candidate would be competent in:

- Querying a SQL (PostgresQL) database
- Data analysis and management skills
- Fluency in using Linux systems, with a good hands-on experience with Bash scripting
- Advanced programming in a scripting language such as Python and/or R

Thisis a great opportunity to study abroad (for international candidates) as Adelaide is a vibrant cosmopolitan city with a Mediterranean climate guaranteeing a great lifestyle. Interested applicants are encouraged to send a resume and a cover letter to either Dr Yassine Souilmi (yassine.souilmi@adelaide.edu.au) or Dr Ray Tobler (raymond.tobler@adelaide.edu.au).

Notethat the Australian Department of Immigration and the University of Adelaide expect international applicants to meet the English Language Proficiency (ELP) requirements. See below for details of the ELP. The ELP is based on high scores in IELTS (International English Language Testing System) or TOEFL (Test of English as a Foreign Language). For further information, please refer to this link .

Universityof Adelaide, North Terrace Campus, South Australia 5005

Phone:+ 61 8 8313 3952

Fullcontact details to our website and social media follow this link adelaide.edu.au/acad/

yassine.souilmi@adelaide.edu.au

UAntwerpen EvolutionParasiteTraits

The Evolutionary Ecology Group has a vacancy for a PhD student in a project on "Evolutionary potential of parasite traits in a bird-tick system". Host-parasite interactions are considered among the most dynamic co-evolutionary processes, as host and parasite exert mutual selective pressures leading to a chain of adaptations and counter-adaptations. To understand this process, a key element is the quantification of heritable individual variation and selection pressures in both host and parasite. This PhD project uses an experimental bird-tick system where hosts have a high degree of tolerance (i.e. minimal harm) towards a specialized parasite. In this system we will explore how parasite traits are shaped by natural selection through the study of genetic variation, trade-offs among traits, and selection pressures related to the host and the environment. Individual ticks will be followed across multiple generation in a strict breeding design, combined with controlled infestations of hosts in the lab and in the field. Using hosts with a known pedigree further allows us to bring in their phenotypic and genetic background as well. Thus, aside from field and lab work the project also involves a strong modelling component for pedigree and fitness analyses. We have ten years of experience with this study system providing a solid basis for a successful project. Profile and requirements: You hold a Master degree in Biology or comparable with a strong background in ecology and evolutionary biology; You can submit outstanding academic results; You have a solid training in both uni- and multivariate statistical analysis; Experience with parasite research, bird ringing and handling, and/or quantitative genetics is an advantage. We offer: A doctoral scholarship for a period of two years, with the possibility of renewal for a further two-year period after positive evaluation; The starting date of the scholarship will be February 1st 2017; You will enrol in the Antwerp Doctoral School training program (www.uantwerpen.be/ads) allowing you to take part in various courses, training programs and conferences within and outside the university; You will work in a team of several PhD students, postdocs and technical staff involved in eco-evolutionary research on birds and bird parasites; You will be member of the Evolutionary Ecology group, a dynamic and internationally-oriented research group that combines field, lab and modelling approaches to study various questions in ecological and evolutionary research, mainly focusing on birds and mammals (www.uantwerpen.be/eveco). Applicants should send their complete CV, a one-page statement of research interests and motivation for this project, and contact information of two referees who can supply letters of recommendation upon our request. Applications should be submitted by email to Prof. Erik Matthysen at erik.matthysen@uantwerpen.be until the closing date: 5 December 2016. For more information, contact Erik Matthysen at the same email adress or at (+32) 3265 3464. The University of Antwerp strives to contribute to an open, democratic and multi-cultural society. We follow an equal-opportunity policy.

Prof. Dr. Erik Matthysen Evolutionary Ecology Group University of Antwerp +322653464

New street address since 10 June 2016: Campus Drie Eiken room D1.32 Universiteitsplein 1, 2610 Wilrijk

Matthysen Erik <erik.matthysen@uantwerpen.be>

UArkansas EvolutionaryEcology

Graduate assistantships are available for Ph.D. positions in the Siepielski Lab https://asiepielski.wordpress.com in the Department of Biological Sciences and Program in Ecology and Evolutionary Biology at the University of Arkansas main campus in Fayetteville, AR (http://biology.uark.edu). Our lab focuses on questions at the intersection of ecology and evolutionary biology. Current projects include examining spatial variation in the mechanisms that maintain species diversity, the role of parasite mediate selection in structuring communities, the contribution of ongoing evolution in shaping the demographic processes regulating populations, and determining the major features characterizing natural selection in the wild. To explore these topics we use a combination of observational, experimental, meta-analytical, and theoretical approaches.

I am looking for students interested in developing their own project on themes broadly related to those listed above. Ideal applicants would have prior research experience in ecology and/or evolutionary biology, previous coursework in statistics, and a genuine passion to conduct research. Depending on availability, students may be funded through a combination of research assistantships for upwards of four semesters, with the remainder of their degree being supported through a teaching assistantship. Graduate research fellowships are also a possibility for highly competitive candidates. Please see http://graduate-recruitment.uark.edu/funding-degree/fellowships.php for additional information on graduate funding opportunities.

The University of Arkansas, Fayetteville, AR, is a Tier I research university located in the Ozark Mountains. The faculty and graduate students at UARK are highly interactive and include an internationally known group of evolutionary biologists and ecologists. We are located in an ideal setting for field-based projects in aquatic systems (AR has more than 2,300 lakes and thousands of smaller ponds, and equally impressive numbers of rivers, streams and creeks). Fayetteville, located in northwest Arkansas, offers a high quality of living at a low cost, an excellent climate, and is a large enough city to offer diverse activities and amenities. Rock climbing, hiking, kayaking, canoeing, and mountain biking opportunities are in close proximity.

Prospective students should check out my website https://asiepielski.wordpress.com for additional information. If interested in joining our lab group, please contact me via email (amsiepie@uark.edu). In your email, please include the following: 1) a brief description of your research interests, career goals, and why you think our lab would be a good fit for you, and 2) contact information for three references. In addition, please attach your CV.

Please note that the deadline for Fall 2017 admission into our program is January 15, 2017. All materials should be submitted well before then.

Adam M. Siepielski Department of Biological Sciences University of Arkansas Fayetteville AR, 72701 Ph: 1-479-575-6357

Adam Michael Siepielski <amsiepie@uark.edu>

UBergen PopulationGenomicsSponges

There is a vacancy for a PhD position in phylogenomics/population genomics of deep-sea sponges at the Department of Biology within the Marine Biodiversity Group. The position is for a fixed term of 3 years.

About the project/work tasks:

The research will be performed in the scope of the EU-funded project "Deep-sea sponge grounds ecosystems of the North Atlantic: an integrated approach towards their preservation and sustainable exploitation - SponGES", a collaborative effort coordinated by the University of Bergen and involving 20 European, Canadian and American partners.

The project's primary goal is to develop an integrated ecosystem-based approach for the preservation and sustainable exploitation of deep-sea sponge ecosystems of the North Atlantic, which requires a deep understanding of their diversity, evolutionary and connectivity patterns.

Phylogenetic and population-level studies performed in sponges have been in most part restricted to shallow-water species, and relatively limited in terms of the nature and number of markers used. In SponGES we will employ a genomic-based approach to investigate the phylogenetic relationships, biogeographic patterns as well as genetic diversity, structure and connectivity of several deep-sea grounds-forming species at different spatial scales.

The candidate will be based at the University of Bergen and enrolled in its PhD programme but have several research stays in the Natural History Museum London (Ana Riesgo's lab), and will further collaborate with researchers from the University of Uppsala (Sweden) and Fisheries and Oceans Canada (Canada).

The activities will entail:

participation in sampling cruises to several case study areas.

development of a suite of genomic resources (e.g. single nucleotide polymorphisms, full mitochondrial genomes) of key structuring species, using next-generation sequencing technologies (NGS).

assessment of the evolutionary, phylogeographic and connectivity patterns of species and populations at various spatial scales.

publishing of scientific work

Qualifications and personal qualities:

The applicant must hold a master's degree or the equivalent in marine and/or molecular ecology/biology (or similar), 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.

Background experience in population genetics/genomics and/or phylogenetics using next-generation sequencing (NGS) platforms, and bioinformatics skills are highly advantageous.

Work independently and in a structured manner, and have the ability to cooperate with others.

Proficiency in both written and oral English.

About the research training:

As a PhD Candidate, you must participate in an approved educational programme for a PhD degree within a period of 3 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 good and professionally challenging working environment.

salary at pay grade 50 upon appointment (code 1017/pay range 20.8). Further promotions are made according to 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.

Your application 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 can 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.

a list of any works of a scientific nature (publication list).

any publications in your name.

The application and appendices with certified translations into English or a Scandinavian language must be uploaded at Jobbnorge.

Closing date for applications: 14 December 2016

General information:

Detailed information about the position can be obtained by contacting:

Professor Hans Tore Rapp, Hans.Rapp@uib.no

Postdoctoral researcher Joana R Xavier, Joana.Xavier@uib.no

*APPLY HERE: * https://www.jobbnorge.no/en/available-jobs/job/131183/phd-position-in-phylogenomics-population-genomics-of-deep-sea-sponges – Joana R Xavier, PhD Postdoctoral researcher & SponGES scientific manager Centre for Geobiology Department of Biology University of Bergen (UiB) Thormohlensgate 53A N-5020 Bergen Norway E-mail: joanarxavier@gmail.com / joana.xavier@bio.uib.no

— / —

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

---

UBristol MorphologicalEvolutionDivTimes

Two PhD positions available at Phil Donogue's group at the University of Bristol, UK, to work on morphological rates of evolution and methods of telling evolutionary time.

*** Project 1: Integrating morphological and molecular methods of telling evolutionary time

Supervisors: Philip Donoghue (Bristol), Ziheng Yang (UCL), Davide Pisani (Bristol), Mario dos Reis (Queen Mary, London)

Deadline: 5th of December of 2016

Info: http://bit.ly/UBristol_MorphologicalRatesTimes Apply: http://www.bristol.ac.uk/study/postgraduate/2017/doctoral/phd-south-west-biosciences—swbio-bbsrc-doctora/ *** Project 2: Patterns, processes, rates, and constraints, in the evolution of morphological disparity

Supervisors: Phil Donoghue (Bristol), Matthew Wills (Bath), Davide Pisani (Bristol), Mario dos Reis (Queen Mary, London), Thomas Guillerme (Imperial College London)

Deadline: 6th of January of 2017

Info: http:bit.ly/BristolU_MorphologicalDisparity Apply: http://www.bristol.ac.uk/study/postgraduate/apply/ *** For enquiries please contact Phil Donoghue at Phil.Donoghue@bristol.ac.uk

http://palaeo.gly.bris.ac.uk/donoghue/ – Mario dos Reis

Lecturer Queen Mary University of London Mile End Road, London, E1 4NS

mariodosreis.wordpress.com

Mario dos Reis <mariodosreis@gmail.com>

UBristol TardigradePhylogenomics

Two PhD student projects are available at the University of Bristol. Only EU students are eligible. The positions are competitively assigned and funded by NERC and BBSRC.

The projects deal with understanding evolution of the Tardigrada and the Vertebrata.

details - follow the links:

http://www.bristol.ac.uk/swbio/media/swbio-dtp-project-48.pdf http://www.bristol.ac.uk/media-library/sites/earthsciences/documents/Critters%20in%20space%20How%20did%20the%20waters%20bears%20evolve%20adaptions.pdf

Davide Pisani Professor of Phylogenomics School of Biological Sciences and School of Earth Sciences University of Bristol Life Sciences Building 24 Tyndall Avenue Bristol, BS8 1TG Email: davide.pisani@bristol.ac.uk Phone: +44 (0) 117 39 41196

Davide Pisani <Davide.Pisani@bristol.ac.uk>

UBritishColumbia MicrobeEvolution

Ph.D. opportunity in the evolution and ecology of host-associated microbial diversity

The Parfrey lab (http://parfreylab.botany.ubc.ca) at the University of British Columbia in Vancouver, Canada is recruiting at least one PhD student to begin in Fall 2017. We study the evolution and diversity of host-associated bacteria and eukaryotes. We are currently working on the following projects: 1) diversity of eukaryotes within the mammalian microbiome; 2) ecological impact co-evolved commensal eukaryotes have on the immune system and gut microbiota in a rat model system; 3) diversity and host-specificity of microbes associated with seaweeds, 4) using the eukaryotic tree of life to make sense of the multitudes of unknown eukaryotes coming from environmental sequencing (eukref.org). The PhD student will have the opportunity to develop his or her own research projects within these topics.

Strong candidates will have a successful track record of conducting research in evolution, ecology, microbiology, or related fields, ideally with evidence of success in the form of a scientific publication. Computational experience in Unix/Linux, Python, or R is an asset.

The PhD student will join a vibrant ecology and evolution community in the Biodiversity Research Centre (http://biodiversity.ubc.ca), and a stellar group of researchers investigating microbial diversity in the Centre for Microbial Diversity and Evolution. Students will have access to a wealth of stimulating discussion group, seminar series, and training opportunities. Vancouver offers a mild climate with abundant opportunities for skiing and outdoor adventures in the nearby mountains and ocean, as well as vibrant city life.

Interested students should email Laura with a 1) summary of research interests and accomplishments, 2) your CV, and 3) unofficial transcripts to Lwparfrey-ATbotany.ubc.ca. Students can apply through either the Botany or Zoology departments. Applicants are strongly encouraged to contact me well ahead of the January application deadlines to ensure full consideration for fellowships.

Laura Wegener Parfrey Assistant Professor, Depts of Botany and Zoology Canada Research Chair in Protist Ecology University of British Columbia 109-2212 Main Mall Vancouver, BC, Canada V6T 1Z4

"Wegener Parfrey, Laura" <lwparfrey@botany.ubc.ca>

UCalgary GenomicsDrugResistanceParasites

PhD Graduate Student Position: "A genomic approach to detect, monitor and track the emergence of anthelmintic drug resistance in Human Soil Transmitted Helminths (STH)".

The University of Calgary, Faculty of Veterinary Medicine (UCVM is seeking a graduate student for a project using genomics approaches to investigate drug resistance in human soil transmitted helminths. The project will apply johnseveral deep amplicon sequencing and genome-wide scanning approaches that we have developed for animal parasites and apply them to track the emergence of benzimidazole drug resistance in human soil transmitted helminths.

What are we looking for an individual with a background in molecular ecology and/or population genomics and bioinformatics skills (or a keen desire and aptitude to learn) with a strong interest in applying their skills to a major human health problem in the developing world. The balance of specific expertise will be considered on a case-by-case basis. The preferred candidate needs to be highly motivated, enthusiastic and good team player with excellent communication skills. The work will be predominantly laboratory based but will involve working with collaborators in endemic regions with the potential fro some field work for the appropriate candidate.

The Project: There are currently 1.5 billion people infected worldwide with soil-transmitted helminths; roundworms such as Ascaris, Trichuris and Hookworms. The World Health Organization is currently undertaking the largest mass drug administration (MDA) program in human history to control these important pathogens. This program is dependent on a single drug class (benzimidazoles such as albendazole and mebendazole) and there is now major concern about the emergence of drug resistance. This PhD project will undertake a number of genomic approaches to detect and monitor the emergence of drug resistance in communities undergoing mass drug administration programs in endemic regions (including Ethiopia, Tanzania and Brazil).

What we offer: The graduate student will be co-supervised by Dr John Gilleard, Professor of Parasitology (http://www.ucalgary.ca/jsgilleard/) and Dr Sam Yeaman, AIHS chair in Computational Biology (http://yeamanlab.weebly.com) at the University of Calgary. They will be part of a large interdisciplinary research group focussed on the study of anthelmintic drug resistance in parasites. The graduate student will also be a member of the NSERC-CREATE Host-parasite Interactions (HPI) graduate program which offers outstanding opportunities to undertake professional development and community outreach activities (see http://www.ucalgary.ca/hpi/).

UCVM is a new and dynamic veterinary faculty in Western Canada that has a strong commitment to comparative medicine and One Health research. UCVM is co-located with the Cummings School of Medicine providing an outstanding infrastructure and academic environment and fostering collaborative research between human and animal health. Descriptions of the Faculty and its departments can be found on the UCVM website (www.vet.ucalgary.ca). Calgary is a vibrant, multicultural city with a population of just over a million people. It is located near the Rocky Mountains, Banff National Park and Lake Louise, and offers an enormous opportunity for outdoor activities both in winter and summer.

The salary will be commensurate with the level of education and experience. For additional information and informal enquiries please contact Dr John Gilleard (jsgillea@ucalgary.ca). Interested individuals should submit a current curriculum vitae and an outline of research interests along with the names of three referees to: Dr John Gilleard. email: jsgillea@ucalgary.ca. Phone +1 (403) 210 6327.

Research Group website: http://www.ucalgary.ca/jsgilleard/

Review of applications will start ASAP and will be ongoing until a suitable candidate is identified.

"jwasmuth@ucalgary.ca" <jwasmuth@ucalgary.ca>

UCaliforniaBerkeley EvolutionMetabolism

The Evolution of Metabolisms that Shaped Life on Earth

Supervisors:

Dr. Patricia Sánchez-Baracaldo (Geographical Sciences, University of Bristol) - Main contact Email: p.sanchez-baracaldo@bristol.ac.uk; Tel: +44 (0) 117 954 6858
Prof. John Huelsenbeck (Dept. of Integrative Biology, University of California, Berkeley)

The bacterial metabolisms of photosynthesis and nitrogen fixation have shaped life on our planet by contributing to the cycling of carbon and nitrogen in the Earth's biosphere. While photosynthesis fixes carbon dioxide using different electron donors into carbohydrates, nitrogen fixation transforms atmospheric nitrogen into a bioavailable source such as ammonium. Geochemical and biological evidence suggests that photosynthesis (1-3) and nitrogen fixation (4,5) evolved shortly after life originated on our planet. Understanding how these metabolisms evolved through the bacterial domain will give insights into how these processes have shaped biogeochemical cycles. How can we study the evolution of photosynthesis and nitrogen fixation given that they evolved billions of years ago? The evolution of these processes must be studied indirectly, through the phylogenetic comparison of a wide diversity of bacterial lineages. Such an analysis can help elucidate the details of how these processes evolved and when they evolved. Lateral gene transfer the transmission of genes between different bacterial lineages has been used to explain the current distribution of these metabolisms on the bacterial tree of life. Alternative explanations might also be possible, such as the differential loss of genes involved in these metabolisms as bacterial lineages diversified.

Using the bacterial tree of life, this project aims to study how and when these fundamental metabolisms evolve. We will use large genomic data sets to study: (1) the evolution of the bacterial linages and (2) the evolutionary patterns for photosynthesis and nitrogen fixation (both vertical and horizontal) across bacterial groups. The Ph.D. student funded by this grant will also have the unique opportunity to not only collect the appropriate data but also to develop new phylogenetic methods.

This student would be co-advised by Dr. Patricia Sánchez-Baracaldo (University of Bristol) who is an expert in the biological/geological data and Prof. John Huelsenbeck (University of California, Berkeley) who is an expert in the development of phylogenetic methods. This is a great opportunity for students interested in evolutionary biology, phylogenetic methods, bioinformatics, and the origin of life.

This is a four-year project funded by the University of Bristol (the host institution) with a stipend of 14,296 + fees for UK and EU students.

How to apply: Please make an online application for this project at http://www.bris.ac.uk/pg-howtoapply. Please select 'Geographical Sciences: Physical (PhD)' on the Programme Choice page and enter the title of the studentship project 'The Evolution of Metabolisms that Shaped Life on Earth' when prompted in the Funding and Research Details sections of the form.

Applications deadline:: 17 February 2017. Interviews are expected to be held in early March 2017

Candidate requirements: At least a 2.1 (Hons) degree or equivalent in a relevant quantitative subject, e.g. microbiology, bioinformatics, population genomics, environmental biotechnology, marine biology, plant molecular biology, genetics, genomics, and computer science. For EU students, English Language IELTS scores of at least 6.5 (no less than 6.0 in any element). A Masters degree in a relevant subject would be desirable but not essential. Computer programming skills in a relevant language, e.g. C/C++, Python, R or Matlab would be an advantage. The award is available for UK or EU students only.

References:

1. Bell, E. A., Boehnke, P., Harrison, T. M. & Mao, W. L. Potentially biogenic carbon preserved in a 4.1 billion-year-old zircon. P Natl Acad Sci USA 112, 14518-14521, (2015). 2. Tice, M. M. & Lowe, D. R. Photosynthetic microbial mats in the 3,416-Myr- old ocean. Nature 431, 549-552, (2004). 3. Blankenship, R. E. Early evolution of photosynthesis. Plant Physiol 154, 434-438, (2010). 4. Thomazo, C., Ader, M. & Philippot, P. Extreme 15N-enrichments in 2.72-Gyr- old sediments: evidence for a turning point in the nitrogen cycle. Geobiology 9, 107-120, (2011). 5. Weiss, M. C. et al. The physiology and habitat of the last universal common ancestor. Nat Microbiol 1, 16116, (2016).

John Huelsenbeck University of California, Berkeley Department of Integrative Biology 3060 VLSB # 3140 Berkeley, CA 94720-3140

E-mail: johnh@berkeley.edu Phone: (510) 502-5887

John Huelsenbeck <johnh@berkeley.edu>

UCincinnati 2 JumpingSpiderEvolution

Hiall,

Iam recruiting two PhD students to join my research group at the University of Cincinnati in the summer or fall of 2017. I am particularly interested in recruiting new students to join our research on the coevolution of jumping spider color vision and coloration.

Oneavailable PhD position, funded through an active NSF grant, will investigate the role of female visual attention/gaze in driving the evolution of complex male displays in the North American jumping spider genus Habronattus. This research project combines intensive field work with lab-based video characterization of male displays and eye-tracking of female gaze responses to video playback of displaying males (the latter in collaboration with Beth Jakob at the University of Massachusetts, Amherst).

Thesecond doctoral position will support a new research initiative in my group to understand the repeated evolution of color vision across jumping spiders. Thus far, we have identified two independent and functionally distinct transitions from dichromacy to tri-/tetrachromacy in jumping spiders, which are, not surprisingly, tightly associated with rapid diversification of male color ornamentation. We are now interested in identifying any additional evolutionary transitions in color vision, characterizing when and why they occurred, and investigating their "downstream" consequences for biodiversity in this group of animals. This work will leverage international field work with molecular, microspectrophotometric, and hyperspectral imaging approaches.

Inaddition to these new research initiatives, we have a number of other research projects that could provide opportunities for incoming students. I am slowly adding more information about these on my lab website: www.morehouselab.com . Studentsinterested in joining the lab should contact me as soon as possible to discuss their interests and fit for the lab. Please include a brief statement of your research interests, how they connect with our current research, and your CV, academic transcripts, and GRE scores if available.

TheUniversity of Cincinnati is emerging as an international center of excellence in sensory ecology. With a strong and growing faculty concentration in Sensory Biology, Behavior, and Evolution (http://www.artsci.uc.edu/departments/biology/-research/Sbbe.html) and an NSF-funded REU program in Sensory Ecology, UC provides a vibrant intellectual environment for research and student training. Plans are afoot for the development of a regional consortium of sensory biologists, including researchers at Purdue and Case Western. Matching research strengths in sensing and sensor technologies in UC's nationally-renowned College of Engineering offer a number of cross-disciplinary training opportunities. In addition, UC's strengths in design and the fine and performing arts provide exciting opportunities for my lab's ongoing involvement in art-science collaborations, including the College of Design, Architecture, Art, and Planning (ranked 3rd internationally) and the Cincinnati Conservatory of Music (ranked 6th nationally). Finally, Cincinnati is a culturally and economically vibrant city with a low cost of living, offering an unbeatable quality of life for our graduate students.

Graduateapplications are due January 1, 2017. More information on the graduate program at the University of Cincinnati and associated application materials can be found here: http://www.artsci.uc.edu/departments/-biology/graduate/future.html . Allmy best,

Nate

NathanMorehouse

AssistantProfessor Departmentof Biological Sciences Universityof Pittsburgh 204CClapp Hall Fifthand Ruskin Avenues Pittsburgh,PA 15260 Office:(412) 624-3378 Lab:(412) 624-3351 http://www.morehouselab.com **TheMorehouse Lab is excited to join the Department of Biological Sciences at the University of Cincinnati, beginning January 2017! Please make note of the new contact info below.**

AssistantProfessor Departmentof Biological Sciences Universityof Cincinnati 711HRieveschl Hall Cincinnati,OH 45221-0006 Office:(513) 556-9700 colorevolution@uc.edu http://www.morehouselab.com "Ily a un autre monde mais il est dans celui-ci." - Paul Ãluard

morehonn@ucmail.uc.edu

UConnecticut EcolEvolutionaryBiol

The Department of Ecology and Evolutionary Biology at the University of Connecticut (UConn) invites applications from prospective graduate students (M.S. and Ph.D.) to begin in Fall 2017. Research in the department includes a wide range of topics in ecology, evolutionary biology, systematics, computational biology, global change biology and conservation biology in a highly collaborative environment at a leading public research university. Applicants should demonstrate a strong commitment to and potential for academic work in ecology and evolutionary biology. Applications from individuals of groups historically underrepresented in STEM fields are particularly encouraged with scholarships available from the university to promote a diverse and inclusive academic community.

Expected Qualifications and Application Process

A Bachelor's or Master's degree in any facet of biology is expected although students with unusual backgrounds are also encouraged to apply if they can demonstrate aptitude and commitment to ecology or evolutionary biology. Because acceptance to the program depends on a good match between the interests of faculty members and students, applicants should communicate about project ideas with potential advisers (see http:/-/eeb.uconn.edu/faculty/) before initiating the on-line application. Applicants are also encouraged to visit UConn to meet faculty members and current graduate students.

We will start reviewing applications on December 15th 2016. The on-line application process requires submission of the formal graduate school application, transcripts, GRE scores (general test required, biology GRE recommended), three letters of reference, a personal essay, and, for non-native speakers of English, TOEFL or IELTS scores.

Funding

Financial support is available through research assistantships, teaching assistantships and university fellowships. Applicants are also encouraged to seek external funding. The UConn Graduate School has funding opportunities for outstanding applicants and groups that are historically under-represented in science (e.g. the NextGenCT Scholarships, Giolas-Harriott and Crandall Cordero Fellowships and Outstanding Scholars Program).

Inquiries

For general inquiries about the application procedure, please contact the admissions coordinator, Anne St-Onge (anne.st_onge@uconn.edu). For more specific questions about research directions, please contact potential advisers directly using the contact information on their webpages (http://eeb.uconn.edu/faculty/).

Jill Wegrzyn <jill.wegrzyn@uconn.edu>

UConnecticut PlantComputationalGenomics

The Plant Computational Genomics lab in the Department of Ecology and Evolutionary Biology at the University of Connecticut seeks motivated PhD and MS students to join the lab in the Summer/Fall 2017. Our research focuses on the computational analysis of genomic and transcriptomic data generated by next-generation sequencing platforms from non-model forest tree species. We implement this through analysis related to gene finding, gene expression, transcriptome assembly, and conserved element identification, through machine learning and computational statistics. We use these methods to address questions related to genome biology and population genomics. In addition, we develop web-based applications that integrate BIG data across domains to facilitate the forest geneticist or ecologist's ability to analyze, share, and visualize their data (http://treegenesdb.org). Such integration requires the implementation of semantic technologies and ontologies to connect genotype, phenotype, and environmental resources.

RESEARCH TOPICS:

Potential research topics in our group include 1) development of visualization tools to support genome-wide association studies in forest trees; 2) application of genomic and transcriptomic techniques to evaluate the impact of climate change on tree populations; 3) development of software solutions to improve assembly and characterization of non-model plant transcriptomes; 4) interrogation of natural genetic variation across populations in large, complex conifer genomes; 5) and your ideas here!

TO APPLY:

Financial support for M.S. and Ph.D. students is available through research assistantships, teaching assistantships, and university fellowships. To learn more about our research, please visit: http://compgenomics.lab.uconn.edu/. Excellent written and oral communication, as well as strong quantitative skills, are required. Backgrounds in genetics/genomics, evolutionary biology, bioinformatics, and computer science are desired. Interested candidates should send an email with a research interest statement (1-2 pages), a CV, unofficial undergraduate/graduate transcripts, and GRE scores to Jill Wegrzyn (jill.wegrzyn@uconn.edu). Qualified candidates will be contacted directly for Skype interviews following review. Applications will be reviewed on December 15th.

ABOUT UCONN:

The University of Connecticut (UConn) has been one of the nation's leading public institutions since its founding in 1881. Located in Storrs, UConn's main campus is situated in the picturesque rolling forests and fields quintessential of New England, yet is only 30 minutes from Hartford, and has close connections to Providence, Boston and New York. The Department of Ecology and Evolutionary Biology consists of over 30 faculty and 60 graduate students with research spanning nearly all major groups of organisms. The Department maintains close ties with the Departments of Physiology and Neurobiology, Molecular and Cell Biology, Marine Sciences, and Natural Resources Management and Engineering, as well as the Center for Environmental Sciences and Engineering and the Institute for Systems Genomics, which together comprise one of the largest groups of biologists in the Northeast.

Jill Wegrzyn <jill.wegrzyn@uconn.edu>

UEastAnglia BirdMigration

PhD at UEA with Aldina Franco on migratory strategies in of partially migratory birds. Terrific project in Spain and Portugal. http://www.enveast.ac.uk/projects/2016-projects/-/asset_publisher/D3hdn
0ff5kVb/content/franco_uenv17ee?inheritRedirectúlse&redirect=http%
2F%2Fwww.enveast.ac.uk%2Fprojects%2F2016-projects%3Fp_p_id%3D101_INSTAN
CE_D3hdn0ff5kVb%26p_p_lifecycle%3D0%26p_p_state%3Dnormal%26p
iew%26p_p_col_id%3Dcolumn-4%26p_p_col_pos%3D2%26p_p_col_count%3D3

PhD at UEA with Aldina Franco tracking white storks to understand how the weather conditions affect their movement and behaviour http://www.enveast.ac.uk/nexuss/nexuss-cdt-projects/-/asset_publisher/D vTPOkhEUkLU/content/the-environmental-determinants-of-dispersal-and-migratory-behaviour-of-long-lived-birds-franco_uenv17nex-?inheritRedirectfalse&redirect=http%3A%2F%2Fwww.enveast.ac.uk%2Fnexuss%2Fnexuss-cdt-projects%3Fp_p_id%3D101_INSTANCE_DvTPOkhEUkLU%26p_p_lifecycle%3D0%26p_p_state%3Dnormal%26p_p_mode%3Dview%26p_p_col_id%3Dcolumn-2%26p_p_col_pos%3D 3%26p_p_col_count%3D6

Aldina M. A. Franco

PGT Director and Course Director at UEA of the International Masters in Applied Ecology (Erasmus MUNDUS)

Senior Lecturer in Ecology | School of Environmental Sciences | University of East Anglia | Norwich | NR4 7TJ, UK | Tel: +44 (0)1603 592721 Web: https://www.uea.ac.uk/environmental-sciences/people/profile/a-franco See also my research and technological developments: Migratory decisions in a changing world

http://www.bto.org/storks http://www.uea.ac.uk/lesser-kestrel-migration/ https://www.uea.ac.uk/movetech/home “Aldina Franco (ENV)” <A.Franco@uea.ac.uk>

UEastAnglia ExptEvolOfReproductiveIsolation

PhD available for Oct 2017 start.

Experimental evolution of reproductive isolation PI: Tracey Chapman, School of Biological Sciences, University of East Anglia, UK Co-Is: Wilfried Haerty, Will Nash, Earlham Institute, Irina Mohorianu, UEA.

Deadline: Jan 8th 2017 The PhD project offers a unique training opportunity to apply novel genetic manipulations and bioinformatics analysis to reveal key mechanisms underlying the evolution of reproductive isolation (RI).

Background The PhD project represents an exciting prospect to investigate the mechanisms underlying Reproductive Isolation (RI) in a global agricultural pest (the medfly, Ceratitis capitata). The student will utilise a unique, long-term evolution experiment in which we have described nascent RI. In this novel project, they will probe the underlying mechanisms involved and test the effect of silencing candidate loci identified from existing transcriptomic data and from new genome scans. They will also profile the expression changes in coding and non-coding transcripts underlying early divergence, to gain much needed insight into the trajectory of early adaptation. The student will benefit significantly from the training they gain from the thriving ENVEast Doctoral Training Partnership. They will also gain highly sought after, transferrable research skills training in genetic manipulations and novel population genetics and bioinformatics analyses of high throughput coding and gene expression data.

Objectives 1. Identifying genes involved in maintaining RI.

Double stranded (ds)RNA gene silencing of candidate loci and tests of altered mating patterns.

2. Profiling the nature of early divergence (i) Analysis of existing transcriptome data to construct gene regulatory networks (GRNs).

(ii) Tracking the genomic and transcriptomic profiles of early divergence.

Training In addition to excellent training in advanced and generic PhD training skills provided by the EnvEast NERC DTP, the student will gain specific research skills in practical genetic / genomic manipulations and in bioinformatics - all of which are in high demand. We have a highly collaborative research ethos and well-equipped insect and molecular labs, spacious CT rooms, wash up, media preparation and dedicated server. The student will attend an EU-wide student-focussed conference, an international conference and national meetings. The student will conduct all the research work and analysis and will increasingly direct the research programme as they progress.

This is a challenging and interdisciplinary project and would suit an ambitious student with a good Honours degree in biological sciences / genetics with a willingness to learn programming.

Funding Notes

This project has been shortlisted for funding by the EnvEast NERC Doctoral Training Partnership, comprising the Universities of East Anglia, Essex and Kent, with twenty other research partners.

Shortlisted applicants will be interviewed on 14/15 February 2017.

Successful candidates who meet RCUK’s eligibility criteria will be awarded a NERC studentship. In most cases, UK and EU nationals who have been resident in the UK for 3 years are eligible for a full award. In 2016/17, the stipend was Â£14,296.

Project Link:

https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=3D78100&LID=3D432
For more details, contact:

tracey.chapman@uea.ac.uk

"Tracey Chapman (BIO)" <Tracey.Chapman@uea.ac.uk>

UEastAnglia SoupInMyFly

The soup in my fly: mechanisms of reproductive plasticity

PI: Tracey Chapman, School of Biological Sciences, University of East Anglia, UK Co-Is: Clive Wilson (Oxford), Matthew Gage, Irina Mohorianu (UEA), Amanda Bretman (Leeds). Deadline: 28th Nov 2016

This PhD project offers a unique training opportunity to understand how male fruitflies respond to their social and sexual environment. The student will gain research skills in cutting-edge genetic, genomic manipulations, bioinformatics and cellular microscopy. They will receive excellent training and career development from the thriving Norwich Biosciences Doctoral Training Partnership and from the collaboration with Professor Clive Wilson at the University of Oxford.

An important part of being successful and competitive is to respond to the rapidly changing environments in which we often find ourselves. A familiar example is 'speech accommodation', where individuals, often unintentionally, adopt the accent or speech patterns of those around them. Fruitfly males have adopted this principle and are able to show highly precise responses to their social and sexual environment. Following detection of conspecific rivals, males transfer more ejaculate proteins to females and sire more offspring. They are even able to alter the composition of the ejaculate 'soup' that they transfer. Males can switch their 'rivals responses' on and off with great accuracy and speed.

The overarching aim is to find out how males can do this. Our recent studies support the hypothesis that males can potentially use different mechanisms, to turn genes on / off, remove inhibitors of gene expression and change the way that ejaculate proteins are made and expelled. The student will test this and determine the temporal sequence of events. They will use phenotypic profiling to assess the effect of genetic manipulations of accessory glands, measure changes to gene and non-coding RNA expression using bioinformatics, and profile structural and signaling changes using high resolution microscopy.

Funding Notes:

For details on how to apply, including eligibility, see: http://biodtp.norwichresearchpark.ac.uk/-how-to-apply Project Link: http://-biodtp.norwichresearchpark.ac.uk/projects/project/the-soup-in-my -fly-mechanisms-of-reproductive-plasticity-chapmanu17dtp

For more details, contact: tracey.chapman@uea.ac.uk

"Tracey Chapman (BIO)" <Tracey.Chapman@uea.ac.uk>

UEdinburgh EvolutionPlantDispersion

As fruits or pollen, plants can fly over a long distance without any muscles; a great example is the dandelion fruit, which is thought to be able to travel over miles by air. The dandelion fruit is only one example of many filamentous flying fruits found in the Asteraceae family, and their morphologies are variations on a common theme. With this PhD research you will resolve the evolutionary origins of key morphological and other design features that enhance the flight capacity of the filamentous flying fruits. In so doing, you will examine the development of these unique fruits and identify the developmental regulators of the evolutionary innovations. The project is highly interdisciplinary and integrates ecology with evolutionary developmental biology, together with functional analyses of specific morphological features using flight assays in the lab and the field. A candidate with immense curiosity about evolutions of biological forms and their functions are encouraged to consider this project. For more information, please go to: (https://www.findaphd.com/search/-projectdetails.aspx?PJID=3D77651). The PhD project is open to candidates from all nationalities. If you are interested in applying, please contact Dr Naomi Nakayama (naomi.nakayama@ed.ac.uk), and she will help you identify the best matching PhD studentship schemes to apply.

Thank you very much,

Naomi

Naomi Nakayama (PhD) Biological Form + Function Lab University of Edinburgh Snail-mail: Rutherford G26, Max Born Crescent, Edinburgh EH9 3BF, UK E-mail: naomi.nakayama@ed.ac.uk Tel: +44 (0)131 650 5924 Web: http://bff-ed-ac-uk.weebly.com/ NAKAYAMA Naomi <Naomi.Nakayama@ed.ac.uk>

UExeter PollinatorPathogenEvolution

Pollinator plagues: the evolutionary ecology of shared infectious diseases in pollinator communities

Honeybees and bumblebees are key pollinators of wild and agricultural flowering plants. Recently, it has become clear that these insects not only overlap in their ecology, but also share many infectious diseases (Fuerst et al. 2014, Manley et al. 2015), which can spread globally (Wilfert et al. 2016). This makes pollinators an excellent ecological model system for emerging diseases, but also potentially impacts how pollinators have to be managed and conserved. In this project, you will be able to study the ecological and evolutionary risk factors driving disease emergence and spread, as well as their impacts on pollinator communities at an ecological and evolutionary level. You will be part of a large collaborative inter-disciplinary research project studying the impacts of agri-environment schemes, designed to improve agricultural landscapes for pollinators, on emerging diseases in pollinators.

In this PhD, you will be trained in experimental ecology in the field and the lab and gain skills in molecular ecology, population genetics and phylogenetics. With your PhD, you will be able to address both fundamental questions on the evolutionary ecology of multi-host pathogen interactions, as well on the applied impacts of these interactions and how they can be mitigated. You will be primarily based at the University of Exeter's Penryn campus, but also spend time at NERC's Centre for Ecology and Hydrology (CEH) in Oxfordshire.

To find out more about our research, visit http://wilfertlabgroup.wixsite.com/wilfertlab and http://biosciences.exeter.ac.uk/cec/research/. For informal enquiries, please contact Lena Wilfert <lena.wilfert@ex.ac.uk>.

Funding: This project is one of a number that are in competition for funding from the NERC Great Western Four+ Doctoral Training Partnership (GW4+ DTP). At least 4 fully-funded studentships that encompass the breadth of earth and environmental sciences are being offered to start in September 2017 at Exeter. The studentships will provide funding for a stipend which is currently £14,296 per annum for 2016-2017, research costs and UK/EU tuition fees at Research Council UK rates for 42 months (3.5 years) for full-time students, pro rata for part-time students. The application deadline is the 6th of January 2017. For full details and to apply, please visit http://www.exeter.ac.uk/studying/funding/award/?id=3D2250 . References 1. R. Manley, M. Boots, L. Wilfert, Emerging viral disease risk to pollinating insects: ecological, evolutionary and anthropogenic factors. Journal of Applied Ecology 52, 331-340 (2015).

2. M. A. Fürst, D. P. McMahon, J. L. Osborne, R. J. Paxton, M. J. F. Brown, Disease associations between honeybees and bumblebees as a threat to wild pollinators. Nature 506, 364-366 (2014).

3. L. Wilfert et al., Deformed wing virus is a recent global epidemic in honeybees driven by Varroa mites. Science 351, 594-597 (2016).

"Bayer-Wilfert, Lena" <L.Bayer-Wilfert@exeter.ac.uk>

UExeter ShrimpVirusEvolution

White Spot Syndrome Virus (WSSV) is a well-studied crustacean virus and has devastating effects on the shrimp farming industry, causing cumulative losses exceeding $10bn since 1993 (Stentiford et al., 2012). Combating this globally important pathogen is a high priority worldwide to promote food security and sustainable food production and to protect the health of wild crustacean species in tropical and temperate areas affected by WSSV. WSSV emerged in 1991 in Penaeus japonicus in China and Taipei, spreading rapidly throughout Asia and the Americas. WSSV is a large dsDNA virus and currently the sole member of the virus family Nimaviridae. Recently, we have isolated a similar virus in wild-caught European shore crab Carcinus maenas and previous studies have also suggested the presence of WSSV-like viruses in other crustaceans. Viral diseases occur in both farmed and wild aquatic animals, and these diseases commonly have their natural reservoir in wild aquatic animals, where population densities are often not sufficient to sustain the natural transmission cycle, which is readily facilitated by aquaculture. To prevent the emergence of novel diseases and to control WSSV, we therefore need to understand the viral epidemiology of wild and farmed crustaceans.

In this project, you will investigate the epidemiology and evolution of viruses in wild and farmed crustaceans in order to better understand the emergence of novel diseases and potentially inform mitigation strategies and therapeutic treatments. You will be part of a large interdisciplinary team and receive training in bioinformatics, evolutionary genetics and experimental and ecological epidemiology in order to identify ancestral hosts of WSSV-like viruses and reconstruct their epidemiology using phylogenetic models.

Using the latest molecular tools, you will analyse high-throughput sequencing datasets derived from existing tissue collections from wild portunid crabs sampled from shrimp farming regions (such as mangrove areas surrounding shrimp ponds in Thailand) to identify WSSV-like viruses with the potential to cause emerging diseases. Furthermore, you will experimentally test for variation in host susceptibility and aim to identify the genetic basis for variation in resistance with the ultimate aim to provide tools for the prevention, mitigation and treatment of WSSV and other novel emerging diseases in farmed crustaceans.

The project will be supervised by Dr Kelly Bateman and Dr Ronny van Aerle (Cefas), Dr Lena Wilfert (University of Exeter) and Dr Kallaya Sritunyalucksana-Dangtip (Centex Shrimp, Thailand). The student will be primarily based at Cefas (Weymouth), but will also spend time at the University of Exeter (Penryn Campus), benefiting from high-quality research environments and the interface between research and its application to policy. For informal enquiries please contact Dr Kelly Bateman (kelly.bateman@cefas.co.uk). To apply, please go to http://www.exeter.ac.uk/studying/funding/award/-?id=3D2517. The application deadline is the 9th of January.

The Strategic Alliance that exists between The Centre for Environment, Fisheries and Aquaculture Science (Cefas) and the University of Exeter is pleased to announce the intention to fund 2 new PhD projects for a September 2017 start. This project is one of six projects that are in competition for funding from the University of Exeter and Cefas. Up to two studentships will be awarded to the best applicants. The new projects will further strengthen the alliance and will contribute towards a developing collective expertise in Aquatic Food Security and Safety. Within the current Cefas Science Strategy, Meeting Food Security and Safety Targets' is one of 5 key evidence challenges. Cefas is focussing its broad aquatic expertise on the growth area of aquatic food production and safety at both national and international levels. As part of this strategy, the strengthening of partner working between government, academia and industry is a major goal.

For eligible students the studentship will cover UK/EU tuition fees plus an annual tax-free stipend of at least £14,296 (2016/17 rate) for 3.5 years, and a research training support grant. This award provides annual funding to cover UK/EU tuition fees and a tax-free stipend. Students who pay international tuition fees are eligible to apply, but should note that the award will only provide payment for part of the international tuition fee and no stipend.

Studentships will be awarded on the basis of merit and are awarded for 3.5 years of full-time study to commence in September 2017.

"Bayer-Wilfert, Lena" <L.Bayer-Wilfert@exeter.ac.uk>

UFlorida FungalEvolution

The Smith Fungal Biology Lab (http://-plantpath.ifas.ufl.edu/faculty/matthew-e-smith/-) and the Hulcr Forest Entomology Lab (www.ambrosiasymbiosis.org) at the University of Florida are recruiting a motivated Ph.D. student to start in Summer or Fall of 2017. We are seeking a student who is broadly interested in fungal systematics, evolutionary biology, and insect-fungi interactions to study ambrosia beetles and their symbiotic fungi as part of an NSF-funded project.

We want someone with: * BS or (preferably) an MS degree in biological sciences * A background that includes evolution, systematics, computational approaches and/or fungal biology * Laboratory and molecular biology experience * Appropriate GPA and GRE scores * Solid English language abilities, strong scientific writing, and demonstrated ability to complete projects.

The following skills and experiences are desired but not required: * Phylogenetic analysis * Isolation and maintenance of fungal cultures * Background in bioinformatics, computer science, and/or genomics * Peer reviewed publications

Interested students should submit a brief cover letter indicating why they are appropriate for the position along with a CV to Dr. Matthew E. Smith (trufflesmith@ufl.edu). Acceptance for the position is contingent upon acceptance to the to the Ph.D. program in the UF Department of Plant Pathology (see http://-plantpath.ifas.ufl.edu/). Applications must be received by 9 December 2016.

Jiri Hulcr, PhD, Assistant Professor UF School of Forest Resources and Conservation 517.256.1894 | www.ambrosiasymbiosis.org http://sfrc.ufl.edu/emergingthreats/

"hulcr@ufl.edu" <hulcr@ufl.edu>

UFlorida SexualSelection

I am looking to recruit graduate students to study (1) the evolutionary interplay of behavior and morphology and (2) the functional morphology of insect weapons. These positions include stipend and tuition, they begin Fall 2017, and they are located at the University of Florida.

Our research focuses on sexual selection in insects, examining the importance of environmental variability both for the expression of sexually-selected traits and for the process of selection itself. We primarily work on leaf-footed bugs, Family Coreidae. These insects wrestle with their hind legs over territories and have a diverse assemblage of hind leg shapes. Ongoing projects in the lab include studies of context-dependent mate choice and male-male competition, testes-weapon trade-offs, and the evolution of allometry. We are currently reconstructing a phylogeny of the group to test hypotheses of weapon shape evolution.

Would you like to apply? Please email me at cwmiller@ufl.edu by December 15th. Include in your email a statement including 1) the kinds of research questions that you would like to pursue, 2) how these fit in with current lab research, 3) a brief overview of your previous academic and research experiences, 4) CV or resume, 5) GRE scores (if you have them), and 6) an unofficial transcript.

Funding including tuition and stipend is available. For more information please visit www.millerlab.net . Information about Gainesville, Florida:

Situated in the rolling countryside of north central Florida, Gainesville is much more than a stereotypical college town. Home of the University of Florida, seat of Alachua County's government and the region's commercial hub, it is progressive, environmentally conscious and culturally diverse. The presence of many students and faculty from abroad among its 99,000-plus population adds a strong cross-cultural flavor to its historic small-town Southern roots. Its natural environment, temperate climate and civic amenities make Gainesville a beautiful, pleasant, and interesting place in which to learn and to live.

Time and time again, Gainesville has been tapped as one of Florida's most liveable cities and ranked among the leaders in the United States - a reputation created by an exceptional combination of local features. Agreeable weather and lovely landscapes, attractive educational and economic opportunities, varied cultural and recreational resources, and a youthful, energetic ambiance all contribute to the standard of living enjoyed by area residents.

"cwmiller@ufl.edu" <cwmiller@ufl.edu>

UGeorgia EvolutionaryBiology

The University of Georgia is seeking graduate students to join a large community of ecology and evolutionary biology researchers through the Integrated Life Sciences (ILS) program.

Admission through ILS allows new graduate students to explore research across 14 participating Ph.D. graduate programs, including over 50 laboratories with diverse ecology and evolutionary biology interests. Over their first semester in the program, graduate students can choose rotations among laboratories from nearly all life science departments.

The application deadline for Fall 2017 admission to the ILS program is December 1, 2016. To learn more about the ILS program and research at the University of Georgia, please visit the website at:

http://ils.uga.edu Potential students are encouraged to explore the ecology and evolutionary biology research underway at UGA through the ILS program and to get in contact with faculty whose research they are interested in:

http://evolutionary.genetics.uga.edu/EvoEcol.html Athens, Georgia is a vibrant college town and is consistently ranked one of the top places to live.

Please contact us or any of the faculty in the ILS program with questions.

Michael White Evolution and Ecology ILS Group Representative Assistant Professor of Genetics whitem@uga.edu

Walter Schmidt Graduate Coordinator of the ILS Program Associate Professor of Biochemistry and Molecular

Biology wschmidt@uga.edu

"whitem@uga.edu" <whitem@uga.edu>

UGhent EvolutionColoration

PhD project on evolution of animal coloration.

Supervisors: Dr. Matthew D. Shawkey and Dr. Liliana D'Alba

Evolution and Optics of Nanostructures (EON) Group, Department of Biology

University of Ghent, Belgium

http://users.ugent.be/˜mshawkey Deadline: February 10, 2017

A fully-funded 4-year PhD position over the broad theme of how coloration affects thermal properties of integument is available in the Evolution and Optics of Nanostructures (EON) group at the University of Ghent, Belgium. Most studies on the colors of animal integument have focused on their roles in camouflage or sexual signaling, but they can also have significant thermal effects. We propose to quantify these thermal effects and determine how nanostructuring that produces bright, iridescent colors affects them. This research will help elucidate evolution of animal coloration and may inspire the design of novel multifunctional materials. Although we primarily work on birds, the study system is open to the student's interest. The student will likely learn and use electron and light microscopy, chemical analyses (Raman and mass spectrometry, etc.), spectrophotometry, phylogenetic and/or optical modeling and fieldwork. We encourage anyone with an interest in multidisciplinary research to apply, including those trained in fields outside biology.

Funding: Four years of funding, including tuition and tax-free yearly stipend of ˜ euro23,800 (with annual increases) are guaranteed. Research expenditures of euro8,900/ year are also provided to the student.

Eligibility: Open to all nationalities. A Bachelor's degree in any field of science (preferably Biology, Physics or Materials Science) is required by the time of admission. Further postgraduate education (e.g. M.Sc.) and/or experience with scientific research will be advantageous. Proficiency with the English language (both written and spoken) is required, and basic skills in Dutch (or a willingness to learn) are advantageous.

Location: The University of Ghent is a large research-oriented university that is consistently ranked within the top 100 Universities worldwide. The Department of Biology has broad research expertise with an active community of faculty, post-docs and students. Ghent is a beautiful small city in the heart of Europe that combines medieval architecture with a thriving arts and food scene.

How to apply: Please first contact Dr. Matthew Shawkey (matthew.shawkey@ugent.be) to discuss your application. A formal application process will then follow.

Matthew Shawkey <Matthew.Shawkey@UGent.be>

UHalle Germany BeeVirusCoevolution

3 year PhD on host-parasite coevolution: bumble bees and their viruses

A PhD position is available for a newly funded project on the evolutionary ecology of viruses in bees, funded by iDiv (www.idiv.de) and within Robert Paxton's lab at the University of Halle, Germany.

The overarching goal of the research is to understand the role of viral evolutionary change for pathogen emergence and host switching as well as host evolutionary response, with a conservation focus on rare and declining species of bumble bee. Research will involve lab and field-based experiments (in Germany) as well as molecular genetic analysis of viruses and their hosts. We seek a highly motivated individual with an interest in host-parasite coevolution and skills or a background in bioinformatics, entomological experimentation, or molecular genetic techniques. Two pre-requisites are a valid driving licence and the ability or willingness to work with bees.

The candidate will be part of iDiv's comprehensive graduate school yDiv (https://www.idiv.de/ydiv.html). The position is available for 3 years commencing April 2017 or soon thereafter. The working language of the lab is English. The neighboring group of Robin Mortiz makes for a strong profile in bee biology and genetics at the University of Halle. Halle is a delightful, historical city approximately 1.5 hours SW of Berlin and 45 minutes from Leipzig, iDiv's seat, to which Halle is connected by several trains per hour. The salary is on the standard German PhD scale of 65% E13, which translates to ca. Euro 30 K per annum.

Further details of the project can be obtained from Robert Paxton (robert.paxton@zoologie-uni-halle.de) and iDiv (https://www.idiv.de/the_centre/-career/flexpool_positions.html#c4681). Applications should be sent on-line to iDiv (apply.idiv.de) by 1 January 2017. Interviews are planned for early February 2017.

Robert Paxton <robert.paxton@zoologie.uni-halle.de>

UJyvaskyla DefensiveSymbiosis

PhD student position available at the University of Jyvaskyla, Finland.

We are looking for a motivated, broad-thinking student interested in pursuing question-driven research. The position may be particularly well suited for students who are skilled at bridging disciplines.

The Doctoral Student will join the project Defensive symbiosis under the supervision of Dr. Juan Galarza and Prof. Johanna Mappes. The project is part of the Centre of Excellence in Biological Interactions (https://www.jyu.fi/bioenv/en/divisions/coe-interactions) funded by the Academy of Finland. The project explores the role of bacterial symbionts in the defensive strategies of chemically defended moths (Arctiinae). The tasks of the Doctoral Student focus on research concerning doctoral thesis, doctoral studies, teaching assistance and other related tasks. The ideal candidate will have basic skills in molecular microbiology and/or gas chromatography techniques, and a good knowledge of evolutionary biology. Entomological knowledge would be an asset. The Doctoral Student is expected to participate in fieldwork, experimental work, microbiological and HPLC assays, as well as conventional and next-generation sequencing. We hope the student to start as soon as possible in 2017, but not later than April 30th 2017.

To learn more about the University of Jyväskylä please visit our web-pages (https://www.jyu.fi/en)

The Doctoral Student job-specific salary component is based on the job demands level 1-4 according to the salary system concerning teaching and research personnel at universities (1.795,12 EUR/month 2.462,01 EUR/month). In addition, a personal performance-based salary component amounting to a maximum of 46,3% of the job-specific salary component is also paid. Starting salary (gross) is typically 2187EUR/month.

For informal enquires about the position please contact Dr. Juan Galarza (juan.galarza@jyu.fi) or Prof. Johanna Mappes (johanna.r.mappes@jyu.fi)

The application (in English) should include 1) A 1-page cover letter, outlining the motivation for applying for the position 2) Contact details of 2 academics who can provide reference 3) Curriculum Vitae 4) Copy of degree certificates Please submit your application as a single pdf file to juan.galarza@jyu.fi no later than 23th December 2016.

Dr. Juan A. Galarza Centre of Excellence in Biological Interactions Dept. of Biological and Environmental Sciences University of Jyväskylä Survontie 9 40500, Jyvaskyla Finland Tel: +358 45 1548044 http://users.jyu.fi/~jugalarz/

“Galarza, Juan” <juan.galarza@jyu.fi>

UKonstanz AvianReproductiveTactics

The International Max Planck Research School for Organismal Biology is a joint cooperation between the Max Planck Institute for Ornithology and the Department of Biology at the University of Konstanz. The research group < http://www.orn.mpg.de/3731861/-Research_Group_Kuepper > Clemens Küpper at the Max Planck Institute for Ornithology in Seewiesen invites applications for a

PhD position (f/m) on < http://www.orn.mpg.de/-3758282/kupper2017 > Alternative Reproductive Tactics in Birds: how to overcome a Ruff handicap

How does behavioural diversity persist over time? The Ruff Philomachus pugnax is a charismatic shorebird with multiple male mating tactics that profoundly differ in display behaviour, aggression and male ornamental plumage. The differences are best visible in males during the breeding season where three morphs can be identified: (i) Independents, large aggressive Ruffs with dark plumage ornaments, who fight other Independents over matings with females; (ii) Satellites, non-aggressive Ruffs with pale plumage ornaments that co-display with Independents and (iii) Faeders, small non-aggressive Ruffs who lack plumage ornaments and actively distract ornamented males from matings whilst stealthily attempting to steal matings with females themselves. Remarkably, these reproductive tactics are fully genetically determined and the three morphs appear to occur in stable frequencies in nature.

We recently found that the underlying genetic differences are entirely encapsulated within a chromosomal inversion region on chromosome 11. This region comprises less than 0.5% of the Ruff genome. This inversion variant is homozygous lethal since one breakpoint interrupts the gene CENPN, whose product is required during mitosis. In addition, long time data from aviary breeding suggest that carrying an inversion allele increases juvenile mortality and therefore the inversion provides a genetic handicap. Our detailed knowledge about the genomic differences has made it possible to develop new diagnostic tools to determine morph frequencies in nature that we want to use to advance our understanding about the persistence of this unusual behavioural diversity and illuminate how the genetic handicap is compensated for.

Your profile: We are seeking a PhD candidate who will take a demographic modeling approach to help us understanding, how the three morphs co-exist in nature. The project will provide opportunities to do fieldwork and sample Ruffs in different parts of Europe, carry out moleculargenetic work (SNP genotyping) and advanced demographic modeling. The student will then integrate already collected data from captivity and the wild with newly collected data and construct a series of state-of-the-art population-matrix models. These models will provide critical morph- and sex-specific parameter estimates, which as such cannot be obtained otherwise. The insights from the modelling will advance our understanding about the maintenance of phenotypic diversity in a textbook example for sexual selection. It will complement other research currently carried out in our group aiming to unravel the proximate mechanisms underlying the three morphs. Applicants should hold a MSc or equivalent degree in biology or a related discipline at the point of enrollment.

Our offer: The PhD project is fully funded for at least 3 years. The salary will be paid according to the collective agreement for civil service employees (TVöD). The program offers a dedicated teaching program, high quality research experience, and outstanding research facilities in an inspiring research and living environment. The working language is English. Each PhD student receives individual supervision and mentoring and is guided in her/his research work by a PhD advisory committee.

Application: Please apply exclusively on our < http://-www.orn.mpg.de/2383/Application > online application portal on no later than Jan 15, 2017. Interviews with the applicants are scheduled for Midâ. Candidates accepted into the program may start latest October 2017.

The Max Planck Society and the University of Konstanz are equal opportunity employers and are committed to increasing the participation of women in its research activities and to employing more individuals with disabilities and especially encourages them to apply.

More information at www.orn.mpg.de/IMPRS and www.facebook.com/OrganismalBiology . Maeggi Hieber Ruiz <maeggi.hieber@uni-konstanz.de>

UKonstanz MicroevolutionHormonalTraits

The International Max Planck Research School for Organismal Biology is a joint cooperation between the Max Planck Institute for Ornithology and the Department of Biology at the University of Konstanz. The research group < http://www.orn.mpg.de/2606/-Research_Group_Hau > Evolutionary Physiology headed by Prof. Michaela Hau at the Max Planck Institute for Ornithology in Seewiesen invites applications for a

PhD position (f/m) on < http://www.orn.mpg.de/-3758082/hau-2017 > Heritability and microevolution of hormonal traits.

Our goal is to unravel evolutionary patterns in flexible physiological traits such as circulating hormone concentrations. Unlike stable traits like morphology, the evolution of highly flexible traits like hormones is still hardly understood. Since hormones regulate a wide range of fitness-relevant traits, it is important to understand their scope for plastic or micro-evolutionary changes to understand the potential of populations to adapt to the rapid ongoing changes in environmental conditions world-wide. We are currently focusing on the â' hormone corticosterone, assessing circulating concentrations as well as responses to environmental and social conditions in wild populations of great tits (Parus major). We are assembling a growing data base of hormone concentrations of individuals taken at multiple times of year, together with measures of fitness and genetic pedigree. We routinely collect correlative data on hormone variation relative to environmental and social variation and have embarked on experimental approaches to establish hormonal reaction norms.

Your profile: We are looking for an enthusiastic PhD candidate to continue and expand the field and data base work to quantify the plasticity and heritability of corticosterone traits. We welcome the use of experimental approaches such as reaction norms to quantify hormonal responses of individuals. We are also able to conduct experiments in captivity. Experience in work with birds, hormones or data bases are advantageous but not required. A driver's licence is required for field work. Applicants should hold a MSc or equivalent degree in biology or a related discipline at the point of enrollment.

Our offer: The PhD project is fully funded for at least 3 years. The salary will be paid according to the collective agreement for civil service employees (TVöD). The program offers a dedicated teaching program, high quality research experience, and outstanding research facilities in an inspiring research and living environment. The working language is English. Each PhD student receives individual supervision and mentoring and is guided in her/his research work by a PhD advisory committee.

Application: Please apply exclusively on our < http://-www.orn.mpg.de/2383/Application > online application portal on no later than Jan 15, 2017. Interviews with the applicants are scheduled for Midâ. Candidates accepted into the program may start latest October 2017.

The Max Planck Society and the University of Konstanz are equal opportunity employers and are committed to increasing the participation of women in its research activities and to employing more individuals with disabilities and especially encourages them to apply.

Interested? For further information and discussion of ideas please contact Prof. Michaela Hau <mailto:mhau@orn.mpg.de> mhau@orn.mpg.de. More information at www.orn.mpg.de/IMPRS and www.facebook.com/OrganismalBiology . Maeggi Hieber Ruiz <maeggi.hieber@uni-konstanz.de>

ULeicester 2 SocialInsectGenomics

The Social Epigenetics Lab at the University of Leicester (http://www2.le.ac.uk/projects/selab) seeks applicants (EU/U.K.) for two funded PhD positions studying various aspects of epigenetics in bees. Please see the attached links for details of the two projects. The Social Epigenetics Lab is a very active research group for new model systems to study epigenetics. This is an exciting time to study epigenetics. For example, the recent use of CRISPR to alter locus specific methylation, opens up a functional approach to epigenetics not possible in the last twenty years. Combining this with more tractable invertebrate systems offers unlimited possibilities to answer many unanswered questions.

BBSRC-MIBTP (8/1/2017)

Uncovering intergenerational epigenetics in the bumblebee using whole genome bisulfite sequencing

https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=37965&LID=775 NERC-CENTA (deadline 23/1/2017)

Epigenetic effects of neonicotinoid pesticides on the important pollinator, the buff tailed bumble bee, Bombus terrestris

https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=80107&LID=2645 Eamonn Mallon Lecturer in Evolutionary Biology Social Epigenetics Lab Lab 219 Adrian Building Department of Genetics University of Leicester LE1 7RH http://www2.le.ac.uk/projects/selab Tel: 01162523488 [cid:61ED6DD1-0C23-43AE-9725-91A8867BDA31]

"Mallon, Eamonn B. (Dr.)" <ebm3@leicester.ac.uk>

ULeicester RecentHumanEvolution

Project supervisors: Dr Ed Hollox and Dr Richard Badge

Project: Gene copy number variation and recent human evolution

Background: Over the past 60,000 years, modern humans have dispersed from Africa into the rest of the world. In the process, humans have adapted to new environments both culturally and genetically. Subsequently, humans have altered the environment themselves, with the development of species domestication, agriculture and spread of urbanisation.

The role of natural selection in recent human evolution remains unclear. There are some well-founded examples, where there is strong genetic evidence for natural selection, a molecular basis for the phenotypic change, and a convincing adaptive evolutionary explanation for the phenotype. An example is the lactase persistence allele enabling digestion of lactose in milk as an adult. Another example is the sickle-cell haemoglobin allele, which is at higher frequencies in populations with endemic malaria because of the protection it confers against severe malarial symptoms. However, such well-validated examples are few.

Because of the recent timescales involved in recent human evolution, it has been argued that subtle changes in allele frequency at multiple loci mediate adaptation. This is likely to be true, certainly in African populations where there is a high level of standing variation, but validating any phenotypic effect of such subtle changes is challenging. As well as single nucleotide polymorphism (SNP), multiallelic copy number variation (mCNV) is another source of genomic variation, where individuals differ in the number of copies of a gene, with several alleles within a population. mCNV is extensive and its evolutionary role is underexplored. Despite this, there are two notable instances where mCNV may underly a recent adaptation. The first is the amylase locus, where it has been claimed that higher copy number of the amylase gene in certain populations is an adaptation to a starch rich diet. The second is the salivary agglutinin gene, which encodes a protein that binds teeth and Streptococcus mutans (the causative agent of dental caries), and where two mCNVs covary with a history of a starch-rich diet https://www.ncbi.nlm.nih.gov/-pubmed/25848046 . Such findings strongly suggest this is an area that will yield new discoveries.

This project will focus on highly-differentiated mCNVs, and the genes within them. In particular we will apply new bioinformatics approaches developed in EJH's group to utilise short read sequencing to call sequence variation with copy number variable regions. This will open up not only the 1000 Genomes samples, which are currently being sequenced to high depth, but other samples, including those in the 100K Genomes project. EJH is a member of the Population genetics Genomics England Clinical Intepretation partnership. We will then use these data to fully explore the evolutionary dynamics of these CNV regions and investigate evidence of recent selection of particular paralogues.

The project is funded by the Midlands Integrative Biosciences Training Partnership by BBSRC. The projects are for four years, with the first year being a rotation between labs across the partner Universities (Leicester, Birmingham, Warwick).

For more details: http://www2.le.ac.uk/colleges/-medbiopsych/research/pg-research/mitbp-at-the-university-of-leicester Please check whether you are eligible for this studentship at https://-www2.warwick.ac.uk/fac/cross_fac/mibtp/pgstudy/-phd_opportunities/application/#Eligibility Deadline for applications is 12 January 2017

Contact for informal enquiries: Ejh33@le.ac.uk

"Hollox, Ed (Dr.)" <ejh33@leicester.ac.uk>

ULeuven EvolutionaryGenomics

A PhD student position in evolutionary genomics is available at the department of Biology, University of Leuven, Leuven, Belgium.

Title: Adaptive responses of an aquatic vertebrate to chemical pollution

Reference: BAP-2016-596

Closing date: 2016-12-23

Starting date: 2017-03-01

Project description: Despite chronic exposure to contaminants at levels known to elicit toxicities in naive animal models, fish populations may thrive at highly polluted sites. Such resistance may involve either intra-generational physiological acclimation or intergenerational genetic adaptation. On the other hand, adaptation doesn't always occur in those situations where it might be expected. While there is a large body of research on acute and chronic toxicant responses in terms of acclimation within generations, the effects of multi-generational exposure on adaptive responses is less well understood and among others requires relevant exposed wildlife populations. The focus of our proposal involves the identification of the genetic and molecular mechanisms that underlie evolutionary processes following multi-generational exposure to biologically relevant chemical pollutants. Model organism is the three-spined stickleback.

The project is part of a larger program that links population genomics, ecotoxicology and modeling. The successful candidate will work in Professor Filip Volckaert's research group (bio.kuleuven.be/eeb/lbeg) in close collaboration with another PhD student at the ecotoxicology research group of Gudrun Deboeck at the University of Antwerpen (B) - https://www.uantwerpen.be/nl/-personeel/gudrun-deboeck/. The group consists of ~12 researchers (senior scientist, postdocs, graduate students and research engineer) with different areas of expertise. Research at the Volckaert lab focuses on population genomics of fish and their parasites, and the lab uses a combination of field data, monitoring data, experiments, modeling and in depth analysis to understand the complex patterns of natural and human-induced genetic variation and their implications for evolutionary history.

Qualifications: A master degree in (applied) biology or a related field is required.

The ideal candidate is highly motivated with thorough education in quantitative disciplines, such as statistical/quantitative/population genetics, bioinformatics, computer science, statistics and with a strong interest in population genetics and evolution in aquatic environments.

For further information about the position please see https://icts.kuleuven.be/apps/jobsite/vacatures/-53997389 of the Arenberg Doctoral School.

or contact Professor Filip Volckaert

mailto:filip.volckaert@kuleuven.be, +32 16 32 39 72.

Filip Volckaert <filip.volckaert@kuleuven.be>

ULiverpool EvolutionHymenopteraImmunity

https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=78293&LID=829 Evolutionary interactions between hosts, pathogens, and microbiomes across multiple origins of sociality in Hymenoptera

Project Description

Sociality produces conditions that are ideal for disease transmission: large, dense populations of closely related individuals. Paradoxically, the genomes of all social insects sequenced to date appear to have a limited immune repertoire, based on homology to Drosophila melanogaster. Is this because there are novel immune pathways in social insects that have no homology to Drosophila? Or is it that immunity in social insects relies more on their microbiome - the community of commensal bacteria they carry around with them? Either way, studies focused solely on the classical immune system are incomplete. This studentship will use transcriptome sequencing of phylogenetically diverse samples across solitary, primitively social, and eusocial Hymenoptera, to understand the connections between eusociality and immune defense, and how the innate immune system and the microbiome evolve across multiple independent origins of sociality. The Hymenoptera have been hugely important to our understanding of fundamental topics in evolutionary biology, including sex allocation, kin selection, and sociality. We aim to resolve longstanding questions about the connection between sociality and immune defense, and link this research to new insights concerning the role of the microbiome in health and disease. Through this we will resolve the fundamental issue of whether sociality leads to depauperate immune systems. This project will suit a student with interests in host-parasite interaction, evolutionary ecology, genetics, bioinformatics, and genomics. Existing skills in any of those areas would be helpful but independence, curiosity, a healthy sense of humor, and a certain amount of grit are usually more important. The successful student will have the opportunity to work closely with collaborators at Harvard University and develop skills in evolutionary ecology, host-parasite interaction, immunology, genomics, transcriptomics, and metagenomics. The Institute of Integrative Biology offers a lively community of researchers to interact with, providing many opportunities for collaboration.

Funding Notes

Competitive funding of tuition fee, research costs and stipend (pounds 14,296 tax-free, 2016-17) from the NERC Doctoral Training Partnership "Adapting to the Challenges of a Changing Environment" (ACCE, http://acce.group.shef.ac.uk/). ACCE - a collaboration between the Universities of Sheffield, Liverpool, and York - is the only dedicated ecology/evolution/conservation Doctoral Training Partnership in the UK. Applications (CV, letter of application, 2 referees) by email to iibapply@liv.ac.uk, deadline: January 9th 2017. Interviews: 15th-17th February 2017. Shortlisted applicants will be interviewed for only one project from the ACCE partnership. This project is also available to self-funded students. A fees bursary may be available

Seth Barribeau <seth.barribeau@liverpool.ac.uk>

ULouisiana Lafayette EvolBiol

Doctoral Fellowships and other assistantships available for entering Ph.D. students in Environmental and Evolutionary Biology at the University of Louisiana

We will be awarding University of Louisiana Fellowships and Board of Regents Fellowships to Ph.D. students entering Fall 2017. UL Fellows are funded for 3-4 years and have limited teaching responsibilities, while BoR Fellows are funded for 4 years and have no formal teaching duties. Stipends are up to $30,000 per year (plus tuition waiver). Eligibility requirements include US citizenship (or permanent residency) or degree from a US institution. We will also have teaching assistantships available for incoming Ph.D. students. Potential applicants are strongly encouraged to directly contact prospective advisors, whose contact information and research interests can be found at our departmental web site (http://biology.louisiana.edu/), which also has a link to our graduate programs (http://biology.louisiana.edu/programs/graduate). The Department of Biology has approximately 75 graduate students and 25 graduate faculty members conducting research on a wide variety of topics. More information on application is available from Dr. Scott C. France (france@louisiana.edu).

Scott C. France france@louisiana.edu Professor & Graduate Admissions Chair Mr. Charles R. Godchaux/BORSF Professorship in Coastal Biodiversity Research Development Department of Biology University of Louisiana at Lafayette P.O. Box 43602 Lafayette, LA 70504

For more information about the graduate program please visit: http://biology.louisiana.edu/programs/graduate Office: (337) 482-6320 Lab: (337) 482-6494 FAX: (337) 482-5834 For information on my research please visit: http://www.ucs.louisiana.edu/~scf4101/ "To learn and from time to time to apply what one has learned - isn't that a pleasure?" - Confucius, 500 B.C.

Scott C France <france@louisiana.edu>

UMississippi SyntheticEcolEvolutionSymbiosis

Graduate Positions in Synthetic Ecology and the Evolution of Symbiosis (Fall 2017)

Graduate assistantships are available to support Masters or PhD students in the Hom Lab at the University of Mississippi (Ole Miss). We are generally interested in understanding how biotic and abiotic factors facilitate the formation, persistence, and evolution of species interactions, notably those that are symbiotic. We are particularly fond of studying interactions involving fungi and algae and use a predominantly synthetic approach to address our questions (see Science 345:94-98). Our lab is seeking bright, highly motivated, and disciplined students with an appetite for discovery and adventure to join us in pursuing research projects of mutual interest in areas that include (but are not limited to): experimental evolution, synthetic ecology, Eco-Evo-Devo, eukaryotic metagenomics, bioinformatics, applied microbiology, and the ecology and biodiversity of microbial consortia in both laboratory and field contexts. We offer students substantial flexibility to define their own research project(s) and/or to contribute to one or more ongoing projects in our growing research portfolio. Members of our lab come from all over the world and we are deeply committed to community outreach and the continual expansion of our international collaborations (e.g., see http://mycophygolife.org). Stipend support will be a combination of research and teaching assistantships, and includes tuition waivers and health benefits. The desired start date for these positions is August 2017.

The University of Mississippi is a Carnegie R1 institution undergoing an exciting phase of growth. The university is located in Oxford, a diverse and idyllic college town in northern Mississippi, about 1 hour south of Memphis, TN. The comedian, Lewis Black, described it best when he said: Oxford is to Mississippi what Austin is to Texas. Oxford is not only about football and baseball, but is also home to a vibrant music, arts, and literary community with strong historic ties to William Faulkner and The Blues.

We strongly encourage women and underrepresented minorities to apply. Those with a particular interest in STEM education and outreach within an underserved region are also highly encouraged to applythere are great opportunities to serve.

For consideration and/or more information, please contact Dr. Hom (erik -at- olemiss.edu< http://olemiss.edu >), +1-662-915-1731, http://darwinsdaemon.com) preferably before January 15, 2017.

Requirements for graduate admissions can be found here: http://goo.gl/t1CfcR . To apply, please send a single PDF file that includes: 1) a cover letter explaining your specific research interest(s) and qualifications/research experience, 2) your curriculum vitae, 3) a scientific writing sample, 4) school transcript(s), 5) GRE scores (note: quantitative and verbal scores should each be >150), and 6) contact information for at least 3 references.

Erik F. Y. Hom Assistant Professor | Department of Biology Program Director, ARISE@UM | http://arise.olemiss.edu University of Mississippi | 401 Shoemaker Hall | University, MS 38677-1848, USA phone: +1-662-915-1731 | mobile: +1-415-480-4780 | http://darwinsdaemon.com "erik@olemiss.edu" <erik@olemiss.edu>

UNottingham CarotenoidsEvolutionImmunity

The effect of diet on oxidative stress, immune gene expression and parasite resistance in fish Project supervisors: Dr Andrew MacColl, Professor Jan Bradley and Professor Simon Avery University of Nottingham, U.K. with Professor Simon Davies, Harper Adams University andrew.maccoll@nottingham.ac.uk http://-ecology.nottingham.ac.uk/AndrewMacColl/index.php Carotenoids are powerful antioxidants often used as dietary additives in aquaculture, and reputed to have effects on immune function, but these, and the consequences for resistance to the parasitic infections that plague farmed fish, are poorly understood. Carotenoids are also commonly used by animals in sexual displays, including the nuptial colouration of three-spined stickleback. The evolutionary significance of these signals remains unclear, but could be associated with the advertisement of immune function. This project will use natural variation in fish populations and manipulations of diet, to investigate the effect of carotenoids on fluorescence-based cellular assays of oxidative stress, proinflammatory immune responses and disease resistance in three-spined stickleback.

The project will work with diverse populations of stickleback on the Scottish island of North Uist, where we have already documented large variation in diet, carotenoid availability, parasite resistance and immune function among lakes. The student will use this variation to investigate carotenoid uptake and use efficiency by fish, its genetic basis and how this relates to diet. The findings will be relevant to the study of aquaculture, to understanding the effects of nutrition on immune function and to the ecology and evolution of wild fish populations.

The project is open to students who qualify for UK Research Council funding.

This project is competitively funded through the 'Agriculture and Food Security' stream of the Nottingham BBSRC DTP (http://www.nottingham.ac.uk/-bbdtp/index.aspx) and applications MUST be submitted through the DTP by Monday 12th December 2016, but applicants should firstly contact Andrew MacColl (andrew.maccoll@nottingham.ac.uk) for more information (http://ecology.nottingham.ac.uk/-AndrewMacColl/index.php).

Applicants should have, or expect to get, a First Class or Upper Second degree or equivalent in a relevant subject. Further experience, including a Masters degree, is likely to be advantageous.

Start date: October 2017, duration 4 years.

Associate Professor of Evolutionary Ecology School of Life Sciences University of Nottingham University Park Nottingham NG7 2RD, U.K. Tel: +44 115 951 3410 http://ecology.nottingham.ac.uk/AndrewMacColl/-index.php Andrew.Maccoll@nottingham.ac.uk

---

UNottingham ChiralityEvolution

Project supervisors: Dr Angus Davison and Dr William Brown, University of Nottingham, UK.

angus.davison@nottingham.ac.uk http://-angusdavison.org/ https://twitter.com/angus_davison/-status/797049668555390976 Applications are open for a PhD position in my lab, formally "The evolution and genetics of being sinister: from chiral shells to chiral cells", but less formally "A chance to study the most famous snail in the world, the shellebrity Jeremy" (highlighted Sunday on BBC R4s Pick of the Week http://www.bbc.co.uk/programmes/b08295z7).

The project is competitively funded through the 'Molecules, Cells and Organisms' stream of the Nottingham BBSRC DTP http://www.nottingham.ac.uk/-bbdtp/index.aspx. Note that applications MUST be submitted through the DTP by Monday 12th December 2016, but applicants should ideally contact me for more information. http://www.nottingham.ac.uk/bbdtp/available-projects/molecules-cells-and-organisms/lifesciences/evolution-and-genetics.aspx Applicants should have, or expect to get, a First Class or Upper Second degree or equivalent in a relevant subject. Further experience, including a Masters degree, is likely to be advantageous. Applications are open to students who qualify for UK Research Council funding.

Project description

While our bodies are bilaterally symmetric on the outside, the internal organs exhibit consistent, directional asymmetries in their position or anatomy, such that left/right positional errors are an important class of human birth defect, and in later life, numerous diseases affect seemingly symmetric organs in a lateralised fashion. However, while invariant left/right asymmetry appears to be the rule in nearly all animals, until recently it has not been clear if the path to asymmetry is conserved, or how/why the left/right axis is consistently set up in the same direction (e.g. heart to the left). In a recent breakthrough published in Current Biology (26: 654-660), the Davison lab and collaborators in Scotland, Germany and the USA identified the one in a billion base pair change that determines mirror image development ("chirality") in the pond snail, finally identifying the first described locus that reverses the whole body structure of an animal. As we also showed that the same gene is similarly involved in setting up asymmetry in the frog, then our work that began in snails ultimately revealed one of the earliest common symmetry-breaking steps across the whole of the Bilateria. The next stage of the project is to 'unravel' symmetry breaking at the molecular and cellular level, in particular to find the set of genes that first establish asymmetry, and ultimately, to define general rules for how this is translated into creating left-right asymmetric snail shells and vertebrate bodies. In this exciting and fast-moving, but quite flexible project, the student will seek to understand why snails routinely vary in their chirality, unlike any other animal group, and how this asymmetry is set up. According to need and specific interests, the student will use the pond snail system, perhaps undertake field work in other countries, and conduct genetic and genomic research, from both developmental and evolutionary perspectives.

Link to the paper: www.cell.com/current-biology/fulltext/S0960-9822(16)00056-7

Lab rotation

The student will receive training in the basic techniques necessary to the project. In the lab, this is likely to include an introduction to some of the core techniques of molecular biology, including DNA extraction, PCR and DNA sequencing, as well as experiments in manipulating embryos. Subsequently, the student will be introduced to bioinformatic and phylogenetic methods, necessary to understand the relationship between the different populations and species. Depending upon the time of year of the rotation, local field work may also be possible.

Start date: October 2017, duration 4 years.

– Dr. Angus Davison Reader and Associate Professor in Evolutionary Genetics School of Life Sciences University Park University of Nottingham NG7 2RD

0115 8230322 angus.davison@nottingham.ac.uk angusdavison.org < http://www.angusdavison.org/ > @angus_davison

Angus Davison <Angus.Davison@nottingham.ac.uk>

UNottingham MitonuclearConflictSpeciation

Mitonuclear conflict and speciation in stickleback

Project supervisors: Dr Andrew MacColl, Dr Lisa Chakrabarti and Dr Sara Goodacre University of Nottingham, U.K. andrew.maccoll@nottingham.ac.uk http://ecology.nottingham.ac.uk/AndrewMacColl/index.php In eukaryotes, 'co-adapted gene complexes' comprised of both nuclear and mitochondrial genes must work closely together in the production of energy by oxidative phosphorylation (oxphos). When this essential biochemical cooperation breaks down, the consequences for cells and organisms are serious. Consideration of the coadaptation of nuclear and mitochondrial genes and the speed with which mitonuclear incompatibilities can evolve has stimulated a novel hypothesis for the process of speciation. This proposes that once gene flow between populations is disrupted, the high mutational rate of mitochondrial genes will lead to rapid and unpredictable divergences between populations in coadaption. The breakdown of nuclear-mitochondrial coadaptation following subsequent secondary contact and hybridisation between divergent taxa may be a common cause of reproductive isolation and speciation. Thus far, this idea has been examined in only a handful of organisms, and only once in vertebrates. This studentship will investigate the contribution of mitonuclear conflict to speciation in stickleback, a small fish with excellent genomic resources.

Three-spined stickleback have repeatedly colonised freshwater from the sea. The contrasting energetic and osmotic demands of marine and freshwater environments exert strong selection on genes involved in oxphos pathways, potentially favouring strong selection on nuclear-mitochondrial coadaptation. On the Scottish island of North Uist there are hybrid zones between marine and freshwater stickleback populations that originate from distinct mitochondrial clades that are ~120,000 years diverged. Hybridisation in these contact zones is strongly asymmetric, with freshwater mtDNA introgressing into marine fish, but not vice versa. This is strongly suggestive of mitonuclear conflict contributing to speciation in these fish. In this project the student will combine traditional analysis of genetic crosses with cutting-edge genomics and assays of mitochondrial function, as well as behavioural and ecological fieldwork, to assess the contribution of mitochondrial dysfunction to speciation in stickleback.

The project is open to students who qualify for UK Research Council funding.

This project is competitively funded through the 'Molecules, Cells and Organisms' stream of the Nottingham BBSRC DTP (http://www.nottingham.ac.uk/-bbdtp/index.aspx) and applications MUST be submitted through the DTP by Monday 12th December 2016, but applicants should firstly contact Andrew MacColl (andrew.maccoll@nottingham.ac.uk) for more information (http://ecology.nottingham.ac.uk/-AndrewMacColl/index.php).

Applicants should have, or expect to get, a First Class or Upper Second degree or equivalent in a relevant subject. Further experience, including a Masters degree, is likely to be advantageous.

Start date: October 2017, duration 4 years.

Associate Professor of Evolutionary Ecology School of Life Sciences University of Nottingham University Park Nottingham NG7 2RD, U.K. Tel: +44 115 951 3410 http://ecology.nottingham.ac.uk/AndrewMacColl/-index.php Andrew.Maccoll@nottingham.ac.uk

---

UNottingham MolluscanBiodiversity

Project supervisors: Dr Angus Davison and Dr Chris Wade, University of Nottingham, UK.

angus.davison@nottingham.ac.uk http://-angusdavison.org/ https://twitter.com/angus_davison/-status/797049668555390976 Applications are open for a PhD position in my lab, " From pests to paradise: control and conservation of molluscan biodiversity".

The project is competitively funded through the "Agriculture and Food Security stream of the Nottingham BBSRC DTP http://www.nottingham.ac.uk/bbdtp/-index.aspx. Note that applications MUST be submitted through the DTP by Monday 12th December 2016, but applicants should ideally contact me for more information. http://www.nottingham.ac.uk/bbdtp/-available-projects/agri-food-security/life-sciences/from-pests-to-paradise.aspx Applicants should have, or expect to get, a First Class or Upper Second degree or equivalent in a relevant subject. Further experience, including a Masters degree, is likely to be advantageous. Applications are open to students who qualify for UK Research Council funding.

Project description

Snails and slugs are a major crop pest, with a few introduced species causing massive worldwide problems. Yet, they are difficult to identify and we have little idea of how this biodiversity has come about, hindering appropriate control and conservation efforts. This project will use next generation sequencing methods to investigate the evolution, speciation and diversification of snails, especially with respect to characters under natural and artificial selection (e.g. shell colour and banding or molluscide resistance), and including methods that may help identify cryptic species, or species of conservation concern. For example, building upon the work of a recent student who investigated the diversity within colour polymorphic Cepaea, the next step may be to investigate the degree of parallelism and convergence between this and other species. Ultimately, the precise project will be determined by the interests of the student, but the overall aim is that he/she will begin to determine if the same modes of speciation and evolution are involved in widely divergent species, with the project having implications for both control and conservation of molluscan biodiversity. Although much of the work will be lab-based, with a concomitant bioinformatics element, field collection will be a necessary component, including probable foreign field work in East Asia or the Caribbean region.

Representative lab publications (both involve former PhD students): www.cell.com/current-biology/fulltext/-S0960-9822(16)00056-7 http://onlinelibrary.wiley.com/-doi/10.1111/mec.12262/full Lab rotation

During the lab rotation the student will receive training in several of the techniques that are a necessary component of the larger PhD project. Depending upon the existing skills of the student, these are likely to include a range of molecular biology techniques (e.g. DNA extraction, PCR, RNA methods), analysis (e.g. mapping genes to chromosomes), simple (e.g BLAST searching) and more advanced bioinformatics (e.g. phylogenetics, introduction to biolinux). Depending upon the precise time of year (snails hibernate in winter), it may also be possible to conduct some field work - e.g. identifying possible field sites for later in depth study.

Start date: October 2017, duration 4 years.

– Dr. Angus Davison Reader and Associate Professor in Evolutionary Genetics School of Life Sciences University Park University of Nottingham NG7 2RD

0115 8230322 angus.davison@nottingham.ac.uk angusdavison.org < http://www.angusdavison.org/ > @angus_davison

Angus Davison <Angus.Davison@nottingham.ac.uk>

UOklahoma ComparativePhylogeography

I am recruiting graduate students to join me at the University of Oklahoma starting Fall 2017! My lab merges comparative phylogeography with biogeography, community ecology and macroecology to explore the patterns of genetic diversity and divergence which underpin the shape and limits of species' geographical ranges, the structure and membership of ecological communities, and how these relate to continental and global biodiversity patterns. We also use species' responses to past environmental dynamics to better predict the consequences of contemporary environmental change. My work includes a blend of field/lab-based and database-oriented research, and I invite students with interests in either or both. Past field work has centered around New Zealand, but in the next few years, we will establish a field program in Oklahoma, which has one of the steepest environmental gradients in the United States. Prospective students can read more about our ongoing projects here:

http://www.ou.edu/content/cas/biology/people/-faculty/katharine-marske.html Geographical ecology is a significant core focus of the OU Department of Biology, where I am part of a Geographical Ecology cluster hire, together with Dan Allen (stream and riparian ecology) and Katie Marshall (physiological ecology). Students will have the opportunity to interact with these and other talented faculty and students in the Geographical Ecology focus group and throughout the department.

http://www.ou.edu/content/cas/biology.html Lab resources include a molecular wet lab for DNA sequencing preparation, a computational lab for genetic and spatial analyses, and a separate 'dirty' space for processing ecological samples. Other Biology facilities on campus include a new Biology Core Genomics lab,the Oklahoma Biological Survey and the Sam Noble Museum of Natural History. OU is also home to state-of-the-art climate and weather research, including the National Weather Center, the Oklahoma Mesonet, the Oklahoma Climatological Survey, and the South Central Climate Science Center.

Funding for graduate students is currently available in the form of 10-month teaching assistantships with stipends, full tuition waivers and excellent health care coverage, and numerous scholarships are available to support graduate student research during the summer.

Interested students should get in touch (kamarske@ou.edu) with a brief summary of your research interests and relevant experiences and attach a resume/CV. All prospective students must also apply through the < http://www.ou.edu/-content/cas/biology/graduate-studies/apply/ > < http://www.ou.edu/content/cas/biology/graduate-studies.html > OU Biology Graduate Program by December 15 2016.Candidates from groups underrepresented in STEM are encouraged to apply.

Find out more here: http://www.ou.edu/content/cas/-biology/graduate-studies.html Join us!

Katharine Marske, PhD Assistant Professor Department of Biology University of Oklahoma (from January 2017)

Web: http://www.ou.edu/content/cas/biology/-people/faculty/katharine-marske.html Google Scholar: https://scholar.google.com/citations?user=-3Dw5AXv0AAAAAJ&hl Twitter: @KAMarske

"Marske, Katharine" <kamarske@ou.edu>

UPennsylvania MacroevolutionPaleontology

PhD Fellowship in Paleontology/Macroevolution at UPenn A PhD fellowship is available in the Department of Earth and Environmental Science at the University of Pennsylvania, starting in Fall 2017. Prof. Lauren Sallan seeks a graduate student to address major questions about the evolution of life. These include: how global change has affected life over time, how life evolves at high levels (macroevolution), the relationships of living and dead animals (phylogeny), and the origins of living biodiversity. While research in the lab has focused on fishes, any suitable group of fossils may be used.

Potential thesis topics include, but are not limited to: the long-term effects of mass extinctions (e.g. the end-Devonian and end-Ordovician), the roles of predation and competition in marine ecosystem evolution, characteristics of adaptive radiations and "living fossils," the effects of long-term climate and environmental changes (e.g. the Late Paleozoic Ice Age) on biodiversity, and major transitions in early vertebrate evolution (e.g. origin of jaws, invasion of land). The student can also develop a novel project that addresses similar questions using quantitative, phylogenetic and/or descriptive methods. This is fully-funded fellowship with stipend and tuition support guaranteed for the length of the PhD. Applicants are encouraged to contact Prof. Sallan (lsallan@upenn.edu) for more details. Additional information on the fellowship is available on the departmental website: www.sas.upenn.edu/earth. Applications for entry in Fall 2017 are due January 15, 2017, with interviews in February. Applications to graduate school at Penn must be submitted online at https://www.applyweb.com/upenng/ Lauren Sallan Assistant Professor Earth and Environmental Science & Evolution Cluster University of Pennsylvania Office: Hayden 154B Phone: (215) 898-5650 lsallan@sas.upenn.edu

Lauren Sallan <laurensallan@gmail.com>

USheffield SexChromosomeEvolution

Evolutionary dynamics of the avian sex chromosomes

We are seeking a highly motivated and enthusiastic PhD student to study the evolution of the avian sex chromosomes.

Lead supervisor: Dr Alison Wright, University of Sheffield Co-supervisors: Prof Jon Slate (University of Sheffield), Prof Steve Paterson (University of Liverpool)

Deadline for applying: 9th January 2017

The PhD project will provide an excellent opportunity to learn state-of-the-art genomic skills to study sex chromosomes and test clear theoretical predictions. Applicants should have strong analytical skills and an enthusiasm for evolutionary genomics. The successful candidate will be trained in cutting-edge bioinformatics and genomic techniques. The applicant will benefit from the diverse range of expertise offered by the co-supervisors and researchers within the Animal and Plant Sciences Department at the University of Sheffield.

Sex chromosomes are the only region of the genome to differ between females and males and are therefore predicted to be hotspots of sexual selection, with important roles in sexually dimorphic phenotypes. As the Y chromosome is inherited from father to son, and the W chromosome from mother to daughter, they are thought to be particularly important for fertility. However, in many species these sex-limited chromosomes have experienced rapid decay of gene content and contain only a handful of genes. Why some genes are retained while the majority are lost is a fundamental question in sex chromosome evolution yet the evolutionary drivers remain unclear. Birds are an ideal system to test key evolutionary theories as avian sex chromosomes have been diverging independently and in parallel across different species over millions of years.

The exact details of the project can be tailored to the particular interests of the student. The student will use next-generation sequencing data to study the evolution of the sex chromosomes across multiple bird species. This will make it possible to test key evolutionary hypotheses about gene expression evolution, sexual conflict and sex chromosome degeneration.

Interested applicants are encouraged to contact Alison Wright before applying (alison.e.wright@ucl.ac.uk) for more details on the project, funding and facilities. For details on current research in the Wright lab, see www.alisonewright.co.uk Funding Notes:

For details on how to apply, including eligibility, see: https://acce.shef.ac.uk/phd-opportunities/-sheffield/ For more details on the project, see: https://acce.shef.ac.uk/evolutionary-dynamics-of-the-avian-sex-chromosomes/ Dr Alison Wright

Department of Animal and Plant Sciences University of Sheffield Sheffield S10 2TN

www.alisonewright.co.uk @alielw < http://-www.alisonewright.co.uk >

"Wright, Alison" <alison.e.wright@ucl.ac.uk>

USheffield StructuralColourEvolution

The evolution of iridescent blue colour in Heliconius butterflies and its role in behaviour Lead supervisor: Dr Nicola Nadeau, Department of Animal and Plant Sciences, University of Sheffield Co-supervisor: Prof Mike Speed, Institute of Integrative Biology, University of Liverpool. Closing date: 9th January

We are seeking an enthusiastic student with interests in evolution and behaviour to work on a project investigating the role of iridescent structural colour in predator avoidance and mate choice in Heliconius butterflies. The bright wing colours of these butterflies act as warnings to predators and mimicry between species facilitates predator learning and reduces attack rates. Wing colours are also used for mate choice and attraction. The main colours used are red, yellow and black, due to pigments, but a small number of species also exhibit iridescent blue/green, due to sub-micron scale structures. The role of these colours in deterring predators and attracting mates is less well understood. The project can be tailored to the interests of the student but would likely involve experiments using captive butterfly populations in South/Central America and the UK, and could involve experiments with wild or captive avian predators or theoretical modelling. The project would also tie in with ongoing work on the genetic basis of these traits. Interested candidates are also welcome to contact Nicola Nadeau (details below) for further information.

If successful, the student would be fully funded for a minimum of 3.5 years, studentships cover: (i) a tax-free stipend at the standard Research Council rate (at least 14,296 per annum for 2017-2018), (ii) research costs, and (iii) tuition fees at the UK/EU rate. Studentship(s) are available to UK and EU students who meet the UK residency requirements. Students from EU countries who do not meet residency requirements may still be eligible for a fees-only award.

This PhD project is part of the NERC funded Doctoral Training Partnership "ACCE" (Adapting to the Challenges of a Changing Environment). This is a partnership between the Universities of Sheffield, Liverpool, York and the Centre for Ecology and Hydrology.

Further information and details of how to apply: https://acce.shef.ac.uk/the-evolution-of-iridescent-blue-colour-in-heliconius-butterflies-and-its-role-in-behaviour/ – Dr Nicola Nadeau Dept. of Animal and Plant Sciences Alfred Denny Building, University of Sheffield Western Bank, Sheffield S10 2TN, UK N.Nadeau@sheffield.ac.uk Tel: +44 (0)114 222 4717 http://nadeau-lab.group.shef.ac.uk/ — This email has been checked for viruses by Avast antivirus software. https://www.avast.com/antivirus "n.nadeau@sheffield.ac.uk" <n.nadeau@sheffield.ac.uk>

USouthampton NHMLondon SpeciationGenomics

Dear Evoldir,

We are currently looking for applicants for a PhD based partly at the University of Southampton and partly at the NHM, London. Please do contact myself (M.Chapman@soton.ac.uk) or Mark Carine (M.Carine@nhm.ac.uk) if you have any questions. Pass on to potential students if you know of some. Application deadline is 2nd January.

This project will analyse speciation genomics in a plant genus found throughout the Canary Islands in a wide variety of habitats. Several species are endemics, showing ecological speciation (the origin of species by adaptation to novel environments) within and between islands. A reference genome is being assembled and annotated and the SPITFIRE project will generate and analyse sequencing data from multiple individuals of all the endemic species.

Specific objectives: 1. Phylogenetic analyses of the dynamics of speciation, including the role of introgression in speciation. 2. Measuring divergent adaptation between species through a reciprocal transplant experiment on Tenerife. 3. Identification of candidate genes underlying ecological speciation. 4. Determining the function of a subset of these candidate genes using transgenics.

If you are interested in this studentship and would like more information (note the nationality requirements, funding situation and other requirements) please take a look at:

http://noc.ac.uk/gsnocs/project/identification-analysis-speciation-genes-island-plants Best wishes, Mark

Dr. Mark A. Chapman M.Chapman@soton.ac.uk +44 (0)2380 594396

Centre for Biological Sciences University of Southampton Life Sciences Building 85 Highfield Campus Southampton SO17 1BJ

Mark Chapman <markchapman4774@gmail.com>

USouthernCalifornia EvolMitochondriaSexAging

Ph.D. position in Mitochondrial Effects on Sex-Specific Aging

The Edmands Lab at the University of Southern California in Los Angeles (https://dornsife.usc.edu/labs/edmands/) is recruiting a Ph.D. student for research developing the copepod Tigriopus californicus as a new model for the effects of mitochondria and mitonuclear interactions on sex-specific aging. The ideal applicant would have a strong interest in evolutionary genetics and aging, with experience in genomics, transcriptomics and/or bioinformatics.

Prospective students should email Suzanne Edmands (sedmands@usc.edu) to discuss project possibilities. In your email please include brief details about your GPA, GREs, research interests, experience and reasons for pursuing a Ph.D.

Applications should be submitted to the Marine Biology and Biological Oceanography Graduate Program at the University of Southern California (https://dornsife.usc.edu/bisc/meb-admissions/). All Ph.D. students in the program will have five years of support (including tuition remission and student health insurance) through a combination of RAships, TAships and fellowships. To receive full consideration for university fellowships, applications must be submitted by January 15, 2017.

Suzanne Edmands Professor Department of Biological Sciences 3616 Trousdale Parkway, AHF 316 University of Southern California Los Angeles, CA 90089 (213)740-5548 http://dornsife.usc.edu/labs/edmands/ edmandss@gmail.com

---

UStAndrews ComputationalBiology

Microbe Wars: Exploring the Maintenance of Microbial Diversity Using Artificial Life

A PhD studentship in computational biology is available at the University of St Andrews in Scotland.

Microbes are the most ubiquitous life form on Earth, found everywhere from exotic locations - black smokers on the ocean bottom - to the inside of every human's gut. They are essential for nearly all life on the planet, driving nutrient cycling in the environment and contributing to the health of plants and animals. Microbes are also critical to industrial biotechnology, especially for fuel, fine chemical and drug production. Thus, understanding how microbial ecosystems are maintained is essential. Evolutionary processes within microbial communities appear fundamentally different than those at play in macro-organisms, requiring specific understanding.

In this studentship, you will develop artificial life simulations to explore evolution and maintenance of biodiversity in microbial communities. You will use machine learning and mathematical modelling to identify and assess strategies leading to stable communities that also maintain biodiversity. You will explore how communities respond to perturbation, corresponding to phenomena such as provision of antibiotics to a patient, and human intervention in industrial and agricultural systems.

Your work will have applications in many areas. It is increasingly clear that the microbial communities within our bodies are key contributors to health: because the beneficial effects of these communities are in danger from both antibiotics and antibiotic-resistant pathogens, understanding how healthy biodiversity can be maintained in the face of perturbation is essential. Maintenance of soil microbial diversity is important for plant health, and ultimately our food security. Microbial populations in all contexts may share essential features of community assembly, and this project will inform multiple topic areas.

You will gain training in artificial life simulations, genetic algorithms, machine learning, game theory, microbial genomics and metabolism, and mathematical modelling, and will acquire a working knowledge of microbial communities and their importance on our planet.

Your project will take place in St Andrews' Centre for Biology Diversity (CBD) in the School of Biology, and will be jointly supervised by Dr V Anne Smith from the School of Biology, Dr John Mitchell from the School of Chemistry, and Dr Leighton Pritchard from the James Hutton Institute. All three groups work in complementary areas of computational systems biology and machine learning. For more information on their research please visit:

Dr V Anne Smith's research pages: http://biology.st-andrews.ac.uk/vannesmithlab/ Dr John Mitchell's research pages: http://chemistry.st-andrews.ac.uk/-staff/jbom/group/ Dr Leighton Pritchard's research pages: http://www.hutton.ac.uk/staff/leighton-pritchard EASTBIO - the BBSRC East of Scotland Bioscience Doctoral Training Partnership - is a partnership between the Universities of Aberdeen, Dundee, Edinburgh and St Andrews; the Scottish Universities Life Sciences Alliance (SULSA); and the Scottish Universities Physics Alliance (SUPA). A fully funded 4-year EASTBIO PhD studentship (fees and stipend at the standard rate) is available for Autumn 2017 for candidates with a strong academic record and that satisfy BBSRC studentship eligibility requirements (see http://www.eastscotbiodtp.ac.uk/how-apply-0 if you are unsure - typically UK citizenship required).

If you are interested, please first make an initial informal enquiry, including a covering letter explaining your interest in the studentship and a CV, to anne.smith@st-andrews.ac.uk.

Formal applications should follow to the University following the procedure available at: http://-www.eastscotbiodtp.ac.uk/how-apply-0 using the forms provided and via the link to St Andrews University.

Complete applications must have been received by the University by 5 December 2016.

Dr V Anne Smith School of Biology Sir Harold Mitchell Building University of St Andrews St Andrews, Fife KY16 9TH United Kingdom +44 (0)1334-463368 anne.smith@st-andrews.ac.uk biology.st-andrews.ac.uk/vannesmithlab/ The University of St Andrews is a charity registered in Scotland : No SC013532

V Anne Smith <vas1@st-andrews.ac.uk>

UStAndrews ToolUsingCrows

TOOL USE IN HAWAIIAN CROWS AND NEW CALEDONIAN CROWS

SUMMARY Why do so few animals use tools, and why are we humans so good at it? Dr Christian Rutzs research group tries to shed light on this fascinating scientific puzzle by studying tool-using crows. The groups discovery that the Hawaiian crow (Corvus hawaiiensis) is a highly proficient tool user – published recently as the cover story of Nature – creates unprecedented opportunities for comparative studies with tool-using New Caledonian crows (C. moneduloides) and naturally non-tool-using corvids. This PhD project will contribute to this exciting new research programme. There is considerable flexibility with regards to specific study objectives, but the successful candidate is likely to conduct both fieldwork and aviary-based experiments, with excellent scope for collaboration with other group members (currently, 2 Postdocs and 3 PhD students). This fully-funded PhD project offers excellent opportunities for a highly motivated student to join a dynamic and prolific research group, to conduct topical research on the evolutionary ecology of animal tool behaviour, and to receive training in state-of-the-art research methodologies.

CENTRE FOR BIOLOGICAL DIVERSITY The Centre for Biological Diversity (CBD) at the University of St Andrews provides a highly interactive and stimulating environment for doctoral studies, with particular strengths in animal behaviour, ecology and evolution. The successful candidate would benefit from frequent interactions with postgraduates, postdocs and PIs, including lab chats, seminars, and discussion groups.

CONTACT For further details on the project and informal inquiries, please contact the supervisor, Dr Christian Rutz (christian.rutz@st-andrews.ac.uk), enclosing a copy of your up-to-date CV. Before you get in touch, please read the references listed below, to get a good understanding of the groups current research activities.

APPLICATION DEADLINE Monday, 05 December 2016

FUNDING NOTES Competition-funded PhD project (European/UK students only); if successful, funding (tuition fees and stipend) will be provided for 3 years. The successful candidate is expected to start in September

2017.

FURTHER APPLICATION DETAILS www.findaphd.com SELECTION CRITERIA + excellent academic track record + excellent analytical, writing and communication skills + demonstrable skill and enthusiasm for behavioural research and fieldwork + high degree of self-motivation and independence + ability and willingness to live and work overseas, for extended periods of time and sometimes under challenging field conditions + clean driving licence + prior research experience is an advantage

REFERENCES (1) Crow study systems + Hunt, G.R. (1996) Manufacture and use of hook-tools by New Caledonian crows. Nature 379, 249251. + Rutz, C. et al. (2016) Discovery of species-wide tool use in the Hawaiian crow. Nature 537, 403407. + Rutz, C. and St Clair, J.J.H. (2012) The evolutionary origins and ecological context of tool use in New Caledonian crows. Behav. Processes 89, 153165.

(2) Other recent papers by the Rutz group + Klump, B.C. et al. (2015) Hook tool manufacture in New Caledonian crows: behavioural variation and the influence of raw materials. BMC Biology 13, 97. + Klump, B.C. et al. (2015) Context-dependent safekeeping of foraging tools in New Caledonian crows. Proc. R. Soc. B 282, 20150278. + Rutz, C. et al. (2016) Tool bending in New Caledonian crows. R. Soc. Open Sci. 3, 160439. + St Clair, J.J.H. et al. (2015) Experimental resource pulses influence social-network dynamics and the potential for information flow in tool- using crows. Nature Communications 6, 7197.

Christian Rutz <cr68@st-andrews.ac.uk>

USussex BalancedPolymorphism

A PhD position is available to investigate the role of balancing selection in the maintenance of genetic variation with Adam Eyre-Walker at the University of Sussex.

Project overview : Almost all organisms have substantial levels of genetic variation, but why there is so much genetic diversity? and why does the quantity differ so little between species? These remain fundamental puzzles in the field of population genetics. It has long been appreciated that balancing selection, either in the form of heterozygous advantage or frequency dependent selection, could potentially maintain large amounts of variation, but both types of selection have received little attention because they are difficult to test for. The aim of the project is to use several novel tests of balancing selection in a broad variety of organisms to test for the signature of balancing selection. Each of these tests will leverage the prediction that neutral and selected genetic variation behave differently, with selected variation being maintained in the population at higher frequency and for longer periods of time. The tests will be applied to those species for which we have population genomic datasets â€“ i.e. the whole genome has been sequenced in multiple individuals. There are now dozens of species for which these data are available, from humans with thousands of genomes to some organisms with just a handful of sequences. The project will build on the supervisors previous work estimating the rate of adaptive evolution between species (James et al. 2016, Castellano et al. 2016, Gossmann et al. 2012, Gossman et al. 2011, Eyre-Walker 2006). Besides shedding light on a fundamental problem in population genetics, the project will give the student experience in computer programming, bioinformatics, population genetic theory and statistics.

James, J., Piganeau, G. and Eyre-Walker, A. (2016) The rate of adaptive evolution in animal mitochondria. Mol. Ecol. 25, 67-78.

Castellano, D, Cnado-Zamora, M., Campos, J.L., Barbadilla, A. and Eyre-Walker, A. (2016) Adaptive evolution is substantially impeded by Hill-Robertson interference in Drosophila. Mol. Biol. Evol. 33, 422-455.

Gossman, T., Keightley, P.D. and Eyre-Walker, A. (2012) The effect of variation in the effective population size on the rate of adaptive molecular evolution in eukaryotes. Gen. Biol. Evol. 4, 658-667.

Gossmann, T., Song, B-H., Windsor, A.J., Mitchell-Olds, T., Dixon, C.J., Kapralov, M.V., Filatov, D.A. & Eyre-Walker, A. (2010) Genome wide analyses reveal little evidence for adaptive evolution in many plant species. Mol. Biol. Evol. 27, 1822-1832.

Eyre-Walker, A. (2006) The rate of adaptive evolution at the molecular level. TREE 21, 569-575

The position is open to UK and EU citizens. It provides a tax-free stipend of approximately Â£14,500 and includes a fee waiver. Applications should be submitted through Sussex University's clunky graduate application system http://www.sussex.ac.uk/study/-phd/apply The applicant should provide a CV and the names and email addresses of two referees. Informal enquiries can be addressed to Adam Eyre-Walker (a.c.eyre-walker@sussex.ac.uk<mailto:a.c.eyre-walker@sussex.ac.uk>). The closing date is November 30th 2016.

a.c.eyre-walker@sussex.ac.uk

UTArlington Evolution

The Department of Biology at the University of Texas at Arlington (http://www.uta.edu/biology/) invites applications for our PhD program beginning in Fall 2017. PhD students are awarded competitive stipends, tuition remission, and health benefits. Research in the department includes a wide range of topics in ecology, evolution, genomics, microbiology, and cell and developmental biology.

For general inquiries about the program, please contact our graduate advisors: Shawn Christensen (shawnc@uta.edu) or Woo-suk Chang (wschang@uta.edu). For more specific questions about research directions, please contact potential advisers directly using the contact information on their webpages (https://www.uta.edu/biology/faculty.php). We will start reviewing applications on December 15th 2016. The on-line application process requires submission of the formal graduate school application, transcripts, GRE scores (general test required), three letters of reference, and, for non- native speakers of English, TOEFL or IELTS scores. Applications can be submitted via the following link: http://www.uta.edu/admissions/graduate/apply/how-to-apply.php . The Department and University have numerous resources including state-of-the-art labs, an Animal Care Facility, a Genomics Core Facility, a Center for Human Genomics, and the newly established Shimadzu Institute for Research Technologies - a major partnership between UT Arlington and Shimadzu Scientific Instruments that offers extensive resources for imaging, proteomics and analytical chemistry. The Department also benefits from access to core UT-system genomics and computational resources at UT Southwestern Medical Center and the Texas Advanced Computing Center (TACC) - one of the leading advanced computing centers in the U.S.

Arlington is a city of approximately 365,000 and is conveniently located in the center of the Dallas-Fort Worth Metroplex. Within a 25-mile radius of the center of Arlington is a workforce of over two million people. The city has 82 public parks, including River Legacy Parks, a 1,300-acre oasis on the Trinity River in the heart of north Arlington. Arlington is the home of the Dallas Cowboys Stadium, the Texas Rangers Ballpark, and Six Flags Over Texas. Cost of living is relatively low for a major metropolitan area. The Dallas-Fort Worth International Airport is the fourth largest airport in the US. More information on the city of Arlington can be found at www.experiencearlington.org . Matthew R. Walsh, Ph.D. Assistant Professor Department of Biology University of Texas at Arlington Arlington TX 76019 Office: 817-272-1546 Lab: 817-272-9079 Email: matthew.walsh@uta.edu

“Walsh, Matthew” <matthew.walsh@uta.edu>

UUppsala PopulationGenomics

A PhD student position in population genomics is available at the department of Organismal Biology, Uppsala University.

Closing date: 2016-12-01.

Project description: The demographic history of many species is currently being addressed with modern computational methods combined with population genomic data, especially humans that often function as a model organism in this respect. In order to understand population divergence processes, concepts of effective population size, population structure and genetic diversity become important. Linking effective population size as a function of time to population divergence and structure is a major challenge for modern population genomics and computational biology. The proposed project focuses on trying to disentangle population structure and divergence from population size (both effective and census) changes. The project will investigate these processes using large-scale population genomic data from humans and archaic humans such as Neandertals.

The project is part of a larger program that links theoretical population genetics, genomics and human evolution. The successful candidate will work in Professor Mattias Jakobsson research group together with Dr. Per Sjödin. The group consists of ~25 researchers (senior scientist, postdocs, graduate students and research engineers) with different areas of expertise. The research at the Jakobsson lab focus on population genetics and human evolution and the lab uses a combination of mathematical studies of population genetic models and computational approaches to understand the complex patterns of large-scale human genetic variation and their implications for human demographic and evolutionary history. In particular, the research focuses on understanding human evolution using genetic information from both recent and ancient individuals, developing statistical methods for analyzing large genomic data, and searching for genes targeted by selection.

Qualifications: A master degree (or equivalent) in a relevant field is required. The ideal candidate is highly motivated with thorough education in quantitative disciplines, such as statistical/quantitative/population genetics, bioinformatics, computer science, statistics, mathematics and with a strong interest in population genetics and human evolution.

For further information about the position please see http://www.iob.uu.se/about-us/join-us/?positionId=-3D3D117081 or contact Professor Mattias Jakobsson mailto:mattias.jakobsson@ebc.uu.se, +46 18 471 6449.

"Per.Sjodin@ebc.uu.se" <Per.Sjodin@ebc.uu.se>

UWesternAustralia AppliedBioinformatics

PhD studentships in Applied Bioinformatics are available at the University of Western Australia

The Laboratory of Applied Bioinformatics is seeking highly motivated PhD students to work on genomics and bioinformatics. With the global population expected to rise to 10 billion by 2050 and climate change already impacting agricultural practices, there is a need for improved crops to meet increasing demand for food and address changing climatic conditions. Genomics and bioinformatics provide novel solutions to accelerate crop improvement and enhance global food security. Plant genomes also differ greatly from animal genomes in complexity and offer fascinating examples of adaptive evolution.

Our lab uses computational methods to investigate the genomic diversity of a broad range of species groups including Brassica, wheat, pulses, as well as environmentally important species such as seagrass. In our research, we perform population genotyping and assembly of complete genomes using cutting-edge genomic technologies, and develop bioinformatic tools and platforms to visualise and interpret genomic data. We are a diverse, international group with backgrounds in evolutionary biology, genomics, bioinformatics and engineering. You can learn more about our research and recent publications on our website (http://www.appliedbioinformatics.com.au/).

Available PhD projects include analysis of genome diversity in Brassica species and pulses such as soybean and chickpea in relation to morphology and agronomic traits, investigation of seagrass genome evolution with a focus on adaptation to the marine environment and comparison of cereal genomes as part of ongoing international efforts to sequence and compare diverse grass genomes related to cereal crop plants. The data underlying these projects can be readily applied to address questions in genome evolution, polyploidization, patterns of diversification and crop improvement, while also providing starting points for the development of bioinformatic tools. In this studentship, you will gain training in applied bioinformatics, genomics, complex data analysis, and will acquire a working knowledge of plant biotechnology and its importance for global food security.

The group receives funding from the University of Western Australia, the Australian Research Council, and several industry partners. Your project will take place in the School of Plant Biology in Perth, which offers an international and dynamic research environment, and has an annual budget of nearly 16 million dollars, 120 postgraduate students and 90 staff members, including numerous highly cited researchers (http://-www.plants.uwa.edu.au/). Perth has been consistently ranked as one of the ten most liveable cities in the world, boastinga Mediterranean climate and relaxed lifestyle in a sophisticated city with beautiful beaches and parks (https://www.lonelyplanet.com/australia/-western-australia/perth).

Candidates must hold a MSc degree or equivalent in Biology, Bioinformatics or Computer Science and have strong interest in computing, complex data analysis, or genomics. Experience in programming (e.g. in Python or R) is not required but is a plus as the project will be computational without wet lab' components. The preferred candidate needs to be highly motivated, enthusiastic and a good team player with excellent communication skills. During the PhD, there will be potential for an internship in Europe with an industry partner. Review of applications will start ASAP, and positions will remain open until filled. PhD studentships can commence from January 2017 but later commencement dates are possible.

A fully funded 4-year PhD studentship is available for candidates with a strong academic record, satisfying UWA eligibility requirements (see http://-www.studyat.uwa.edu.au/research/admission).

Any inquiries about the positions and full applications should be sent to: Dave Edwards (Dave.Edwards@uwa.edu.au). Applicants should send documents (as a single pdf) including: A cover letter stating their research interests and motivation to apply, a complete curriculum vitaeand a reference letter of at least one referee.

Armin Patrick Scheben
<armin.scheben@research.uwa.edu.au>

UYork AntHybridisationSpeciation

Hybridisation, speciation and genetic structure in a woodland specialist

Supervisor: Dr Elva Robinson < http://www.york.ac.uk/biology/research/ecology-evolution/elva-robinson/ >

Co-supervisors: Dr Joan Cottrell (Forest Research), Dr Kanchon Dasmahapatra < http://www.york.ac.uk/biology/research/ecology-evolution/kanchon-dasmahapatra/ > , Dr Kevin Watts (Forest Research)

Project description:

Britain's forests offer key habitat for woodland species; however, maintaining biodiversity under the demands of timber production can be challenging. The highly fragmented nature of British woodlands is a further challenge because fragmentation leads to isolation, usually reducing genetic diversity of woodland dwelling species, particularly in species with poor dispersal abilities and exacting habitat requirements such as wood ants (*Formica rufa* group). These species, threatened across Europe, are key components of woodland ecosystems and offer an ideal study system to explore the impact of habitat fragmentation on genetic diversity of a woodland species.

This study will clarify the conservation status of a genetically unusual wood ant population in the North York Moors (NYM) and will use wood ants to study how dispersal and habitat fragmentation influence the formation of hybrids and new species. We will do this by comparing the genetic diversity of the NYM population to samples from across the UK and Eurasia. The data will explain what creates the unusually high diversity in the NYM and allow investigation of how wood ants spread and diversified at the continental scale after the last glacial period.

Research team The collaboration involves the University of York, CASE partner Forest Research, and a project partner (University of Helsinki). The supervisory team provide a range of skills, including genetic techniques, fieldwork skills, landscape analysis, and expertise in forest management and invertebrate ecology/evolution. This combination offers a challenging and well-supported training environment and enables the student to acquire a diverse skill-set with excellent employment prospects.

Applications The results of our research will set the NYM wood ant population in its broader European context which will inform foresters, including Forestry Commission practitioners, and DEFRA policy-makers, in the development of appropriate management strategies for the conservation and promotion of this key woodland species group.

*Funding: *This is a NERC Industrial CASE studentship fully funded for 4 years and covers: (i) a tax-free stipend at the standard Research Council rate (pounds 14,296 for 2016-2017, to be confirmed for 2017-2018), (ii) research costs, and (iii) tuition fees at the UK/EU rate.

Start date: October 2017

The studentship is available to UK and EU students who meet the UK residency requirements.

To discuss your suitability for this project please email: elva.robinson@york.ac.uk <elva.robinson@york.ac.uk>

For more information, see: http://www.york.ac.uk/biology/postgraduate/research/funding/funded-studentships/fullyfundedproject2-robinson/ *CLOSING DATE FOR APPLICATIONS: Sunday 22nd January 2017*

Other related available PhD and MSc projects listed here:

https://pure.york.ac.uk/portal/en/researchers/elva-joan-hilda-robinson(9c6bafea-ffbb-444c-8d9f-63b9312b9dce).html

– EJH Robinson University of York Elva.Robinson@york.ac.uk Twitter: @Elva_Robinson < http://twitter.com/Elva_Robinson >

Home page < http://www.york.ac.uk/biology/research/ecology-evolution/elva-robinson/#research > Publications list < http://scholar.google.co.uk/citations?user=FZZX_koAAAAJ&hl=en > Email disclaimer < http://www.york.ac.uk/docs/disclaimer/email.htm >

Biology at York holds an Athena Swan Gold Award < http://www.york.ac.uk/biology/about/athena-swan/ >

Elva Robinson <ejhr500@yccsa.org>

UZurich PlantEvolEpigenome HIVimmunology

University of Zurich will have a several open PhD positions of interdisciplinary evolutionary projects supported by the University Research Priority Program in Evolution in Action. http://www.evolution.uzh.ch/en.html Among them are: 1. New statistical tools for allele- or homeolog-specific epigenomics data, with applications to rapid adaptation of polyploid species to environmental niches 2. Evolutionary epidemiology and immunology of HIV 3. Plant Mating Systems Evolution

The deadline through the PhD program of Evolutionary Biology of Life Science Graduate School Zurich is 1 Dec. Through this site, you will be considered not only for the positions below but also for other positions. http://www.evobio.uzh.ch/en.html You are welcome to contact each PI below.

1. PhD position: New statistical tools for allele- or homeolog-specific epigenomics data, with applications to rapid adaptation of polyploid species to environmental niches PhD position is available from January 2017 jointly at the Department of Evolutionary Biology and Environmental Studies, and the Department of Molecular Life Science, University of Zurich, for a period of four years. Allopolyploidization, or genome duplication with hybridization, is a mechanism of rapid speciation and would be a suitable model to study evolution in action. Artificial allopolyploids have shown rapid genetic changes and epigenetic silencing by DNA methylation. We have developed a new bioinformatic workflow for polyploid RNA-seq analysis. By extending this, we will collect genome-wide bisulphite sequencing data from the preserved tissue and develop new statistical tools for homeolog-specific DNA methylome analysis. These tools would be also applicable to other research areas, such as allele-specific methylome in cancer or sexual reproduction. Supervised by Rie Inatsugi (rie.inatsugi@ieu.uzh.ch, http://www.ieu.uzh.ch/en/staff/leaders/inatsugi.html), Mark Robinson (mark.robinson@imls.uzh.ch, http://www.imls.uzh.ch/en/research/robinson.html), Kentaro Shimizu (kentaro.shimizu@ieu.uzh.ch, http://www.ieu.uzh.ch/en/staff/professors/shimizu.html) The successful candidate will experience both wet and dry studies of evolutionary biology, including bioinformatics, lab work and common garden transplantation in Switzerland and Japan. A candidate with bioinformatic experience has a priority.

2. PhD position: Evolutionary epidemiology and immunology of HIV

We are looking for a highly motivated PhD-Student on a project at the interface of evolutionary biology, immunology, and infectious-disease epidemiology. The project combines computational modeling with the analysis of complex clinical and immunological data in order understand HIV transmission and its adaption to the immune system. Accordingly, the candidate should have in addition to a strong computational background, skills to deal with complex and diverse data, and a strong interest in infectious-diseases and evolution. The PhD student will carry out his project in the context of the University of Zurich's Research Priority Program "Evolution in Action: From Genomes Ecosystems" (http://www.evolution.uzh.ch/en.html) and the Swiss HIV Cohort Study (www.SHCS.ch). These collaborations represent the ideal setting for this project since they provide the necessary evolutionary and clinical background. The student will work on a range of specified research projects, but will also be highly encouraged and expected to develop and investigate his/her own research questions.

The applicant should hold a Masters degree in a discipline relevant to the project (e.g. Evolutionary Biology, Epidemiology, Statistics, Mathematics, Biomedical Sciences, Physics, Computer Science). The PhD will take place within the PhD-Program Evolutionary Biology of the Life Science Zurich Graduate School (run jointly by the University of Zurich and the ETH Zurich). Research will be conducted at the Division of Infectious Diseases at the University Hospital of Zurich; University of Zurich (supervision: Roger Kouyos). The Division of Infectious Diseases provides a highly interdisciplinary and translational research environment with links both to clinical practice and basic science. Moreover, we are strongly interconnected with a variety of other research institutes in Zurich and beyond. In particular, we maintain strong collaborations with the Institute of Medical Virology at the University of Zurich, and the Institutes of Theoretical Biology and Computational Biology at the ETH Zurich.

Contact: roger.kouyos@uzh.ch.

3. PhD position: Plant Mating Systems Evolution

— / —

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

UZurich PlantMatingSystemEvolution

A PhD position funded by the University Research Priority Program (URPP) "Evolution in action" is available from January 2017 at the Department of Systematic and Evolutionary Botany/Plant and Microbial Biology, University of Zurich, for a period of four years. The position is to study the molecular bases of mating system evolution using Brassica rapa as a model, co-supervised by Prof. Florian Schiestl and Prof. Ueli Grossniklaus. You should have a Master degree in any field of (molecular) biology and a thorough interest in evolutionary biology. A good knowledge of molecular and bioinformatics techniques is required. The successful candidate will work in an exciting research environment, offered by the two departments and the URPP, comprising research groups from several different biological disciplines. Our departments are located in the botanical gardens and house modern molecular and ecological labs, including greenhouses and climate chambers for plant cultivation. The University of Zurich has a very broad coverage of organismal and molecular biology, and several research groups work on evolutionary topics (www.lifescience-zurich.ch). The city also offers excellent quality of life through cultural programs and infrastructure, as well as an attractive surrounding.

If you are interested in the job, please send by e-mail a letter describing your motivation, C.V., copy of degrees, publications (manuscripts), and e-mail addresses of two academic referees, by 20^th of December 2016. If you have any further questions, don't hesitate to contact me (florian.schiestl@systbot.uzh.ch).

Florian Schiestl <florian.schiestl@systbot.uzh.ch>

Vienna PopulationGenetics

The 2017 call for PhD students at the Vienna Graduate School of Population Genetics (Twitter @PopGenViennaPhD) is now open:

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, 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:

- Evolution of gene expression

- Understanding thermal adaptation

- The impact of new transposable element insertions on adaptation to a new environment

- *Wolbachia* infection dynamics in evolving *Drosophila* populations

- The adaptive value of diversity produced by recurrent whole genome doubling

- Epigenetic variation in *Arabidopsis*

- Genetic footprints of adaptive introgression

- New methods for modelling and analysis of data from experimental evolution

- Maximum likelihood inference of population genetic parameters using genome-wide data from nearly neutral sites

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics *in a single pdf*) received by *January 08, 2017* will be considered. Two letters of recommendation need to be sent directly by the referees.

All information about the about available topics, the training program and the application procedure can be found at www.popgen-vienna.at Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator www.popgen-vienna.at https://twitter.com/-PopGenViennaPhD c/o Institut für Populationsgenetik Veterinärmedizinische Universität Wien (Vetmeduni Vienna) Veterinärplatz 1, 1210 Wien

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

http://www.vetmeduni.ac.at/en/population-genetics/ https://twitter.com/PopGenVienna julia.hosp@gmail.com

Wageningen InsectPestEvolution

Wageningen.InsectPestEvolution

Insects have an amazing ability to adapt to diverse food resources, often by shifting to new host-plants and/or by overcoming plant defenses. So called “insect pest species” are of particular interest due to the growing demand for human food production worldwide and the challenges for agriculture to deal with losses due to herbivorous insects. But, what makes a pest a pest? As a PhD student, you will study the genetic basis of “pestiness” using a comparative phylogenomic framework. You will combine insect feeding assays of closely related moth species with next-generation sequencing-based transcriptional analysis to identify putative candidate genes involved in “pestiness” and to trace their evolutionary origins using phylogenomic approaches.

The PhD project is funded by The Graduate School Experimental Plant Sciences (EPS) under the supervision of Dr. Sabrina Simon in the Biosystematics Group, Wageningen UR. The inter-university Graduate School ’Experimental Plant Sciences’ (EPS) is a collaborative research and teaching institution of Wageningen University (WU), Radboud University (RU), Vrije Universiteit Amsterdam (VU), Leiden University (LU), University of Amsterdam (UvA), Utrecht University (UU) and University of Groningen (RUG). The mission of EPS is to organize the training of PhD students and postdocs to become self-reliant researchers.

Requirements The successful candidate will have an MSc degree in Biology. Students with an interest in transcriptomics, gene expression analyses, phylogenomics, comparative phylogenetics, evolutionary biology, and bioinformatics are encouraged to apply.

We are looking for a highly motivated insect biologist who can work in a multidisciplinary team in a collaborative spirit with the willingness to learn programming languages as well as next-gen sequencing methods and insect feeding assays. The candidate will be proficient in the English language. Within the Biosystematics group, PhD students have the opportunity to assist in teaching of undergraduates and/ or two courses Biodiversity of the Netherlands and Webs of Terrestrial Diversity. Therefore knowledge or experience on the taxonomy/ systematics of arthropods/ plants is desirable.

Working conditions We offer a full-time position (38 hours), initially for 1 year after which a go/no go decision will be taken on extension with another three years. Gross salary per month euro 2191,- in the first year rising to euro 2801,- per month in the fourth year, for a full-time appointment. The candidate will be based at the Biosystematics group. Further information and application details: http://www.wur.nl/en/Jobs/Vacancies/-Show/PhD-position-Insect-pest-evolution.htm Deadline: November 19, 2016

“Simon, Sabrina” <sabrina.simon@wur.nl>

WageningenUR Netherlands SexDeterminationEvolution

Background One of the most important stages during development is the sex determination. After all, the consequence of being male or female has a profound effect on the biology of the individual, affecting many aspects of its life-history. On a species level, sex determination systems also affect the evolution of reproductive modes which are one of the driving forces of speciation. Even though the occurrence of only two sexes is universal in plants and animals, the molecular mechanisms for sex determination are extraordinarily variable, especially in insects. However, despite the variety of sex determining mechanisms in insects, within the haplodiploid Hymenoptera still only two mechanisms are molecularly understood: the Complementary Sex Determiner (CSD) mechanism in Apis mellifera, and the parental imprinting mechanism (MEGISD) in Nasonia vitripennis. It is unknown how many different systems are present within the Hymenoptera and if the expected divergence in sex determining mechanisms is related to the phylogenetic distances of organismal groups. The genus Muscidifurax is a close relative of Nasonia. It contains the sister-species M. uniraptor, which is infected with the intracellular endosymbiont Wolbachia, causing asexual reproduction, and M. raptorellus, which is uninfected and reproduces sexually. We currently have a poor understanding of the mechanisms by which Wolbachia achieves asexual reproduction in its host in general and M. uniraptor in particular, as we have hardly any knowledge of the plethora of sex determining mechanisms. Therefore, research into the sex determining mechanisms of the Wolbachia-infected M. uniraptor and the uninfected M. raptorellus will greatly advance our understanding of the mechanisms that Wolbachia can employ to alter its host reproduction.

To elucidate the sex determining mechanism of M. raptorellus and M. uniraptor and compare this system to Nasonia vitripennis and other insects, we have a vacancy for a PhD position. The PhD student will aim to identify homologs of the known sex determination genes and perform functional analyses to determine the sex determining mechanism. In addition, the PhD student will study the role of Wolbachia in manipulating sex determination in M. uniraptor.

We ask: The successful candidate has an MSc degree in Biology or Molecular Life Sciences with a specialization in molecular biology, molecular ecology, molecular development and gene regulation, biological chemistry or similar. You have an affinity to working with insects and having some experience with bioinformatics will be a bonus. The candidate will be proficient in the English language. We are looking for highly motivated candidates who can work in a multidisciplinary team in a collaborative spirit. Within the Laboratory of Entomology, PhD students are encouraged to supervise MSc thesis students when such opportunities arise. The candidate will be based at the Laboratory of Entomology in Wageningen.

We offer: We offer a full-time position (38 hours), initially for 1 year after which a go/no go decision will be taken on extension with another three years. Gross salary per month Â€2191,- in the first year rising to Â€2801,- per month in the fourth year, for a fulltime appointment. The candidate will be based at the Laboratory of Entomology in Wageningen.

More information: Information on the research: Dr. Eveline Verhulst (eveline.verhulst@wur.nl) Information on the selection procedure: Mrs. Dorien Wissink (dorien.wissink@wur.nl).

You can apply up and until 28 November 2016 For this position you can only apply on line: http://www.wageningenur.nl/career Don't email directly to the people mentioned above but use the website to apply. Stuur uw sollicitatie niet naar de genoemde contactpersoon, maar solliciteer via de website.

We are: At the Laboratory of Entomology the research team consists of ambitious scientists and we aim at an interdisciplinary approach from cellular to community level to unravel biological phenomena underlying the functioning of insect sex determination, plant-insect communities, insect vectored diseases, insect neurobiology and insects as food and feed. The Laboratory of Entomology is part of the Plant Sciences Group of the Wageningen University and Research Centre.

Wageningen University and Research Centre Delivering a substantial contribution to the quality of life. That's our focus - each and every day. Within our domain, healthy food and living environment, we search for answers to issues affecting society - such as sustainable food production, climate change and alternative energy. Of course, we don't do this alone. Every day, 6,500 people work on 'the quality of life', turning ideas into reality, on a global scale.

Could you be one of these people? We give you the space you need.

For further information about working at Wageningen UR, take a look

— / —

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

---

WakeForestU PlantEvolution

Wake Forest University Department of Biology is seeking outstanding graduate applicants to join our plant ecology and evolution group. Our research spans a broad spectrum of topics in ecology and evolution, including phylogenomics, speciation, physiology, plant-animal interactions, demography and biodiversity. Our group is focused on investigating core questions in ecology and evolution with an emphasis on modern and novel techniques. Students in the program come from a variety of backgrounds (botany, zoology, evolution, ecology, informatics, etc.). Opportunities exist to start new projects, or join on-going research projects at field sites in Peru, Tanzania and Wyoming, and work with large-scale datasets (genomics, camera-trap networks, remote sensing, etc.).

*James Pease (http://peaselab.github.io) works with phylogenomic datasets to disentangle complex evolutionary patterns of hybridization and adaptation. Current projects involve using multi-genomic datasets from a diverse set of plant groups (ranging from the Andes to local species) to characterize molecular patterns of speciation and adaptation, and develop new computational methods and approaches to large-scale data analysis (peasejb@wfu.edu).

*Michael Anderson (http://wfu.me/andersonlab/ and https://www.snapshotserengeti.org/) conducts research in the Serengeti, one of the last great "grazing ecosystems" remaining on earth and a magnificent natural laboratory to study interactions among soil, vegetation, large herbivores and carnivores across a striking natural environmental gradient. (anderstm@wfu.edu)

*Miles Silman (http://users.wfu.edu/silmanmr/labpage/) works in the wilds of the Andes and Amazon and focuses on understanding biodiversity distribution and the response of forest ecosystems to climate and land use changes, past and future. Current projects include using an Andes-to-Amazon gradient as a natural laboratory for understanding tropical forest responses to climate change and private- and public-sector ecosystem services projects that encourage sustainable land use by generating revenue for conservation and enhancing governance. (silmanmr@wfu.edu)

*Bill Smith lab (http://users.wfu.edu/smithwk/smithwk.htm) is a plant ecopysiologist with experience working in more extreme environments such as deserts, the alpine, and coastal barrier islands. A current focus is on ecophysiological mechanisms driving the elevation of alpine treelines in the Rocky Mountains and the critical involvement of seedling establishment in the treeline ecotone. (smithwk@wfu.edu)

Wake Forest University, located in the friendly, affordable city of Winston-Salem NC, is a top-ranked private university with a vibrant graduate program in biology (currently with 35 graduate students). Situated between the Blue Ridge Mountains and the Atlantic Ocean, Winston-Salem provides abundant outdoor and recreational opportunities. The position includes a competitive stipend and comes with a minimum of five years of guaranteed TA support. Positions are available starting August 2017.

Interested candidates should submit a brief letter of introduction, CV and contact information for two references to one or more potential faculty mentors listed above.

“peasejb@wfu.edu” <peasejb@wfu.edu>

Wisconsin EvolutionaryGenomics

Ph.D. Positions in Evolutionary Genomics

The Genetics PhD program at the University of Wisconsin - Madison welcomes applications from students with interests in population genetics, evolutionary genomics, and related topics.

The Genetics program has an especially strong contingent of faculty with evolutionary interests: http://www.genetics.wisc.edu/EvoPopGenetics.htm A broader list of evolution faculty at UW Madison is available through the J. F. Crow Institute for the Study of Evolution: http://www.evolution.wisc.edu/ Students are encouraged to contact faculty of particular interest before applying. Students typically rotate in three labs during their first semester before choosing an advisor.

Financial support for Genetics PhD students is available from NIH training grants, research assistantships, and teaching assistantships (most students TA for one semester).

Madison is nestled amongst beautiful lakes and offers exceptional quality of life: http://www.visitmadison.com/media/rankings/ Interested students should apply by December 1: http://www.genetics.wisc.edu/PHDProspective.htm
“jpool@wisc.edu” <jpool@wisc.edu>

Jobs

AdelphiU NY EvolutionaryPhysiology

We highly encourage physiologists who have an evolutionary focus to their research to apply.

Adelphi University invites applications for a tenure-track position for an organismal physiologist to begin fall 2017. A Ph.D is required and postdoctoral experience is highly preferred. Teaching responsibilities will include undergraduate and graduate physiology, human anatomy & physiology and could include courses such as comparative physiology, animal behavior, pathophysiology for nursing students, introductory biology, and/or additional specialty courses for upper-level undergraduates and master's students in the area of expertise. The successful applicant will have a commitment to teaching students from diverse cultural backgrounds and excellent potential as a teacher, plus a record of significant research accomplishment and the potential to develop a fundable independent research program involving undergraduate and master's students. Some research release time is available. The successful applicant will join an active, engaged, and collegial department spanning all areas of biology. Opportunities for collaboration exist within the university as well as in the NY metropolitan area.

Applicants should submit the following, all merged into one document: cover letter, CV, statement of teaching interests and philosophy, statement of research background and interests, and the names and contact information for 3 references. For more information about the department, visit http://academics.adelphi.edu/artsci/bio/ We are strongly committed to achieving excellence through cultural diversity. Adelphi is a private university with the spirit of a liberal arts college, committed to combining teaching and scholarship, and located in suburban Long Island within easy reach of New York City.

Deadline for applications: November 15, 2016. Applications should be submitted at: http://chm.tbe.taleo.net/chm02/ats/careers/requisition.jsp?org=ADELPHI&cws=3&rid=1732
Andrea Ward Associate Professor Department of Biology Adelphi University 1 South Avenue Garden City, NY 11530

Email: award@adelphi.edu Office Phone: 516-877-4204

Fax: 516-877-4209 http://home.adelphi.edu/~aw17333/-index.html Andrea Ward <award@adelphi.edu>

ArizonaStateU EvolutionMedicine

Assistant/Associate Professor (JOB #11741) Arizona State University School of Life Sciences Center for Evolution and Medicine Faculty Positions Closing date Nov 30

The Center for Evolution & Medicine (CEM) and the School of Life Sciences (SOLS) at Arizona State University (ASU) invite applications for tenure-eligible faculty positions in the area of evolution and medicine. Rank and tenure status will be commensurate with experience. The anticipated start date is August 2017. These positions are part of an institutional initiative to advance the field of evolutionary medicine. Under the direction of Randolph Nesse, the Center for Evolution & Medicine (CEM) seeks to improve human health by establishing evolutionary biology as a basic science for medicine, worldwide. In an institution that rewards transdisciplinary research, the CEM currently includes faculty from the School of Life Sciences, School of Human Evolution and Social Change, the Department of Psychology, and the School of Mathematical and Statistical Sciences, as well as researchers from ASU's Complex Adaptive Systems Initiative and clinical partnerships with the Mayo Clinic and Banner Hospitals. For more information on the CEM, please visit http://evmed.asu.edu/ . Newly remodeled space for CEM offices and laboratories encourages collaborations between members of its highly interdisciplinary group. The CEM provides support for visiting speakers, workshops, research collaborations, and extensive web resources for the world's evolution and medicine community.

The research focus for this search can be in any area that has a high likelihood of demonstrating how the principles of organic evolution can improve human health. All approaches are welcome including field, clinical, and/or lab-based research. Preferred topics include, but are not limited to, physiological systems, immunology, infectious disease, or aging. Preference will be given to candidates whose research plans hold promise of major advances that demonstrate why evolutionary biology is essential for medicine or public health. Clinical relevance and potential collaborations in clinical settings are encouraged. Experience or an interest in teaching evolutionary medicine and otherwise contributing to developing the field is desired.

Successful candidates will be expected to develop or maintain an innovative, independent, extramurally funded research program, provide excellent classroom instruction, contribute to curriculum development, mentor students and postdoctoral fellows, and interact with a transdisciplinary group of colleagues. Salary and start-up packages are competitive.

Minimum Qualifications: a doctoral degree or an MD by the time of appointment, and a track record of research that uses evolutionary biology to address questions about health and disease. Candidates for Associate Professor rank must have a demonstrated record of significant extramural funding.

Desired Qualifications: postdoctoral experience, publications in refereed journals, demonstrated excellence in teaching and/or mentoring, experience working in a transdisciplinary environment; demonstrated success meeting the needs of diverse student populations and/or reaching out to diverse communities.

To apply, please submit the following materials within a single PDF document tosolsfacultysearch1@asu.edu: (1) a cover letter that specifies the rank for which you seek consideration and why this position is a good fit for you, (2) curriculum vitae, (3) three representative publications, (4) a statement of research vision and plans, (5) a statement of teaching philosophy/experience and (6) contact information (name, email and telephone number) for three references. Only electronic applications will be considered.

The initial closing date for receipt of complete applications is November 30, 2016; if not filled, review will continue every week thereafter until the search is closed. A background check is required for employment. For additional information, please feel free to contact Randolph Nesse (nesse@asu.edu) or James Collins (jcollins@asu.edu).

Arizona State University is a VEVRAA Federal Contractor and an Equal Opportunity/Affirmative Action Employer. All qualified applicants will be considered without regard to race, color, sex, religion, national origin, disability, protected veteran status, or any other basis protected by law. ASU's full nondiscrimination statement (ACD 401) is located on the ASU website athttps://www.asu.edu/aad/manuals/-acd/acd401.html and https://www.asu.edu/titleIX . rmnesse@gmail.com

Australia ConservationGeneticist

http://www.antarctica.gov.au/jobs/vacancies/-conservation-geneticist Conservation Geneticist Antarctic Conservation and Management

Research Scientist (APS Level 6) - Senior Research Scientist (Executive Level 2) - Ongoing

Salary: $76,224 - $141,071 pa Duties: The Conservation Geneticist will develop and lead research projects with high levels of alignment to the Australian Antarctic Strategic Plan, the 20 Year Antarctic Strategy and Action Plan, and Science Branch and Section Business plans. This role will also closely collaborate with other researchers, the Science Branch Executive and other Branches of the Division to provide expert input on the best use of genetics, molecular biology and bioinformatics techniques to address strategic research questions. The Conservation Geneticist will lead a small group of 2-4 technical and research staff and ensure genetic samples are processed in a cost-effective manner either using the laboratories at the AAD or through subcontracting.

The Conservation Geneticist may also be required to lead teams to collect samples in the Antarctic or sub-Antarctic in ship and land-based campaigns.

Ben Raymond <Ben.Raymond@aad.gov.au>

BowdoinC EvolBiology

The job advertisement describes the position as targeting an ecologist (broadly defined), but any sort of evolutionary ecologist would be fine as well.

Bowdoin College, located along the coast in Brunswick, Maine, invites applications for the position of Assistant Professor of Biology and Director, Bowdoin Scientific Station on Kent Island beginning Fall 2017. The successful candidate will play a leadership role in fostering a thriving intellectual environment at Bowdoin College's Scientific Station on Kent Island (https://-www.bowdoin.edu/kent-island/). The station, located on Kent Island, New Brunswick, Canada (44 35'N, 66 45'W), was established in 1935 as a research facility and sanctuary for nesting seabirds, and has been a member of the Organization of Biological Field Stations since 1988. Population, community and behavioral ecologists are encouraged to apply and applicants should demonstrate that their research takes advantage of this unique island setting.

We are particularly interested in candidates who are committed to the instruction and support of a diverse student population and who will enrich and contribute to the ethnic, cultural, and socio-economic diversity of the Department and College faculty.

The summer research season typically includes 6-10 fellowship students conducting research during the summer months under the guidance of the Director, an Assistant Director - the search for whom will be led by the successful candidate - and a vibrant community of international researchers. We especially welcome applications from those with quantitative strengths in, for example, statistical analyses, demographic modeling, or the use of genomic and bioinformatic approaches to ecological questions. The yearly teaching load on the main campus includes a core course in general ecology, participation in introductory biology or non-majors biology and an upper level course in Biology. Bowdoin faculty are committed to providing research opportunities for undergraduate students and the successful candidate will be expected to mentor student-led independent projects and to actively encourage student involvement in research.

Excellent opportunities exist for disciplinary and interdisciplinary interactions and collaborations with Bowdoin faculty in Biology, Earth and Oceanographic Science, and Environmental Studies along with other departments and programs at the College, and for synergies with Bowdoin's Marine Lab and Coastal Studies Center on Orr's Island ME. The Coastal Studies Center, a 20-minute drive from main campus, is a 114 acre facility that includes over 100 acres of coastal forest, a marine laboratory with flowing seawater, access to 5 miles of coastline, and a small boat fleet to access Casco Bay and the greater Gulf of Maine.

Ph.D. required; postdoctoral experience preferred. Bowdoin College offers strong support for faculty research and teaching. We recognize that recruiting and retaining faculty may involve considerations of spouses and domestic partners. To that end, where possible, the College will attempt to accommodate and respond creatively to the needs of spouses and partners of members of the faculty.

Bowdoin College accepts only electronic submissions. Please visit https://careers.bowdoin.edu to submit a cover letter, curriculum vitae, statement of research plans, statement describing teaching philosophy/experience, a statement of directorial vision for the Bowdoin Scientific Station on Kent Island, and the names and contact information for three references who have agreed to provide letters of recommendation upon request. Review of applications begins February 1, 2017.

A highly selective liberal arts college on the Maine coast with a diverse student body made up of 31% students of color, 5% international students and approximately 15% first generation college students, Bowdoin College is committed to equality and is an equal opportunity employer. Bowdoin College does not discriminate on the basis of age, race, creed, color, religion, marital status, gender identity and/or expression, sexual orientation, veteran status, national origin, or disability status in employment, or in our education programs.

Michael Palopoli <mpalopol@bowdoin.edu>

CaliforniaInstTech EvolutionaryBiol

The Division of Biology and Biological Engineering at the California Institute of Technology is seeking outstanding candidates for a tenure-track professorial position in the general area of multicellular organismal biology. Research areas of interest include, but are not restricted to development, physiology, behavior, biomechanics, and evolution. Applicants whose research covers different scales of biological organization - from cellular mechanisms to ecosystems - are particularly encouraged to apply.

Successful applicants are expected to develop innovative research programs and to be committed to high quality teaching. Preference will be given to candidates at the assistant professor level; however, under extraordinary circumstances, applicants at the associate or full professor level may also be considered. The term of an initial untenured appointment is for four years and is contingent upon completion of the Ph.D. degree.

Please submit on-line application at http://bbe.caltech.edu/Positions and include a brief cover letter, curriculum vitae, relevant publications, a description of proposed research, and a statement of teaching interests. Instructions will be given for submission of letters of reference when you apply on-line.

Positions will remain open until filled; however, applicants for the assistant professor level should plan on completing an application by Dec 16, 2016, in order to attend a recruiting symposium at Caltech on Feb 2, 2017, where they will present their research and future directions.

We are an equal opportunity employer and all qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, or national origin, disability status, protected veteran status, or any other characteristic protected by law.

Michael Dickinson, Ph.D. Zarem Professor of Biology and Bioengineering California Institute of Technology 1200 E. California Blvd. Pasadena, CA 91125 626-395-5775

Michael Dickinson <flyman@caltech.edu>

CollegeOfCharleston EvolutionaryMicrobialGenetics

Microbial Genetics

The Department of Biology at the College of Charleston invites applications for a tenure-track position in Microbial Genetics at the Assistant Professor level to begin August 2017. Candidates must have a Ph.D. in Biology or a related field and a strong commitment to teaching and maintaining an active research program involving undergraduates. The area of research is open to any microbial system (eukaryotic, prokaryotic, viral) but we are targeting a microbiologist who asks evolutionary or environmental questions and seek a colleague interested in developing collaborations with existing faculty (http://biology.cofc.edu/about-the-department/faculty-staff-listing/index.php). Primary teaching responsibilities include undergraduate courses in Genetics, Microbiology, introductory biology and perhaps specialty courses in an area of expertise. The College of Charleston, located in Charleston, SC, is a public liberal arts and sciences institution of 12,000 students, with MS programs in Marine Biology and Environmental Studies, and a commitment to excellence in teaching and research. Information about the department is available at http://biology.cofc.edu/ .Applicants should submit electronic (pdf) copies of their curriculum vitae, statements of teaching and research interests, up to three relevant publications, and a list with names and contact information for three referees, to the following site: http://jobs.cofc.edu/postings/5577 .Questions regarding this position can be directed to Dr. Christine

Byrum, search committee chair, at byrumc@cofc.edu. This is a nine-month appointment; salary is competitive and commensurate with experience and qualifications. Review of applications will begin Dec 14, 2016 and will continue until the position is filled. The College of Charleston is an Affirmative Action, Equal Opportunity Employer and does not discriminate against any individual or group on the basis of gender, sexual orientation, gender identity or expression, age, race, color, religion, national origin, veteran status, genetic information, or disability.

"Rutter, Matt" <RutterM@cofc.edu>

CSIC UPF Barcelona LabTech Adaptation

We are seeking a lab technician to join our research team at the Institute of Evolutionary Biology(CSIC-UPF). Our laboratory focuses on understanding how organisms adapt to the environment. Wecombine -omics approaches and functional assays to identify the genes, molecular mechanisms, andphenotypic effects relevant for adaptation.

The successful candidate must be familiar with or able to be trained in all methods employed in the lab,including Drosophila culture and handling, DNA and RNA extraction and amplification, qRT-PCR,sequencing, cloning, ChIP-PCR, Drosophila cell culture, Drosophila embryo microinjection, and datamanagement and analysis.

The position requires attention to detail, good organizational skills, independence, and the ability towork well with others. Evening and weekend hours may sometimes be necessary for time-sensitivesample collections and experiments.

Starting date February 2017 but alternative dates can be discussed.

Application: Please send your CV and a brief letter of motivation before 9th December 2016 to:josefa.gonzalez@ibe.upf-csic.es

Dr Jordi Lanuza Masdeu Communication manager Institut de Biologia Evolutiva (IBE) (CSIC-UPF) Despatx P85, Edifici CMIMA Passeig MarÃtim de la Barceloneta 37-49 08003 Barcelona comunicacio@ibe.upf-csic.es Tel. 932309645 (Ext. 6050) Web: http://www.ibe.upf-csic.es Follow us on Twitter: @IBE_Barcelona Follow us on Facebook: IBEvolutiva Follow us on LinkedIn

Jordi Lanuza Masdeu <comunicacio@ibe.upf-csic.es>

Estonia PhD-PDF-GroupLeader HumanPopGenomics

Hello,

Please find attached three open positions at the Estonian Biocentre in Tartu in the fields of modern and ancient human population genomics. Deadline for all applications is 31st January 2017.

See www.ebc.ee (current vacancies) for details.

Please spread the information to anybody you think might be interested.

I'm sorry for spam as some of you might get this e-mail from multiple sources.

The Estonian Biocentre Evolutionary Biology group is interested in human genetic diversity and reconstructing human evolutionary history through migrations, population splits and admixture as well as adaptation. We generate modern and ancient DNA genomic sequences and genotype data from around the world and share all the published data (www.ebc.ee/free_data) to the scientific community.

1) Pre-Doc: a four years position with one year probationary period.

The candidate will chose one of three research areas in the realm of modern human population genomics (see attachment for full details) and will apply for a PhD at the University of Tartu, starting in fall 2017.

Salary: negotiable up to 15 600 EUR/year depending on experience level.

Net salary after all taxes (incl. coverage of medical insurance and pension) is up to 15 600 EUR/year.

2) Post-Doc: a three years Post-Doc position on modern human population genomics. Candidates are encouraged to submit a short research proposal along with their CV, or to choose one of the proposed research themes (see attachment for full details). Salary: negotiable up to 24 000 EUR/year depending on experience level. Net salary after all taxes (incl. coverage of medical insurance and pension) is up to 20 000 EUR/year.

3) Group Leader: a 3-years Senior Research Fellow position as head of the Ancient DNA group and lab. The candidate will be responsible for establishing a research

group of ancient population genomics and hiring and supervising postdocs and graduate students as well as managing the newly built aDNA lab. Salary: up to 42 000 EUR per year (Net salary after all taxes incl. coverage of medical insurance and pension is up to 35000 EUR/year.).

Potential candidates are encouraged make informal contact with Luca Pagani (lp.lucapagani@gmail.com), Senior Researcher in human population genomics or with Mait Metspalu (mait@ebc.ee), Director of the Estonian Biocentre.

Mait Metspalu, PhD director Estonian Biocentre Tartu, Estonia +372 5283315 www.ebc.ee Mait Metspalu <mait@ebc.ee>

InovaMedInst CompBiol

The Inova Translational Medicine Institute (ITMI) is leading the transformation of healthcare into personalized medicine using technological innovation, pioneering research, and sophisticated information management. The work of ITMI is enabling Inova to translate advances from genomics and molecular sciences directly to patients, optimizing individual health and well-being. We offer a unique opportunity to work on integration of high-throughput omics data, individual health records, and individual environment factors – ideal for those wanting to make an impact transforming translational research.

As a member of the multidisciplinary bioinformatics team, you may participate, but not necessarily be limited to, the following activities: §Lead and undertake innovative research that utilizes ITMI's large collection of internal multi-omics data and public data resources. Make significant contributions to journal papers on data analysis and/or novel method development. §Big genomic data algorithm and analytics development on Hadoop/Spark platforms. §Support research and high-throughput omics data analysis for internal clinical lab and other institutes within the Inova Health Systems. §Microbiome projects using 16S or shotgun metagenomics.

Desirable qualifications and skill: §PhD in Statistics, Statistical Genetics, Computer Science or related fields. §Experience of techniques used in bioinformatics, genomics and statistical genetics, with particular expertise in computational approaches to genomic analyses. Previous experience with large-scale association studies is highly desirable. §Experience also expected in working with large-scale biomedical data and hands on experience developing software or information systems to manage and analyze biomedical data. Previous experience with Next and Third generation sequence data, proteomic data and microarray data is highly desirable. §Excellent computational skills, including statistical programming (ideally R) and ideally also a programming language such as Python, Java, and C++. Experience with Linux and use of a High-Performance Computing Linux cluster. §Ability to work independently and also as part of a team. §Excellent written and oral communication skills.

Please email your application to Jeanne.Bridges-Findling@inova.org or apply electronically at http://www.inovacareers.org/ (JobID: 25285BR)

wendy.wong@gmail.com

KentStateU EvolutionaryBiologist

Tenure-track Faculty Position in Ecology or Evolutionary Biology Assistant or Associate Professor

Kent State University's Department of Biological Sciences invites applications for a tenure-track position at the Assistant or Associate Professor rank to be appointed on the main Kent campus. We seek collaborative individuals who address cutting-edge research questions in Ecology or Evolutionary Biology. The Department of Biological Sciences is the largest in the College of Arts and Sciences, with over 80 MS and PhD students, over 1200 undergraduate majors, and 40 faculty. Departmental resources include natural areas for research, as well as local, regional and international affiliations for research, teaching and outreach. The Kent State system has a total enrollment of nearly 42,000 students, and is ranked as 'high research' by the Carnegie Foundation.

Based on our department's strategic vision, we especially encourage applicants with expertise in: ecoinformatics and ecological modeling, urban ecology, plant ecological or evolutionary physiology, or 'omics' approaches. We expect these fields will complement and expand the department's current research strengths in plant population biology, microbial ecology, community ecology, and biogeochemistry (www.kent.edu/biology/kent-campus-faculty-research-expertise). Successful candidates will hold a Ph.D. with postdoctoral experience. Faculty are expected to establish a highly competitive, externally funded research program, to demonstrate teaching excellence, and participate in graduate training. Candidates at the Associate Professor level are expected to have a history of sustained extramural funding. Salary and startup funds are competitive and commensurate with academic qualifications and experience.

Facilities and resources include 18 managed natural areas available for research activities, an experimental wetland facility, an active herbarium, plant conservatory, and an interdisciplinary Center for Ecology and Resource Sustainability (CENRS). The Department has formal affiliations or active collaborations with non-academic organizations across northeast Ohio, including: the Holden Arboretum, the Cleveland Botanical Garden, Cuyahoga Valley National Park, Cleveland Metroparks, Cleveland Museum of Natural History, the Cleveland Water Alliance, and the Nature Conservancy of Ohio. International opportunities for teaching, training, and research are supported by: extension programs in Florence, Italy; a formal agreement with the University of Costa Rica; membership in OTS; and a field course to South Africa.

The city of Kent combines the eclectic atmosphere of a small Midwest college town with easy access to major metropolitan centers, including Cleveland, Akron, Columbus, and Pittsburgh. The student population increasingly reflects the diversity of the region and beyond. Kent State University is an EEO/AA employer with strong commitments to building a diverse faculty and fostering working, teaching and learning in an inclusive environment (www.kent.edu/diversity). We seek a diverse applicant pool for this position, including women, members of underrepresented minority groups, veterans, persons with disabilities, and the LGBTQ community.

Applicants should send the following materials to BioSearch@kent.edu with 'Ecology/Evolution Search' in the subject line: (1) letter of application; (2) CV; (3) a 2-3 page statement of research interests, accomplishments, and plans; (4) a 1-2 page statement of teaching interests and experience; and (5) contact information for at least three referees.

Review of applications will begin on December 1, 2016 and will continue until the position is filled. Specific inquiries may be directed to Dr. Darren Bade (dbade@kent.edu), chair of the search committee.

acase@kent.edu

Kew London ResAssist PlantEvolution

https://careers.kew.org/vacancy/research-assistant-data-state-of-the-worlds-plants-285102.html Research Assistant - Data (State of the World's Plants)

As a Research Assistant you will support two Senior Research Leaders (Ilia Leitch and Richard Buggs) responsible for chapters on plant evolution, plant genomes and plant health in Kew's annual "State of the World's Plants" report. You will be responsible for identifying data sources, searching databases, mining data, surveying literature and conducting primary data collection and analyses. You will assist with administrative tasks.

You must hold a degree in a subject relevant to plant evolution, plant health and/or genomics. You must have post-graduate or work experience in data mining and analysis. You need experience of using a range of genomic bioinformatics tools. You need excellent communication skills, especially in writing.

Kew is the world's leading botanic gardens, at the forefront of plant and fungal science, a UNESCO World Heritage Site and a major visitor attraction. We want a world where plants and fungi are understood, valued and conserved - because our lives depend on them. We use the power of our science and the rich diversity of our gardens and collections to provide knowledge, inspiration and understanding of why plants and fungi matter to everyone. Closing Date 14/11/2016

Richard Buggs <R.Buggs@kew.org>

LeipzigU SystematicBotany

The Faculty of Biosciences,Pharmacy and Psychology, Institute of Biology, Professorship for MolecularEvolution and Plant Systematics, offers the following position from April 1st,2017: Research Assistant (Postdoc)(time-limited position)Salary: Entgeltgruppe 13 TV-LTasks:-research in the field ofsystematics, evolution and biogeography of flowering plants-application of existing andestablishment of new methods in the research field-supervision of scientific andtechnical staff-preparation of manuscripts forpublication-application of research grantsand supervision of projects (e.g. DFG, BMBF)-teaching at BSc and MSc levelsConducting a"Habilitation" (formal German postdoctoral qualification) will beencouraged.Requirements:-university degree and excellentdoctoral degree in biology, with specialisation in botany or relateddisciplines-several years of experience inconcepts and methods in the field of systematics, evolution and biogeography offlowering plants-several years of experience insupervising scientific and/or technical staff-track record showingpublication activity-experience in raising researchfunds-experience in conception andperformance of teaching activities-very good spoken and writtenEnglish skills-relevant knowledge of modernmolecular biological techniques and in-depth knowledge in phylogenetics andtaxonomy of flowering plants as well as field experience are desirable-knowledge of the Germanlanguage will be of advantageApplications in English languagewill be accepted until November 25th, 2016. Applications should make referenceto the file number 218/2016, include a cover letter, curriculum vitae, copiesof educational certificates, and names and addresses of two references.Applications should be directed to:Universität LeipzigFakultät für Biowissenschaften,Pharmazie und PsychologieHerrn Dekan Professor Dr. TiloPompeTalstraße 3304103 LeipzigGermanySeverely disabled persons areencouraged to apply and will be given preference in the case of equalsuitability.Note: Please additionally sendan electronic copy of your application as a single pdf by email to Prof. Dr.Alexandra Muellner-Riehl (muellner-riehl@uni-leipzig.de). Further informationon the working group may be found at http://www.biphaps.uni-leipzig.de/en/sysbot/-molecular-evolution-and-systematics-of-plants.html .This is a temporary position of up to five years duration, depending on thequalification of applicants. Inquiries about this position may be directed tomuellner-riehl@uni-leipzig.de. Interviews for this position are likely to beconducted in December 2016 (or January 2017).

muellner_alexandra@yahoo.de

LouisianaStateU ComparativePhysiology

Assistant Professor in Comparative/Integrative Physiology http://www.lsu.edu/science/biosci/resources/-employment.php The Department of Biological Sciences at Louisiana State University invites applications for a tenure-track position in Comparative or Integrative Physiology. Biological Sciences is a large and dynamic department with research ranging across all levels of biological organization from molecules to ecosystems. Information about the department is available at http://www.lsu.edu/science/biosci. Preference will be given to individuals with a record of achievement in physiology at levels of biological organization ranging from molecules to organ systems. The successful candidate will be expected to develop a vigorous, extramurally funded research program and contribute to undergraduate and graduate teaching; participate in service activities pertaining to the mission of the Department and advancement of the profession.

50% Develop and maintain an independent and vigorous research program that emphasizes comparative integrative physiology.

50% Teach undergraduate and/or graduate level courses in a biological sciences discipline and direct/supervise graduate students; participate in University service, including committee activities, supervision of teaching/research assistants and student advising; maintain professional standards and level of competence.

Required Qualifications: Ph.D. or equivalent in Biology or related field; and post-doctoral research experience are required.

Special Instructions: Candidates should attach curriculum vitae, including email address, statement of research and teaching interests. A copy of your transcript(s) may be attached to your application (if available). If unable to scan and electronically attach, please provide an original transcript at the time of interview. Please provide 3 professional references including name, title, phone number and e-mail address.

Additional Position Information:

Background Check - An offer of employment is contingent on a satisfactory pre-employment background check.

Benefits - LSU offers outstanding benefits to eligible employees and their dependents including health, life, dental, and vision insurance; flexible spending accounts; retirement options; various leave options; paid holidays; wellness benefits; tuition exemption for qualified positions; training and development opportunities; employee discounts; and more!

Essential Position (Y/N): No

EEO Statement:

LSU is committed to diversity and is an equal opportunity / equal access employer.

HCM Contact Information: Questions or concerns can be directed to the LSU Human Resources Management Office at 225-578-8200 or emailed

Morgan Kelly <morgankelly@lsu.edu>

MaxPlanckInst Ploen ResTech AdaptationBiologicalClocks

Technical Assistant / Research Technician in Adaptation of Biological Clocks

The Kaiser Lab at the Max Planck Institute for Evolutionary Biology in Ploen (Germany) combines evolutionary genomics and molecular biology with behavioral experiments and ecological fieldwork, aiming to uncover the yet unknown molecular basis of circalunar clocks.

Starting from 1st January 2017 we are seeking to hire a technical assistant/research technician (full time = 39h/week, initially for 2 years).

Tasks: - Independent work on (sub)projects in genetics, molecular biology and immunohistology - General laboratory work and laboratory organisation, including ordering and management of databases - Participation in the rearing of non-biting marine midges

Required qualifications: - Completed relevant apprenticeship (e.g. BTA or MTA in Germany) or equivalent qualifications (e.g. BSc in Biology) - Practical experience with techniques in molecular biology and immunohistology - Proficiency in English and good written and oral communication skills - Flexibility and ability to work in an international team

Salary is commensurate with experience and qualification (according to “TVöD Bund”).

Applications should include (1) a cover letter describing your motivation to join our team and your relevant experience, (2) a detailed CV and copies of relevant certificates, and (3) the contact details of two academic or professional referees. Please send the above as a single PDF file to kaiser@evolbio.mpg.de.

Review of applications will start on 1st December 2016 and will continue until the position is filled.

The Max Planck Society is committed to also employing handicapped individuals and encourages them to apply. The Max Planck Society seeks to increase the number of women in those areas where they are underrepresented and therefore explicitly encourages women to apply.

For further information feel free to contact Tobias Kaiser (kaiser@evolbio.mpg.de).

Dr. Tobias Kaiser Max Planck Research Group “Biological Clocks” Max Planck Institute for Evolutionary Biology August-Thienemann-Str. 2 24306 Plön Germany Phone +49-4522-763-224 Web: http://www.evolbio.mpg.de/biologicalclocks

“kaiser@evolbio.mpg.de” <kaiser@evolbio.mpg.de>

MiamiU PlantEvoDevo

Biology: Tenure-track Assistant Professor in Plant Development Biology to start August 2017. We seek candidates who study the development, anatomy, or morphology of whole plant systems with expertise in areas such as gene expression analysis at the molecular and developmental level, molecular and whole plant analysis of gene function, comparative genomics, advanced microscopy techniques, plant structural analysis, or molecular systematics. We are especially interested in candidates who will address key questions in the evolution of plant vegetative or reproductive development and morphology (i.e. plant evolutionary development or evo-devo).

The successful candidate will teach at the graduate and undergraduate levels, maintain an active research program, and provide service to the institution. Teaching may include introductory biology for majors or nonmajors, cell biology, biotechnology, and advanced plant biology courses in the candidate’s area of expertise, including plant anatomy and development.

Required: Ph.D. in biology, botany, or a related field.

Consideration will be given to candidates with postdoctoral experience, and demonstrated commitment to developing an externally funded research program and teaching at the undergraduate and graduate levels.

The Department of Biology (http://www.miamioh.edu/-biology) has over 40 faculty with excellence in undergraduate and graduate teaching and research. The department offers bachelors, masters, and PhD degrees in the biological sciences, as well as multidisciplinary, interdepartmental graduate degree programs in cell, molecular, and structural biology (http://miamioh.edu/cmsb) and ecology, evolution and environmental biology (http://miamioh.edu/eeeb). Research and teaching are supported by outstanding core facilities, including the Willard Sherman Turrell Herbarium, the Center for Bioinformatics and Functional Genomics, the Center for Advanced Microscopy and Imaging, the Ecology Research Center, and a Laboratory Animal Resources Center. Miami is a top-ranked public university for its commitment to excellence in both undergraduate and graduate education.

Submit letter of application, curriculum vitae, statement of research plans, and teaching philosophy to https://miamioh.hiretouch.com/job-details?jobID=3466. Department will request letters of references from references listed in application. For inquiries about posting, contact Thomas Crist at biology@miamioh.edu. Screening of applications will begin November 11, 2016 and will continue until the position is filled.

The University is committed to equal opportunity, affirmative action, and eliminating discrimination and harassment. Miami University does not discriminate on the basis of age, color, disability, gender identity or expression, genetic information, military status, national origin, pregnancy, race, religion, sex, sexual orientation or protected veteran status in its application and admission processes, educational programs and activities, facilities, programs or employment practices. Requests for all reasonable accommodations for disabilities related to employment should be directed to ADAFacultyStaff@miamioh.edu or 513-529-3560.

Miami University's Annual Security and Fire Safety Report with information on campus crime, fires, and safety may be found at: http://www.MiamiOH.edu/campus-safety/annual-report/index.html. Hard copy available upon request. A criminal background check is required. All campuses are smoke- and tobacco-free campuses.

Richard Moore <moorerc@miamioh.edu>

MontrealBotanicalGardens EvolPlants

Though the add does not explicitly say so, evolutionary plant cell biologists are encouraged to apply. The successful applicant's lab will be located with my botany colleagues at the Montreal Botanical Gardens, which curates the second largest plant collection on the planet. There are extensive green houses, and Genome Quebec is just around the corner. Come join me in the cultural capital of Canada, Montreal.

Chris Cameron

Département de sciences biologiques Faculté des arts et des sciences

Professor in Plant Cellular Biology

The Département de sciences biologiques is seeking applications for a full-time tenure-track position at the rank of Assistant Professor in Plant Cellular Biology.

- Responsibilities

The appointed candidate will be expected to teach at all three levels of the curriculum, supervise graduate students, engage in ongoing research and publication, and contribute to the academic life and reputation of the University. The appointed candidate will also be responsible for the management and development of the microscopy platform at the Plant Biology Research Institute (IRBV).

- Requirements

§Ph.D. in cellular biology or in a related field §Postdoctoral experience in a related field §High quality publication record in international journals with very good impact factor §Interest in cross-disciplinary research and capacity to develop collaborations with members of the Département de sciences biologiques and other departments of Université de Montréal §Excellent abilities to teach at the undergraduate and graduate levels §Elaboration of a novel research programme that uses leading-edge experimental approaches in microscopy and cellular biology to study plant cell function §Large experience in advanced imagery, such as live-cell imaging, is an asset §Proficiency in French within a reasonable period

Linguistic Policy: Université de Montréal is a Québec university with an international reputation. French is the language of instruction. To renew its teaching faculty, the University is intensively recruiting the world's best specialists. In accordance with the institution's language policy [http://secretariatgeneral.umontreal.ca/fileadmin/user_upload/secretariat/doc_officiels/reglements/administration/adm10-34_politique-linguistique.pdf], Université de Montréal provides support for newly-recruited faculty to attain proficiency in French.

- Salary

Université de Montréal offers a competitive salary and a complete range of employee benefits.

Salary scale < http://fas.umontreal.ca/fileadmin/Documents/FAS/fas/Documents/Affaires_professorales/dossier_personnel/%C3%89chelle_salariale.pdf >

- Starting Date

On or after June 1st, 2017.

- Constitution of application

§The application must include the following documents:

- a cover letter
- a curriculum vitÃ
- copies of three recent publications and research
- a description of the teaching philosophy
- a description of the research programme

§Three letters of recommendation are also to be sent directly to the Chair of the Département de sciences biologiques by the referees.

- Deadline

Application and letters of recommendation must be sent to the Chair of the Département de sciences biologiques by November 25th, 2016 at the following address:

M. Daniel Boisclair, Chair Département de sciences biologiques Faculté des arts et des sciences Université de Montréal C. P. 6128, succursale Centre-ville Montréal (QC) H3C 3J7

The complete application may also be sent at the following e-mail: daniel.boisclair@umontreal.ca.

For more information about the Department and about the IRBV, please consult their respective Web site at http://www.bio.umontreal.ca/ and http://www.irbv.umontreal.ca/ . - Confidentiality The Université de Montréal application process allows all regular professors in the Department to have access to all documents unless the applicant explicitly states in her or his cover letter that access to the application should be limited to the selection committee. This restriction on accessibility will be lifted if the applicant is invited for an interview.

- Equal Access Employment Program Université de Montréal promotes diversity in its workforce and encourages members of visible and ethnic minorities as well as women, Aboriginal people, persons with disabilities and people of all sexual orientations and gender identities to apply.

— / —

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

---

Namibia CheetahConservation LabTechConsGenetics

Genetics Laboratory Technician or Manager Cheetah Conservation Fund, Namibia

The Cheetah Conservation Fund (CCF), Namibia, is currently looking for a highly motivated individual to join its genetics laboratory staff in the position of Laboratory Technician.

The specific title and remuneration are dependent on the applicant's level of experience. The successful applicant should have a Master's degree in a relevant field of research or a minimum of 3 years of professional experience. The position is available immediately, with expected start date on or as close as possible to December 15th, 2016. Namibian residency is preferred. Applicants should send their CV, letter of motivation, and contact details of 3 references to genetics@cheetah.org.

The successful candidate should have a strong background in best laboratory practices in molecular biology, and have excellent organizational and communication skills. His/her main responsibilities will include maintenance and operation of our genetic analysers and supervision of interns and students, ensuring that good laboratory practices and protocols are followed. Other responsibilities will be curation of databases, development of laboratory services, writing of permit applications and reports, and keeping the laboratory adequately stocked at all times. Prior experience in these particular tasks is not required; however, willingness to learn and attention to detail are essential. This position will also provide opportunities for direct participation in research projects as time permits.

The genetics laboratory is at the CCF research centre, about 40 km east of Otjiwarongo, Namibia. Staff members live on CCF property and housing is provided. Meals are prepared by CCF kitchen staff and are eaten communally. Further information regarding CCF and its mission to conserve cheetahs in the wild may be found at www.cheetah.org.

Anne Schmidt-Küntzel, DMV, PhD Assistant Director for Animal Health and Research Life Technologies Conservation Genetics—Laboratory Email: genetics@cheetah.org Tel: +264 67 306 225 Fax: +264 67 306 247 Cheetah Conservation Fund (CCF) www.cheetah.org

Anne Schmidt-Kuentzel <genetics@cheetah.org>

NewYorkU AbuDhabi EvolutionaryBio

FACULTY POSITION

Biology

New York University Abu Dhabi

New York University (NYU) Abu Dhabi invites applications for faculty positions at the associate professor, professor or equivalent level, potentially with tenure, for appointments as faculty in biology. We particularly encourage applications from candidates with research interests in genomics, computational biology and synthetic biology. Research interests in biology at NYU Abu Dhabi include evolution, development, neuroscience and environmental biology. Candidates will be expected to have active research programs and to participate in the division's teaching activities at the undergraduate andgraduate level.

Successful candidates will find a vibrant research and teaching environment that includes supportive and highly motivated colleagues, access to significant resources, a competitive startup package, and broad opportunities for interdisciplinary work at NYU Abu Dhabi and across campuses of the NYU system. Successful candidates will also have access to state-of-the-art core facilities that include next-generation sequencing, robotics, advanced microscopy, and high performance computing facilities with more than 6,400 computing cores and a peak performance of 70 TFLOPS. To obtain further information about research at NYU Abu Dhabi, please visit our website: http://nyuad.nyu.edu/en/research/faculty-research.html . The terms of employment are highly competitive. Appointments can begin as soon as September 1, 2017, but candidates may elect to start as late as September 1, 2018, pending budgetary approval.

Applications are due by November 15, 2016; however, the search will remain open until an appointment is made. Applicants should submit, in PDF format, a cover letter, curriculum vitae, a description of research interests (not to exceed five pages), a teaching philosophy statement (not to exceed three pages), and up to three representative publications. Applicants should also arrange to have three letters of reference uploaded to the web site by independent referees. Please visit our website at http://nyuad.nyu.edu/human.resources/open.positions.html for instructions and other information on how to apply. If you have any questions, please e-mail nyuad.science@nyu.edu.

NYU has established a multi-site, organically connected network encompassing key global cities and idea capitals. The network has three foundational degree-granting campusesâYork, Abu Dhabi, and Shanghaiâby a network of eleven research and study-away sites across five continents. Our students are drawn from around the world and surpass all traditional recruitment benchmarks, both US and global. Our goal is to develop a cohort of international students attuned to and educated for an inclusive global society. Students and Faculty will circulate within the global network in pursuit of common research interests and the promotion of cross-cultural and interdisciplinary solutions for problems both local and global.

NYU Abu Dhabi has recruited a cohort of faculty who are distinguished in their research and teaching. Its students are drawn from around the world and surpass all traditional recruitment benchmarks, both in the United States and globally. NYU Abu Dhabi's highly selective liberal arts enterprise is complemented by an institute for advanced research, sponsoring cutting-edge projects across the arts, humanities, social sciences, sciences, and engineering.

EOE/AA/Minorities/Females/Vet/Disabled/Sexual Orientation/Gender Identity Employer Stephane Boissinot, Ph.D. Professor of Biology NYU Abu Dhabi Saadiyat Island campus P.O. Box 129188 Abu Dhabi, United Arab Emirates http://www.boissinotlab.squarespace.com Office (UAE): +971 2 628 4790 Mobile (UAE): +971 56 305 2592

Stephane Boissinot <stephane.boissinot@nyu.edu>

NHM London ResAssist FishEvolution

Job: Research Assistant, Leverhulme Novelty

Vacancy reference: JM/NHM/RALN Location: South Kensington Employment type: Fixed Term Area of business: Life Sciences Closing date: 28/11/2016

Role description: We are seeking to appoint a Research Assistant (RA) to work on a Leverhulme Trust funded project on the development and evolution of the priapium fishes based in the Department of Life Sciences at the Natural History Museum, London. The project is managed by the Principal Investigator (PI) and a Postdoctoral Research Assistant (PDRA) in London, and a Co-investigator (Co-I) in Sheffield. This is an exciting project that requires application of molecular techniques primarily used in evolutionary developmental biology to investigate the morphological development of one of the most astonishing organ novelties in vertebrates and its genetic basis. To be successful in this role, you will be will be proficient in practical molecular biology and be able to implement techniques such as PCR based methods and RNA extraction. The ideal candidate may be familiar with fish husbandry or anatomy and may have experience with imaging techniques such as confocal microscopy or micro/nano CTscanning. Salary: 24,745 per annum plus benefits Contract: 34 months fixed term contract Closing date: 9am on Monday 28 November

Role competences: BEFORE beginning your application - Please read the section below about the 'Online Application Process' carefully.

If you wish to be considered for this role you will need to address each of the following competences in the 'other information' section of your online application:

Essential 1. Bachelor's degree in Life Science 2. Postgraduate Research experience 3. Experience working in a laboratory

Desirable 4. Advanced molecular biology lab techniques - especially RNA extraction/qPCR /next gen library prep/in situ hybridisation 5. Experience with confocal microscopy and/or micro/nano CT scanning 6. Experience with fish husbandry 7. Knowledge of fish anatomy/dissection 8. Ability to work independently on a day-to-day basis 9. Ability to work in a team 10. Excellent organization and communication skills

Apply here: https://nhm.irecruittotal.com/CONFIG/NHM/StaticPages/CAC/SearchVacancy.aspx?EmploymentTypeID=0&Intranet=0 "R.Britz@nhm.ac.uk" <R.Britz@nhm.ac.uk>

NorthCarolinaMuseum Raleigh CuratorPaleontology

The North Carolina Museum of Natural Sciences (Raleigh, NC) is searching for a Research Curator of Paleontology. This position has several areas of responsibility, including:

+ Development of an original scientific research program in Paleontology (vertebrate, invertebrate, or paleobotany; taxon unspecified, but non-archosaur focus is preferred); research could involve systematics (taxonomy, phylogenetics), evolution, ecology, and/or related fields; research may have local, regional, and/or international focus and will include pursuit of external research funding, data generation and analyses, and publication/dissemination of results; some aspects of this research should, ideally, include collaborations with other agencies, universities, and/or citizen scientists.

+ Curatorial responsibilities for the Paleontology Research Collection, including maintenance and growth of collection, migrating collections data to database format, specimen loan activities, and setting curatorial best-practice guidelines for collection.

+ Assisting Paleontology Unit Head with the operational management and administration of the Paleontology Unit, a subdivision of the Research & Collections section; duties may include supervision of laboratory with oversight of equipment, budgets, and personnel.

+ Participation in science communication initiatives, including participation in Museum educational programming, delivering public science-based presentations, conducting tours, interacting with Museum visitors, serving as a role model for students and citizen scientists, and creating programmatic themes that raise the science literacy of visitors.

The successful candidate will have:

+ Considerable taxonomic/systematic knowledge of Paleontology, in general, and of some taxonomic groups (vertebrate, invertebrate, or paleobotany, but non-archosaurian preferred), specifically experience applying principles and practices of research, with special expertise in at least one aspect of Paleontological systematics (taxonomy, phylogenetics), evolution, ecology, and/or related fields.

+ Demonstrated mastery of materials, equipment, and techniques used in relevant research (laboratory based protocols and fieldwork) and specimen collection curatorial activities.

+ Demonstrated track record of effective and creative science communication to diverse audiences.

+ Experience managing/supervising research projects, a research laboratory, and/or personnel.

+ Experience in preparing grant proposals to fund paleontological research and/or administering budgets supporting research or collections-related activities.

+ Experience in publishing technical science papers in peer-reviewed journals.

Possession of a master's degree in biology, zoology, or a science curriculum related to area of expertise and three years of experience in specialty area; or an equivalent combination of education and experience.

Preferred: A Ph.D. in paleontology or related science field. Additional Information to include: Applicants should attach: a current CV; contact information for 3 personal references; and a vision statement outlining their short and long term research goals, their approach to collection curation, and their philosophy and objectives regarding science communication.

Supplemental and Contact Information To apply for this position, please click the APPLY link provided above. In order to receive credit for your work history and credentials, you must list the information on the online application form. Any information omitted from the application cannot be considered for qualifying credit. Attached or incorporated resumes will be accepted, but will not be used for screening for qualifying credit. Using "See Resume" or "See Attachment" instead of completing the education and experience portion of the profile is not acceptable and will result in an incomplete application. Other attachments (except a DD-214 copy) will also be accepted, but not used in screening for qualifying credit. Applicants are required to scan and attach a copy of their DD- 214 or discharge orders if they wish to obtain veterans preference. Applicants requesting and receiving an accommodation under the Americans with Disabilities Act (ADA) are eligible to submit paper applications via mail or by fax. Please call the human resources office for assistance.

— / —

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

---

SaintLouisU 2 TeachingEvolution

Saint Louis University, a Catholic, Jesuit institution dedicated to student learning, research, health care, and service is seeking broadly trained applicants for two non-tenure track Assistant Professors in the Department of Biology. The successful candidates will be responsible for teaching Introductory Biology and Evolution in the Spring Semester 2017. In the fall, the successful candidates will participate in Introductory Biology lecture and/or labs and teach 1 or more courses in their specialty. Applicants should have a Ph.D., post-doctoral experience, a record of research productivity, and a commitment to undergraduate and graduate student mentoring in Biology. Experience teaching courses such as those listed above is highly desirable.

All applications must be made online at https://jobs.slu.edu and include a cover letter, curriculum vitae, a research statement, and a statement of teaching experience and philosophy. In addition, please have three letters of reference sent to Dr. John Kennell, Department of Biology, Saint Louis University, 3507 Laclede Avenue, St. Louis, MO, 63103-2010. Review of applications will begin onDecember 1, 2016 and continue until suitable candidates are identified.

Additional information on the Department of Biology can be found athttp://bio.slu.edu Saint Louis University is an equal opportunity/affirmative action employer. All qualified candidates will receive consideration for the position applied for without regard to race, color, religion, sex, age, national origin, disability, marital status, sexual orientation, military/veteran status, gender identity, or other non-merit factors. We welcome and encourage applications from minorities, women, protected veterans, and individuals with disabilities (including disabled veterans). If accommodations are needed for completing the application and/or with the interviewing process, please contact Human Resources at 314-977-5847.

Kasey Fowler-Finn, Ph.D. Assistant Professor Department of Biology Saint Louis University http://bio.slu.edu/fowlerfinn/ Kasey Fowler-Finn <fowlerfinn@slu.edu>

SciLifeLab Sweden Bioinformatics

1-2 positions providing advanced bioinformatics support, located at the SciLifeLab Bioinformatics Platform, Stockholm, Sweden.

Science for Life Laboratory (SciLifeLab, www.scilifelab.se) in Sweden serves as a national infrastructure to support advanced high-throughput life science research, and is currently one of the fastest-growing life science research establishments in Europe. The SciLifeLab bioinformatics platform (www.nbis.se) is a national infrastructure in rapid development, now looking for a 1-2 staff members to join the Bioinformatics Long-term Support team (WABI), placed in Stockholm. The Bioinformatics Long-term Support team provides advanced bioinformatics analyses to some of the most scientifically exciting projects across Sweden, and with 24 full-time senior bioinformaticians, the team is one of the strongest units for analysis of large-scale genomics and integrative omics in Sweden.

We are looking forward to your application at the latest December 14, 2016 http://www.su.se/english/about/vacancies/vacancies-new-list?rmpage=job&rmjob=2274&rmlang=UK Pär Engström, par.engstrom@scilifelab.se Björn Nystedt, bjorn.nystedt@scilifelab.se Joint Heads of SciLifeLab Bioinformatics Long-term Support

http://www.nbis.se/support/longtermsupport.html
http://www.scilifelab.se/platforms/bioinformatics/

StonyBrookU EvolInfectiousDiseases

As part of a new initiative in Planetary Health, Stony Brook University's Department of Ecology and Evolution and Global Health Institute invite applications for a faculty position. The successful candidate will hold a tenured or tenure-track appointment in the Department of Ecology and Evolution, and will be affiliated with the Global Health Institute (GHI), with additional potential affiliations as desired with the Centre ValBio, the Center for Infectious Diseases, the Division of Infectious Diseases, the Program in Public Health and/or the School of Dental Medicine. While open to all ranks, only exceptional candidates will be considered at the Assistant Professor level. The successful candidate will teach at the undergraduate and/or graduate level, generate external funding to support their research, and perform services to support the Department of Ecology and Evolution and the interdisciplinary mission of the GHI. Required qualifications include a Ph.D. in biological sciences or a related field, and an active and funded research program in ecology and/or evolution of infectious disease agents of relevance to human health. Preferred qualifications include demonstrated ability to develop international and interdisciplinary collaborations, strategic program building, development or use of quantitative approaches to model infectious disease dynamics, and an interest in developing research projects consistent with the mission of the GHI in Madagascar.

Stony Brook University has deep expertise in ecology, evolutionary biology, conservation biology, biodiversity, public health, and infectious diseases. The Global Health Institute's Planetary Health program seeks to simultaneously improve human and ecosystem health. The university supports field research at the Centre ValBio, located at the edge of Ranomafana National Park, Madagascar. Centre ValBio facilitates basic research in conservation biology and infectious disease ecology, but is also pioneering innovative methods for rural health care delivery. The successful candidate is expected to contribute to this long-standing research program in Madagascar.

The Department of Ecology and Evolution is a dynamic and growing department in a Tier I, Association of American Universities (AAU) university. Information about department faculty and our strong graduate training program is available at http://www.stonybrook.edu/ecoevo/. Areas of strength in our program include population genetics, conservation biology, molecular evolution and phylogenetics, evolutionary genomics, species interactions, invasion ecology, biogeography, mathematical ecology, and marine and freshwater ecology. The Department has recently benefited from new University initiatives that include faculty hiring in a new cross-departmental human evolution major and a campus-wide genomics cluster hire.

In addition to being a member of the prestigious AAU, Stony Brook University is co-manager of nearby Brookhaven National Laboratory, a multidisciplinary research laboratory supporting world-class scientific programs utilizing state of-the-art facilities. Stony Brook Medicine is Suffolk County's only academic medical center and tertiary care provider. Collaborations are also possible with Cold Spring Harbor Laboratories. The campus is close to marine and terrestrial research sites, including 50,000 acres of legally protected Pine Barrens and woodlands. While in the New York metropolitan area, Stony Brook is located on the north shore of eastern Long Island, NY, with access to farmlands, vineyards, miles of beaches, and convenient access to the cultural resources of New York City.

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. Anticipated Start Date: July 1, 2017. Stony Brook University is 100% tobacco-free as of January 1, 2016. See our policy and learn more at stonybrook.edu/tobaccofree. The selected candidate must successfully clear a background investigation.

Application Procedure: Those interested in this position should submit a State Employment Application: https://www.asa.stonybrook.edu/asa/ASAForms/Department/HRS/Document/HRSF0113, cover letter, resume/CV, a statement of research interests, and a statement of teaching interests to Academic Jobs

Online at: https://academicjobsonline.org/ajo/-jobs/8616 Applicants should arrange to have three letters of recommendation submitted on their behalf. Electronic submission via Academic Jobs Online is highly preferred.

Alternatively, submit above materials to:

Chair of Search Committee Department Ecology and Evolution Life Sciences Building, Room 650 Stony Brook University Stony Brook, NY 11794-5245

— / —

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

---

SussexU EvolutionBehaviourEnvironment

We are advertising for a Professor or Reader in the area of Evolution, Behaviour and Ecology, with a closing date of December 12th

http://www.sussex.ac.uk/aboutus/jobs/1302-1421 Could you draw this to the attention of anyone you think may be interested? I am happy to respond to informal questions.

Best wishes

Daniel Osorio

Subject Chair: Evolution, Behaviour and Environment

School of Life Sciences University of Sussex Brighton. BN1 9QG.

Tel: -44-(0)-1273-877440 Mobile: -44-(0)-7713083215

"abriscoe@uci.edu" <abriscoe@uci.edu>

UBath MathematicalBiology

The Department of Mathematical Sciences is seeking to appoint a professor in the research area of Mathematical Biology. Applications are welcome in any area of Mathematical Biology, which naturally includes evolutionary theory (with opportunities to interact with members of the Milner Centre for Evolution, see http:/-/www.bath.ac.uk/groups/milner-centre-for-evolution/).

Note that there is also a second position available in statistics (https://www.bath.ac.uk/jobs/-Vacancy.aspx?ref=SF4413).

The full announcement for the position in Mathematical Biology follows (see also https://www.bath.ac.uk/jobs/-Vacancy.aspx?ref=SF4447_.

—

The appointee will provide strategic leadership for Mathematical Biology both at a departmental level and across the institution where collaborative activity has traditionally been facilitated through the Centre for Mathematical Biology.

The appointee should also have a strong interest in pursuing excellence in undergraduate and postgraduate teaching and in supervising graduate students.

Doctoral training activities are supported by the Centre for Doctoral Training in Statistical Applied Mathematics at Bath (SAMBa), which has an annual intake of 10-15 research students, and with a broad applications spectrum which includes Mathematical Biology.

The successful applicant will join a vibrant department with over 70 staff across all of Mathematical Sciences and various cross disciplinary centres including the Centre for Mathematical Biology and the Centre for Networks and Collective Behaviour.

The Bath Institute for Mathematical Innovation helps businesses solve complex mathematical and statistical problems, and promotes cross-campus research activities and international collaborations. The recently established Milner Centre for Evolution, brings together the University's research in evolutionary biology. The superb location of the UNESCO-designated World Heritage City of Bath offers outstanding facilities and an excellent quality of life.

Applications from all groups currently under-represented in academic posts are particularly encouraged. We are working to improve the present gender balance within the Department, and particularly welcome applications from women. Both the Department and the University are committed to providing a supportive and inclusive working environment. Flexible working options will be considered wherever possible. For more information, visit http://www.bath.ac.uk/hr/working/flexible-working/ Alongside completion of the online application form, candidates should upload:

- a full Curriculum Vitae, - a statement of research interests of up to 3 pages - a one-page summary of teaching experience

Interviews will be held in the week of 20 February 2017.

Informal enquiries may be addressed to: Professor Paul Milewski (p.a.milewski@bath.ac.uk) Dr. Ben Adams (b.adams@bath.ac.uk) Dr. Jane White (k.a.j.white@bath.ac.uk)

The University of Bath is an equal opportunities employer and has an excellent international reputation with staff from over 60 different nations. To achieve our global aspirations, we welcome applicants from all backgrounds.

Salary: Competitive package Placed On: Friday 18 November 2016 Closing Date: Monday 09 January 2017 Interview Date: See advert Reference: SF4447

jason@evolutionarygenetics.org

UCalfornia LosAngeles ResTech OakGenomics 2

UCLA Genomics Technician/Lab Manager for Oak Genomic Studies

We are inviting applications for an enthusiastic and experienced biologist with a bachelor's degree to conduct molecular and genetic analysis of oaks and to manage a laboratory with on-going genomic and field studies related to the evolutionary and conservation questions on oaks. This position is funded in part by a multi-investigator NSF-funded project to assemble and annotate the genome of valley oak. The individual will join a diverse and stimulating scientific team and will be included in weekly lab meetings and social events.

Working in the laboratory of Victoria Sork, the technician and lab manager (classified as Staff Research Associate III) will be responsible for laboratory methods in support of research in plant genomics, genome annotation, and gene expression studies. This work requires knowledge of molecular research tools and skill in high throughput genomic techniques. The technician will also provide data management for research in these areas. The necessary molecular techniques include: DNA extraction, PCR, RNAseq, epigenetics, preliminary data analysis; and sequencing sample design. S/he will also oversee a website that presents research findings and datasets for our research group. Other duties include: oversee day-to-day management of laboratory including purchase of supplies and equipment; insure proper operation and maintenance of laboratory equipment; entering and managing electronic data files; supervise undergraduate research assistants; and occasional training of students.

Any interested individuals should review the job listing for further details: hr.mycareer.ucla.edu/applicants/Central?quickFindi406 Applications submitted through the link above will be reviewed as submitted. Reviews will begin November 15, 2016 and continue until position is filled. Desired start date is: January 9, 2017

If you have questions, please write Victoria Sork (sorklab@gmail.com).

"Sork, Victoria" <vlsork@ucla.edu>

UCalifornia LosAngeles ResTech OakGenomics

Hello,

Please post the following ad for a research tech position in Oak Genomics at UCLA.

I am not sure if all the job postings note who the person posting it is, but if so we would like it to have been from Dr. Victoria Sork who is the PI for this position.

Thank you for your help, -Krista

Job:UCLA.ResTech.OakGenomics

UCLA Genomics Technician/Lab Manager

Plant population genomics of trees

We are inviting applications for an enthusiastic and experienced biologist with a bachelor's degree to conduct molecular and genetic analysis of oaks and to manage a laboratory with on-going genomic and field studies related to the evolutionary and conservation questions on oaks. This position is funded in part by a multi-investigator NSF-funded project to assemble and annotate the genome of valley oak. The individual will join a diverse and stimulating scientific team and will be included in weekly lab meetings and social events.

Working in the laboratory of Victoria Sork, the technician and lab manager (classified as Staff Research Associate III) will be responsible for executing experiments in support of research in plant genomics and population genetics. This work requires a combination of journey level knowledge of molecular research tools and skill in both high throughput biology genomic techniques and some bioinformatic expertise. The incumbent will also provide data management for research in these areas.

This individual will conduct molecular analyses, including DNA extraction, PCR, RNAseq, epigenetics and other high throughput techniques; analyze preliminary data; and help design new experiments based on the data. S/he will also oversee a website that presents research findings and datasets for our research group. Other duties include: oversee day-to-day management of laboratory including purchase of supplies and equipment; insure proper operation and maintenance of laboratory equipment; entering and managing electronic data files; supervise undergraduate research assistants; occasional training of students.

Any interested individuals should review the job listing for further details: hr.mycareer.ucla.edu/applicants/Central?quickFindi406

If you have questions, please write Victoria Sork (sorklab@gmail.com).

Applications submitted through the link above will be reviewed as submitted. Reviews will begin November 15, 2016 and continue until position is filled.

Desired start date is: January 9, 2017

"klbeckley@g.ucla.edu" <klbeckley@g.ucla.edu>

UCentralFlorida 4 Genomics

The University of Central Florida (UCF) has recently established six interdisciplinary clusters to strengthen its academic and research missions. We are building a new Genomics and Bioinformatics Cluster (GBC) (http://www.ucf.edu/research/genomics), staffing for which should be completed by Fall 2017. As part of the GBC, we are currently seeking to hire four tenure-earning assistant professors; however, exceptionally well-qualified individuals will be considered at the rank of tenured associate or full professor. Candidates must have a strong research publication record and demonstrated independent research, with either existing research funding, or strong potential to initiate and obtain funding for their research program. The GBC emphasizes multidisciplinary research in genomics that cover at least two disciplines among biology, biomedical sciences, and computer science. In particular, the GBC is looking to expand research programs in genomics that are enabled by next-generation sequencing technologies and that address one or more areas among molecular evolution, biodiversity, microbiome research (environmental and plant/animal health), new biological model systems, cancer genetics, infectious diseases, computational biology, systems biology, machine learning and data mining. Strong candidates in other areas of genomics will also be considered.

The GBC members will be expected to strengthen their individual tenure homes as well as the cluster. A strong advantage of this position is the ability of the candidate to choose a tenure home, with mutual consent, among units involved in the cluster. The list of host departments includes Biomedical Sciences (College of Medicine), Biology (College of Sciences), or Computer Science (College of Engineering and Computer Science). A candidate may also be jointly appointed among these as appropriate to qualifications and interest. All GBC faculty members (and their students) will be housed jointly to facilitate collaboration.

Candidates must have a Ph.D. or M.D./Ph.D. from an accredited institution in an area appropriate to the cluster at the time of appointment. Postdoctoral research training experience is also strongly preferred.

The University of Central Florida is the nation's second-largest university with more than 63,000 students. UCF has grown substantially in size, quality, diversity, and reputation in its first 50 years. Today, the university offers more than 200 degree programs at its main campus in Orlando and more than a dozen satellite locations. UCF is an economic engine, attracting and supporting industries vital to the region's future while providing students with real-world experiences that help them succeed after graduation. For more information, visit http://www.ucf.edu/faculty/ . Candidates must apply online at https://www.jobswithucf.com/postings/47009 and provide the following materials: a cover letter, curriculum vitae, teaching statement, research statement, and contact information for three professional references. In the cover letter, candidates should address their background in genomics and/or bioinformatics and identify the anticipated department(s) for their potential tenure home. In the research statement candidates should include descriptions of their successful interdisciplinary research collaborations and how their current and future research can contribute to the cluster's overall interdisciplinary objectives. Please have all documents ready when applying so they can be attached at that time. Once the online submission process is finalized, the system does not allow applicants to submit additional documents at a later date.

UCF is an equal opportunity/affirmative action employer. All qualified applicants are encouraged to apply, including minorities, women, veterans and individuals with disabilities. As a Florida public university, UCF makes all application materials and selection procedures available to the public upon request.

The search committee will begin reviewing applications in November 2016 and continue until the positions are filled.

For more information about these positions, please contact the Cluster Search Chair, Shibu Yooseph, at GenomicsCluster@ucf.edu.

Eric Hoffman

Associate Professor and

Undergraduate Program Coordinator

UCF Department of Biology

Eric Hoffman <Eric.Hoffman@ucf.edu>

UCincinnati MicrobialMetagenomics

Environmental Microbiology of Aquatic Systems

We seek to hire an Assistant Professor with research interests in environmental microbiology. Emphasis is placed on understanding the broad factors affecting aquatic ecosystems in natural and urban settings from local to regional scales. Specific areas of interest may include natural and human-influenced dynamics of microbial communities, the detection and mitigation of waterborne pathogens, algal blooms, and/or biofilms. Candidates using metagenomics/bioinformatics approaches to these questions are particularly encouraged to apply. The successful candidate will complement the three broad areas of interest within the water cluster, including human impacts on the global hydrologic cycle, urban water and wastewater systems, and linkages between water and energy systems.

Full ad:

WATER CLUSTER - Environmental Microbiology of Aquatic Systems

Tenure-Track Position

UNIVERSITY OF CINCINNATI

The University of Cincinnati is pleased to announce a tenure-track faculty position in the area of environmental microbiology of aquatic systems. This position is part of the second round of hiring for the Water Cluster Initiative that will hire a total of six new tenure-track faculty members to strengthen interdisciplinary programs in water research, education and outreach. The Water Cluster hires represent a joint initiative between the College of Engineering and Applied Science (CEAS), the College of Arts & Sciences (A&S), and the College of Design, Architecture, Art and Planning (DAAP).

Building on our research and innovation strengths, UC's Cluster Hiring Initiative supports existing and emerging partnerships within and between colleges, divisions and areas. In partnership with the Vice President of Research, the Provost's cluster hiring investments harness the power of faculty members focused on solving the world's biggest challenges through leading-edge research and interdisciplinary collaborations that erase boundaries and embrace creative, bold ideas.

Designed to attract top-quality faculty from around the world, UC's Clusters represent the university's commitment to investing in faculty and interdisciplinary problem-solving. UC's Water Cluster establishes our region as a national and global leader in water research, education and outreach centered on integrated water resources management within and across natural and engineered systems. By bringing water planning and management experts together, the Water Cluster provides a supportive platform for new approaches to environmental sustainability.

A job description for the specific position follows. Please see the Provost's website http://www.uc.edu/provost /clusters for more information about the Cluster Hiring initiative, and visit https://jobs.uc.edu for a listing of all open positions.

Environmental microbiology of aquatic systems. We seek to hire an Assistant Professor with research interests in environmental microbiology. Emphasis is placed on understanding the broad factors affecting aquatic ecosystems in natural and urban settings from local to regional scales. Specific areas of interest may include natural and human-influenced dynamics of microbial communities, the detection and mitigation of waterborne pathogens, algal blooms, and/or biofilms. Candidates using metagenomics/bioinformatics approaches to these questions are particularly encouraged to apply. The successful candidate will complement the three broad areas of interest within the water cluster, including human impacts on the global hydrologic cycle, urban water and wastewater systems, and linkages between water and energy systems.

Responsibilities The successful candidate will be expected to develop and maintain an internationally-recognized externally funded research program; provide excellence in undergraduate and graduate teaching and education; and contribute to scholarly activities performed within academic communities across the university. The successful candidate will also be expected to contribute in meaningful ways to interdisciplinary research and educational activities that complement and are synergistic within the Water Cluster.

Qualifications A Ph.D. degree in biology/microbiology or a closely related field is required. Candidates will be evaluated based on their alignment within the Water Cluster and on their academic credentials, their record of research, teaching and scholarly activities and potential for success in developing a funded research program and making contributions in research, teaching and service to the field.

Appointment The position is anticipated to be filled at the rank of Assistant Professor. However, exceptional Associate and full Professor candidates will be considered based upon credentials. Successful candidates are expected to have a primary appointment in either the Department of

— / —

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

UCollegeLondon NatureInspiredUrbanism

We are seeking Postdoctoral RA, with a PhD in Life Sciences, Science Communication or related field, to work on a short-term project on Nature Inspired Urbanism. The basic aim of the project is help systematically evaluate the biological analogies, many of which are evolutionary in nature, used in the Urbanisation literature. This post is well suited to someone to wishing to expand their scientific horizons beyond the life sciences. The closing date is 15 November 2016 and with a starting date of 1st December 2016 or soon after.

https://naturbanism.wordpress.com/2016/11/01/job-opportunity-research-associate/ Dr Katrina Lythgoe | Sir Henry Dale Fellow | University of Oxford, Department of Zoology, OX1 3PS | +44 (0)1865 281 896 | website< http://www.zoo.ox.ac.uk/people/view/lythgoe_k.htm > I work part time and am usually in Oxford on Mondays and Wednesdays; please don't expect a reply after 3pm on other days.

Katrina Lythgoe <katrina.lythgoe@zoo.ox.ac.uk>

UCologne PlantBiodiversity

The Faculty of Mathematics and Natural Sciences of the University of Cologne invites applications for a tenured Full Professorship (W3) in Plant Ecology and Biodiversitystarting by March 01, 2017.

Candidates should have proven achievements in the field of Experimental Plant Ecology and Biodiversity. Outstanding research on processes influencing ecologically relevant phenotypes, ecosystem composition or population dynamics in natural conditions is of particular importance. The successful candidate should contribute to broaden the spectrum of species studied at the Botanical Institute and have an interest in applying molecular, genomic and genetic approaches to ecological research questions. He/she is expected to teach at undergraduate and graduate levels in Biology, especially in the field of organismic biology. Teaching can initially be conducted in English; all graduate-level courses in biology are taught in English.

The professorship is located at the Biocenter, which provides state-of-the-art plant growth infrastructure, excellent facilities for molecular and genomic research and hosts a rich and diversified panel of experts in Plant Biology. Conditions of employment are, beside the ones named in Â§36 HG NRW, excellent scientific qualifications, experience and competence in teaching, proven ability to acquire external funding and the motivation to participate in interdisciplinary collaborations with groups in the Biocenter, the Cluster of Excellence on Plant Sciences (CEPLAS), the Max Planck Institute of Plant Breeding Research in Cologne and the Faculty of Mathematics and Natural Sciences of the University of Cologne.

The University of Cologne particularly encourages applications from disabled persons. Disabled persons are given preference in case of equal qualification. Women are strongly encouraged to apply. Preferential treatment is given to women if their professional qualifications and abilities are equivalent to those of other applicants.

Applications should include a letter of motivation with a research statement and the usual documents (CV, publication list, information on external funding, teaching experience, academic achievements and honors). Applications should be submitted via our Academic Job Portal (https://berufungen.uni-koeln.de) no later than December 20, 2016 to

Professor Dr. Ansgar BuÌschges Dean of the Faculty of Mathematics and Natural Sciences University of Cologne Albertus-Magnus-Platz, 50923 Cologne, Germany E-Mail mnf-berufungen@uni-koeln.de

Juliette de Meaux <jdemeaux@uni-koeln.de>

UExeter Tech GuppyEvolutionaryGenetics

We are currently seeking a technician to join the Wilson group at the University of Exeter (Cornwall Campus), UK. The post will primarily be working in the fish lab, joining a team studying evolutionary and behavioural genetics in the Trinidadian guppy

https://biosciences.exeter.ac.uk/cec/staff/index.php?web_id=Alastair_Wilson The position is part-time (50% FTE) with funding in place for 24 months (proposed start date Jan 1 2017). For a suitably qualified candidate the position could be combined with part time study for a Master's degree in the group (with a fee-waiver provided). More information and links to online application process (deadline 21/11/2016) can be found at

https://jobs.exeter.ac.uk/hrpr_webrecruitment/wrd/run/ETREC107GF.open?VACANCY_ID=532414GC0p&WVID=3817591jNg&LANG=USA Note funding restrictions mean applicants must be UK/EU citizens (or have an existing right to work in the UK). For more information please contact a.wilson@ex.ac.uk.

"Wilson, Alastair" <A.Wilson@exeter.ac.uk>

UHelsinki EcolEvolution

Job: University of Helsinki, Professor in Ecology

The Department of Biosciences at the Faculty of Biological and Environmental Sciences invites applications for a

PROFESSOR / ASSOCIATE PROFESSOR / ASSISTANT PROFESSOR IN ECOLOGY

The successful applicant may be appointed to a permanent professorship or a fixed-term associate / assistant professorship (tenure track) depending on his or her qualifications and career stage.

The professorship is based in the Division of Ecology and Evolutionary Biology of the Department (http://www.helsinki.fi/biosciences/ecologyandevolutionarybiology/index.htm). The areas of strength of the division include population, molecular and evolutionary ecology, to the advancement of which the professor is expected to contribute. Demonstrated excellence and scientific leadership in the fields of ecology and/or evolutionary biology is a requirement. The appointee is also expected to be experienced in empirical field work or laboratory work.

According to the Government Decree on Universities, professors / associate / assistant professors must be proficient in Finnish. They must also have at least satisfactory spoken and written skills in Swedish. Foreign citizens, non-native Finnish citizens or citizens who have not been educated in Finnish or Swedish may be exempted from this requirement without a separate application. To successfully attend to the duties of the position, the appointee must also have good English skills.

For full description of position and instructions how to apply, please see:

https://www.helsinki.fi/en/open-positions/professor-associate-assistant-professor-in-ecology-department-of-biosciences Juha Merilä Ecological Genetics Research Unit Department of Biosciences PO Box 65 (Biocenter 3, Viikinkaari 1) FIN-00014 University of Helsinki Finland

E-mail: juha.merila@helsinki.fi Gsm: +358-(0)50-416 0561 ResearchGate: https://www.researchgate.net/profile/Juha_Merilae?ev=hdr_xprf Google Scholar: https://scholar.google.fi/citations?user=cZJ7ifQAAAAJ&hl=en Publons: https://publons.com/author/341551/juha-merila#profile Juha Merilä <juha.merila@helsinki.fi>

UHouston MathematicalBiology

The Department of Biology and Biochemistry at the University of Houston invites applications for a tenure-track faculty position at the rank of Assistant or Associate Professor. Applicants with research interests and a record of accomplishment in dynamic models of biological systems are encouraged to respond. Possible specialties include, but are not restricted to, biochemistry, biological networks, cell biology, cancer biology, developmental biology, ecology, evolution, gene regulation, infectious diseases, molecular dynamics, neurobiology, and systems biology. Successful applicants will complement existing departmental strengths in evolutionary genetics, genomics, developmental and stem cell biology, and cancer biology. The position requires a Ph.D. and significant relevant academic experience. Hiring at the Associate Professor rank requires a record that includes scientific achievement, external funding, and graduate or undergraduate instruction.

Faculty members are expected to establish and maintain nationally competitive externally funded research programs and to participate in graduate and undergraduate teaching. The department is seeking outstanding candidates with the potential for exceptional research, excellence in teaching, and a clear commitment to enhancing the diversity of the faculty, graduate, and undergraduate student population.

The Department of Biology and Biochemistry has state-of-the-art laboratory space, well-equipped core facilities and broad opportunities for research collaborations within the University of Houston as well as with other member institutions of the Texas Medical Center. The University of Houston has excellent high-performance computing resources.

Interested applicants should submit a curriculum vitae, research plan, statement of teaching philosophy, list of references with contact information, and cover letter. Review of applications will begin on November 15 and continue until the position has been filled.

UH is an Equal Opportunity/Affirmative Action Employer. Minorities, women, veterans, and persons with disabilities are encouraged to apply.

The University of Houston is responsive to the needs of dual career couples.

Ricardo

Ricardo B. R. Azevedo, PhD Associate Professor Dept. Biology & Biochemistry University of Houston 369 Science & Research 2 Houston, TX 77204-5001 Tel: 713-743 4149 Fax: 713-743 2636 Email: razevedo@uh.edu

“razevedo@Central.UH.EDU”
<razevedo@Central.UH.EDU>

UIowa PredictiveGenomics

FACULTY POSITION IN PREDICTIVE GENOMICS AND EPIGENOMICS

The Department of Biology at the University of Iowa invites applications for a tenure-track faculty member at the rank of Assistant Professor. This position is part of a campus-wide Informatics Initiative and is targeted towards researchers who can bring together multiple genome-scale datasets (transcriptomes, chromatin states, population genomics) to generate predictive descriptions of phenotypes using statistical and machine learning approaches. We are particularly interested in computational biologists with wet lab experience or a track record of collaboration with experimentalists to investigate the effects of stressors (genetic, molecular, cellular or environmental) on behavior, population dynamics, aging, or susceptibility to diseases and cancer using model systems.

The Department of Biology (https://biology.uiowa.edu/-) represents a unique and rich combination of basic and applied research. Biology faculty use all the standard experimental model systems (Drosophila, Zebrafish, C. elegans, Xenopus, yeast, mice and rats), study diverse levels of organization (from genes and genomes to cells, organisms, and populations) and are engaged in complementary areas of research including overarching disciplines such as molecular genetics, cell and developmental biology, neurobiology and evolution. Subspecialties include genomics, transcriptomics and epigenetics, population biology and speciation, and the genetic basis of behavior, aging, human disease and stress responses, amongst others. The University's Iowa Informatics Initiative UI3 (http://informatics.uiowa.edu/) is a multidisciplinary initiative designed to establish the University of Iowa as a center of excellence in the rapidly evolving field of informatics. Together with a number of Colleges, Departments and Programs, the Department of Biology and UI3 offer opportunities for a wide range of research collaborations, leadership roles, and teaching and mentoring of graduate students and postdoctoral fellows.

Applicants must have a PhD or terminal degree in either computer science or statistics, genetics, biology, or a related discipline, a recognized record of accomplishment as reflected in publications in leading journals, and demonstrate the potential to develop and maintain an internationally-recognized, externally-funded research program. Candidates will also contribute to the teaching mission of the Department of Biology and should be committed to excellence through teaching Genomics or Biology-related courses at graduate and undergraduate levels, including the development of an upper level course in "Big Data Analysis" with a focus on genomic approaches. Postdoctoral experience and published record of expertise in high-dimensional data analysis applied to next-generation sequencing (NGS) data is highly desired. Competitive salary, start-up package, laboratory, and computational facilities will be provided.

Applications must be submitted online at http://-jobs.uiowa.edu/ (Requisition #69710). Applicants should submit a cover letter, curriculum vitae, and separate statements of research objectives and teaching interests. A statement within the cover letter indicating how the candidate's research may fit in and contribute to Biology and the UI3 initiative is desirable. Applicants should also include the names and contact information of three references to be fully considered.

Review of applications will begin on November 15th and will continue until the position is filled. The target starting date for this position is August 2017.

The Department of Biology and the College of Liberal Arts & Sciences are strongly committed to diversity; the strategic plans of the University and College reflect this commitment. All qualified applicants are encouraged to apply and will receive consideration for employment free from discrimination on the basis of race, creed, color, national origin, age, sex, pregnancy, sexual orientation, gender identity, genetic information, religion, associational preference, status as a qualified individual with a disability, or status as a protected veteran. The University of Iowa is an equal opportunity/affirmative action employer.

John Manak (john-manak@uiowa.edu), Josep M. Comeron (josep-comeron@uiowa.edu). Search Committee Co-Chairs Department of Biology. The University of Iowa. Iowa City, IA 52242-1324

"Comeron, Josep M" <josep-comeron@uiowa.edu>

ULouisiana Lafayette EvoDevo

Assistant Professor Position in Evolutionary Developmental Biology

The Department of Biology (http://-biology.louisiana.edu) at the University of Louisiana Lafayette seeks to fill a tenure-track position at the Assistant Professor level. We are looking for an outstanding scientist studying the interplay of genetic and developmental mechanisms that mediate the origin and diversification of complex traits and functions. Scientists with a research focus on gene regulation or epigenetics are highly encouraged to apply.

Minimum qualifications are a Ph.D. in a relevant field, a significant publication record, and postdoctoral experience. Successful applicants will be expected to establish a vigorous, externally-funded research program, provide instruction to undergraduates and graduate students and participate in our Ph.D. program in Environmental and Evolutionary Biology. Cover letter, curriculum vitae, statement of research interests, statement of teaching interests, and a list of three references (including postal and email addresses) should be emailed as a single pdf attachment to: EvoDevo.search@louisiana.edu. Please refer to "EvoDevo search" in the subject line. To ensure full consideration, applications should be received by December 5, 2016.

The University of Louisiana at Lafayette is a public research university with High Research Activity with accreditation from the Southern Association of Colleges and Schools Commission on Colleges. With an enrollment of over 18,000 students and 800 full-time faculty members, UL Lafayette is the largest of nine universities in the University of Louisiana System. The University offers degree programs in 55 undergraduate disciplines, 15 post-bachelor certificates, seven graduate certificates, the master's degree in 28 disciplines, and the doctorate in 10 disciplines. Further information about the University is available on the University's webpage at http://louisiana.edu. With approximately 30 faculty members and 70 graduate students, the biology program is one of the largest of its kind on the Gulf Coast.

For information about safety at the University of Louisiana at Lafayette, and to review the Annual Security Report, which contains information about crime statistics and other safety and security matters, please go tohttp://police.louisiana.edu/jeanne-clery-act, where you will also find details on requesting a hard copy of the Annual Security Report.

UL Lafayette is an EEO/AA employer.

Paul Leberg John E. and Joretta Achee Chance Professor of Biology and Department Head Department of Biology University of Louisiana at Lafayette http:/-/biology.louisiana.edu/ https://www.facebook.com/-ullafayettebiology/ http://leberglab.weebly.com/ PO Box 43602 Lafayette, LA 70504 Leberg@Louisiana.edu

337-482-6637 337-482-5660 (Fax) 452 Wharton Hall

Paul Leberg <leberg@louisiana.edu>

UMississippi QuantitativeEcologyEvolution

Please note: While the official job title is in Ecology, the position is equally open to candidates pursuing research in Evolutionary Theory.

The Department of Biology at The University of Mississippi invites applications for two tenure-track Assistant Professor positions, in Cell Biology and Quantitative Ecology.

*Quantitative Ecology. *We seek candidates who bring cutting-edge mathematical, modeling, and computational tools to the development of ecological and evolutionary theory. Areas of interest include behavioral ecology, multilevel selection theory, sexual selection, life history ecology, metabolic scaling, spatial and temporal structure, species coexistence, and community assembly. Applicants with transdisciplinary interests who integrate theoretical development with empirical tests, whether alone or in collaboration, are encouraged to apply.

The successful candidate will be expected to develop an innovative, externally funded research program and to teach graduate and undergraduate courses in their areas of expertise. They will join a vibrant and broad-based Biology department (biology.olemiss.edu) at The University of Mississippi, a Carnegie-designated R1 University with Highest Research Activity. Applicants are required to have a Ph.D. in a relevant field, postdoctoral experience, and a record of published work related to their research area. Women and individuals from underrepresented groups are strongly encouraged to apply.

These appointments are part of a strategic growth initiative to complement departmental strengths in species interactions and symbiosis, genetics and biodiversity, and neuroscience and behavior. The University of Mississippi has been recognized by the Chronicle of Higher Education as a "Great College to Work For" and is located in Oxford, Mississippi, a beautiful college town well known for its outstanding educational and cultural opportunities.

To apply, please visit our Online Employment Service at jobs.olemiss.edu. Applications should include: (1) cover letter outlining interest and suitability for the position, (2) curriculum vitae, (3) a two-page statement of current and future research interests, (4) a one-page statement of teaching interests and qualifications, (5) copies of up to five publications or submitted manuscripts, and (6) names and contact information for four references. Review of applications will begin on December 15, 2016 and continue until the positions are filled. The University of Mississippi is an EOE/AA/Minorities/Females/Vet/Disability/Sexual Orientation/Gender Identity/Title VI/Title VII/Title IX/504/ADA/ADEA employer.

Inquiries about these positions can be directed to Dr. Stephen Brewer, Chair of the Quantitative Ecologist Search Committee, at jbrewer@olemiss.edu.

Susan Balenger <balenger@olemiss.edu>

UMontana GeneticsLabTech

GENETICS LAB TECHNICIAN and ENVIRONMENTAL DNA MONITORING PROGRAM COORDINATOR

Project: Aquatic invasive species monitoring and eDNA detection

Principal Investigators: Gordon Luikart and Steve Amish, Flathead Lake Biological Station and Montana Conservation Genomics Laboratory, Division of Biological Sciences, The University of Montana. gordon.luikart@umontana.edu (406-982-3301 x249), stephen.amish@mso.umt.edu (406-243-6749)

Start Date & Duration: January 2016; 1 year with likely extension

Project Description/Summary: Aquatic Invasive Species (AIS) such as zebra and quagga mussels, Euarasian watermilfoil, rainbow trout, brook trout, New Zealand mudsnails, Asian carp and many others are spreading across North America and causing massive economic and ecological problems. Sensitive eDNA tests are urgently needed for early detection, monitoring, and preventing the spread of these AIS. eDNA tests are also needed for monitoring endangered species such as bull trout and salmon. This position will oversee and organize existing monitoring work and lab testing, and help develop new lab protocols, eDNA assays, and field sampling protocols. The project will also develop and compare PCR technologies (digital and real time) and perhaps next gen sequencing methods to quantify their relative sensitivity and specificity on many of the most insidious AIS and the most threatened salmonids in

North America. We are especially interested in and concerned about stopping the spread of zebra mussels which were discovered in Montana last summer (2016). The applicant may also work on additional exciting population genomics projects including trout and stonefly adaption to extreme environments (captivity, climate change), and travel to conduct fish and eDNA sampling in beautiful areas such as Glacier National Park, Yellowstone National Park, Flathead Lake, and streams across Montana. Skills required: The applicant should have substantial experience conducting qPCR and ideally eDNA analyses or noninvasive or ancient DNA analyses (including sample extraction). The applicant should have demonstrated ability to write and publish papers, organize and manage lab supplies, and ideally to oversee and train others. Proven ability to communicate with others from diverse groups (e.g. agencies, managers, researchers, the public), establish collaborations, and write small grant proposals are highly desirable.

Applications: Send a brief letter (< 1 page) describing your motivation and background, your CV, and the names and contact information for three references to both G. Luikart and S. Amish. Review of applications will start November 29th and remain open until a suitable candidate is hired.

Salary: Negotiable, but likely approximately $26,000 to $33,000 the first year depending on experience and CV. We would consider hiring a postdoc with higher salary if the applicant has demonstrated high productivity, experience, and is passionate about preventing AIS invasions (including by pathogens killing our native fish).

Key references: see our web pages, this eDNA video: <https://flbs.umt.edu/giving/default.aspx?id=3D1 >; & contact us.

"Luikart, Gordon" <gordon.luikart@mso.umt.edu>

UNAM MexicoCity SystematicBotanist

Position opening - Instituto de Biologia, Universidad Nacional Autonoma de Mexico: Systematic Botanist/Mycologist

The Instituto de Biologia (IB), Universidad Nacional Autonoma de Mexico (UNAM), whose main mission is the study of national biodiversity and houses the national biological collections, invites applications for a tenure-track, full-time position at the level of Associate Researcher "C", in Systematic Botany or Systematic Mycology at UNAM's main campus in Mexico City.

Requirements for candidates: 1. A Ph.D. degree or equivalent, preferably in botany, mycology, systematics, evolutionary biology, or a related discipline. 2. Experience in systematic research of plants or fungi, demonstrated by original, high quality publications, commensurate to age and academic trajectory. 3. Knowledge of the vascular flora or mycota of Mexico and/or the Neotropics, particularly in one or more groups whose diversity is exceptional in Mexico, as well as experience in the curation of scientific collections, techniques of field collecting, morphology, molecular systematics, and/or evolutionary biology. 4. A commitment to participate in activities complementary to research, including teaching in educational programs at UNAM, and the direction of theses at the undergraduate and graduate level, activities of science outreach, and institutional participation. 5. Willingness to integrate immediately into the academic activities of the IB-UNAM, practice leadership in his or her area of investigation, and demonstrate capacity to form or integrate into a research group. 6. Proficiency in Spanish.

Applicants should submit a letter addressed to the Academic Secretary of the IB-UNAM with a detailed statement of proposed activities; a full curriculum vitae with contact information (supporting documentation is not necessary at this stage); PDFs of publications that the applicant considers the most important of her/his professional trajectory (a maximum of five); a brief proposal of her/his activities for the first year at the IB-UNAM (5 pages maximum); and a letter of recommendation. Applications with the required documentation will be received from September 1st, 2016 until December 2nd, 2016. Shortlisted candidates will be contacted for a personal interview.

Inquiries regarding this announcement should be addressed to Dr. Atilano Contreras-Ramos, Academic Secretary of IB-UNAM, e-mail: acontreras@ib.unam.mx. Applications should be sent to the email addresses sacademica@ib.unam.mx or vinculacion@ib.unam.mx.

Convocatoria - Instituto de Biologia, Universidad Nacional Autonoma de Mexico: Botanico/Micologo Sistematico

El Instituto de Biologia de la Universidad Nacional Autonoma de Mexico (IB-UNAM), cuya mision principal es el estudio de la biodiversidad nacional y albergar las colecciones biologicas nacionales, a través de la Secretaria Academica convoca a los interesados en ocupar una posicion como Investigador Asociado "C" de Tiempo Completo, con posibilidad de posicion permanente, en las areas de Botanica Sistematica o Micologia Sistematica en el campus de Ciudad Universitaria, Ciudad de Mexico.

Requisitos. 1. Tener el grado de Doctor en Ciencias o equivalente (Ph.D.), preferentemente en Botanica, Micologia, Sistematica, Biologia Evolutiva o una disciplina afin. 2. Poseer experiencia de investigacion en sistematica de plantas u hongos, demostrada mediante publicaciones originales y de calidad, proporcionales a su edad y trayectoria academica. 3. Preferentemente, tener conocimiento de la flora vascular o la diversidad fingica de Mexico y/o el Neotropico, particularmente en uno o mas grupos cuya diversidad sea sobresaliente en el pais, asi como conocimientos de curacion de colecciones cientificas, tecnicas de recolecta de campo, morfologia, sistematica molecular y/o biologia evolutiva. 4. Tener el compromiso de participar en actividades complementarias a la investigacion, incluyendo la formacion de recursos humanos de alto nivel mediante docencia en los programas educativos de la UNAM y la dirección de tesis de licenciatura y posgrado, activida des de difusión y participación institucional. 5. Tener disposición para integrarse de manera inmediata a las actividades académicas del IB-UNAM, ejercer liderazgo en su línea de investigación y demostrar la capacidad de formar y/o integrarse a grupos de investigación. 6. Dominio de la lengua española.

Solicitud: 1. Carta del candidato dirigida al Secretario Academico del IB-UNAM con una detallada exposicion de motivos. 2. Curriculum vitae completo y actualizado; no es necesario incluir en esta fase la documentacion probatoria completa, pero si los datos de contacto y PDFs de publicaciones (maximo cinco) que, a juicio del solicitante, sean las mas importantes de su trayectoria profesional. 3. Sintesis del plan de trabajo anual que desarrollaria como primera responsabilidad en el IB-UNAM, de ser contratado (5 cuartillas maximo). 4. Una carta

— / —

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

---

UNebraska Lincoln DirectorBiologicalSciences

Director, School of Biological Sciences, University of Nebraska-Lincoln.

We are seeking an extraordinary individual to serve as Director of the School of Biological Sciences at the University of Nebraska-Lincoln (UNL), a public land grant research university and member of the Big 10/Committee on Institutional Cooperation, with a total enrollment of over 25,000 students. The School of Biological Sciences (SBS) is part of the College of Arts and Sciences, and plays a central role in undergraduate and graduate education and research at UNL. SBS faculty attract $12 million annually in competitive extramural research support, primarily from NIH and NSF. SBS has over 500 undergraduate majors and nearly 80 graduate students. Our 44 faculty members pursue research across the full spectrum of biology from molecules to ecosystems, and theory to empiricism. Research by SBS faculty members is highly collaborative, and benefits from strong linkages with other campus units.

We seek a Director who will promote faculty collaboration and integration across levels of biological organization - from genes, cells, and physiology through organisms to populations, communities, and ecosystems - and between biology and other STEM and non-STEM disciplines. The Director will provide strategic leadership and vision to promote SBS excellence in research, education, and outreach; will effectively manage the School's resources; will be instrumental in fund raising and alumni relations; and will play a key role in developing strong relationships between SBS and other units across the campus and the university system.

UNL is committed to achieving academic excellence and continued growth and development within the Life Sciences. The successful candidate will be a dynamic individual with outstanding scientific credentials, a commitment to quality education, and the desire, ability, and vision to lead the School. Candidates for this position must have a PhD; an outstanding record, including accomplishments as a scientist, educator, and in service to their institution; an understanding of the strengths and opportunities offered by a School encompassing the breadth of biology; and demonstrated commitment to excellence. Candidates must qualify for the rank of Professor with tenure. Candidates with research interests in any recognized biological discipline will be considered. The successful candidate will receive a competitive salary and start-up package.

Additional qualifications include: proven success in academic leadership in the context of shared governance and transparent decision-making; excellent communication skills; an understanding of opportunities and challenges in the current funding climate; an interest in working with the university foundation, donors, and alumni to support fund raising; an appreciation of the SBS teaching mission and an awareness of the importance of innovation in instruction; a commitment to diversity; and experience managing financial and human resources.

Information about the department can be found at http://www.biosci.unl.edu . For consideration, applicants must complete the on-line Faculty/Administrative form and submit application materials at http://employment.unl.edu, requisition F_160169. Application materials should include a cover letter describing administrative experience and philosophy; a curriculum vitae with a full list of publications and a summary of past, current, and pending research support; the names of three references; and brief statements of research, educational, and service interests. Inquiries regarding the position or the application process should be directed to: BioSciDirectorSearch@unl.edu, or SBS Search Committee Chair, College of Arts and Sciences, University of Nebraska-Lincoln, 1223 Oldfather Hall, Lincoln, NE 68588-0312 (Fax: 402-472- 1123).

Review of applications will begin November 14, 2016 and continue until the position is filled.

The University of Nebraska-Lincoln is committed to a pluralistic campus community through affirmative action, equal opportunity, work-life balance, and dual careers. See http://www.unl.edu/equity/notice-nondiscrimination . cmeiklejohn@gmail.com

UOklahoma ResAssist Bioinformatics

Title of Position: Assistant Research Professor

University of Oklahoma's Laboratories for Molecular Anthropology and Microbiome Research (LMAMR.ORG) is seeking an Assistant Research Professor | Adjunct Lecturer. LMAMR is an NIH and NSF funded leader in anthropologically focused microbiome research. The position requires PhD Degree and five years of experience in bioinformatics with experience working in the area of NGS and metagenomics. Experience with programming and shell scripting languages Perl or Python and R is required, with the addition of C or C++ preferred. The Research Professor's primary effort will be working within currently funded projects that study human microbiome variation; there will be opportunities for independently lead research. Salary is $75k plus fringe.

Start date: Position open until filled

Inquiries and applications (CV and three references) directed to Dr. Cecil M. Lewis (cmlewis AT ou.edu) with "Assistant Research Professor | Adjunct Lecturer" in the subject line.

OU is a Carnegie Very High Research institution that comprises three campuses. The University was established in 1890 and enrolls over 30,000 students and more than 2600 full time faculty. It ranks first among all universities in the number of National Merit Scholars enrolled and has developed an award-winning Research Campus, contiguous to the Main Campus, that houses more than a dozen private companies, several Federal agencies, and numerous research programs in a unique synergistic ecosystem. More than a million square feet of new, fully-occupied space now exists on the Research Campus, with the latest additions including a Radar Innovations Laboratory, Life Sciences Complex, and an Innovation Hub that will open in about a year. Norman, with a population of 110,000 has a vibrant arts community with outstanding public schools and a variety of recreational resources. It was ranked #6 among the best places to live by CNN/Money Magazine on America's best small cities.

Located in Norman, Oklahoma, University of Oklahoma's Laboratories for Molecular Anthropology and Microbiome Research (LMAMR.ORG) specializes in anthropological genomics and metagenomics. Current projects include characterizing the ancestral state of the human metagenomics using extraordinary biological samples from traditional indigenous communities, non-human primates, and archaeological "ancient" materials. Our labs are located in the SRTC (http://srtc.ou.edu/index.php), a newer building with several research groups working in environmental genomics (e.g., http://ieg.ou.edu/). Our building also houses part of OSCER, OU's supercomputer (http://www.oscer.ou.edu/). This broad, multidisciplinary research and education consortium is well situated on OU's award winning Research Campus (http://urc.ou.edu/video).

The University of Oklahoma is an Equal Opportunity Employer. Protected veterans and individuals with disabilities are encouraged to apply.

"Lewis, Cecil M. Jr." <cmlewis@ou.edu>

URochester Evolution

Faculty Position in Evolution, Ecology, Genetics, and Genomics at the University of Rochester

The Department of Biology at the University of Rochester (http://www.rochester.edu/College/BIO/index) invites applications for a faculty position (open rank) in evolution or ecology. We are seeking candidates that extend our program in Evolution, Ecology, Genetics, and Genomics (http://blogs.rochester.edu/EEB/). Candidates working with systems and/or approaches not currently represented in our group are particularly encouraged to apply.

Candidates with a strong record of accomplishment should upload application materials to our online application system (https://www.rochester.edu/faculty-recruiting/positions/show/4382). Complete applications include: a CV; a statement of research interests/plans; pdfs of three publications; and a statement of teaching experiences and interests. Instructions for supplying three letters of recommendation are provided on the application website. Review of applications will begin December 1st and continue until the position is filled.

The University of Rochester is an Equal Opportunity Employer, has a strong commitment to diversity, and actively encourages applications from candidates from groups underrepresented in higher education. EOE Minorities / Females / Protected Veterans / Disabled

http://www.rochester.edu/College/BIO/index http://blogs.rochester.edu/EEB/ https://www.rochester.edu/faculty-recruiting Amanda M. Larracuente, PhD Assistant Professor University of Rochester Department of Biology 343 Hutchison Hall Rochester, NY 14627 alarracu@bio.Rochester.edu<mailto:alarracu@bio.Rochester.edu> 585-273-1693 (office) http://blogs.rochester.edu/larracuente/ "Larracuente, Amanda" <alarracu@UR.Rochester.edu>

USussex EvolutionBehaviourEcol

The School of Life Sciences at the University of Sussex wishes to appoint an outstanding individual in the area of Evolution, Behavioural Biology and Ecology who will establish an internationally recognised research programme to complement existing activities in the School. The School is at the forefront of research in the biological sciences in the UK, coming in the top 10 in the REF 2014, with an impressive profile across a broad range of subjects; particular strengths include Conservation Biology, Evolutionary Biology, Neuroscience, and Genome Damage and Stability (seehttp://www.sussex.ac.uk/lifesci/research). We have state of the art facilities for microscopy and analytical chemistry, as well as access to field sites in the South Downs National Park. The appointment will be in the Reader or Professorial range, depending on qualifications and experience, applicants should clearly state which post they are applying for.

The appointee will be expected to offer teaching according to their expertise. The School has a vibrant PhD programme, and its taught B.Sc. and M.Sci. Degrees include Biology, Zoology, Environment and Ecology, Genetics and Neuroscience. M.Sc. and M.Res courses include Animal Behaviour, Evolution, Conservation and Neuroscience.

Potential candidates are encouraged make informal contact with the Chair of the Evolution, Behaviour and Environment subject, Prof. Daniel Osorio, (d.osorio@sussex.ac.uk) or the Head of the School of Life Sciences, Prof. Laurence Pearl FRS (Laurence.pearl@sussex.ac.uk).

Applications should be accompanied by a full CV, a statement of research interests and aspirations (not more than 4 pages), and the names of three academic referees.

The School is committed to equality and valuing diversity, and currently holds an Athena SWAN Silver Award. Applications are particularly welcomed from women and black and minority ethnic candidates, who are under-represented in academic posts in science and engineering at Sussex. The School of Life Sciences welcomes applications to academic posts from candidates who wish to work part-time or as job-sharers.

The University offers various schemes to provide real benefits to parents, these can be found athttp://www.sussex.ac.uk/humanresources/personnel/-

familyfriendlypolicies When submitting your application please ensure that you state the reference number for the position that you are applying for on the front page of the application form.

Adam Eyre-Walker Professor of Biology School of Life Sciences University of Sussex Brighton BN1 9QG

a.c.eyre-walker@sussex.ac.uk

Adam Eyre-Walker <a.c.eyre-walker@sussex.ac.uk>

VirginiaTech InfectiousDiseaseDynamics

Infectious Disease Dynamics in the Context of Global Change

As part of a new university-wide emphasis on Global Systems Science, Virginia Tech is hiring five faculty members in the area of infectious disease across four colleges. The Department of Biological Sciences (www.biol.vt.edu) in the College of Science invites applications for a tenure-track faculty position in the area of infectious disease dynamics and global change. The appointment is expected to be at the rank of assistant professor, but senior applicants will be considered. We seek a scientist who uses predominantly computational approaches to address how global change from environmental or anthropogenic sources influence infectious disease dynamics. Potential research questions may include, but are not limited to, the effects of global change on population and community dynamics of pathogens, vectors, and hosts; within-host dynamics between microbes and the immune system as a result of anthropogenic activities; evolutionary dynamics of disease-causing agents in response to changing selection pressures; and coevolutionary interactions between pathogens and their hosts/vectors.

The successful candidate's research should complement existing strengths in our department and university in microbiology, disease ecology, ecological modeling, and computational biology. The faculty member in this position is expected to help establish and grow the new Global Systems Science Destination Area (http://provost.vt.edu/destination-areas/-da-global-systems.html). Opportunities to work with university-level programs such as the Global Change Center (http://www.globalchange.vt.edu/) as well as the Interfaces of Global Change (IGC), the Genetics, Bioinformatics, and Computational Biology (GBCB), and Integrated Microbiology (IMP) graduate programs are also encouraged.

Building on its motto of Ut Prosim (that I may serve), Virginia Tech is dedicated to InclusiveVT–serving in the spirit of community, diversity, and excellence. Virginia Tech actively seeks a broad spectrum of candidates to join our community in preparing leaders for the world. Applicants should submit a cover letter that includes a brief statement of how they can contribute to promotion of diversity and inclusion on the Virginia Tech campus, a curriculum vitae, and separate statements of research (3 page limit) and teaching interests (2 page limit) emphasizing career goals; they should also arrange for three letters of reference using our on-line system (https://listings.jobs.vt.edu/postings/70723). Inquiries about the position should be directed to the chair of the search committee, Dr. Dana Hawley (hawleyd@vt.edu). Review of applications will begin on Dec 1.

Dana M. Hawley Associate Professor Department of Biological Sciences Virginia Tech Derring Hall Room 4036 1405 Perry Street Blacksburg, VA 24061 (540) 231-8946 HawleyD@vt.edu

Dana Hawley <hawleyd@vt.edu>

WashingtonStateU Vancouver LabTech PlantMicrobeEvol

The Porter lab at Washington State University, Vancouver, is recruiting a research technician. Our lab explores the evolutionary and ecological dynamics of plants and their microbial symbionts to test fundamental theory about cooperative interactions. We focus on environmentally acquired symbioses between plants and microbial mutualists such as nitrogen-fixing rhizobium bacteria. Our research projects range from the field, to the lab to the greenhouse and integrate approaches from quantitative genetics, ecological genetics, and genomics.

The technician will be based at WSUV and will participate in a collaborative multi-year NSF-funded project with the Friesen lab at Michigan State University to investigate evolutionary and ecological shifts in plant-symbiont mutualism during plant invasions. The Porter lab supports diverse projects ranging from the importance of microbes to plant adaptation, to quantifying natural selection on cooperation (https://labs.wsu.edu/-stephanie-porter/)

The technician will have a flexible start date and the appointment will be for one year with a second year of employment contingent on satisfactory performance in year one. WSUV is a vibrant, rapidly growing institution located in the greater Portland/Vancouver metropolitan area, near the Columbia River, Cascade Mountains and coastal ocean, and as such offers an exceptional quality of life.

Interested candidates should send a cover letter, resume, and unofficial copy of transcripts to stephanie.porter@wsu.edu. Please include the words “Lab tech application” in the subject line of your email.

Stephanie S. Porter Assistant Professor, School of Biological Sciences Washington State University, Vancouver

Stephanie Porter <stephanie.porter@wsu.edu>

YaleU ResAssoc Evolution

Our labs focus on both ecology and evolution (we're only housed in the Forestry and Environmental Studies dept - these are not our areas of research).

—-

The Research Associate will support a newly renovated, shared lab facility serving three ecologists on the faculty of the Yale School of Forestry & Environmental Studies. The investigators are pursuing research topics aimed at understanding functional mechanisms underlying ecological patterns. They work on a range of taxa including insects, amphibians and plants and they use both laboratory and field based experimentation in their research programs. The Research Associate will officially report to one of the investigators but will have responsibilites across the research programs of all three. This position will provide the incumbent with the opportunity to learn new techniques and to investigate xylem structure and function, the dialogue between ecosystem and population level processes, or the role of landscape conversion in the reproductive ecology of amphibians.

For more information and how to apply: http://newhaven.jobing .com/yale-university/rsrch-assoc-sch-of-for-env-stu

Essential Duties 1. Recommends the design and implementation of procedures and protocols under the direction of a higher-level authority. 2. Investigates, analyzes, and reaches preliminary scientific conclusions related to research planning 3. Ensures data results are compiled, analyzed, and presented properly. 4. Analyzes, develops and interprets scientific results. Maintains clear documentation of results. Prepares scientific reports and papers for research proposals and published reports. 5. Performs independent research and laboratory techniques and participates in experimental research planning. 6. Interacts with internal contacts including the PI, research assistants, graduate students, Radiation Safety and Biological Safety officers, and Animal Care personnel to discuss and evaluate research results and to ensure the smooth and safe operation of the laboratory. 7. Interacts with external contacts such as researchers at other institutions, staff at biotechnology and reagents companies to consult on research methods and to keep abreast of product information and developments. 8. May perform other duties as assigned.

Required Education and Experience Master's Degree in a scientific discipline and one year experience or an equivalent combination of education and experience.

Required Skill/Ability 1: Ability to multi-task effectively with demanding time constraints; ability to work well under pressure with conflicting demands, deadlines & emergencies. Strong attention to detail & well-developed organizational, analytical, and interpersonal skills.

Required Skill/Ability 2: Demonstrated ability to work well in a team environment with co-workers, faculty, and others; ability to work independently as well as part of a team. Independent work includes time spent alone at remote field locations. References must indicate an excellent attendance record.

Required Skill/Ability 3: Demonstrated willingness to absorb incidental responsibilities and contribute to special projects in order to ensure smooth functioning of the laboratory. Research experience with one or more of the following taxa: insects, herps (amphibians and reptiles) or vascular plants.

Required Skill/Ability 4: Ability to track work and follow up when necessary. Demonstrated editing and proofreading skills. Superior arithmetic statistical skills. Proficiency with email, MS Office programs, and Adobe products, especially strong knowledge of Excel, Word, Access, Outlook, PowerPoint, and Photoshop

Required Skill/Ability 5: Ability to compile database extractions. Proficiency with document formatting, editing & design. Highly developed & demonstrated customer service skills, both in person & on the telephone. Excellent oral and written communication skills. Ability to problem-solve and exercise independent judgment.

Preferred Education, Experience and Skills: Master's degree in Ecology, Physiology or associated environmental sciences.

Weekend Hours Required? Occasional

Evening Hours Required? Occasional

Drug Screen No

Health Screening No

Background Check Requirements All candidates for employment will be subject to pre-employment background screening for this position, which may include motor vehicle, DOT certification, drug testing and credit checks based on the position description and job requirements. All offers are contingent upon the successful completion of the background check. Click here

< http://www.yale.edu/hronline/careers/screening/faqs.html >for additional information on the background check requirements and process.

Posting Disclaimer The intent of this job description is to provide a representative

— / —

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

Other

AcademicMentoringSurvey

Post Title: Participate in a survey on academic mentoring

Post Text: Hello! I am recruiting scientists at all levels and in any STEM field to participate in an anonymous online survey about mentoring. The mentor-mentee relationship is a central component of scientific training. I am interested in what kind of training mentors receive and the impact mentoring has on both mentor and mentee. This survey is open to anyone who has participated in a mentoring relationship, as either mentor or mentee, in an academic setting. The goal of this survey is to document how mentoring affects STEM academics and to propose training methods based on responses. Participation is anonymous but respondents are invited to contact me after participating at sierra.lovestowell@colorado.edu, to receive or share additional information. You can find the survey here: https://cuboulder.qualtrics.com/SE/?SID=-3DSV_5j6ww9dQyqDyHOd. Please share the link with others you think might be interested. Thanks for considering!

Sierra Love Stowell <lovestow@colorado.edu>

CEBA CallProposals AmazonBiodiversity

Annual call for proposals CEBA 2017, French Guiana

The CEntre for the study of Biodiversity in Amazonia (CEBA) is a Laboratory of Excellence based in French Guiana aimed at fostering knowledge on terrestrial biodiversity. The Labex CEBA aims to coordinate research capacity in France on the topic of Amazonian terrestrial biodiversity, and to reinforce collaborations with South American and other international partners. Details are available at http://www.labex-ceba.fr The Labex CEBA opens an annual competitive call for proposals to encourage innovative research on biodiversity in French Guiana. Projects will be evaluated by the Scientific Board and by external referees. The submission deadline is February 10^th, 2017. To access the call for proposals form: http://www.labex-ceba.fr/en/appel-a-projets-annuel-ceba/ Amaia IRIBAR-PELOZUELO

Chargee de coordination scientifique CEBA

Laboratoire Evolution et Diversite Biologique UMR 5174 Universite Paul Sabatier, bat 4R1, bureau 124 118 route de Narbonne, 31062 Toulouse Cedex 9 - France

tel : + 33 (0)5 61 55 64 95 fax : + 33 (0)5 61 55 73 27

link: www.labex-ceba.fr Amaia Iribar-Pelozuelo <amaya.pelozuelo@univ-tlse3.fr>

CORBEL OpenCall Infrastructure

I'm contacting you on behalf of the H2020 project CORBEL (www.corbel-project.eu). This cluster project of 11 research infrastructures aims to support European researchers from academia and industry and their advanced interdisciplinary research projects by establishing a platform of aligned customised services. Beginning of October we launched an Open Call for research projects from academia and industry; selected researchers will then have the unique opportunity to gain open access to state-of-the-art technologies and services offered by these research infrastructures across biological and medical sciences. In order to distribute this Open Call to the scientific community, I would like to ask whether it is possible that you communicate the announcement to your members.

A brief summary of the CORBEL Open Call: CORBEL - Coordinated Research Infrastructures Building Enduring Life-science services - is an EC Horizon2020 project uniting 11 Biological and Medical Science Research Infrastructures (RIs). In CORBEL, the participating RIs expand their cooperation in order to harmonise researchers' access to their cutting-edge technologies and services by establishing a sustainable platform of aligned services that will enable faster admission to and a wider portfolio of technologies and services to boost research projects from academia and industry.

The CORBEL Open Call invites researchers to apply to access technologies and services from more than 15 facilities from eight different research infrastructures across Europe. Selected projects will be allocated to so-called Access Tracks and gain unprecedented opportunities to utilise a wide range of high-end technologies and services. These include state-of-the-art offers from the fields of advanced imaging, biobanking, curated databases, marine model organisms, mouse mutant phenotyping, screening and medicinal chemistry, structural biology as well as systems biology.

Projects will be supported at every stage, with CORBEL project managers on hand to help scientists navigate between different service providers and exploit the full potential of the offers available. The CORBEL consortium already launched its Innovation Office, consisting of a well-experienced team dealing with the special needs of industry (e.g. regarding IP issues, confidentiality agreements).

Learn more about the CORBEL Open Call by visiting our website (http://www.corbel-project.eu/1st-open-call.html).

Deadline: 30 November 2016

Best regards, Manuela Schuengel

Dr. Manuela Schüngel Leibniz Institute DSMZ-German Collection of Microorganisms and Cell Cultures Inhoffenstraße 7 B 38124 Braunschweig Germany

E-Mail: Manuela.Schuengel@DSMZ.de http://www.dsmz.de http://www.mirri.org http://www.corbel-project.eu Director: Prof. Dr. Jörg Overmann Local court: Braunschweig HRB 2570 Chairman of the management board: RD Dr. David Schnieders

DSMZ - A member of the Leibniz Association (WGL) www.leibniz-gemeinschaft.de

CrowdFunding InsecticideEffectBees

Dear list, We are a team of three Postdoctoral Researchers working in the Department of Biological Sciences at North Dakota State University. We are interested in how insecticide exposure may affect nest construction in the alfalfa leafcutter bee, a critical pollinator used in many agricultural crops. We are raising funds through a crowdfunding campaign in order to pay for an undergraduate assistant this summer: https://experiment.com/beenesting . This work will have critical implications for the management of the alfalfa leafcutter bee. Furthermore, it will help lay the groundwork for using nest architecture to study the behavior and fitness of other solitary bees, including crop pollinators such as mason bees .We hope this research will help us better understand how insecticide exposure affects solitary bee fitness, as indicated by nest size and structure, and elucidate important gaps between individual and population level dynamics.

You can find more information on the Bee Grant Challenge that this project is part of here: https://experiment.com/grants/bees. We are already funded at 20% through this platform and have until December 8th to reach our funding goals.

We sincerely appreciate any help with our campaign. If you are unable to donate, please consider sharing this project with your colleagues. Every little bit helps! Best,

Raphael Royaute Bryan Helm Rachel Mallinger

-- Raphaël Royauté Postdoctoral Fellow Dept Biological Sciences North Dakota State University Evolutionary Ecology of Variation Lab 701-231-8993 < https://sites.google.com/site/neddochtermann/ >

raphael.royaute@gmail.com

Crowdfunding UndergroundEvolution

Title: Challenge grant campaign "groundwater and caves" needs your support

Dear EvolDir community: This is to alert you of the ongoing challenge grant crowdfunding campaign "groundwater and caves" which was launched last week: https://experiment.com/grants/groundwater/ The initiative features 11 projects, most of them with significant ecological or evolutionary components. Challenge grants offer prizes to supplement existing crowdfunding campaigns. Partway through the campaigns, the project with the highest number of backers will receive an additional $500. There are two runners-up prizes of $200 each. So if you feel strongly for one of the projects you can help by even modest amounts of contributions, simply by boosting the backer numbers. Of course, any contribution to science will be greatly appreciated by any of the projects.

Other ways to help includes helping the campaign to snowball further by sharing with friends, enthusiasts, or posting on social media like facebook, twitter, etc...

Further questions can be directed to: Dr. Markus Friedrich Department of Biological Sciences Wayne State University 5047 Gullen Mall Detroit, MI 48202

office: BSB 3117 office phone: 313 577 9612 lab phone: 313 577 5120 http://friedrichlab.googlepages.com/home Markus Friedrich <friedrichwsu@gmail.com>

Crowdfunding UndergroundEvolution 2

Hello everyone,

My apology to everyone who received this before. And my apology to anyone who received this before and already backed!

No reason to back out, quite the opposite...The newest backer numbers reveal that we are three backers short from garnering the $500.00 award of the challenge grant campaign by experiment.com with the theme "groundwater and caves". As you may remember, the project with the highest number of backers receives an additional $500 and there are two runners-up prizes of $200 each.

Unlike last week today, the cave beetle campaign ranks not only solidly at second place but just three backers away from first place in this competition: https://docs.google.com/-spreadsheets/d/1VnINc2gx0gYqvyjr5Abi qSuetU1H4mzOHIRk_nLCnuw/edit?usp=sharing So things heated up quite a bit. As stated before, it doesn't need to be a big amount. A single dollar does already make a huge difference.

And spreading the news among nature enthusiasts is equally important and appreciated.

Three new backers may be all we need in the next 36 hours. That's bc the winners of the challenge grant will be announced at 6pm EDT on November 23rd. Clearly, we can do this.

One more time for your convenience: https://-experiment.com/cavebeetles Let me know in case you have questions or comments or suggestions of science social media outlets to put this on!

Thanks much in advance for your time and effort!

Dr. Markus Friedrich Department of Biological Sciences Wayne State University 5047 Gullen Mall Detroit, MI 48202

office: BSB 3117 office phone: 313 577 9612 lab phone: 313 577 5120 http://friedrichlab.googlepages.com/home Markus Friedrich <friedrichwsu@gmail.com>

ExtractingDNA BirdBlood

Dearlist members,

Iwas wondering if anyone had any suggestions for getting the best DNA yield from bird blood samples stored in ethanol?

Itypically extract DNA using a slightly modified Qiagen DNeasy Blood and Tissue protocol. Our samples are usually stored in Queen's Lysis buffer so the yield is high and the sample digestion step is straightforward.

Wouldbe great to hear the experiences of others and I'll happily post responses to the list.

Manythanks in advance

Mark

MarkRavinet Researcher CEESOslo mark.ravinet@ibv.uio.no

mark.ravinet@ibv.uio.no

ExtractingDNA BirdBlood answers

Dearll,

Manyhanks for the excellent replies to my query on extracting DNA from ethanol stored bird blood samples. They were extremely helpful and I have copied them below to redistribute to the list as promised!

Allhe best

Mark

Markavinet Researcher CEESslo mark.ravinet@ibv.uio.no

*** Iave had amazing results using the Phenol:Chloroform extraction method. I have been doing this for over 10 years and always end up with so much DNA I need to keep diluting it! I do an ethanol precipitation at the final step and re suspend my pellet in water.

*** Iave always used the proteinase K/phenol:chroloform protocol, and is quite good (better than any kit I have ever tried). You just need to clean the blood from the alcohol with some TE before starting

*** When have to deal with avian blood samples in ethanol, I always have two phases clearly separated in my tubes. Iemove the most ethanol I can, then take blood cells (with fine tweezers for example) and put them in the new tube I will use for extraction. I let this tube open for a few minutes to evaporate ethanol (which could interfere with the extraction steps). Then use the Qiagen DNeasy Blood and Tissue standard protocol (for nucleated blood cells

*** Iave used two protocols for this. Usually you get the highest amount with a phenol-chloroform protocol. The problem I faced there was that I had difficulties getting the DNA into solution again. You'll usually get this with high molecular weight DNA. However, this was not a problem for Illumina sequencing for the few birds for which we used this DNA. For most samples I then used a modified protocol of the DNeasy Blood and Tissue protocol. What proved important with this was to do the proteinase digest in double the volume and to ensure the blood is properly digested. For this, I usually put one volume of pK at 56^{o}C an hour or two before leaving for the night, and then added another volume just before leaving and leaving the digestion run at 37^{o}C overnight. If there was still some coagulate left in the morning, I added yet another volume of pK to 56^{o}C until it was digested.

*** Ineneral, for high yield AND high molecular weight DNA, I usually go for phenol-chloroform extraction, as it is efficient and can render really good quality (if youre careful). Therotocol is optimized for blood collected in SET buffer, but Ive modified it for samples stored in EtOH, i.e. picking out blood, quickly letting the EtOH evaporate, and putting it in SET to proceed with the protocol. Its important to only letting the EtOH evaporate rather briefly, or the blood will turn rock solid if it is left to dry for long. Now were on details, but some blood samples form chunks similar to coarse sawdust: these samples are great and simple to handle, pieces can easily be picked out with a toothpick or similar. Some blood samples instead behave as more or less dissolved, and these are a bit trickier. I usually centrifuge them down properly, and use a mini shovel (I really have no idea about what the tool is called, but something spoonish that is small enough to reach the bottom of a tube) to scoop up blood along the wall of the tube. In either case, just let the blood evaporate in the air, or gently press a tissue against the sample to suck up ethanol (especially for the latter type of sample).

Now dont remember the lysis step in the B&T kit, but if you want to continue with that just put the blood in the whatever-buffer-is-used-for-lysis and continue. This is at least what I did some five years ago for some 200 samples used for RADseq, with reasonably good results.

Therere also further optimizations that can be made for obtaining ridiculously long DNA molecules, such as picking out the precipitated DNA cloud from the ice-cold EtOH using a glass staff etc. Let me know if youre interested in a description of this and the subsequent washing.

(And,s you will also know, if you are going to RNase A treat your samples, do it during the lysis step to avoid the risk of DNA degradation by the enzyme [or make sure to boil it before use, as DNase most often co-purifies with the RNase].)

*** Wetore most of our blood samples in ethanol. It doesn't matter what extraction method you use: chelex, kit, phenol=chloroform. The main thing is you need all the ethanol to evaporate before you start the extraction. We typically take 10 ul of blood ethanol mix and put it in a 1.5 ml tube. Leaving the lid on the tube open, put the rack in an incubator (37-55C) for 15-30 min or leave it on the bench. The ethanol will take longer to evaporate at room temp, but both work.

*** Iope everything is going well with you. I have seen your post in evoldir. Is it because you have experienced problems with the DNA extraction? It is usually very straightforward as well. I usually pick up a piece of blood with a wood dental stick (but it should be flat). See for instance this

— / —

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

---

Hokkaido VolResAssist SeabirdBehaviour

Behavioural Ecology of seabirds by using bio-logging techniques.

Location: Teuri and Rishiri Islands, Hokkaido, Japan. Duration: 2 months. Job Type: Volunteer.

We use bio-logging devices (e.g. geolocators, GPS recorders) on two species (Rhinoceros Auklets and Black-backed Gulls) to study behavioural ecology of colonial seabirds. Most work will involve assisting a long-term monitoring project and behavioural studies of post-doc fellows and graduate students from Hokkaido University coordinated by Yutaka Watanuki, with the daily monitoring breeding birds and their chicks, and the deployment and retrieval of tracking devices. It will also involve entering data collected in the field into databases.

We are looking for an enthusiastic, hardworking young biologist to work as a voluntary Research Assistant to help with our seabird research on Teuri/Rishiri Island, Hokkaido, Japan, between May 1st and June 30th 2017. Previous experience in the field or in harsh conditions is desirable, but not essential. Work on Teuri/Rishiri requires long hours (with some work at night and at dawn) spent in a cold and wet environment and considerable manual work. A successful candidate should be able to work independently and have a reasonable level of fitness. Planning to embark on further research degrees in the future would be preferable. It is also important that the assistant feels comfortable sharing sometimes crowded accommodation with a number of colleagues over long periods of time, and can cope with the occasional untidiness inevitably associated with fieldwork.

Unfortunately we cannot provide a stipend but accommodation (shared and basic) on Teuri/Rishiri will be covered. However, the project is a great opportunity to gain valuable experience in modern field ornithology, with bio-logging techniques. There will also be opportunities for the assistant to learn some analytical techniques applied to animal movement data or chemical analytical techniques in the wet-lab. Teuri/Rishiri has mobile coverage and some access to Internet, however movements to and from the mainland are limited because of unpredictable wind conditions. Teuri/Rishiri is an inhabited island and there are small restaurants and grocery stores. There is a small community of other researchers, ringers and volunteers at our shared accommodation.

If you are interested, please email a CV and a statement of interest and arrange for two letters of reference to be emailed to akikosho@gmail.com (with ywata@fish.hokudai.ac.jp in cc). The deadline for submitting applications (including reference letters) is the 10th January 2017. We will interview the shortlisted candidates (on Skype) shortly after and we expect to make a decision by late January.

Akiko Shoji <akikosho@gmail.com>

Instrumentl grantOpportunities

Hi EvolDir-ers,

Instrumentl is the place to find grants if you're in the fields of biology, ecology, evolution, and natural resources. And we just launched a new plan you can use entirely for free.

Try it out yourself at: www.instrumentl.com < https://www.instrumentl.com/?utm_source=-3DFreemium_Launch&utm_campaign=-3DTest_Campaign_Name&utm_medium=-email&utm_content=Listserv_evoldir >

Best,

Katharine

PS - Questions? please email: katharine@instrumentl.com

Katharine Corriveau Co-founder Instrumentl (510) 684-4978

Follow us on Facebook < https://www.facebook.com/-Instrumentl > and Twitter < http://twitter.com/-BeInstrumentl > Visit us at: www < http://-goog_1148219688 >.instrumentl.com

katharine@instrumentl.com

InternalFertilisation EggLayingFish

"Dear All

Internal fertilisation in an egg-laying fish.

I would be interested to hear whether anyone has ever recorded, or is aware of any records in the literature of, *fertilised* embryos (ie not parthenogenetic or hermaphroditic) inside a female of a normally egg laying fish species.

Best wishes

Andrew MacColl"

Associate Professor of Evolutionary Ecology School of Life Sciences University of Nottingham University Park Nottingham NG7 2RD, U.K.

Tel: +44 115 951 3410

http://ecology.nottingham.ac.uk/-AndrewMacColl/index.php Andrew Maccoll <Andrew.Maccoll@nottingham.ac.uk>

MaxPlanckInst Seewiesen Vol SexualSelectionParrots

MaxPlanckInst_Seewiesen.SexualSelectionParrotsVolunteers

Where: Tenerife, Spain When: mid-January until end of August (at least 2 months, but preferable for the entire period) What: Volunteer field assistants - Parrot sexual selection

The Department of Behavioural Ecology and Evolutionary Genetics at the Max Planck Institute for Ornithology in Seewiesen, Bayern, Germany (see http://www.orn.mpg.de/2622/Department_Kempenaers), is seeking three volunteers to start working mid-January and until the end of August 2017 (the position requires a minimum of 2 months, but preferable for the entire period).

The volunteers will assist in the collection of courtship displays and egg-laying data. This work would be part of a project that aims to understand sexual selection in parrots of the world. The work will be done with captive animals that are held in the facilities of the Loro Parque Fundacion, located in Tenerife, Spain.

Work will include: - recording courtship displays - following up reproduction (sexual displays, mating, and egg laying) - maintenance of electronic equipment - setting up experimental equipment - data collection, entry, and management

Successful candidates should have experience with video-recording equipment. Experience with monitoring animals is desirable. Applicants should also be highly motivated and well organised, with capabilities of working both in a group and independently. Work will be 5-6 days per week.

The working language at the Institute is English, so good knowledge of the language is required. A basic working knowledge of the Spanish language would be advantageous. Eligibility is sadly restricted to UK and EU students. The Max Planck Institute for Ornithology employs a dynamic, dedicated, and international group of researchers who are focused on exploring the fields of evolution, ecology, genetics, and neurobiology.

Benefits will include accommodation and travel-related expenses in Tenerife.

Please apply (including your CV and cover letter) via email to lcarballo@orn.mpg.de. Deadline: 06 January 2017 or until the positions are filled.

Luisana Carballo Department of Behavioural Ecology and Evolutionary Genetics Max-Planck-Institute for Ornithology Eberhard-Gwinner-Straße, House 8 82319 Seewiesen Germany

“L. Carballo” <lcarballo@orn.mpg.de>

Nouragues TravelGrants

Nouragues Travel Grants Program 2017

The Nouragues annual call for proposals is aimed at facilitating access to the Nouragues station for scientists of all research fields. Graduate students, post-doctoral researchers, and established scientists may apply.

Submitted proposals will be evaluated by a Science Advisory Board and selected based on their excellence, the quality of expected publications, and the feasibility of the project. The grants will not exceed 10,000euro in total, and will be for a duration of one year. Reapplications will be evaluated based on the achievements of the previous projects. Grant recipients will be expected to provide a scientific and financial report one month after the end of the fieldwork. They will also be expected to contribute to the dissemination of knowledge in French Guiana, via participation in outreach programs of the Nouragues Natural Reserve. In 2017, experimental projects and projects related to the COPAS instrument (Canopy Operational Permanent Access System) will be considered in priority.

Deadline for application: February 10th, 2017. For further information: http://www.nouragues.cnrs.fr/ – Amaia IRIBAR-PELOZUELO

Chargee de coordination scientifique CEBA

Laboratoire Evolution et Diversite Biologique UMR 5174 Universite Paul Sabatier, bat 4R1, bureau 124 118 route de Narbonne, 31062 Toulouse Cedex 9 - France

tel : + 33 (0)5 61 55 64 95 fax : + 33 (0)5 61 55 73 27

link: www.labex-ceba.fr Amaia Iribar-Pelozuelo <amaya.pelozuelo@univ-tlse3.fr>

Phyloseminar LauraHug Dec13

Next talk:

Microbial diversity through a total community sequencing lens Laura Hug University of Waterloo Tuesday, December 13, 2016, 10:00 AM PST

Total community approaches (omics) provide a blueprint of the microbial functions and community diversity within an environment. With genome-resolved metagenomics, this view can be refined, identifying an organism's specific contributions to pathways and processes as well as their interactions with other community members. This approach has led to a recent explosion of genome sequences for uncultured and uncharacterized microbial lineages, many with previously-unknown roles in biogeochemical cycles. My work explores the environmental importance of these novel organisms and the emerging view of the Tree of Life that stems from our new understanding of microbial diversity.

For more information on this talk, see http://-phyloseminar.org/ ematsen@gmail.com

Seeking GBS facilities

Dear Evoldir members

In our group we seek to use GBS of restriction-enzyme reduced genomes to find SNPs for population genetics of non-model organisms. We are aware of patent problems when using this technique, that's why I would like advice about facilities or companies that are adequately licensed and that offer the service of library preparation (with preliminary enzyme checking and selection) and sequencing. Infos about prices are also welcome

Thanks for your answers, I will prepare a post with them

Regards

Xavier Turon xturon@ceab.csic.es

–

Xavier Turon Dept. of Marine Ecology Center for Advanced Studies of Blanes (CEAB, CSIC) Accés a la Cala S. Francesc 14 17300 Blanes (Girona) Spain

E-mail: xturon@ceab.csic.es Phone: +34 972 336101 Fax: +34 972 337806 http://www.ceab.csic.es/ http://www.ub.edu/beb/english/invertebrates/turon/-turon.htm Xavier Turon <xturon@ceab.csic.es>

Software BuddySuite

Dear Evolution Community,

I am pleased to announce the release of BuddySuite, an open-source project for the manipulation and analysis of sequence, alignment, and phylogenetic tree data on the command line. These cross-platform, general-purpose, toolkits are implemented in Python and will streamline your day-to-day interactions with common file types (e.g., FASTA, GenBank, NEXUS, PHYLIP, Newick, and more).

Features include automatic detection and processing of records in any supported format, the ability to pipe data freely among the BuddySuite programs (and any other command-line program that reads/writes stdout), file format-agnostic wrapping of popular alignment and phylogenetic inference software, and sophisticated handling of feature annotations in rich formats like GenBank.

Over 100 tools have been written to date and each tool is fully documented in wiki format (https://github.com/-biologyguy/BuddySuite/wiki), complete with usage examples and a detailed explanation of all arguments.

Installation is easy with pip: $ pip install buddysuite $ buddysuite -setup

Alternatively, the GitHub repository can be cloned from https://github.com/biologyguy/BuddySuite If you run into any issues with installation or general usage, I would truly value the feedback.

Kind regards,

Steve Bond Visiting Fellow Computational and Statistical Genomics National Human Genome Research Institute National Institutes of Health

"Bond, Steve (NIH/NHGRI) [F]" <steve.bond@nih.gov>

StomatalTraitEstimationTool

Hello Plant Biologists, Paleoecologists, & Ecophysiologists & Evolutionary Biologists of the World!

I have been wrestling with various methods to automatically estimate stomatal density and stomatal pore size in my own research. With the help of a colleague in the computer vision world, we have identified a method that faithfully automates estimation of stomatal densities from Populus leaves.

In an effort to determine if public dissemination of such a tool is needed and would be welcomed by the community, I'd like to ask you to consider how this tool may impact your own research.

If you're interested in automatic stomatal estimation, please take a moment to visit the survey link provided below and answer a few questions.

https://goo.gl/forms/c3Lu7AOAaYDm0Snb2 Please only respond once and feel free to share this link with your colleagues and friends who may be interested.

Thanks very much for your time.

Sincerely,

Karl Fetter

Graduate Student Keller Lab Department of Plant Biology University of Vermont kfetter@uvm.edu

Karl Fetter <kfetter@uvm.edu>

SwissInstBioinform Seminar Nov23

Dear all,

We are pleased to announce the next speaker at the SIB Swiss Institute of Bioinformatics Virtual Computational Biology Seminar Series:

Henrik Kaessmann, ZMBH - Center for Molecular Biology, Heidelberg University, Germany The evolution of mammalian gene expression programs Wednesday 23 November 2016 at 16:00 - Genopode Auditorium C - UNIL campus

The seminar will be broadcast live for those unable to attend it physically (https://collab.switch.ch/sib-cbss/). For more information about these seminars as well as the upcoming speakers list and previous screencasts, please visit the SIB virtual seminar series webpage: http://www.sib.swiss/training/virtual-seminars-series Important: If you want to remain informed about our upcoming seminars, please subscribe to the dedicated mailing list:http://lists.isb-sib.ch/mailman/listinfo/sib-virtual-seminars Looking forward to seeing you all there.

Best regards, Diana Marek

*Diana Marek, PhD *Vital-IT - Training & Outreach * **SIB | Swiss Institute of Bioinformatics* Quartier Sorge - BÃ'timent Genopode - CH 1015 Lausanne - Switzerland t +41 21 692 40 77 - f +41 21 692 40 65 New email: Diana.Marek@sib.swiss www.vital-it.ch - www.sib.swiss/training

"Diana.Marek@sib.swiss" <Diana.Marek@sib.swiss>

TeachingWithData

Reminder: Announcing Two Faculty Mentoring Networks

The Ecological Society of America (ESA) and the Quantitative Undergraduate Biology Education Synthesis (QUBES) Project are inviting applications for two upcoming Faculty Mentoring Networks (FMNs). These online communities are professional development opportunities where participants work collaboratively to discover new teaching materials, pedagogical techniques, and quantitative content.

All faculty are welcome. We are actively seeking participation from faculty teaching at all undergraduate levels at diverse institution types and serving diverse student populations, including non-science majors.

Benefits to Participants in Both Networks

§Support for further development of pedagogical material focused on bringing research data into the biology/ecology classroom

§Access to peer mentors on lecture/classroom/lab effective tips and strategies in small group virtual meetings every two weeks

§Recognition as an ESA Education Scholar upon completion of all network requirements.

Check out this blog about the 2016 ESA Education Scholars (http://esa.org/fed/2016scholars/).

The Spring 2017 ESA Data Discovery FMN is seeking applicants who are interested in adapting existing Teaching Issues in Ecology and Evolution (TIEE) modules for use in their Spring 2017 courses. Faculty participants will implement two selected modules with a focus on providing students with the quantitative skillset needed to 'scale up' to large ecological datasets. This FMN will begin in January and run through the Spring semester. For more information on the selected modules and to apply, please visit https://qubeshub.org/groups/datadiscovery_2017. Application deadline has been extended to December 2nd.

Questions? Contact Gaby Hamerlinck at gaby.hamerlinck@bioquest.org.

The new DIG into Data for the Biology Classroom FMN is seeking applicants who have experience in bringing data-driven activities into the introductory biology or ecology classroom and are interested in further refining their own teaching modules or developing new ones. Our data partners include DryadLab and the National Ecological Observatory Network (NEON). As a group, participants in this network will work towards developing polished teaching resources suitable for submission as a teaching data set to a special issue of TIEE. Please visit the DIG data incubator group website for more details and to apply (https://qubeshub.org/groups/dig). Applications are due by December 2nd.

Questions? Contact Kaitlin Bonner at kbonner@sjfc.edu or Kristine Grayson at kgrayson@richmond.edu.

"kbonner@sjfc.edu" <kbonner@sjfc.edu>

Tjarno VolResAssist SeaweedFly

Chromosomal inversions and Evolution

Location - Tjärnö, Sweden

We study the seaweed fly (Coelopa frigida), which has one of the largest maintained chromosomal inversions in the animal kingdom (10% of the genome). This inversion is under strong selection resulting in strong heterosis in most known populations (generally more than 60% of individuals are heterokaryotypes) and a cline in the frequency of the inversion from the North Sea to the Baltic. Our group is investigating the natural factors that drive this cline, the genetic causes of heterosis, and the genetic signatures of selection on the inversion.

We are looking for 1-2 enthusiastic and motivated young biologists for internships (2-3 months) with our group. Candidates should have some research experience and be able to work somewhat independently. Successful candidates will get experience with fly culturing, field collections, and molecular lab work. Previous experience in a molecular lab is desirable.

Unfortunately, we cannot provide a stipend but accommodation and travel costs will be covered. Interns will be based at the Sven Loven Center in Tjärnö (http://loven.gu.se/english) a research station with an international group working on diverse topics.

Candidates MUST have demonstrated proficiency in English by one of the following: 1. Coming from an English speaking country, 2. Having completed courses taught only in English, or 3. Getting the minimum result necessary in an internationally ranked English test (see https://www.universityadmissions.se/en/All-you-need-to-know1/Applying-for-studies/English-requirements/Internationally-recognized-English-test/)

We will accept applications until January 1st 2017. Please send a CV, proof of English proficiency, and a statement of interest to emma.berdan@gu.se. Successful candidates will be notified mid-January.

"emma.berdan@gu.se" <emma.berdan@gu.se>

UNewSouthWales Vol ZebrafishEvolution

Job: UNSW_Sydney.Internship.EvolBiol Scientific Internship/Apprenticeship in Evolutionary Biology at i-deel, E&ERC, UNSW, Australia

Our lab (www.i-deel.org) is offering one scientific internship/apprenticeship (or volunteer position) for up to 10 months in 2017 to help conduct behavioural and physiological experiments on zebrafish. We are located at the Evolution & Ecology Research Centre (E&ERC) within the School of Biological, Earth and Environmental Sciences (BEES) at the University of New South Wales (UNSW), Sydney, Australia. The intern will be engaged in variety of scientific work (mainly, running zebrafish behavioural and metabolic experiments, helping in fish breeding and database management). We expect that the apprentice will learn essential skills as well as gain experience necessary for conducting their own projects. As such, an ideal candidate would be someone who plans to undertake a PhD in the future, within the fields of Evolutionary Biology, Ecology and Behavioural Sciences (i.e. someone with BSc or MSc). We will provide an allowance to cover accommodation and food (~up to AU$2000 per month).

Importantly, the intern needs to be an Australian or New Zealand resident. Please read our webpage to see what kind of research we conduct (www.i-deel.org). If you are passionate about our science and would like to join our team, please contact Daniel Noble (daniel.noble@unsw.edu.au) or Shinichi Nakagawa (s.nakagawa@unsw.edu.au) with your CV and a one page letter of motivation.

Dr Shinichi Nakagawa (Associate Professor / ARC Future Fellow) Deputy Director of Research, Evolution & Ecology Research Centre, EERC (Visiting Scientist at Garvan Institute of Medical Research) Room 568, Biological Sciences Building (D26) 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>

USussex FieldAssist WaspBehaviourEvol

Job: Two Field Assistants Required for Study of Social Behaviour on Tropical Wasps

January 9^th- April 7^th 2016

Applications are invited for highly motivated field assistants to work with a PhD researcher from Prof. Jeremy Field's research lab in the department of Life Sciences at the University of Sussex (http://www.sussex.ac.uk/-lifesci/fieldlab/).

Two field assistants are required to help with a field-based project to investigate the effects of environmental conditions on social behaviour in Microstigmus wasps. The fieldwork will be conducted in the Choco region of NW Ecuador, and will run from early January until early April 2017 (three months in total). This is a great opportunity to visit some very unique places in a beautiful part of the world as well as gaining valuable tropical fieldwork experience. Successful applicants will obtain excellent experience of cutting-edge insect behavioural ecology.

The work will involve hiking an altitudinal transect in a tropical climate. Applicants should therefore be physically fit, enthusiastic about fieldwork, hard-working and able to maintain a positive attitude when tired. The work entails assisting a PhD student with data-collection, marking live wasps (they are very small and can't sting!), setting up video cameras on specific observation nests as well as some simple manipulation experiments. There will be some early mornings and travelling to and from research sites using local transport. Applicants are expected to have a degree in biological sciences and some background or keen interest in behavioural ecology and/or social evolution. Previous work-experience with social insects and/or in the tropics would be an advantage. A clean driving licence and some basic knowledge of Spanish also desirable although not essential. The applicants must be committed to working the entire 3-month field season. Because the work involves recording colour marks on individual animals, the job would not be suitable for someone who is colour-blind

All work-related costs in Ecuador will be paid, including accommodation. Whilst in the field there will be basic but comfortable accommodation in a house/ lodge with hot showers and basic kitchen facilities (although meals are provided by the reserves). We also hope to have separate housing in a nearby village to use as a base during our days off. In addition, each assistant will receive Â£500 towards travel costs (air ticket) and a further Â£750 contribution towards their expenses/food whilst not in the field.

Any queries can be sent to Rosa Bonifacii (R.bonifacii@sussex.ac.uk) and/or Prof. Jeremy Field (j.Field@sussex.ac.uk). Applicants should send a covering letter explaining why they would like to work on the project and a CV, including contact details (e-mail addresses/telephone numbers) for the applicant and 2-3 referees. Applications should be e-mailed as a single word document to Rosa Bonifacii by November 21^st 2016. Shortlisted applicants will be notified by e-mail, and will be invited for interview either in person or over skype/phone soon afterwards.

Many thanks, Rosa Bonifacii

Rosa Bonifacii <R.Bonifacii@sussex.ac.uk>

UTelAviv Israel VolResAssist IrisPollination

Opportunity available to participate in an ongoing project on Floral Evolution and Ecology of the Royal Irises in Dr. Yuval Sapir's lab (http://labsapir.wix.com/-labsapir) at Tel Aviv University, Israel. We are seeking one or two motivated volunteer research assistants to help with pollination experiments in field and assist in data analyses.

The positions are most suitable for graduates in Biology seeking to gain further research experience in pollination biology. Candidates who are still undergraduates will be also considered. Candidates should have good organizational skills, high interest to work in the field. Fluency in English and an International driving license is essential. Positions start early February and will continue until early April, but a partial term is also possible. There is also a possibility to carry out genetic studies on Royal irises in the lab.

Tel Aviv University (https://english.tau.ac.il/) is among the top universities for life sciences in Israel. The University has a wide representation of International students and is located in the vibrant coastal city of Tel Aviv.

Israel is culturally and ecologically diverse. The country has approximately 3000 plant species growing along a climate gradient, from sub-alpine mountain through Mediterranean maquis to extreme desert. Alongside the natural settings, Israel is rich in history, with archaeological sites dated thousands years old and sites that are sacred to three religions.

The volunteer will have an opportunity to travel throughout the country during the project work and experience the diversity in vegetation, especially the coastal and desert vegetation, as well as the culture.

If you are interested please e-mail your cv to Dr. Mahua Ghara (mahuaghara[at]gmail.com) on or before 30 November, 2016 . You could also write to Dr. Ghara for further information and queries regarding the opportunity.

Mahua Ghara PBC Post-Doctoral Research Fellow, Dept. of Molecular Biology and Ecology of Plants Tel-Aviv University, Tel Aviv, 69978 Israel. http://labsapir.wix.com/labsapir Botanical Garden, Tel Aviv University, Ramat Aviv, Tel Aviv 69978 http://botanic.tau.ac.il/ Mahua Ghara <mahuaghara@gmail.com>

UTelAviv Israel VolResAssist Iris Pollination

Opportunity available to participate in an ongoing project on Floral Evolution and Ecology of the Royal Irises in Dr. Yuval Sapir's lab (http://labsapir.wix.com/-labsapir) at Tel Aviv University, Israel. We are seeking one or two motivated volunteer research assistants to help with pollination experiments in field and assist in data analyses.

The positions are most suitable for graduates in Biology seeking to gain further research experience in pollination biology. Candidates who are still undergraduates will be also considered. Candidates should have good organizational skills, high interest to work in the field. Fluency in English and an International driving license is essential. Positions start early February and will continue until early April, but a partial term is also possible. There is also a possibility to carry out genetic studies on Royal irises in the lab.

Tel Aviv University (https://english.tau.ac.il/) is among the top universities for life sciences in Israel. The University has a wide representation of International students and is located in the vibrant coastal city of Tel Aviv.

Israel is culturally and ecologically diverse. The country has approximately 3000 plant species growing along a climate gradient, from sub-alpine mountain through Mediterranean maquis to extreme desert. Alongside the natural settings, Israel is rich in history, with archaeological sites dated thousands years old and sites that are sacred to three religions.

The volunteer will have an opportunity to travel throughout the country during the project work and experience the diversity in vegetation, especially the coastal and desert vegetation, as well as the culture.

If you are interested please e-mail your cv to Dr. Mahua Ghara (mahuaghara[at]gmail.com) on or before 30 November, 2016 . You could also write to Dr. Ghara for further information and queries regarding the opportunity.

Thanks in advance, Dr. Mahua Ghara Post-Doctoral Fellow, Tel Aviv University, Israel

mahuaghara@gmail.com

PostDocs

Aarhus EvolBiol

12 to 15 AIAS-COFUND Marie Curie fellowships are available at the Aarhus Institute of Advanced Studies, AIAS, for talented junior and senior researchers from all academic disciplines within this fourth Call for Applications.

The application deadline is 3 February 2017.

Commencement date: 1 October 2017 and 1 February 2018.

Duration: up to 3 years

Read about the fellowship programme, the Guide for Applicants, and AIAS on our website:

www.aias.au.dk http://aias.au.dk/aias-fellowships/aias-cofund-fellowships/ Contact:

Helle Villekold, Programme Manager

helv@au.dk

Jessie Barker <jbarker@aias.au.dk>

ArizonaStateU EvolutionMedicine 1

Evolution & Medicine Postdoctoral Fellowship Arizona State University, The Center for Evolution & Medicine

Salary: $60,000 Reference # 11751 Full time

The Center for Evolution & Medicine (CEM) at Arizona State University (ASU) invites applications from exceptional early career scientists for the Evolution & Medicine Research Fellowship. The Fellowship brings talented researchers with a recently awarded M.D. or Ph.D. to the ASU campus to develop and extend their own independent research agendas with opportunities to collaborate with CEM faculty and other members of their laboratories. Additionally, fellows will spend time working with their mentor to develop skills in the areas of outreach, education and grant writing. Possible research areas include, but are not limited to, co-evolution and infectious diseases, regulation of inflammation and other defenses, autoimmune disorders, cancer, genomics, reproductive health, lactation, and factors that influence disease susceptibility. The proposed research project must advance evidence based science for evolution and medicine.

Fellows will receive a salary of $60,000 and will have access to funding of up to $10,000 per annum to support their research, of which $1500 may be allocated for moving expenses. The initial closing date for receipt of complete applications is December 1, 2016; applications will be reviewed weekly thereafter until the search is closed. The earliest anticipated start date is June, 2017, the latest is January, 2018. This is a fulltime (1.0 FTE) benefits eligible, fiscal year (July 1 June 30) appointment. The fellowship is granted for a period of two years, with a possible third year. Renewal for the second and possible third year is contingent on satisfactory performance, and the availability of resources. For additional information and policies regarding postdoctoral scholars at ASU, please see http://provost.asu.edu/postdoc . The successful fellow(s) will be an outstanding scientist with a specific independent research plan, wide-ranging interests in evolutionary biology related to disease and health, and an appreciation for interdisciplinary research. Selections are based on academic achievement, creativity, goodness of fit, overlap of interests with multiple CEM faculty, and the likely success and impact of the research project. Fellows cannot have had more than five years of previous postdoctoral experience, nor have been employed previously as an assistant professor, associate professor or professor on the tenure track. Nominees who are non-US citizens are encouraged to apply, and will need to be eligible for a J-1 Scholar visa status for the duration of the Fellowship. The CEM does not support H1B visa status. A background check is required for employment.

The Center for Evolution & Medicine is a university-wide Presidential Initiative directed by Randolph Nesse. Its mission is to improve human health by establishing evolutionary biology as an essential basic science for medicine, worldwide. It supports research that demonstrates the power of evolutionary biology to advance the understanding, prevention, and treatment of disease, as well as teaching and outreach initiatives. See http://evmed.asu.edu for details and information on Core Faculty. As an interdisciplinary unit, the CEM provides postdoctoral fellows with opportunities collaborate with faculty from a wide-range of disciplines including anthropology, biology, complex systems, computational informatics, genetics, infectious disease, psychology, and virology.

Arizona State University is a new model for American higher education, an unprecedented combination of academic excellence, entrepreneurial energy and broad access. This New American University is a single, unified institution comprising four differentiated campuses positively impacting the economic, social, cultural and environmental health of the communities it serves. Its research is inspired by real world application blurring the boundaries that traditionally separate academic disciplines. ASU serves more than 80,000 students in metropolitan Phoenix, Arizona, the nation's fifth largest city. ASU champions intellectual and cultural diversity, and welcomes students from all fifty states and more than one hundred nations across the globe.

By the start date, candidates must have completed a Ph.D. in anthropology, biology, psychology or another natural science field that provides an extensive background in evolutionary biology, or an MD, DVM, DrPH or equivalent level health professional degree.

To apply, please email a single pdf document to evmedsearch @asu.edu that contains:

-a one page statement explaining your interest in this position, which faculty members you would like to work with (and to have act as your postdoctoral sponsor/advisor(s)), and how it could advance your career plans,

— / —

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

---

ArizonaStateU EvolutionMedicine 2

The Center for Evolution & Medicine (CEM) at Arizona State University (ASU) invites applications from exceptional early career scientists for the Evolution & Medicine Research Fellowship. The Fellowship brings talented researchers with a recently awarded M.D. or Ph.D. to the ASU campus to develop and extend their own independent research agendas with opportunities to collaborate with CEM faculty and other members of their laboratories. Additionally, fellows will spend time working with their mentor to develop skills in the areas of outreach, education and grant writing. Possible research areas include, but are not limited to, co-evolution and infectious diseases, regulation of inflammation and other defenses, autoimmune disorders, cancer, genomics, reproductive health, lactation, and factors that influence disease susceptibility. The proposed research project must advance evidence based science for evolution and medicine.

The initial closing date for receipt of complete applications is December 1, 2016; applications will be reviewed weekly thereafter until the search is closed.

Full information at http://evmed.asu.edu/faculty-and-postdoctoral-positions-available-evolution-medicine-arizona-state rmnesse@gmail.com

---

ArizonaStateU ForensicGenetics

Postdoctoral Research Associate in forensic genetics/genomics, Stone Laboratory, Arizona State University

The Stone Lab at the Arizona State University is recruiting one Postdoctoral Research associate in forensic genetics and genomics to assist with a National Institutes of Justice funded project that partner researchers at ASU with the Maricopa County Office of the Medical Examiner in assessing new methods appropriate for forensic samples of burned bone, tooth roots, and dental calculus. Specifically, our goals are to examine questions about the relationship between different degrees of charring/burning and DNA recovery for different skeletal elements, the success rate of the different extraction methods and different analytical methods (STR analysis, genomic SNPs), and the extent of fragmentation and damage in DNA recovered from different tissues with different levels of burning. The anticipated start date is in January 2017. The full-time, benefits-eligible position is renewable on an annual basis (July 1 - June 30), contingent upon satisfactory performance, availability of resources, and the needs of the university. Applicants must be within five years of receipt of their Ph.D. to be considered for initial appointment of for subsequent annual renewal. Minimum qualifications include a Ph.D. in anthropology, evolutionary biology, or a related field by the time of appointment. Desired qualifications include experience in ancient DNA, forensic genetic or population genetic laboratory research and the ability to analyze large NGS datasets using scripts and analysis pipelines.

For more information about the Stone Lab, please see http://stone.lab.asu.edu/. The position will be based in the School of Human Evolution and Social Change at the Arizona State University with links to the CBR and CEM. The mission of the CBR is to advance problem-based research that seeks to discover and communicate new knowledge about past peoples' life experiences, including health and disease, cultural contexts, and environmental adaptations well as to address critical contemporary problems through innovative approaches to the analysis of the physical evidence of our past human biology (See https://shesc.asu.edu/research/centers/-center-bioarchaeological-research for more details). The Mission of the CEM is to improve human health by establishing evolutionary biology as an essential basic science for medicine, worldwide. It supports research that demonstrates the power of evolutionary biology to advance the understanding, prevention, and treatment of disease, as well as teaching and outreach initiatives (See http://evmed.asu.edu for details). SHESC, CBR and CEM provide postdoctoral fellows with opportunities collaborate with faculty from a wide-range of disciplines including anthropology, biology, complex systems, computational informatics, genetics, infectious disease, psychology, and virology.

To apply, please submit a single pdf document that contains: 1) a cover letter outlining qualifications and previous research, 2) a current curriculum vitae, and 3) contact information (including email addresses) for three professional references. General questions about this initiative should be directed to Dr. Anne Stone (acstone@asu.edu). Applicants can apply here: https:/-/academicjobsonline.org/ajo/jobs/8530 Initial deadline for complete applications is December 7, 2016; if not filled, review of complete application will occur every two weeks thereafter until the search is closed. A background check is required for employment.

The fiscal year (12-month) salary for this position is $47,476 along with competitive benefits through ASU including health insurance, paid vacation, sick leave, and holidays. The associate must be in residence in the greater-Phoenix metropolitan area during the appointment.

Arizona State University is a VEVRAA Federal Contractor and an Equal Opportunity/Affirmative Action Employer. All qualified applicants will be considered without regard to race, color, sex, religion, national origin, disability, protected veteran status, or any other basis protected by law. ASU's full nondiscrimination statement (ACD 401) is located on the ASU website at: https://www.asu.edu/aad/manuals/acd/acd401.html https://www.asu.edu/titleIX/ KRISTEN DRESCHLER Department HR Specialist, Sr. School of Human Evolution and Social Change College of Liberal Arts and Sciences Arizona State University | P.O. Box 872402 | Tempe, Arizona 85287 (480) 965 - 0102 | Fax: (480) 965 - 7671 | kristen.dreschler@asu.edu

Kristen Dreschler <Kristen.Dreschler@asu.edu>

Austria AquaticMolecularEvolution

University assistant - Postdoc (40 hours per week) - (BIO-9109)

at the Research Institute for Limnology, Mondsee, Austria, start from 1 March 2017, with a duration of 2 years.

Main tasks: International and grant-based research including grant-holding as Principal Investigator in the field of molecular evolutionary ecology of aquatic organisms. Co-Supervision of Master- and bachelor theses as well as PhD theses. Practical guidance of technical assistance. Administrative tasks include management of research.

Qualification: PhD in biology/molecular biology/genetics. Research experience in single cell analysis, population genetics or functional genetics. Specific scientific achievements, such as international Post-Doc experience, international research net-working and (inter)national research grant acquisition. Publications in high-ranking journals documenting achievements in the field of aquatic ecology. Foreign country experience. Experience in teaching and supervision of BSc, MSc, PhD candidates is required. Integrative abilities in team-leading and team-playing are essential.

Job profile: The description associated with this job duties and requirements can be found at http://www.uibk.ac.at/universitaet/profile-wiss-personal/postdoc.html Salary: The minimum gross salary (stipulated by collective agreement) for this position amounts to euro 3.591 per month (14 times). Furthermore, the university has numerous attractive offers (http://www.uibk.ac.at/universitaet/zusatzleistungen/).

Application: We are looking forward to receiving your online application by December 14^th, 2016. Please apply online via the Career portal of the University of Innsbruck https://orawww.uibk.ac.at/public/karriereportal.details?asg_id_in=3D9109 We would be very grateful. Please let us know if it is not possible.

Kind regards,

Sonja Burggraf Institutsreferentin / Secretary University of Innsbruck Research Institute for Limnology, Mondsee Mondseestrasse 9, A-5310 Mondsee Phone: +43 512 507-50201 / Fax: +43 512 507-50299 E-Mail: sonja.burggraf@uibk.ac.at / Homepage: www.uibk.ac.at/limno "Burggraf, Sonja" <Sonja.Burggraf@uibk.ac.at>

BangorU MolecularEvolution

Dear All

In light of recent global events, notwithstanding Brexit and the forthcoming UK-Euro negotiations, the UK has received very clear guidance from the UK Government on the guaranteed funding of EU research programs at least until the final Brexit process is complete. This adds increasing focus to existing and operational research streams that are available and it would be remiss of me not to remind the EvolDir community the opportunities afforded by the multimillion pound investment by the EU and Welsh European Funding Office (WEFO) under the European Regional Development Fund (ERDF) in the Sêr Cymru (Welsh Stars) scheme. In a nutshell, Wales needs more excellent researchers to build critical mass and attract further research funding into Wales and there are number of schemes available:

https://businesswales.gov.wales/expertisewales/s=EAr-cymru-ii-early-career-fellowships-and-rising-star'-scheme

Funding competitive, but prestigious Postdoctoral Fellowships from 3-5 years (3-5 years post PhD) and other support schemes. If anyone is interested in molecular ecology/genomics/evolution in the broadest sense and would like to join the MEFGL group at Bangor University, to take advantage of these opportunities, please don't hesitate to get in touch with myself or another MEFGL team member and we can explore the possibilities to help you join existing researchers that have benefitted from the funding.

http://mefgl.bangor.ac.uk Cheers and best

Si Creer

Simon Creer Professor of Molecular Ecology Molecular Ecology and Fisheries Genetics Lab Environment Centre Wales Building School of Biological Sciences Bangor University Bangor Gwynedd LL57 2UW UK

e-mail: s.creer@bangor.ac.uk Tel: +1248 382302 Fax: +1248 382569 Home Page: http://mefgl.bangor.ac.uk/staff/si.php Skype: spideycreer Twitter: @spideycreer

Simon Creer <s.creer@bangor.ac.uk>

BangorU MolecularEvolution 2

Dear All (url link now fixed hopefully)

In light of recent global events, notwithstanding Brexit and the forthcoming UK-Euro negotiations, the UK has received very clear guidance from the UK Government on the guaranteed funding of EU research programs at least until the final Brexit process is complete. This adds increasing focus to existing and operational research streams that are available and it would be remiss of me not to remind the EvolDir community the opportunities afforded by the multimillion pound investment by the EU and Welsh European Funding Office (WEFO) under the European Regional Development Fund (ERDF) in the Sêr Cymru (Welsh Stars) scheme. In a nutshell, Wales needs more excellent researchers to build critical mass and attract further research funding into Wales and there are number of schemes available:

https://businesswales.gov.wales/expertisewales/s%C3%AAr-cymru-ii-early-career-fellowships-and-%E2%80%98rising-star%E2%80%99-scheme Funding competitive, but prestigious Postdoctoral Fellowships from 3-5 years (3-5 years post PhD) and other support schemes. If anyone is interested in molecular ecology/genomics/evolution in the broadest sense and would like to join the MEFGL group at Bangor University, to take advantage of these opportunities, please don't hesitate to get in touch with myself or another MEFGL team member and we can explore the possibilities to help you join existing researchers that have benefitted from the funding.

http://mefgl.bangor.ac.uk Cheers and best

Si Creer

Simon Creer Professor of Molecular Ecology Molecular Ecology and Fisheries Genetics Lab Environment Centre Wales Building School of Biological Sciences Bangor University Bangor Gwynedd LL57 2UW UK

e-mail: s.creer@bangor.ac.uk Tel: +1248 382302 Fax: +1248 382569 Home Page: http://mefgl.bangor.ac.uk/staff/si.php Skype: spideycreer Twitter: @spideycreer

Rhif Elusen Gofrestredig 1141565 - Registered Charity No. 1141565

Simon Creer <s.creer@bangor.ac.uk>

Barcelona PDF PhD EvoDevoGenomics

University of Barcelona Department of Genetics

Our group working on Chordate Evo-Devo and Genomics in the Department of Genetics at the University of Barcelona is looking for both DOCTORAL and POSTDOCTORAL motivated candidates to join our recently granted project 2017-2020 and to apply to the soon-coming fellowship calls

Our main research interest is to understand the impact of gene loss on Evo-Devo (Albalat and Cañestro, Nat. Rev. Genet 2016), focusing on Wnt, Fgf signaling, during muscle and heart development. Our main subject of study is Oikopleura dioica, a newly emergent model within our own phylum, with the smallest chordate genome size known so far (Denoeud et al., Science, 2010; Marti-Solans et al., Mol Biol Evol 2016). The project will include gene manipulation by CRISPR and DNA interference, RNAseq transcriptomic analyses, imaging, as well as the development of novel tools.

Positions are available for immediate incorporation, but medium long term incorporations during our newly granted project 2017-2020 will be also considered.

Interested candidates, please send an email to Cristian Cañestro (canestro@ub.edu), including a brief letter of interest, a brief CV, including list of publications with their impact, and technical skills for post-doc applications, and official scores for PhD candidates, all together in ONE single pdf file.

For more information please visit our web site: http://evodevogenomics-unibarcelona.weebly.com/join-the-lab.html Cristian Cañestro and Ricard Albalat

Departament de Genètica Facultat de Biologia, Universitat de Barcelona Av. Diagonal 643, 08028, Barcelona, Spain canestro@ub.edu http://evodevogenomics-unibarcelona.weebly.com/ @evodevogenomeUB

Cristian Cañestro <oikocris@gmail.com>

CalAcademy 2 CoralReefGenomics

TWO POST-DOCTORAL FELLOWSHIPS IN CORAL REEF ECOLOGY AND GENOMICS

The Institute of Biodiversity Science and Sustainability and the Steinhart Aquarium, California Academy of Sciences, are recruiting two (or a total of four) post-doctoral fellows to be a part of our 5-year Coral Reefs Initiative. The candidates will be supervised by Drs. Rebecca Albright and Luiz Rocha and will work closely with other scientists within the Institute of Biodiversity Science and Sustainability and Steinhart Aquarium with generous support for laboratory and fieldwork. The positions will focus on: (Position 1) establishing a coral reproductive model at Steinhart Aquarium (in conjunction with aquarium staff and global partners), and documenting carbonate chemistry dynamics and reef metabolism at various field sites; (Position 2) coral reef genomics and bioinformatics. There is additional flexibility to propose research projects that complement the California Academy of Science's current initiatives. Public outreach through in person and online interactions will be encouraged. Applicants with expertise in any area of coral reef biology and conservation will be given full consideration. However, preference will likely be given to candidates with experience in the following areas: field expertise, coral reproduction, larval biology, seawater carbonate chemistry, ocean warming and acidification, bioinformatics, and genomics.

Applicants should possess a PhD in a relevant discipline at the time of hiring, be able to work collaboratively across the different laboratories and departments involved, and have strong academic publication and outreach records. California Academy of Sciences post-docs are expected to participate in a wide variety of outreach programs, both online and in our public museum.

To apply, please follow instructions at CalAcademy's SnapHire (http://calacademy.snaphire.com/jobdetails?ajid=3D4pVR8) by December 16, 2016. Please specify your desired start date (which can be as soon as January 2017) in your letter of interest. General inquiries should be sent to Rebecca Albright (ralbright@calacademy.org) or Luiz Rocha (lrocha@calacademy.org).

The California Academy of Sciences is a scientific and educational institution dedicated to exploring, explaining, and sustaining life on Earth. Based in San Francisco's Golden Gate Park, it is home to a world-class natural history museum, aquarium, and planetarium-all under one living roof.

Luiz A. Rocha, PhD Associate Curator and Follett Chair of Ichthyology California Academy of Sciences p. 415.379.5370 f. 415.379.5731 LRocha@calacademy.org http://www.luizrocha.com/academic/ 55 Music Concourse Drive Golden Gate Park San Francisco, CA 94118

lrocha@calacademy.org

CornellU HumanPopulationGenomics

Postdoctoral position in human population genomics

The postdoctoral position is with Alon Keinan in the Department of Biological Statistics and Computational Biology at Cornell University. The Keinan lab studies the effects of demographic history and natural selection on patterns of human genetic variation and their role in common, complex disease risk. We address these questions while developing computational and statistical methods in human population genomics and sequence-based association studies. Current lab members have backgrounds in computer science, genetics, nutrigenomics, statistics, and physics, which facilitates a collaborative environment optimized for conducting all stages of a study, from method development, their genomic application, and interpretation of results. Below are representative publications from the lab of related projects from this year, while specific projects will be based on the interests of the successful candidate.

The ideal candidate will have a strong track record in either population genetics or statistical genetics, as well as strong programming and statistical skills, with a Ph.D. in computational biology , computer science, statistics, mathematics, genetics, or a related field. The starting date is flexible and can be as early as January 2017. Applications will be accepted until the position is filled. Competitive salaries commensurate with experience and skills, as well as a very generous benefits package will be offered.

Relevant projects can be as part of the lab's ongoing collaborations with Andrew Clark, Erez Levanon, John Novembre, Harry Ostrer, Yun Song, Haiyuan Yu and several consortia.

Interested applicants should send a PDF with CV, a brief description of research interests and experience, and contact information for three references to the attention of Ms. Sue Bishop, administrative assistant (skp5@cornell.edu), indicating “position 208” in the subject line. Informal inquiries are also welcome.

Representative publications from the lab from 2016 (for additional recent publications, check the google scholar page at https://scholar.google.com/citations?user=-rS0EX5EAAAAJ&hl=en) “ Positive selection on a regulatory insertion-deletion polymorphism in FADS2 influences apparent endogenous synthesis of arachidonic acid. Molecular Biology and Evolution (2016). ” Inference of super-exponential human population growth via efficient computation of the site frequency spectrum for generalized models. Genetics (2016). “ Clustered mutations in hominid genome evolution are consistent with APOBEC3G enzymatic activity. Genome Research (2016). ” The genetic history of Cochin Jews from India. Human Genetics (2016). “ Strong constraint on human genes escaping X-inactivation is modulated by their expression level and breadth in both sexes. Molecular Biology and Evolution (2016).

Alon Keinan, PhD Associate Professor Department of Biological Statistics & Computational Biology 102C Weill Hall | Cornell University | Ithaca, NY 14853 alon.keinan@cornell.edu | 607-254-1328 phone | 607-255-2323 fax http://keinanlab.cb.bscb.cornell.edu/ | @AlonKeinan

Alon Keinan <alon.keinan@cornell.edu>

DalhousieU MajorTransitionsInEvolution

A funded postdoctoral research position (2 years, potentially renewable for a 3rd) is available in the laboratories of Andrew J. Roger and W. Ford Doolittle at Dalhousie University to study the major evolutionary transitions in the history of Life using comparative genomic, molecular evolutionary, bioinformatic and phylogenomic methods. Roger and Doolittle are part of the world-renowned Centre for Comparative Genomics and Evolutionary Bioinformatics (CGEB) - a vibrant collaborative group of 12 P.I.’s and ˜70 trainees with research interests in deep evolution, comparative genomics, phylogenetics, microbiomics and computational biology (cgeb.dal.ca)

The successful candidate will conduct analyses with microbial genome and metagenome data from the three (two?) domains of Life to reconstruct the gene contents (and infer cellular and biochemical properties) of the last universal common ancestor (LUCA), the last archaeal common ancestor (LACA), the last eukaryotic common ancestor (LECA) and the alphaproteobacterial endosymbiont that gave rise to mitochondria. The overarching goal is to clarify the evolutionary transitions between these primary types of cells. The ideal candidate would have a Ph.D. in a related field and extensive knowledge/expertise with statistical phylogenetic, phylogenomic and comparative genomic methods and computational functional annotation/prediction of genes. Expertise in analyzing microbial transcriptome/genome data, metagenomic data, bioinformatics scripting languages (e.g. Python and/or Perl) and familiarity with the R statistical package is also an asset.

For more information about the Roger and Doolittle labs and the CGEB Centre see rogerlab.biochem.dal.ca, www.biochem.dal.ca/faculty-staff/faculty/doolittle.php and cgeb.dal.ca

To apply please send an application package consisting of: i) a cover letter that describes why you are interested in this position and highlights your expertise, ii) your curriculum vitae (CV), and iii) the names and contact details of 2 or more individuals who have agreed to write reference letters.

The package should be sent by email to Wanda Danilchuk, Email: wanda.danilchuk@dal.ca

Initial deadline for complete applications is December 7th, 2016; if not filled, review of complete application will occur every two weeks thereafter until the search is closed. Please note, only those candidates chosen to continue on through the selection process will be contacted.

Dalhousie University is committed to fostering a collegial culture grounded in diversity and inclusiveness. The university encourages applications from qualified Aboriginal people, persons with a disability, racially visible persons, women, persons of minority sexual orientations and gender identities, and all qualified candidates who would contribute to the diversity of our community.

Andrew Roger <Andrew.Roger@Dal.Ca>

DukeU DiseaseEvolution

The Koelle lab in the Department of Biology at Duke University and the Ke lab in the Department of Mathematics at North Carolina State University have multiple openings for postdoctoral researchers between the two collaborating research groups. The post-docs will work on a DARPA-funded human influenza virus project that aims to understand the functional organization of influenza viruses at multiple scales and develop novel evolution-proof antivirals. We encourage applications from highly motivated and creative individuals who have backgrounds in one or more of the following: mathematical modeling (ideally infectious disease modeling), statistically fitting models to data, theoretical biology (including multi-level selection theory and theory on the evolution of multicellularity), population genetics, population ecology, and viral sequence analysis. The project involves modeling influenza at multiple scales of organization, including intracellular dynamics, within-host dynamics, and between-host dynamics. Opportunity will be present to interact with the experimental labs at UIUC, Rutgers, and Montana State University that belong to the multidisciplinary team.

To apply, please send a brief statement of research interests, a CV, and up to 3 publications to both Katia Koelle (katia.koelle@duke.edu) and Ruian Ke (rke2@ncsu.edu) by December 15, 2016 at the latest. We will review applications on a rolling basis.

"katia.koelle@duke.edu" <katia.koelle@duke.edu>

Ghent PlantComparativeNetworkBiol

The Comparative & Integrative Genomics lab (Klaas Vandepoele) and the Systems Biology of Yield la b (Dirk Inze) of the VIB Department of Plant Systems Biology, is currently looking for a

Postdoc in 'Comparative Network Biology in Plants'

Our mission

Our objective is to extract and validate biological knowledge related to plant growth and yield from large-scale experimental data sets using data integration, comparative sequence and expression analysis, and network exploration. In this international project, including academic and industrial partners, we aim to identify novel regulators of growth using the cross-species analysis of gene regulatory networks and gene function prediction.

Job description

- Fully funded Postdoc position for 2 years in the framework of an international research project.

- Tackle specific research questions about plant growth and yield in different plant species through the integration of experimental omics data types (e.g. RNA-Seq, phenotypes, GO functions) and computational biology methods (e.g. comparative genomics, network analysis).

- Interpretation of network biology results using scientific literature, unpublished experimental datasets and current working hypotheses.

- Work in close collaboration with computational and experimental colleagues, both in Ghent and abroad (through short-term visits within Europe).

- Reporting of results to international partners and publish in peer- reviewed international journals.

Your profile

- You have PhD degree in Bioinformatics, Plant Biotechnology or related.

- You are enthusiastic about scientific research and have a strong interest in studying plant biology using genomics and systems biology approaches.

- Through international peer-reviewed publications, you have a track record in plant genomics or systems biology research.

- You are familiar with Linux/Unix and have knowledge of Python/Perl or another programming/scripting language.

- You have good communication and writing skills.

- You are proficient in English. Apply? http://www.vib.be/en/jobs/Pages/Postdoc-in-%E2%80%98Comparative-Network-Biology-in-Plants%E2%80%99.aspx Prof. Dr. Klaas Vandepoele Tel. 32 (0)9 33 13822 VIB Department of Plant Systems Biology, Ghent University Technologiepark 927, 9052 Gent, Belgium

Lab website: http://bioinformatics.psb.ugent.be/cig/- BIG N2N: http://www.bign2n.ugent.be/ Twitter: http://twitter.com/plaza_genomics

Klaas Vandepoele <klpoe@psb.vib-ugent.be>

Glasgow Evodevo Epigenetics

We seek a theory-driven postdoc to join us to focus on questions related to evolutionary developmental biology and genomics including the genetic and epigenetic basis of phenotypic change. We offer a highly interdisciplinary group and generous funding support from a recently awarded NERC Highlight topics grant to Dr Kevin J. Parsons (PI), Prof. Neil B. Metcalfe, Dr Shaun S. Killen and Dr Jan Lindstrom.

The project provides an opportunity to take evo-devo and genomics in a new direction by investigating the impact that long-term increases in temperature can have on evolution. The postdoc will be in charge of leading and applying large-scale population genomic and QTL mapping approaches to sticklebacks that have evolved within geothermally-heated and ambient temperature locations in Iceland. A substantial portion of this research will also involve the use of genomics to understand patterns of methylation in response to temperature in both wild and lab-reared populations. While these genomic approaches will be used, the lab is phenotype-first orientated and works at the intersections of ecology, evolution, physiology, and development. The postdoc will therefore also have the opportunity to take part in the design of experiments used to assess developmental changes in a range of phenotypes.

You will have previous postdoc experience or be near to completing a relevant PhD and be experienced with genomics, developmental genetics, and/or epigenetics. Interest and experience with questions surrounding parallel evolution and phenotypic plasticity would be an asset. As part of a team funded by this NERC grant, you will work closely with another postdoctoral scientist who will focus on running lab experiments and behavioural assays, and a full-time technician who will aid in the running of a breeding programme and lab work.

Passion for research, team spirit and enthusiasm are essential. Our team is multidisciplinary with additional major projects funded by the European Research Council (ERC) and NERC. Additional PhD student projects in the lab of the PI involve collaborations with engineers, statisticians, and physicists demonstrating the highly active and collaborative research environment in the University of Glasgow. Further information on the post can be obtained from Dr. Kevin Parsons (kevin.parsons@glasgow.ac.uk). Formal applications are due by January 8th, 2017, and can be made at:

reference # 015558 http://www.gla.ac.uk/about/jobs/vacancies/ Dr. Kevin Parsons Lecturer, Institute of Biodiversity, Animal Health, and Comparative Medicine University of Glasgow https://sites.google.com/site/kevinparsonslab/home http://www.gla.ac.uk/researchinstitutes/bahcm/staff/kevinparsons/ Dr. Kevin Parsons Lecturer, Institute of Biodiversity, Animal Health, and Comparative Medicine University of Glasgow https://sites.google.com/site/kevinparsonslab/home/people http://www.gla.ac.uk/researchinstitutes/bahcm/staff/kevinparsons/ Kevin Parsons <Kevin.Parsons@glasgow.ac.uk>

Harvard InfectiousDiseaseGenomics

Summary

The Department of Biomedical Informatics (DBMI) at Harvard Medical School and the Farhat Lab are looking for a Postdoctoral Fellow in infectious disease genomics.

Pathogens display a remarkable range of variability in phenotypes relevant to disease including transmissibility, organ tropism, and antibiotic resistance. Elucidating the biological mechanisms for these differences is a fundamental question in the study of infectious diseases and creates new avenues for surveillance, diagnosis and personalized treatment. The heritability of disease phenotypes within pathogen species and their evolution over generations indicates that they should be genetically encoded. As a result, the study of pathogen whole genome sequence (WGS) data is expected to further our understanding of these traits. The Farhat lab was one of the first to use phylogenetic convergence to test for association between genes and the drug resistance phenotype on a genome wide scale, and is continuing in this path for both methodological development and application to large scale datasets.

Responsibilities

The Postdoctoral Fellow will be responsible for developing and applying computational methodologies to identify novel infectious disease genomic markers.

Basic Requirements

We are an interdisciplinary lab. Candidates may have an MD or PhD degree in epidemiology, bioinformatics, computational and evolutionary biology, biostatistics, or a related field. The candidate interested in this position must be highly motivated and demonstrate initiative in assigned tasks.

Additional Requirements

Experience in programming R, Python, and/or Perl and statistical analysis or at least an interest in learning these skills will be necessary. The candidate and PI can work together to delineate the fellow's training needs and develop a program to fulfill this, utilizing the department and university's wide range of resources.

Terms

The position is available immediately and can be renewed annually.

How to apply

Email applications including curriculum vitae, summary statement of personal objective and research interests, PDFs of the best two papers, and the names and email addresses of three references to mrfarhat@partners.org. Maha R Farhat, MD MS

"Farhat, Maha R.,M.D." <MRFARHAT@partners.org>

IGC LisbonPortugal GeneticsGenomics

A postdoctoral research fellowship is available in the host-microorganism interactions lab at Instituto Gulbenkian de Ciência (http://www.igc.gulbenkian.pt/-lteixeira). This position is integrated on a FCT project, led by Nelson Martins and Luis Teixeira, focused on antiviral resistance in Drosophila melanogaster. We are interested in understanding functionally how genetic variation leads to differences in antiviral immunity and how the antiviral Toll pathway is activated. Our research group works not only on antiviral immunity but also on the interaction of Drosophila with intracellular bacteria (Wolbachia) and gut bacteria. We are looking for an enthusiastic candidate with a collaborative spirit that wants to join our group. Experience in Drosophila genetics and genomics, Drosophila infection and immunity, molecular biology or tissue cell culture are a plus.

To apply send a letter of motivation, Curriculum Vitae, and contacts of two previous supervisors, in one PDF file, by e-mail, with subject "Postdoc fellowship antiviral immunity", to Luís Teixeira (lteixeira@igc.gulbenkian.pt). Deadline for applications is 30th November 2016. More details at http://www.igc.gulbenkian.pt/mediaRep/igc/files/-uploads/recruitment/Bolsa_postodoc_PTDC-BEX-GMG-3128-2014-1.pdf nelson.e.v.martins@gmail.com

IndianaU ExperimentalMicrobialEvolution

Three postdoctoral research positions are available in the epartment of Biology at Indiana University. Positions will be supported with a five-year Multidisciplinary University Research Initiative (MURI) grant from the US epartment of Defense (DoD) program on "Innovation in Prokaryotic Evolution". The goals of the project are to reveal the molecular causes and consequences of evolution in highly replicated lines of a phylogenetically diverse range of microbial taxa in response to changes in the internal population-genetic environment (e.g., population size) and the external natural environment (i.e., starvation and cross-feeding interactions). We seek individuals with expertise in microbiology, bioinformatics, and evolutionary theory. We are also looking for individuals that have the ability to design long-term evolution experiments and analyze whole-genome sequences and other omics data.

Postdocs will be appointed to one of the following three laboratories: - Michael Lynch: www.indiana.edu/-˜ lynchlab/ - Jay T. Lennon: www.indiana.edu/-˜ microbes/ - Jake McKinlay: www.indiana.edu/-˜mckinlab/ The epartment of Biology at Indiana University in Bloomington has excellent infrastructure for conducting microbiological, evolutionary, and ecological research (http://www.bio.indiana.edu/). Postdocs will have ample opportunity to interact and collaborate with partnering labs including Pat Foster (https://-goo.gl/dviOS7) at Indiana University and Allan rummond (drummondlab.org/) at the University of Chicago. Interested parties should email a cover letter containing a brief statement of research interests, a CV, and the names and contact information for three potential letter writers to microevo@indiana.edu. These positions are available immediately, although the start dates are somewhat flexible. Preference will be given to applications received prior to ecember 1, 2016, but we will consider applicants until the positions have been filled. https://goo.gl/IZala7 megbehri@indiana.edu

JamesCookU LobsterPopulationGenomics

Postdoc position Rock lobster population genomics

JamesCook University, Townsville, North Queensland, Australia

Weare seeking a Post-doctoral Research Fellow to conduct research activities on an Australian Research Council (ARC) funded project focused on investigating fine-scale population differentiation in a range of closely related rock lobster species and identify signatures of adaptive genetic diversity. The incumbent works with a team of researchers using a range of population genomic, phylogenomics and transcriptomic methods to investigate and report on population genomic processes in commercially important rock lobsters with long larval durations.

Theprincipal accountabilities of the position include:

- Co-design and conduct population genomic experiments genetic analyses using reduced representation sequencing in order to investigate and analyse neutral and adaptive genetic variation in rock lobsters.

- Use bioinformatic approaches to distinguish between factors causing population differentiation in lobsters (e.g. self-recruitment, larval cohesiveness, sweepstake reproduction).

Requirementsinclude:

1. PhD qualification in Biological Sciences or Genetics. 2. Demonstrated experience in designing and conducting population genetic experiments. 3. Demonstrated experience working with next generation sequencing and reduced representation genomic Single Nucleotide Polymorphism (SNP) techniques. 4. Experience in using the command line and running analyses remotely on a High Performance Computer (HPC). 5. Experience working in a multidisciplinary environment, and an ability to work both in a team environment and also independently. 6. Demonstrated proficiency to carry out high-quality research, and a record of professional achievement in the relevant discipline area in both publications and oral presentations.

7. Strong interpersonal, time management and organisational skills, with an ability to manage a number of competing priorities.

Applicationprocedure:

Interestedcandidates should apply through the James Cook University jobs website prior to 23 November:

https://www.jcu.edu.au/jobs/research-jobs Referencenumber 15816

Anyqueries please contact A/Prof Jan Strugnell jan.strugnell@jcu.edu.au

AssociateProfessor Jan Strugnell Centrefor Sustainable Tropical Fisheries and Aquaculture, Collegeof Science and Engineering, JamesCook University, Townsville, 4811 QLD, Australia. Ph: +61-7-4781 6357 Email: jan.strugnell@jcu.edu.au

jan.strugnell@jcu.edu.au

LeipzigU PlantSystematics

Research Assistant (Postdoc) position the field of systematics, evolution and biogeography of flowering plants available at Leipzig University in Germany - application deadline Nov 25th, 2016

For further information, please visit:

http://www.zv.uni-leipzig.de/universitaet/stellen-und-ausbildung/stellenausschreibungen/wissenschaftliches-personal.html#c178111 http://www.zv.uni-leipzig.de/universitaet/stellen-und-ausbildung/stellenausschreibungen/wissenschaftliches-personal.html#c178113 Note: Please additionally send an electronic copy of your application as a single pdf by email to Prof. Dr. Alexandra Muellner-Riehl (muellner-riehl@uni-leipzig.de). Further information on the working group may be found at http://www.biphaps.uni-leipzig.de/en/sysbot/molecular-evolution-and-systematics-of-plants.html .This is a temporary position of up to five years duration, depending on the qualification of applicants. Inquiries about this position may be directed to muellner-riehl@uni-leipzig.de. Interviews for this position are likely to be conducted in December 2016 (or January 2017).

muellner_alexandra@yahoo.de

LouisianaStateU SystematicsPopGenetics

Postdoctoral Researcher Museum of Natural Science College of Science Louisiana State University

Candidate will conduct research in coordination with one or more of the Curators. The candidate will also be responsible for helping with the laboratory supervision of graduate and undergraduate research assistants and management of the Museum molecular genetics core facility. Ongoing projects in the lab include systematics and population genetics studies of birds, fish, mammals, reptiles and amphibians.

Duties: 70% Conduct active lab research on a semi-independent basis. To prepare and publish scientific manuscripts under the direction of a Curator. To attend, contribute, and where necessary lead relevant meetings. To take the responsibility for planning and developing research methods and techniques within the framework of the research program. Bring new expertise to the research program. To undertake any other duties relevant to the program of research, including field work. To collaborate with research colleagues and support staff internally as appropriate to the research and to actively develop appropriate external contacts and networks relevant to the project and to future funding opportunities. The person in this position is expected to be part of the Museum's vibrant academic community, attending seminars, participating in journal clubs, etc.

30% Responsible for helping with the laboratory supervision and training of graduate, undergraduate, and high school research assistants, and management of the Museum's shared molecular genetics facility. Ongoing projects in the lab include systematics and population genetic studies of birds, mammals, reptiles and amphibians, and fishes. Monitor laboratory cleanliness and safety. Order general lab supplies for the department. Establish and enforce lab rules and regulations, and indoctrinate new staff/students in same at beginning of each semester. Attend regular meetings with the research team and investigators as required. Work with external collaborators as agreed with the investigators.

Minimum Qualifications: Ph.D. in Biology or related discipline; Experience in molecular methods, evolutionary biology, and computational biology, strong publication record, ability to manage an active laboratory.

An offer of employment is contingent on a satisfactory pre-employment background check. Application review will begin November 29, 2016 and continue until a candidate is selected.

LSU IS COMMITTED TO DIVERSITY AND IS AN EQUAL OPPORTUNITY/EQUAL ACCESS EMPLOYER

Quick link at ad URL: https://-lsu.wd1.myworkdayjobs.com/LSU/job/LSU—Baton-Rouge/Postdoctoral-Researcher_R00007345 Thank You,

Monica Morvant |Office of Human Resource Management|Recruiting Analyst 110 Thomas Boyd Hall| Baton Rouge, LA 70803 O: 225.578.8292| M: 225.578.8200 | F: 225.578.6571 Email: mmorvant@lsu.edu www.lsu.edu/hrm LSU HRM: Employment Resources for Student Success

Monica E Morvant <mmorvant@lsu.edu>

MNHN Paris PlantBiodiversity

Post-doctoral position at Museum National d'Histoire Naturelle, Paris France.

The Institut de Systematique Evolution et Biodiversite seeks applicants for a full-time Post-doctoral position in macroecology focussing on land plants functional diversity in islands.

Islands have always intrigued biologists, due to their remarkable biodiversity. They are considered natural laboratories of evolutionary specialization and adaptation, because life in isolation has allowed evolution to take its own course, giving rise to many innovations and leading to peculiar faunas and floras (Losos and Ricklefs 2009).

Although much of island biology has been well explored, we still lack documented patterns at large scale in order to understand the main drivers shaping island biodiversity. Factors such as distance from a source of colonizers (continents or other islands), size and age are recognized to be important determinants of species richness in islands.

But, is it true at large scale and for every group of organisms? What does it mean in terms of other biodiversity features such as Phylogenetic Diversity (PD) or Trait Diversity (TD)? Our aim is to answer these questions using our dataset of curated occurrences and trait diversity for land plants, representing a large proportion of plant diversity on earth. However, several operational problems appear when dealing with such a large data set. The main contribution of this project is dealing with this data to provide an overall understanding of phylogenetic and trait diversification in islands. In addition to that, this will also contribute to finding solutions and designing scripts that can further be applied to any kind of study of this type.

The specific objectives will be: i) Assessment of the spatial correlation of phylogenetic diversity with trait diversity. The aim will be to detect if there is an overall match, and to investigate the factors that could explain those matches and mismatches.

ii) Verification of the relationship between island endemicity, phylogenetic and trait diversity. Are there common trends shared by species endemic of island when compared to species also occurring in continental areas (here after called widespread for convenience)? The idea is to test whether island endemics tend to have more original traits than widespread species, and how this is associated with phylogenetic diversity. Are original traits associated with particular branches? Are there tendencies for appearance of original traits in particular places of the phylogenetic tree? Did they appear by convergence? A second step in both studies will be the analysis of diversification drivers in islands.

We are looking for a passionate scientist with solid background in macroecology and demonstrated skills in R and Python languages, desirably applied to manipulating and analyzing large amounts of data replaced in a spatial perspective, or very large phylogenies. There is no language prerequisite. This offer is for a 24 months full-time position, funded by the Labex BCDiv (Diversites Biologiques et Culturelles). Salary will be commensurate with the experience of the candidate. For a first job after PhD, gross salary is 30000 Euros/Year (2500 Euros Month). Funds are already secured for the whole duration of the contract and the successful candidate shall begin on January 1st 2017.

Candidates' Ph.D. should have been defended and awarded at November 30th 2016. Candidates will be selected for an oral presentation at the very beginning of December. All charges related to the trip to the oral examination will be taken in charge by our project. We can also use Skype or other videoconference media for this audition.

A full CV and a cover letter, with two recommendation letters from previous employers or supervisors, should be sent by e-mail to Thomas Haevermans haever@mnhn.fr Roseli Pellens pellens@mnhn.fr and Maud Mouchet maud.mouchet@mnhn.fr. The deadline is November 5th 2016, midnight Paris (FR) time.

Thomas Haevermans

Dr. Thomas Haevermans Institut de Systematique, Evolution, Biodiversite - http://isyeb.mnhn.fr Head of System-C Team - ISYEB UMR 7205 CNRS/MNHN/EPHE/UPMC Museum national d'histoire naturelle, CP39 - 57, rue Cuvier, 75231 Paris cedex 05 - France.

Thomas Haevermans <euphorbiaman@me.com>

Montpellier MicrobialGenomics

A funded postdoctoral position in bacterial genomics and phylogenomics is open at the CEFE (Centre for Functional and Evolutionary Ecology) in Montpellier, France.

Project: The recruited postdoc will conduct research in the framework of the ERC CoG HGTCODONUSE project. The main goal is to investigate the impact of codon usage preferences on the success of horizontal gene transfer and on post-transfer gene evolution, with different bacteria and antibiotic resistance genes as model systems. The results gathered will in particular help understand the role of codon usage preferences in shaping the propagation routes of antibiotic resistance. The project has a strong experimental component, including characterization of mutant collections, experimental horizontal transfer and experimental evolution of the resulting bacterial populations. This experimental part will employ NGS-assisted fitness measurements and analysis of whole genome sequences after experimental evolution. The experimental core of the project will be completed by comparative approaches: taking advantage of the large whole genome data sets currently available we will investigate the long-term evolutionary consequences of HGT at the genomic level. The postdoc recruited will work both on the experimental component (by taking part in the fitness and genomic data analysis) and on the comparative genomic aspects of the project.

Scientific environment: The postdoc will work in the "Evolutionary Genetics and Ecology" team within the Centre for Functional and Evolutionary Ecology (CEFE), Montpellier, France. http://www.cefe.cnrs.fr/fr/recherche/ee/gee The CEFE is the largest French institute for ecology and evolution. It gathers numerous recognized research groups, particularly in experimental evolution. It also hosts shared platforms with high-level equipment in microbiology, rearing facilities, molecular biology and ecological chemistry. The "Evolutionary Genetics and Ecology" team is a lively, dynamic and stimulating working environment. The group is composed of 10 permanent researchers and 10 to 15 PhD students and postdocs working on a diversity of topics: reproduction system evolution, life-history trait evolution, mechanisms of adaptation, community evolution and antibiotic resistance evolution. Finally, Montpellier is a medium-size lively student city in the south of France, close to the Mediterranean Sea and to the Cevennes mountains.

Profile: We seek a motivated and enthusiastic scientist with a PhD degree in Evolutionary Biology and with strong knowledge and experience in bioinformatics analysis: NGS data analysis, whole-genome assembly and phylogenomics. Expertise in theoretical evolutionary biology would be appreciated. Candidates should be fluent in written and oral English.

Application: Application with CV (including a publication list), a brief statement of research interests and contact information for two professional references should be submitted in an electronic form to Stéphanie Bedhomme (stephanie.bedhomme@cefe.cnrs.fr) before December 11th. The expected starting date is spring 2017. The position is open for 2 years. The salary will depend on the past experience with a minimum net salary of 2040 euros. Do not hesitate to contact me for further details or questions.

Stéphanie Bedhomme CR CNRS Equipe "Génétique et Ecologie Evolutive" Centre d'Ecologie Fonctionnelle et Evolutive Montpellier

BEDHOMME Stéphanie <Stephanie.BEDHOMME@cefe.cnrs.fr>

Moulis EvolutionaryGenomics 2

Post-doctoral fellowship in Evolutionary Genomics

A post-doctoral position is available for two years at the Station for Theoretical and Experimental Ecology (Moulis, France) in the field of evolutionary genomics.

Project objectives

The main objective of the project is to determine the molecular bases of organisms response to environmental changes using an Evolve and Resequence framework. To do so, we are currently running experimental evolution on species of the genus Tetrahymena (ciliated protozoa) submitted to divergent environmental treatments. The candidate will be in charge of the genomic part of the project and will compare the patterns of genome/transcriptome evolution of the evolved lines. By relating whole genome/transcriptome profiles to the phenotypic changes observed both between and within species, and by searching for footprints of selection, the candidate would determine some of the molecular mechanisms responsible for phenotypic response to environmental variation. The candidate will also develop SNPs to allow discrimination of our laboratory lines of Tetrahymena thermophila, which have been used in several microcosm experiments. In particular, he/she will analyze the genetic composition of experimental metapopulations that were confronted to different climatic scenarios in a fragmented landscape. The candidate will lead a genomic network within the Station for Theoretical and Experimental Ecology. He/she will organize regular meetings with members of the lab performing analyses of NGS datasets in order to share information on bioinformatics and biostatistics pipelines. The candidate will thus collaborate on several ongoing genomic projects including the transcriptomic analysis of individuals with different dispersal abilities in butterflies. In addition, it would be relevant if the candidate is interested in participating in the ongoing thought in Moulis about the impact of the use of omics in ecology (e.g. much increased environmental footprint or increased disconnection with non-scientists).

Candidate profile

The ideal candidate should have a PhD in the field of genomics with expertise in bioinformatics and biostatistics. Good knowledge in evolutionary ecology and the molecular basis of evolution is strongly recommended. The candidate should also have good communication skills, and should be autonomous and organized.

Contact

The closing date is fixed to the 16th of December. The candidate should begin in the first half of 2017. To apply, please send a cover letter, CV, summary of past work, and two letters of recommendation to Hervé Philippe and Delphine Legrand.

Hervé Philippe Email: herve.philippe@sete.cnrs.fr http://www.cbtm-moulis.com/m-176-herve-philippe.html Delphine Legrand Email: delphine.legrand@sete.cnrs.fr https://sites.google.com/site/delphinelegrandresearch/home Representative publications:

Rodrigue N and H Philippe (2010) Mechanistic revisions of phenomenological modeling strategies in molecular

evolution. Trends in Genetics, 26: 248-252.

Philippe H, et al. (2011) Resolving difficult phylogenetic questions: Why more sequences are not enough. Plos Biology 9(3)e1000602.

Amemiya CT, Philippe H, (2013) The African coelacanth genome provides insights into tetrapod evolution. Nature 7445, 311-316.

Telford MJ, Budd GE, Philippe H (2015) Phylogenomic insights into animal evolution. Current Biology, 25 R876-R887.

Baguette, M., Legrand D, Stevens, V.M. (2015) An individual-centered framework for unravelling genotype-phenotype interactions. Trends in Ecology and Evolution, 30: 709-711.

Altermatt F, Legrand D, (2015) Big answers from small worlds: a user's guide for protist microcosms as a model system in ecology and evolution. Methods in Ecology and Evolution, 6(2): 218-231.Chang ES, Philippe H, (2015) Genomic insights into the evolutionary origin of Myxozoa within Cnidaria. Proceedings of the National Academy of Sciences, 112:14912-14917.

Legrand D, Larranaga N, Bertrand R, Ducatez S, Clavez O, Stevens VM, Baguette M (2016) Evolution of a butterfly dispersal syndrome. Proceedings of the Royal Society Biological Sciences, 283: 20161533.

Jacob S, Wehi P, Clobert J, Legrand D, Schtickzelle N, Huet M, Chaine AS (in press) Cooperation-mediated plasticity in dispersal and colonization. Evolution.

Dr Delphine LEGRAND CNRS Researcher Station d'Ecologie Théorique et Expérimentale, UMR5321 2 route du CNRS, 09200 Moulis, France +33 (0) 5 61 04 03 77 delphine.legrand@sete.cnrs.fr

LEGRAND Delphine <Delphine.LEGRAND@sete.cnrs.fr>

MountSinai NewYork PopulationGenetics

ICAHN SCHOOL OF MEDICINE AT MOUNT SINAI Open Post-Doc Position in Dr. Ron Do Lab

A computational postdoctoral position is available immediately in Population Genetics and/or Statistical Genetics in Dr. Ron Do's lab. The Do lab is in the Department of Genetics and Genomic Sciences, Icahn School of Medicine at Mount Sinai, New York and is situated in the Charles Bronfman Institute for Personalized Medicine.

Dr. Do's lab focuses on determining the genetic and biological bases of complex disease. The group pursues these interests by utilizing approaches from statistical genetics, population genetics, human genetics and genetic epidemiology.

Current lab research areas include: (1) Causal inference of biomarkers with complex disease; (2) Identification of biological processes of complex disease using functional data; (3) Testing for natural selection in medically relevant loci; (4) Rare variant association studies using sequencing data; (5) data mining in electronic health records.

The successful candidate will have the opportunity to work on large-scale cutting-edge sequencing, genotyping (including Mount Sinai's BioMe Biobank) and high-throughput functional data. Importantly, the candidate will have substantial input to the specific nature of their research project but should broadly fit within the lab's overall research goals.

Lab members will benefit from collaborations with neighboring labs in the Charles Bronfman Institute for Personalized Medicine, the Center for Statistical Genetics, and the Icahn Institute for Genomics and Multiscale Biology.

The term for this position is for 2-3 years with possibility of an extension depending on successful progress and available funding. A competitive salary, benefits and travel opportunities will be offered commensurate with experience and qualifications.

Job Qualifications: 1. Candidates should have a Ph.D., M.D. or equivalent doctorate in statistical genetics, population genetics, computational biology and/or human genetics. 2. Candidates should have proficiency in programming (e.g. Perl or Python) and statistical computing (e.g. R). 3. Candidates should have a track record of scientific productivity and/or leadership.

Please send inquiries, including a CV and two references, to Dr. Ron Do via email ron.do@mssm.edu.

Ron Do, Ph.D.

Assistant Professor in Genetics and Genomic Sciences Member, The Charles Bronfman Institute for Personalized Medicine Member, The Center for Statistical Genetics Member, The Icahn Institute for Genomics and Multiscale Biology Icahn School of Medicine at Mount Sinai Tel: 212-241-6206 Email: ron.do@mssm.edu Website: www.rondolab.org "Do, Ron" <ron.do@mssm.edu>

NIMBioS Knoxville SpatialModeling

*Postdoctoral Fellowship in Spatial Modeling at NIMBioS*The National Institute for Mathematical and Biological Synthesis (NIMBioS), located at the Univ. of Tennessee, Knoxville, is currently accepting applications for a two-year postdoctoral fellowship in spatial modeling with an interest in GIS, remote sensing, large spatial datasets and spatial analysis.

An applicant may propose to make advances on conceptual or methodological problems related to spatial modeling or to the application of spatial analyses to advance management of the environment and natural resources or of human or environmental health and diseases. Possible topics include, but are not limited to:

- Developing new tools for handling and analyzing Big Data (e.g., NEON) - Spatial, landscape explicit transmission of diseases - Linking fine scale and large scale ecological processes - Physiology trait mapping and links with climatic changes or extreme weather events - Spatial modeling of biodiversity and ecosystem services

Reflecting the interdisciplinary nature of this position, candidates with a PhD or equivalent in biology, mathematics, statistics, computer science, geography, environmental science, epidemiology, civil or environmental engineering, or any other relevant field will be considered.

*Support: *annual stipend of $51,000, full University of Tennessee employee fringe benefits, and an annual travel allowance of $3,000.

Deadline: The deadline is *December 18, 2016*, for fellowship research beginning late spring 2017. All letters of recommendation must be submitted before the request deadline.

*How to apply: *Follow the guidelines at http://www.nimbios.org/postdocs/ . Brian O'Meara, http://www.brianomeara.info, especially Calendar < http://brianomeara.info/calendars/omeara/ >, CV < http://brianomeara.info/cv/ >, and Feedback < http://brianomeara.info/teaching/feedback/ >

Associate Professor, Dept. of Ecology & Evolutionary Biology, UT Knoxville Associate Head, Dept. of Ecology & Evolutionary Biology, UT Knoxville Associate Director for Postdoctoral Activities, National Institute for Mathematical & Biological Synthesis < http://www.nimbios.org/ > (NIMBioS) Communication Director, Society of Systematic Biologists

omeara.brian@gmail.com

OhioStateU SnakeVenomEvolution

POSTDOCTORAL POSITION IN SNAKE VENOM EVOLUTION

The Gibbs Lab (https://u.osu.edu/gibbslab/) in the Department of Evolution, Ecology and Organismal Biology, Ohio State University has an opening for an NSF-funded Postdoctoral Research Associate for research on snake venom evolution. The postdoc will join a collaborative research group of US and Brazilian scientists funded through a joint NSF-FAPESP grant to study venom evolution in snakes at micro- to macroevolutionary timescales. Members of the group include D. Rokyta (Florida State University), C. Parkinson (University of Central Florida) and L. Gibbs (Ohio State University), I. Avezedo, A. Moura, E. Hingst-Zaher (Instituto Butantan) and H. Zaher (Universidade de Sāo Paulo). The specific project will focus on using comparative analyses to explore the links between venom variation at the molecular level and rates of speciation in venomous snakes but will also be involved in research assessing links between the genomic, proteomic and functional variation in venom across species. There will be the chance to visit participating laboratories in the US and Brazil and participate in field work.

MINIMUM QUALIFICATIONS:

- PhD in evolutionary biology, phylogenetics. bioinformatics or a related field

- Expertise in comparative analyses and/or molecular evolution

- Fluency in a programming language such as Perl or Python

- Record of publication

DESIRED QUALIFICATIONS:

- Experience with analyzing genomic, transcriptomic and proteomic data

- Experience with the use of high performance computing resources

START DATE AND DURATION The position is available 15 September 2017. The initial appointment is for one year with the possibility of reappointment for three additional years pending satisfactory performance. Salary is $47.5K with full benefits.

APPLICATION PROCESS Interested candidates should send the following to H. Lisle Gibbs (gibbs.128@osu.edu): 1) a CV, 2) Statement of research interests and how current professional abilities match possible project goals, 3) Names and contact information for three references. Review of applications will start 15 January 2017 with interviews taking place in February. I hope to offer the position to a candidate by March 2017.

ABOUT COLUMBUS The Ohio State University campus is located in Columbus, the capital city of Ohio. Columbus is the center of a rapidly growing and diverse metropolitan area with a population of over 1.5 million. The area offers a wide range of affordable housing, many cultural and recreational opportunities, excellent schools, and a strong economy based on government as well as service, transportation and technology industries (see http://liveworkplaycolumbus.com/). Columbus has consistently been rated as one of the Top U.S. cities for quality of life, and was selected as one of the Top 10 cities for African Americans to live, work, and play by Black Enterprise magazine. Additional information about the Columbus area is available at http://www.columbus.org. The Ohio State University is an equal opportunity employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation or identity, national origin, disability status, or protected veteran status.

“gibbs.128@osu.edu” <gibbs.128@osu.edu>

OregonStateU ExperimentalEvolution

A postdoctoral position is available in Molly Burke’s lab in the Department of Integrative Biology at Oregon State University, Corvallis, Oregon. Work in our lab examines broad evolutionary questions that can be interrogated with long-term selection experiments in model systems, integrating approaches in molecular/functional genetics, population genetics/genomics, and bioinformatics. Current areas of interest in the lab include the relative contribution of standing genetic variation vs. de novo beneficial mutation to long-term evolutionary change, the influence of population size on genomic signatures of selection, and the evolutionary genetics of aging. The successful candidate will work with the lab’s primary study system, Saccharomyces cerevisiae, and will also be encouraged to develop independent projects on new questions and/or other model systems within the general area of evolutionary genomics.

The candidate must have a Ph.D. in evolutionary biology or a related field.

Preferred qualifications:

1) experience with yeast genetics and genomics

2) experience generating and analyzing Next-Gen data

3) fluency in at least one programming language

Corvallis is located in the beautiful Willamette Valley in western Oregon, about 90 miles south of Portland. It has a charming college-town feel, great schools, and is surrounded by wilderness areas ideal for hiking and camping. The Department of Integrative Biology is a collegial group of biologists with diverse interests including geneticists, ecologists, and organismal biologists, and the university’s Center for Genome Research and Biocomputing provides state-of-the-art resources and training for genomic projects.

Please visit the P.I.’s homepage for more details on the lab’s research: www.burkelabosu.org Additional information:

Job posting: https://jobs.oregonstate.edu/postings/34909 Dept. of Integrative Biology: http://ib.oregonstate.edu/ Center for Genome Research and Biocomputing: http://cgrb.oregonstate.edu/ Applicants should upload a CV, a brief cover letter describing experience and interests, and contact information for 3 references to the job posting. Inquiries about the position also welcome by e-mail (molly.burke@oregonstate.edu).

Review of applicants will begin on November 30, though the position will remain open until filled. Start date is flexible, but could begin as early as January 2, 2017.

Molly K. Burke Assistant Professor Department of Integrative Biology Oregon State University 2094 Cordley Hall 541-737-5861 www.burkelabosu.org “Burke, Molly Kathleen” <Molly.Burke@oregonstate.edu>

RoyalOntarioMuseum CetaceanGenomics

The Royal Ontario Museum in Toronto invites applications for a Rebanks Postdoctoral Research Fellowship in the Department of Natural History starting ideally in February 2017. The successful candidate will work full time in the lab of Dr. Mark Engstrom developing a program on whale genomics and bioinformatics of mammals.

This is a two-year fellowship with an annual salary of $50,000 that provides Canadian citizens or Canadian landed immigrants who have obtained their doctorate degree in the last five years the opportunity to pursue their research with the support of one of Canada's leading research institutions. The ROM is a superlative showcase of the world's cultural and natural history - a place of discovery, learning, inspiration and imagination for visitors and staff alike.

With the salvaging of two blue whales from Newfoundland by the ROM in 2014, we have the unprecedented opportunity to sequence the first complete genome of this endangered species, to investigate questions concerning their evolution, phylogeny, historical demography, and conservation in relation to other cetaceans and mammals in general. The candidate will be able to interact with various collaborating labs and will be part of the active and diverse community of evolutionary biologists at the ROM and the University of Toronto.

We seek applicants with excellent skills in de novo next-generation genome assembly and analysis of genomic data with strong programming experience with R, Perl, or Phython, and statistical skills. Other required experience includes molecular laboratory skills such as primer design, PCR optimization, DNA sequencing, and sequence editing and alignment. Familiarity with theoretical phylogenetics, including current developments in tree reconstruction methods and experience with phylogenetic analysis software is needed for the position.

Candidates should electronically submit a letter of application detailing their research experience, interest in the position, preferred start date, curriculum vitae, and names with contact details of three references to: Dr. Mark Engstrom (marke@rom.on.ca), Deputy Director of Collections & Research and Senior Curator of Mammalogy, Royal Ontario Museum, 100 Queen's Park, Toronto, Ontario, M5S 2C6, Canada. Application materials must be received by January 6, 2017 for consideration. We especially encourage applications from women and members of minority groups.

[Chihuly. Now Open. ? l'affiche.] < https://www.rom.on.ca/chihuly >

Burton Lim <burtonl@rom.on.ca>

TexasAM PopGenomics

A postdoctoral research position is available in the Hurtado and Mateos Lab at Texas A&M University to study evolutionary and conservation genomics of marine and coastal organisms. The successful candidate will perform independent and team oriented studies on population genetic structure and ecological genomics using SNPs and DNA sequence data. S/he will conduct population genetics analyses of the blue crab using SNPs generated by ddRADseq. The lab also has ongoing projects on conservation genomics of the Critically Endangered Kemp's ridley sea turtle, evolution/phylogeography of coastal isopods, symbiosis, and there may be opportunities for collaboration with other projects.

The ideal candidate will be passionate about evolutionary and conservation genomics, and have excellent organization and communication skills. S/he must have demonstrated experience in generating and analyzing RADsequencing data to study population genomics. Other preferred experience includes: generation and analyses of transcriptomics data; DNA anchored hybridization data; phylogenomics; genome assembly/annotation; and/or microsatellites. The successful applicant is expected to conduct fieldwork in coastal habitats, have excellent verbal and written skills, and a successful population genomics research track indicated by publications in peer-reviewed journals and/or dissertation. S/he is also expected to lead outreach activities, multitask and work cooperatively with others, as well as assist, train and mentor students and other laboratory personnel.

Texas A&M University is in College Station, which offers an excellent living and work environment within easy reach of Houston and Austin. We strongly encourage women and members of underrepresented groups to apply. This position is eligible for health insurance benefits as well as retirement.

To apply and to obtain the full position description, visit greatjobs.tamu.edu/applicants/Central?quickFind3398 (NOV# 09910). In your application, please include a cover letter that describes why you are interested in this position and highlights your expertise, as well as the names and contact details of 2-3 references. Please also submit a research statement summarizing your major research accomplishments to date. Review of applications will begin Nov. 3rd and continue until position is filled. The expected start date is January 2017 or earlier. The position is available for one year. An additional year is contingent upon funding and satisfactory performance.

For questions about this position please contact Luis A. Hurtado (lhurtado@tamu.edu) or Mariana Mateos (mmateos@tamu.edu).

https://www.researchgate.net/profile/Luis_Hurtado5 http://people.tamu.edu/˜mmateos/mateoslab/Home.html Mariana Mateos, Ph.D. Associate Professor Department of Wildlife and Fisheries Sciences (wfsc.tamu.edu) Ecology and Evolutionary Biology PhD. Program (eeb.tamu.edu) Faculty of Genetics (genetics.tamu.edu) Texas A&M University 320B Heep Laboratory Building 2258 TAMUS College Station, TX 77843-2258 Phone(office/lab): 979-847-9463 Fax 979-845-4096 Email: mmateos@tamu.edu http://people.tamu.edu/˜mmateos My ResearcherID: http://www.researcherid.com/rid/B-5235-2008

"mmateos@tamu.edu" <mmateos@tamu.edu>

TexasTechU MicrobialGenomics

1. Postdoc Position in Microbial Symbiosis Genomics at Texas Tech

We are pleased to announce a Postdoctoral Research Associate position in metagenomics/bioinformatics in the laboratory of Dr. A.M.V. Brown (see http://www.amvbrown.com) in the Department of Biological Sciences (http://www.depts.ttu.edu/biology) at Texas Tech University, to begin in Fall 2017. Dr. Brown's lab investigates how host-associated bacteria and other microbes interact to limit or facilitate species invasions, disease outbreaks, or biomass production. We use a wide range of approaches including shotgun metagenomics and metatransciptomics, functional comparative genomics, and advanced bioinformatics. Systems include agricultural and medically related microbial communities.

We seek applicants who have completed, or will soon complete a PhD in any of these areas: symbiosis/host-microbe metagenomics, next-generation sequencing and bioinformatics, microbial genetics and ecology/evolution, or related fields. We especially encourage applicants with specialized skills and training in more than one -omics approach or with bioinformatics software development (programming) ability. To contribute to the scholarly excellence in Dr. Brown's lab, applicants should be self-motivated, insightful and ambitious in setting research goals, have excellent time management and organizational skills, demonstrated ability to complete projects and communicate science effectively, and be committed to enhancing the positive and diverse collaborative research community at Texas Tech.

Dr. Brown's lab will provide the successful applicant with a competitive salary and benefits for up to two years in accordance with national and university policy for postdocs, as well as cutting-edge training in important areas of biological research. Applicants will be mentored in career skills such as grant and fellowship application, and will be encouraged to seek additional funding support as part of their training. Texas Tech is a large university, growing in research strength and status, located in a sunny region with cool winters and plenty of outdoor and cultural activities, close to important centers for agriculture, medicine, and genomics. We welcome applicants of all backgrounds, without discrimination on the basis of an applicant's race, ethnicity, color, religion, sex, sexual orientation, gender identity, national origin, age, disability, genetic information or status as a protected veteran.

To apply for this postdoctoral position, please prepare a single pdf that includes: (1) a cover letter, (2) your up-to-date CV, with contact information for 3 persons who may be contacted for academic reference letters, and (3) a short statement of research interests (maximum 2 pages) describing your research goals, skills and expertise, and highlighting the impact of your academic achievements. Please send this to amanda.mv.brown@ttu.edu and contact this email address for questions.

Dr. Amanda M.V. Brown Assistant Professor Department of Biological Sciences, Texas Tech University Biological Sciences MS3131, Lubbock, TX 79409 Work Ph: 806-834-0984

Amanda Brown <amanda.mv.brown@ttu.edu>

UAarhus PlantKinInteractions

A two year post doc position in plant evolutionary ecology focusing on kin response in plant-plant interaction

The post doc position will focus on intraspecific variation in kin interaction and its impact for coexistence using annual Medicago species as model system and setting up experiments both under controlled and field conditions.

The position will be available from 1st March 2017. Application deadline 20th January 2017.

Place to work: Plant and Insect Ecology section at the Department of Bioscience, Aarhus University, Vejlsøvej 25, 8600 Silkeborg (Jutland), Denmark.

Further information can be obtained from Senior Scientist B. K. Ehlers, e-mail: boe@bios.au.dk and from the link: http://www.au.dk/om/stillinger/videnskabelige-stillinger/stillinger/Vacancy/show/867004/5285/ Thomas Bataillon <tbata@birc.au.dk>

UBasel EvoDevoNeuroEvolution

Postdoc: UBasel.EvoDevoNeuroEvolution A fully funded postdoctoral position is available in the Laboratory of Regulatory Evolution (Tschopp group) at the Zoological Institute, University of Basel, Switzerland.

The lab's research interests focus on how developmental processes can get modified, to give rise to morphological diversification on an evolutionary time-scale. As a model system, we are studying the development of the vertebrate skeleton with its associated neuromuscular system.

Vertebrate autopods (hands and feet) display the highest degree of morphological diversification in the appendicular skeleton, reflecting e.g. distinct modes of locomotion. While digit loss in the autopod has occurred in multiple vertebrate lineages, there seems to be a strong constraint to maintain the maximum number of digits at five, even though extra digits might prove beneficial in certain species.

The present project will investigate the potential for developmental plasticity in the limb neuromuscular system in response to changes in dactyly, i.e. altering digit numbers. Specific questions we will address include: How are muscle patterning and motorneuron axonal pathfinding coping with changes in digit numbers in vertebrate hands and feet? How is motorneuron pool complexity in the spinal cord affected by additional digit targets in the periphery? We will use a range of methods, including experimental embryology in chicken, genetic mouse models, axonal backfilling, NextGeneration-Sequencing and functional experiments using gene knock-down and overexpression.

The project builds on a solid foundation of confirmed preliminary data. For more information please visit http://evolution.unibas.ch/tschopp/research/ We offer a highly interactive and interdisciplinary research environment, attractive employment conditions and a very competitive salary by international standards. Full funding is available for 2 years The successful candidate will have a PhD in developmental biology and/or neurobiology, and will have skills in embryology, molecular biology and NextGeneration-Sequencing. Experience in axonal backfilling techniques will be a big plus. A basic understanding of Unix and the R language for statistical computing would be beneficial. You are interested in learning and using new technology to address longstanding questions in developmental and evolutionary biology.

Please send your application with a brief statement of motivation, a current CV and contacts for references to patrick.tschopp@unibas.ch Evaluation will begin on Dec. 1st 2016 and suitable candidates will be contacted shortly after. Earliest starting date is 1 January 2017.

Patrick Tschopp <patrick.tschopp@unibas.ch>

UBergen Bioinformatics

There is a vacancy for a postdoctoral fellow position at the Department of Biology within bioinformatics. The position is for a period of 4 years, and is connected to the Marine Biodiversity Group.

About the project/work tasks: The Marine Biodiversity Group of UiB has been focusing on the taxonomy, systematics and biogeography of marine invertebrates and algae of both shallow and deep-sea habitats of the Boreo-Arctic region, using a range of approaches from classical taxonomy to next-generation-sequencing technologies. The research will be in great part performed in the scope of the *EU-funded project SponGES* on the "Deep-sea sponge grounds ecosystems of the North Atlantic: an integrated approach towards their preservation and sustainable exploitation", a collaborative effort coordinated by the University of Bergen and involving 20 European, Canadian and American partners. The project's primary goal is to develop an integrated ecosystem-based approach for the preservation and sustainable exploitation of deep-sea sponge ecosystems of the North Atlantic, which requires a deep understanding of their diversity, evolutionary and connectivity patterns. Phylogenetic and population-level studies performed in sponges have been in most part restricted to shallow-water species, and relatively limited in terms of the nature and number of markers used. In SponGES we will employ a genomic-based approach to investigate the phylogenetic relationships, biogeographic patterns as well as genetic diversity, structure and connectivity of several deep-sea grounds-forming species at different spatial scales. Metagenomic and metatranscriptomic approaches will also be used to assess the composition and infer the function of sponges-associated microbial communities.

The candidate will be based at the University of Bergen but collaborate with researchers from several partner institutions of the SponGES consortium.

The activities will entail: assisting in data and sampling design development of data analyses pipelines analyses of genomic and transcriptomic datasets training and co-supervision of MSc and PhD-level students publishing in internationally recognized journals

Qualifications and personal qualities: The applicant must hold a PhD degree in biological sciences or bioinformatics, or have submitted his/her doctoral thesis for assessment prior to the application deadline. It is a condition of employment that the PhD has been awarded. The applicant must have a strong background in phylogenomics / population genomics Experience in developing and analysing genomic / transcriptomics datasets (e.g. GBS, RADseq, RNAseq) from non-model organisms, experience working in a Linux/Unix environment, and competence in scripting languages (e.g. Python, Perl) Work independently and in a structured manner, and have the ability to work as part of a large collaborative team. Proficiency in both written and oral English

About the position of postdoctoral fellow The position of postdoctoral fellow is a fixed-term appointment with the primary objective of qualifying the appointee for work in top academic positions. The fixed term period for this position is 4 years, of which 25 per cent of the employment period comprises required duties associated with research, teaching and dissemination. Individuals may not be hired for more than one fixed-term period as a postdoctoral fellow at the same institution. Upon appointment, applicants must submit a project proposal for the qualifying work. The project proposal must be prepared in cooperation with the project manager/supervisor and must also include a schedule. It is a requirement that the project is completed in the course of the period of employment.

We can offer: a good and professionally challenging working environment. salary at pay grade 57 (Code 1352) in the state salary scale. This currently amounts to an annual salary of NOK 486 100,-. Further promotions are made according to 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.

Your application 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 references. One of these may be the main advisor for the PhD thesis. CV transcripts and diplomas, and official confirmation that the doctoral thesis has been submitted. relevant certificates. a list of any works of a scientific nature (publication list). any publications in your name. The application and appendices with certified translations into English or a Scandinavian language must be uploaded at Jobbnorge.

Closing date for applications: 14 December 2016

General information: Detailed information about the position can be obtained by contacting Professor Hans Tore Rapp, Hans.Rapp@uib.no, or Postdoctoral Researcher Joana R Xavier, Joana.Xavier@uib.no

— / —

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

UBristol PlantEvolutionaryGenetics

Three year NERC postdoctoral position in plant ecological genetics and evolutionary rescue available at the University of Bristol, UK We are looking for an enthusiastic postdoctoral researcher for a NERC project on "evolutionary rescue and the limits of phenotypic plasticity", beginning in April 2017. This project will transplant ecologically divergent but closely related Senecio ragwort species on the slopes of Mount Etna, Sicily.

This project is a new collaboration between the Universities of Bristol, Oxford, Napoli (Italy), Catania (Sicily) and CNRS Montpellier.

It will combine extensive field transplant experiments with ecological and demographic analysis, quantitative genetics, and transcriptomics, in order to develop and test theory for the role of phenotypic plasticity in helping or hindering evolutionary responses at ecological margins.

The successful candidate will be based in Sicily for the first 15 months of the project, and then at the University of Bristol. A major part of the research will involve the extensive propagation and transplant of large numbers of Senecio seedlings along an elevational gradient, monitoring their fitness, and quantifying variation in their traits and phenotypes. This will be followed by extensive ecological and quantitative genetic analysis, and transcriptomic analysis of the genomic basis of adaptive and non-adaptive plastic responses.

The post will involve working closely with a field assistant based in Sicily, as well as a postdoctoral bioinformatician based at Oxford, and a Bristol-based technician to assist with morphometric and molecular analysis. Experience in extensive field experiments (particularly in plants), plant propagation and quantitative genetics would be highly desirable. A passion for evolutionary biology and the interaction between population genetics and genomics with population ecology is essential. Demonstrated experience in management, and proficiency in Italian would also be a big advantage.

Applications are invited from applicants regardless of their citizenship or country of origin.

More details are available here http://www.bristol.ac.uk/jobs/find/-details.html?nPostingId5337&nPostingTargetId 019&id=Q50FK026203F3VBQBV7V77V83& LG=UK&mask=uobext The closing date for applications is 4th January, 2017 Please direct informal enquiries to Dr Jon Bridle (jon.bridle@bristol.ac.uk), Prof Simon Hiscock (simon.hiscock@obg.ac.uk), or Prof Dmitry Filatov (dmitry.filatov@plants.ox.ac.uk) in the first instance.

Dr Jon Bridle School of Biological Sciences 2A03, Life Sciences Building University of Bristol, BS8 1TQ Tel. (+44) 117 394 1174 (internal 41174) jon.bridle@bristol.ac.uk http://-www.bristol.ac.uk/biology/people/jon-r-bridle/ Jon Bridle <bzzjrb@bristol.ac.uk>

UBritishColumbia Biodiversity

Postdoctoral Fellowship Opportunity

The next application round begins November 1, 2016. The deadline is January 13, 2017.

We seek applicants for a 2-year postdoctoral fellowship in the U.B.C. Biodiversity Research Centre (www.biodiversity.ubc.ca). The Centre is made up of over 60 faculty members with interests in ecology, evolution, systematics, biodiversity and conservation. Preference will be given to candidates with bold ideas, demonstrated research ability, and strong communication skills. The successful candidate will be expected to conduct original research on core problems in biodiversity, foster interactions within the Centre, run a seminar series, and organize a retreat. Postdoctoral fellows funded by the Biodiversity Research Centre typically interact with several lab groups. Candidates are welcome to contact potential collaborating labs in the Centre to inquire about current and potential research activities, but it is not necessary to apply to work with a specific faculty member.

Starting date, 1 September 2017. Salary $48,000 per yr. Research stipend: $7,000 per yr. Application requirements: curriculum vitae, a statement of overall scientific goals and interests (approximately 2 pages), and the names and contact information for three references All of the material should be submitted to biodiversity.centre@ubc.ca as a single PDF (please name your file using this format: Lastname_Firstname_PDF2017.pdf) Closing date for application, 13 January 2017.

The University of British Columbia hires on the basis of merit and is committed to employment equity. We encourage all qualified candidates to apply.

Katie Beall <brcadmin@biodiversity.ubc.ca>

UCalifornia Berkeley MicrobiotaHostEvolution

A postdoc position is available at the lab of Michael Shapira at UC Berkeley's department of Integrative Biology (https://ib.berkeley.edu/labs/shapira/).

We have recently established C. elegans as a new model for studying Host-Microbiota Interactions and we are interested (not exclusively) in using it to characterize factors that shape microbiota composition, microbiota contributions to host evolution, and modes of commensal transmission, or preference. All motivated researchers are welcome to apply; preference will be given to candidates with experience in molecular biology/microbiology, knowledge in python and/or R, and/or experience in C. elegans Biology.

Applications are welcome effective immediately. Please contact Michael Shapira directly: mshapira@berkeley.edu

Michael Shapira UC Berkeley Department of Integrative Biology Valley Life Sciences Bldg room 5155A Berkeley, CA 94720-3140 (510) 643-2579

mshapira@berkeley.edu

UCalifornia LosAngeles ConservationBiol

Title:

2017-2019 La Kretz Center Postdoctoral Fellowship Call for Applications Body:

The UCLA La Kretz Center for California Conservation Science (http://www.environment.ucla.edu/lakretz/) invites applications for its 2017 Postdoctoral Fellowship. Consistent with our mission, we seek one or more postdoctoral scholars who conduct innovative research that interfaces with the conservation and management agencies that direct and lead California conservation. Our emphasis is on biological conservation, and the successful candidate(s) could work in any discipline that provides the scientific research critical to the preservation, protection, management, or restoration of at-risk species, environments, or ecological communities in California. We will consider candidates who have completed their PhD, or will have completed it by August 2017. We envision hiring at least one Fellow each year, building a team of conservation scientists with a passion for California and its biodiversity.

The La Kretz Fellowship is for two years, subject to review after the first year. Our expected start date is late summer, 2017. The successful applicant will be expected to identify and work with at least one UCLA faculty member La Kretz affiliate (https://www.ioes.ucla.edu/-lakretz/people/?ioesrole=affiliates). Successful applications will identify research that addresses priority science concerns of resource management agencies (broadly defined) in California. The position has an annual salary of approximately $50,000 plus full benefits and modest research support ($5,000 over the two-year fellowship) that may be supplemented by individual mentors. Fellows have the option to reside at the newly renovated La Kretz Field Station (http:/-/www.environment.ucla.edu/lakretz/fieldstation/), located in the Santa Monica Mountains about 25 miles from campus, should it fit with their research and lifestyle objectives.

A requirement of the La Kretz Postdoctoral program is that candidates identify both a UCLA faculty mentor and an off-campus agency mentor. Our goal is to fund the most creative and innovative science that is of greatest interest both to our faculty and the applied conservation community. Several of our partner agencies have expressed particular interest in a series of high-priority projects, including some with potential co-funding. This list is neither comprehensive nor representative of projects that stand the highest chance of successful support. Rather, it provides one set of projects with strong interest from our partners and could form a starting point for developing collaborative projects. Visit our website at https://www.ioes.ucla.edu/lakretz/-our-work/fellowships/ for our La Kretz Center Partner Collaborative Projects & Funding list.

Several of our partners have expressed interest in co-sponsoring a La Kretz Center fellow, including possible co-funding opportunities, including:

Name: Sophie Parker

Organization: The Nature Conservancy

Email: sophie_parker@TNC.ORG

Name: Luis Chiappe

Organization: LA Natural History Museum

Email: lchiappe@nhm.org

Name: Robert Fisher

Organization: U.S. Geological Survey

Email: rfisher@usgs.gov

Name: Mike Westphal

Organization: US Bureau of Land Management

Email: mwestpha@blm.gov

Name: Cat Darst

Organization: US Fish and Wildlife Service

Email: cat_darst@fws.gov

Name: Katy Delaney

Organization: National Park Service

Email: katy_delaney@nps.gov

Name: Seth Riley

Organization: National Park Service

Email: seth_riley@nps.gov

Name: Robert Lovich

Organization: Department of Defense

Email: robert.lovich@navy.mil

Name: Mike White

Organization: Tejon Ranch Conservancy

Email: mwhite@tejonconservancy.org

Name: Milan Mitrovich

Organization: OC Natural Communities Coalition

Email: mitrovich@naturereserveoc.org

Name: Danielle Lefer

Organization: CA State Parks

Emai: Danielle.LeFer@parks.ca.gov

Interested candidates should submit 1) cover letter, 2) CV, 3) short 1-2-page description of their research and management accomplishments, 4) 2-page proposal describing their proposed research including potential faculty and agency mentors (single spaced, 2 page limit includes figures but not references), and 5) copies of two research publications, all as a single PDF file to Mario Colon, Administrative Assistant, at mario.colon@ucla.edu. You should also have three letters of recommendation, including one from your Ph.D. advisor, sent under separate emails with the subject line "La Kretz Postdoc letter for XXX (your last name)". The deadline for completed applications is 20 November 2016. E-mail questions to Mario or to Brad Shaffer (Director

— / —

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

---

UCambridge EvolutionaryGenomics

We are currently advertising two postdoc positions in 1) Chemical Ecology and 2) Mathematical and Evolutionary Genomics

http://www.jobs.cam.ac.uk/job/11915/ http://www.jobs.cam.ac.uk/job/11884/ These are part of an ERC grant to study speciation in Heliconius butterflies. This is an exciting opportunity to understand speciation in a well studied system with great genomic resources. See the links above for more details of individual positions or contact me for more information. The broader goals of the grant are outlined below:

The Heliconius butterflies offer an excellent opportunity to gain novel insights into the genetic architecture of speciation and its genomic consequences, by integrating genomic data from the well-studied ecological and behavioural processes that underlie speciation in this group. This ERC-funded project aims to study patterns of selection and introgression at wing patterning loci, in order to understand the process of genome divergence and adaptive radiation. The main goals of the wider project are as follows:

1) Characterise patterns of genetic divergence and gene flow along the speciation continuum. Using whole-genome resequencing of population samples in sympatry and allopatry, we will quantify the extent of gene flow between hybridising taxa. Wing pattern genes provide an example of adaptive introgression among populations and between species.

2) Are speciation genes clustered in the genome? Speciation theory predicts clustering of barrier genes, and we will test this by conducting the first genome-wide quantitative trait locus studies of reproductive isolation in Heliconius, replicated in two hybridising species pairs. Taking advantage of well-characterized ecology and behavior, we will determine the distribution of barrier genes accumulated where hybridizing species pairs are sympatric. In particular the focus is on the role of pheromonal signals in mate choice.

3) Are chromosomal rearrangements favoured by selection, and what is their impact on patterns of recombination? Theory predicts CRs should be favoured in association with barrier genes between sympatric species. We will determine the presence of chromosomal rearrangements in both sympatric hybridising pairs and

their allopatric relatives. Recombination will also be measured directly from crosses in both F1 and pure species genomes, to directly determine the influence of CRs on recombination rate. Finally we will determine the extent to which regions of high divergence (Goal 1) between species are explained by the known distribution of barrier genes (Goal 2) and patterns of recombination. This work will offer new insights into speciation, a process fundamental to evolution and biodiversity, but also has wider implications for our understanding of the processes that drive genome evolution.

Chris Jiggins Professor of Evolutionary Biology Department of Zoology University of Cambridge Tel: (+44)(0)1223 769021 Mob: (+44)(0) 7549-524-481 http://www.heliconius.org/ http://heliconius.zoo.cam.ac.uk/ @mel_rosina Fellow of St John's College, Cambridge, UK. CB2 1TP

Chris Jiggins <c.jiggins@zoo.cam.ac.uk>

UCollegeLondon StatisticalPhylogenetics

Research Associate in Statistical Phylogenetics in University College London, - Ref: 1607396

Research Associate in Statistical Phylogenetics at Department of Genetics, Evolution & Environment, UCL Grade: 7 Hours: Full Time Salary: Grade 7 (pounds 34,056 - pounds 41,163) per annum including London Allowance

Duties and Responsibilities

Working in Professor Ziheng Yang's group at UCL, the post holder will work on a project developing statistical methods and computer software to estimate specifies divergence times integrating information in genomic sequence data and in the fossil record. The project involves close collaborative work with Professor Phil Donoghue FRS of the University of Bristol.

The successful candidate will develop Bayesian inference methods and implement computer software for analysing genomic sequence and morphological character data incorporating information from living and fossil species. They will be required to participate in developing theory, designing and implementing computational algorithms, conducting simulation, compiling and analysing genomic datasets, and writing up the results for publication in international peer-reviewed journals.

The post is funded by the BBSRC for 32 months in the first instance. Starting date is 1 January 2017 or as soon as possible thereafter.

Key Requirements

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

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

Please note: Appointment at Grade 7 is dependent upon having been awarded a PhD; if this is not the case, initial appointment will be at research assistant Grade 6B (salary pounds 29,809 - pounds 31,432 per annum) with payment at Grade 7 being backdated to the date of final submission of the PhD thesis (including corrections).

Further Details

Full details on the role and the person specification can be accessed at https://goo.gl/C5e0jh .Please read these carefully before applying for the post. Your application should include: a brief personal statement (within two pages), explaining how your qualifications and experience make you a good candidate for this job, a CV and names and email addresses of at least two referees.

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

For any queries regarding the application process, please contact Biosciences Staffing on biosciences.staffing@ucl.ac.uk and quote the reference 1607396.

Closing Date: 13 December 2016

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

UConnecticut PlantComputationalGenomics

The Computational Plant Genomics Lab invites applications for a Postdoctoral position in the Department of Ecology and Evolutionary Biology at the University of

Connecticut. The group is focused on developing computational approaches that integrate next generation sequence data to address questions in non-model plants, particularly forest trees. We have the following ongoing projects: 1) Understanding the evolution of alternative translation initiation using RNA-seq data 2) Integrating new and existing approaches to gene prediction to improve the annotation of complex genomes 3) Analysis of gene family evolution and related comparative genomics questions 4) Detecting variation in populations from GBS and related sequence data.

Qualifications: * Ph.D in Genetics, Plant Genetics, Evolutionary Biology, Bioinformatics, Computational Biology, or other related field. * Track record of publications in comparative genomics. * Programming skills in Python, Perl, Java, C++, R or other languages. * Experience with Linux and high performance computing environments. * Experience in genome scale data analysis including RNA-Seq data, genome annotation, biological sequence analysis or other relevant computational genomics experience. * Highly motivated for interdisciplinary research, excellent communication skills, and the ability to work independently as well as within a research group.

About the University of Connecticut The University of Connecticut (UConn) has been one of the nation's leading public institutions since its founding in 1881. Located in Storrs, UConns main campus is situated in the picturesque rolling forests and fields quintessential of New England, yet is only 30 minutes from Hartford, and has close connections to Providence, Boston and New York City. The Department of Ecology and Evolutionary Biology consists of over 30 faculty and 60 graduate students with research spanning nearly all major groups of organisms. The Department maintains close ties with the Departments of Molecular and Cell Biology, Physiology and Neurobiology, Plant Science and Landscape Architecture, Animal Science, Marine Sciences, and the Institute for Systems Genomics, which together comprise one of the largest groups of biologists in the Northeast.

To Apply: Initial appointment is one year, with possible extension. Interested applicants should send their C.V., 2-3 page research statement, available start date, and contact information for three references to: jill.wegrzyn@uconn.edu. Applications that do not contain all materials will not be considered. Please submit application by Jan 1.

“jill.wegrzyn@uconn.edu” <jill.wegrzyn@uconn.edu>

UFederaldeMatoGrossodoSul Brazil SpeciesInteractions

Call for application to post-doctoral fellowship

(PNPD/CAPES)

In compliance with procedures of the Brazilian National Program of Post-Doctorate (PNPD/CAPES), the Ecology and Conservation Graduate Program (ECGP) calls for application from candidates willing to conduct research at the Universidade Federal de Mato Grosso do Sul (UFMS) as post-doctoral fellow.

*General information *

One fellowship grant will be provided through the selective process described here, open for PhD holders interested in participating in the ECGPs ongoing research and activities, hosted in the UFMS at the city of Campo Grande, capital of Mato Grosso do Sul state, southwestern Brazil.

The fellowship duration will be initially one year, renewable annually to a maximum of five years. Monthly stipends will be paid by CAPES in Brazilian currency (presently 4,100.00). The post-doctoral fellow should reside in Campo Grande.

Candidate profile

Preference will be given to candidates with PhD in ecology or related areas, with experience in conducting research and scientific publications. Expertise with species interaction networks is particularly welcome, nonetheless candidates with experience in other fields of ecology are also invited to apply.

Activities

The post-doctoral fellow will undertake research within the long-term research program (PELD/CNPq) conducted by ECGPs members in the carstic region of Serra da Bodoquena, in Mato Grosso do Sul. This research program hosts several projects with focus on different aspects of biological dynamics associated to a landscape gradient of habitat loss. The post-doctoral fellow can also be involved in undergraduate and graduate lecturing, laboratory instruction, tutorials, and supervision of undergraduate projects.

How to apply

Applications must be submitted by e-mail to the ECGPs secretariat (ecologia.ccbs@ufms.br) until January 15,

2017. The e-mail should contain the title post-doctoral fellowship and include in attachment, in PDF format, the following documents (in English, Portuguese or Spanish):

Letter of intention pointing out the background, interests and motivations for applying. It should concisely describe the main research lines and skills of the candidate, and present the academic activities in which the candidate would like to get involved.

Curriculum vitae containing relevant academic activities, with full name, birthday, present institutional affiliation (if any) and residential address. Brazilian candidates must send a CV copy generated in the Plataforma Lattes, and foreign candidates can use the form available in http://www.capes.gov.br/bolsas/-bolsas-no-pais/pnpd-capes, or alternative formats containing the same fields of information.

Note: additional documents will be required after approval. Additional procedures and detailed information is available in Portuguese at http://www.capes.gov.br/-bolsas/bolsas-no-pais/pnpd-capes . *Selective process*

The ECGPs board members will evaluated applications based on the CV and letter of intention of the candidates. They will consider the general academic experience of candidates, but mainly the experience showed through recent publications in high audience international journals. The research lines of the candidates will be evaluated according to the interest of the ECGP, which includes conciliating the input of new lines of study but not so distant from the ongoing lines already associated to the graduate program. As anticipated above, the ECGP will give preference for candidates with high expertise with species interaction networks. However, candidates with experience in other fields of ecology can be accepted instead, through comparative evaluation of CVs along with the letters of intention. The ECGPs board through voting of their members will decide a final rank of candidates. Each candidate will be informed on the results by e-mail. The ECGP reserves the right to publish a new call for application if no candidates were approved, as well as to offer the fellowship grant to subsequent ranked candidates in case of waiver by first classified ones.

*Implementation of fellowship grant *

The grant can be implemented immediately after the selective process, on February 2017, or later according to time required for arrangements of residence in Campo Grande. Once implemented, the post-doctoral fellow will discuss and schedule his research activities within the long-term research program in the Serra da Bodoquena, and other academic activities as well.

*Calendar *

Application deadline: January 15, 2017

Conclusion of the selective process: January 25, 2017 Beginning of activities: preferably February to early March 2017 (depending on time required for establishing residence in Campo Grande)

Nicolay Cunha <nicolaycunha@gmail.com>

— / —

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

---

UFlorida CladeDefinitions TreeOfLife

We are seeking a second postdoctoral fellow to support the Phyloreferencing project. Our ideal candidate is a biologist by training, and has strong expertise in systematic biology. The focus of your work would be on working with select NSF GoLife projects to develop meaningful phyloreferences and to use these in proof-of-concept applications for aggregating trait and other domain-relevant data. In addition, you would work with the ARBOR project to research integrating phyloreferences into trait-based analysis and visualization workflows.

The Phyloreferencing project is a collaboration between Dr. Nico Cellinese (Florida Museum of Natural History, University of Florida) and Hilmar Lapp (Center for Genomic and Computational Biology, Duke University) newly funded by the National Science Foundation. The postdoc will be based in the lab of Dr. Cellinese, but will work closely with both PIs. Starting date is negotiable. Salary is $50,000.

Why phyloreferencing?

The ability to freely and precisely communicate organism-linked data suffers serious limitations from the traditionally used taxon names based in Linnaean nomenclature. The semantics of such names are too often ambiguous, subject to divergent interpretation, and unavailable to computation. And with the advent of next-generation sequencing, metagenomics, and other modern biological data collection technologies, many groups of organisms for which we have interesting data do not yet, and may never have a Linnaean name.

Our project aims to overcome these limitations by defining ontology-based references (phyloreferences) to elements on the Tree of Life that are unambiguous and the semantics of which are amenable to powerful machine reasoning. One of the foundations of phyloreferencing is formed by the decades of theoretical and applied work on phylogenetic taxonomy. Ongoing computational work involves researching and developing OWL models and ontologies, tools for converting existing data into OWL format, and online proof-of-concept applications for using machine reasoning to navigate biodiversity data by clade semantics.

You can read the full grant proposal here: https://figshare.com/articles/-An_Ontology_Based_System_for_Querying_Life_in_a_Post_Taxonomic_Age/-1401984 Postdoctoral project responsibilities

You will work closely with the project PIs, existing postdoc and graduate students to generate the major project deliverables, focus on extending proof-of-concept tools to data integration use-cases beyond the Open Tree of Life project as the main phylogeny provider. Specifically, you will work with other projects funded by NSF's GoLife program to obtain large phylogenies, gather sources for meaningful phyloreferences, and develop phylorefer-encing proof-of-concept applications for these. These applications will include aggregating trait and other domain-relevant data. You will also work with the ARBOR Evolutionary Workflows project to prototype ways for integrating phyloreferences into trait-based analysis and visualization workflows that can be executed within the ARBOR framework.

While working with us on this project, you will gain familiarity with ontology development and ontology-enabled applications, including generating phyloreferences at a Tree-of-Life scale. You will also have the opportunity to explore, develop and test alternative approaches to clade definitions at every taxonomic level and at the broadest possible scales. You will have opportunities to publish both empirical and theoretical work.

Qualifications:

* PhD in Biology or a related field. * Strong background in Systematic Biology required. You should be well versed in all aspects of theoretical phylogenetics and related topics. * Programming experience in languages frequently used in scientific computing and for managing or converting scientific data (e.g., Python) is useful (and thus preferred) but not required. * Excellent communication and writing skills, and ability to interact productively with other projects' PIs and personnel.

How to apply:

Please submit a letter of interest and CV, together with the names and contact information of three academic references, to Dr. Nico Cellinese (ncellinese@flmnh.ufl.edu). All other inquiries should also be directed to Dr. Cellinese. The position will remain open until filled.

Nico Cellinese, Ph.D. Associate Curator, Botany & Informatics Joint Associate Professor, Department of Biology

University of Florida Florida Museum of Natural History 354 Dickinson Hall, 1659 Museum Rd. Gainesville, FL 32611-7800, U.S.A. Tel. 352-273-1979 Fax 352-846-1861 http://www.flmnh.ufl.edu/museum-voices/-nico-cellinese/ Twitter @ncellinese

"Cellinese,Nico" <ncellinese@flmnh.ufl.edu>

UIllinois ViralEvolution

The Brooke Lab (https://mcb.illinois.edu/faculty/-profile/cbrooke/) at the University of Illinois at Urbana-Champaign is looking to hire 2 postdoctoral research associates to work on a DARPA-funded project to study how collective interactions within influenza virus populations influence viral replication, transmission, and evolution. This project will be part of the DARPA INTERCEPT (INTERfering and Co-Evolving Prevention and Therapy) program, which aims to explore the potential of defective interfering particles as escape-resistant anti-viral therapeutics.

Studies in our lab will include using cutting-edge population sequencing and analysis approaches to examine influenza virus evolution in high resolution, the molecular dissection of viral replication at the cellular level, and in vivo studies of viral transmission. Candidates will be part of a multidisciplinary team that includes mathematicians/theoreticians (Ruian Ke at NC State and Katia Koelle at Duke), computational biologists, engineers (Connie Chang at Montana State), and chemists (Laura Fabris at Rutgers), all working together to develop ground-breaking approaches to explore influenza virus biology and population dynamics.

These positions will be fully funded for 1-4 years, and come with full benefits. Highly motivated, creative individuals with experience in molecular virology, experimental evolution, population sequencing, and/or animal models of viral infection are encouraged to apply. Ideal candidates will be highly motivated and creative, with strong interpersonal skills and command of written and spoken English. Applicants must have published in high quality peer-reviewed journals, and must have a PhD or have successfully defended their thesis prior to starting the position. Experience with bioinformatics/programming is highly desirable but not essential.

Applications will be reviewed until the positions are filled. The desired start date for these positions is early 2017, though accommodations can be made for the right candidate. Interested candidates should contact Chris Brooke (cbrooke@illinois.edu) with a cover letter and CV.

The University of Illinois at Urbana-Champaign is a world class public research institution located in idyllic Urbana, Illinois. We have all of the amenities of a thriving college town, paired with a low cost of living and relaxed, family-friendly atmosphere. Urbana is a 2 hour drive from Chicago, and a 3 hour drive from St. Louis.

“Brooke, Christopher Byron” <cbrooke@illinois.edu>

ULausanne BigDataBioinformatics

Postdoctoral associate in big data bioinformatics University of Lausanne & Swiss Institute of Bioinformatics

Start date: 01.01.2017 (or as soon as possible thereafter)

Contract: 1 year renewable (funding readily available for 3 years)

One of the major promises of Big Data lies in the simultaneous mining of multiple sources of data. This is particularly important in life sciences, where different and complementary data are scattered across multiple resources. To overcome this issue, the use of RDF/semantic web technology is emerging, but querying these systems often proves to be too complex for most usersâ€“thereby hampering wide development and adoption of these technologies.

This project is a collaboration between bioinformaticians from the Swiss Institute of Bioinformatics in Lausanne and Zurich, and information system engineers at the Zurich University of Applied Sciences (ZHAW), funded by the Swiss National Priority Programme ”Big Data“. It aims at enabling sophisticated semantic queries across large, decentralized and heterogeneous databases via an intuitive interface. The system will enable scientists, without prior training, to perform powerful joint queries across resources in ways that cannot be anticipated and therefore goes far beyond the query functionality of specialized knowledge bases.

The successful candidate will be based at the University of Lausanne, under the supervision of Prof. Christophe Dessimoz (OMA database), Dr. Heinz Stockinger (CTO of the Swiss Institute of Bioinformatics), and Prof. Marc Robinson-Rechavi (Bgee database). S/he will be responsible to implement interfaces to the OMA orthology database and Bgee gene expression database, and to establish a catalogue of sample cross-resources queries.

The successful candidate will also have the opportunity to gain teaching experience (e.g. via student project supervision and contribution to undergraduate or graduate teaching) and to contribute to other ongoing projects in the host labs.

At least 50% of the regular working hours will be devoted to personal research work.

Working conditions in Lausanne are extremely competitive, and include access to state-of-the-art computing and sequencing facilities. The environment is highly international, and all activities are conducted in English.

Profile Sought

Essential: - Doctorate degree in computer science, or bioinformatics with solid database or ontology experience in life sciences - Solid programming experience (min. 4 years) with languages such as Python, C/C++, Java, or R - Excellent spoken and written English proficiency - High level of motivation - Ability to collaborate in an interdisciplinary environment

Desirable: - Publications in peer-reviewed journals - Experience with bioinformatic databases - Experience with ontologies - Experience with semantic web technology - Experience with web technologies (Javascript, HTML, CSS)

How to apply

The application should consist of a single PDF file containing the following elements: - Motivation letter - Curriculum vitae including list of publications - Reference to best paper accompanied by a brief supporting statement (approx. 200 words) - The names and contact details of 2-3 references - Copy of official PhD certificate

Applications should be sent to Prof. Christophe Dessimoz (Christophe.Dessimoz@unil.ch) with subject line ”Big data postdoc job“.

For informal information, please contact Prof. Dessimoz, Prof. Marc Robinson-Rechavi (Marc.Robinson-Rechavi@unil.ch), or Dr. Heinz Stockinger (Heinz.Stockinger@sib.swiss).

Committed to promoting equal employment opportunities among its staff members, the University of Lausanne and the Swiss Institute of Bioinformatics particularly encourages applications by women.

To ensure full consideration, applications should be received by 10 Dec 2016

More info:

Dessimoz lab: http://lab.dessimoz.org Robinson-Rechavi lab: http://bioinfo.unil.ch/ < https://www.unil.ch/physiologie/home/menuinst/groupes-de-recherche/ana-claudia-marques-1.html > SIB Technology group: https://www.sib.swiss/sibt/ National Research Programme Big Data: http://www.nfp75.ch/en/ Christophe Dessimoz <Christophe.Dessimoz@unil.ch>

ULausanne ComparativeGenomics

Postdoctoral position in comparative genomics

Universtity of Lausanne, Department of Ecology and Evolution

We are looking for a highly motivated candidate to work on the comparative genomics of socially polymorphic ants. Previous work showed that social organization in the fire ant Solenopsis invicta is under the control of a social chromosome. The aim of this project is to reconstruct the evolutionary history of the social chromosome. The same genomic region has been shown to regulate social organization in 6 closely related fire ant species. Comparative analyses will be conducted to characterize the gene content, putative regulatory regions, and extent of synteny in the supergene among species and determine the routes and mechanisms of gene gain/loss and identify the nature of selection acting on the genes in the nonrecombining region. The proposed studies will thus permit to reconstruct the evolutionary history of a supergene involved in mediating a major social innovation. This work is of general significance because there are increasing number of examples of supergenes being involved in the regulation of important and diverse evolutionary phenomena such as the origin of sex chromosomes, mimicry, reproductive morphs and self-incompatibility.

The positions will be funded by a grant from the Swiss NSF. The duration will be 1-5 years.

Our group (www.unil.ch/dee/home/menuinst/research/keller-group.html) is part of the Department of Ecology and Evolution of the University of Lausanne, a well-funded and vibrant research institution, with superb facilities. The work will be conducted in collaboration with Kenneth Ross from the University of Georgia.

Inquiries and applications can be sent to laurent.keller@unil.ch. Applications should comprise

1) A CV and a list of publication

2) 1 page describing precisely why you are interested in joining our group and why you are competent for the proposed studies

3) Contact information for three referees.

Only applications with all these information will be considered.

Laurent Keller Department of Ecology and Evolution Biophore University of Lausanne 1015 Lausanne Switzerland www.unil.ch/dee/home/menuinst/research/keller-group.html Laurent Keller <Laurent.Keller@unil.ch>

ULausanne FungalGenomics

Postdoctoral position - Genetic and epigenetic variation in mycorrhizal fungi and its effects on plant growth (Uni. Lausanne, Switzerland)

A postdoctoral position is available in the Sanders' group to study the role of genetic and epigenetic variation in mycorrhizal fungi on plant growth. Our research indicates that genetic variation in mycorrhizal fungi is associated with large differences in plant growth. We will study this in more detail to find out which aspects of genetic or epigenetic variation in these fungi causes high growth rates in plants (especially cassava).

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.

Candidates must be highly motivated, have a PhD (or expect to have very soon), and have knowledge in at least two of the following fields: genomics; bioinformatics; epigenetics; evolutionary genetics; transcriptomics. 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, Dr Marco Pagni at the Vital-IT center of the SIB Swiss Institute of Bioinformatics and Prof. Alia Rodriguez at the National University of Colombia.

The position is available as soon as possible and is initially for 1 year. It is renewable for a maximum of 4 more years (depending on the number of years after receiving your PhD).

To apply send a CV and motivation letter in English, by email to ian.sanders@unil.ch. Please include the names of at least 2 people who I can contact for a reference. Applications must be received not later than 30th November 2016.

Prof. Ian R. Sanders Dept. of Ecology & Evolution University of Lausanne Biophore Building 1015 Lausanne Switzerland Tel (direct): +41 21 692 4261 Tel (Secretary): +41 21 692 4260 Fax: +41 21 692 4265 Email: ian.sanders@unil.ch http://www.unil.ch/dee/page7238_en.html **See my new website** http://people.unil.ch/iansanders/ Ian Sanders <ian.sanders@unil.ch>

ULiverpool EvolutionDrosophilaFertility

Header: ULiverpool.EvolEcol.DrosophilaFertility

Evolutionary Ecology Postdoctoral position available at the University of Liverpool, UK.

We are seeking a highly motivated individual to investigate how extreme temperatures impact on fertility in Drosophila, and whether this is likely to affect how species will respond to climate change. The thermal limits of species have often been used to predict how species are likely to respond to increasing global temperatures. These thermal limits are typically based on the temperatures at which organisms die or lose mobility. However, in a great many organisms, sterility occurs at temperatures far less extreme than those required to kill the organism. We aim to systematically investigate the links between fatal thermal limits and the temperatures at which flies become infertile, across a suite of Drosophila species.

You will join the research group of Dr Tom Price at Liverpool, and this NERC funded project will be co-supervised by Dr Amanda Bretman (Leeds) and Dr Rhonda Snook (Sheffield). You will be responsible for running laboratory experiments alongside a full-time technician. You should have a PhD degree in Ecology, Evolution or a related discipline, and practical experience working with invertebrates in a laboratory setting is required. You should possess excellent statistical analysis and communication skills, and be able to work in a collaborative environment. The post is available until 2020.

Unfortunately, due to funding restrictions, this post is only available to UK or EU citizens.

The deadline for applications is the 30th of November.

For enquiries email t.price@liverpool.ac.uk To apply go to: https://recruit.liverpool.ac.uk and search for job number 003144

Tom Price Institute of Integrative Biology Biosciences Building, Crown Street University of Liverpool Liverpool L69 7ZB 0151 795 4523

"Price, Thomas" <T.Price@liverpool.ac.uk>

ULyon EvolutionaryGenomics

A post-doctoral position in bioinformatics is available in the Laboratory of Biometry and Evolutionary Biology, at the University of Lyon, France. The selected candidate will join the Bioinformatics, Phylogeny and Evolutionary Genomics group and will work with Anamaria Necsulea on the evolution and functionality of long non-coding RNAs in mammals. The position is funded for 12 months (potentially renewable), starting in January 2017.

The ideal candidate has a PhD in bioinformatics, biostatistics and/or genomics and has experience in the analysis of high-throughput transcriptome sequencing data (RNA-seq). Applications from candidates with a Master degree will also be considered for a research assistant position.

The selected candidate will work on the evolution and functionality of long non-coding RNAs. It is now well established that long non-coding RNA (lncRNAs) transcription is pervasive in mammals. Thousands of lncRNA transcripts are now routinely detected with high-throughput transcriptome sequencing approaches. However, lncRNA functionality remains an important open question. Evolutionary approaches can bridge the gap between the mere evidence of transcription and lncRNA functionality, by identifying lncRNA genes that are subject to purifying natural selection to maintain their functional properties, or to positive selection following the acquisition of new functions. Here, we propose to use an evolutionary genomics and transcriptomics approach to explore lncRNA functionality. The project will entail comparative analyses of genomics and transcriptomics data, from several mammalian species.

Contact:

Anamaria Necsulea

anamaria.necsulea@univ-lyon1.fr

https://lbbe.univ-lyon1.fr Laboratoire de Biométrie et Biologie Evolutive

UMR CNRS 5558, Université Claude Bernard - Lyon 1

43 Bd du 11 Novembre 1918

Bâtiment Gregor Mendel

69622 Villeurbanne CEDEX

France

Anamaria Necsulea

Chargée de recherche CNRS Laboratoire de Biométrie et Biologie Evolutive UMR CNRS 5558, Université Claude Bernard - Lyon 1

43 Bd du 11 Novembre 1918 Bâtiment Gregor Mendel 69622 Villeurbanne CEDEX France

“anamaria.necsulea@univ-lyon1.fr” <anamaria.necsulea@univ-lyon1.fr>

UPennsylvania BehavioralGenomics

Two postdoctoral positions based at the University of Pennsylvania are available for sociogenomic projects using social spider and honey bee study systems.

1. The first project is a NIH-funded project that seeks to elucidate the molecular and behavioral mechanisms underlying collective behavior and disease transmission, using social spiders (Stegodyphus dumicola) as a study system. This project is a close collaboration between the Pinter-Wollman lab at UCLA (pinter-wollmanlab.eeb.ucla.edu), the Pruitt lab at UC Santa Barbara (labs.eemb.ucsb.edu/pruitt/jonathan), and the Linksvayer lab at U Pennsylvania (sites.sas.upenn.edu/linksvayer-lab). The post-doc would be based in the Linksvayer lab but would have opportunities to work in the Pinter-Wollman and Pruitt labs, as well as to participate in field collections and field work with spider colonies in South Africa and Namibia.

We seek enthusiastic, talented, and driven individuals to carry out the funded research project as well as to conduct related research. Candidates must have experience and expertise with one or more of the following: RNA sequencing, comparative or population genomics, evolutionary genetics, and bioinformatics (regardless of study system); experience studying animal behavior and social spiders or social insects is not required.

We will begin reviewing applications November 15, 2016, and continue considering applications as they arrive until the position as filled. The start date is flexible but can begin January 2017. Funding is available for multiple years, contingent on satisfactory progress. To apply, please send your CV, a short statement of research interests, and 1-3 representative papers or manuscripts to Tim Linksvayer at tlinks@sas.upenn.edu. Please contact Tim Linksvayer for further information.

2. The second project is a USDA-funded project that seeks to elucidate the genetic and social mechanisms regulating honey bee (Apis mellifera) traits associated with queen reproductive quality. This project is a close collaboration between the Linksvayer lab (sites.sas.upenn.edu/linksvayer-lab) in the Department of Biology at the University of Pennsylvania and the Tarpy lab (www.cals.ncsu.edu/entomology/apiculture) in the Department of Entomology at North Carolina State University.

We seek enthusiastic, talented, and driven individuals to carry out the funded research project as well as to conduct related research in the Linksvayer and Tarpy labs. We are especially interested in candidates with expertise in one of the following two broad categories: 1) RNA sequencing, comparative genomics, evolutionary genetics, and bioinformatics (regardless of study system); or 2) honey bee behavioral ecology and behavior. Depending on the candidate's expertise, the position will be housed in either Philadelphia at the University of Pennsylvania or Raleigh at NC State University, with the opportunity to work at both universities to gain expertise in these and other approaches.

We will begin reviewing applications November 15, 2016, and continue considering applications as they arrive until the position as filled. The start date is flexible but can begin January 2017. Funding is available for multiple years, contingent on satisfactory progress. To apply, please send your CV, a short statement of research interests, and 1-3 representative papers or manuscripts to Tim Linksvayer at tlinks@sas.upenn.edu. Please contact Tim Linksvayer or David Tarpy (david_tarpy@ncsu.edu) for further information.

Timothy Linksvayer Assistant Professor Department of Biology, University of Pennsylvania 225 Leidy Laboratories, 433 South University Avenue Philadelphia PA 19104-6018 tlinks@sas.upenn.edu phone +1 215 573 2657 https://sites.sas.upenn.edu/linksvayer-lab <

http://www.bio.upenn.edu/faculty/linksvayer/ >

tlinksvayer@gmail.com

UTexas Austin PlantPollinatorInteractions

Postdoctoral Position in Fire Ecology and Pollination

Funding is available through a multi-university USFWS State Wildlife Grant Program to examine the impact of prescribed fire and wildflower seeding on plant-pollinator populations and interactions across the US Southern Central Plains. The postdoctoral position will be supported by the Jha Lab at the University of Texas at Austin (https://w3.biosci.utexas.edu/-jha/) and the Baum Lab at Oklahoma State University (http://kabaum.wix.com/home), with residence in Austin, Texas for the first two years. A third year of funding is available and contingent upon research progress.

The postdoctoral project involves coordinating prescribed burn and wildflower seeding treatments to restore prairie systems across northern Texas and southern Oklahoma and evaluating the impacts of these treatments on native plant recovery, pollinator communities, and pollinator foraging ecology. The project will include one year of implementing the treatments (including pre and post-fire fuel load analyses) and two or more years of plant and pollinator population monitoring (including assessment of monarchs, native bees, and other species of conservation need). The objective is to characterize the impact of local restoration practices on plant and pollinator communities and their interactions to inform regional and national restoration practices.

Qualified candidates are required to have a Ph.D. in ecology, wildlife biology, entomology, or a related field of study. Candidates with background in fire ecology are strongly encouraged to apply; hands-on experience with prescribed fires is especially desirable. The research project will have a large field component, and thus some type of relevant field expertise (such as prescribed fire, vegetation surveys, bee community surveys, or wildland seeding) is required. Excellent communication skills, including effective writing, are also required. Prior experience supervising undergraduate students, working with landowners, and/or identifying native bees is a plus. It is expected that the appointee will be involved in the management of a large field crew and the mentoring of graduate and undergraduate students, as well as outreach/extension activities.

This is full-time postdoctoral researcher position with excellent benefits. Interested applicants should send (1) a letter of interest (˜1 page) describing previous research experience and their interests in working on the project, (2) a CV, and (3) contact information for three references willing to provide a recommendation. Please send any questions regarding the position to sjha@austin.utexas.edu (Subject line: “Postdoc position”). To apply, go to https://utdirect.utexas.edu/-apps/hr/jobs/nlogon/search/0/ and search for job # 16-11-16-01-0712. Review of applications will begin Dec 20th 2016, and will continue until the position is filled; however, applications received by the deadline will be given priority consideration.

The University of Texas at Austin is home to a vibrant research community, with strengths in population and community ecology, fire ecology, behavior, molecular biology, population genetics/genomics, multi-species interactions, and evolutionary biology. Opportunities exist to learn a range of both field-based and lab-based experimental techniques and to develop grant proposals for additional research projects. The University of Texas at Austin is an equal opportunity employer and is committed to providing employment opportunities to all qualified applicants without regard to race, color, religion, age, sex, sexual orientation, gender identity, national origin, disability or protected veteran status.

“Jha, Shalene” <sjha@austin.utexas.edu>

UToronto EEB Fellowship

The Department of Ecology and Evolutionary Biology at the University of Toronto invites applications for the 2017-18 EEB Postdoctoral Fellowship position.

Posting Date: November 8, 2016 Closing date: December 10, 2016 Area of Research: Ecology and/or Evolution, broadly defined. Description of duties: The Fellow will collaborate with the advisor(s) on research that is mutually agreed upon by all parties and the Fellow will publish the results in scientific journals. The Fellow will be a fully participating member in the Department. The Fellow may be asked to organize a workshop for graduate students, postdocs and faculty. Salary: $40,500/year Required qualifications: Applicants must have a PhD in ecology and/or evolution or a related area of study, and field-specific qualifications as set by the faculty advisor(s).

Application Instructions: All individuals interested in this position must first contact and obtain the agreement of a faculty advisor (or co-advisors); full-time faculty members at the St. George (downtown) campus of the University of Toronto are eligible to serve as advisors (see a list of potential supervisors at the bottom of this webpage: http://www.eeb.utoronto.ca/about-us/-employment/postdocs/eebpostdoc.htm). Afterwards, applicants must submit a cover letter clearly indicating the proposed faculty advisor(s) and the date that they will be available to begin the position, a curriculum vitae, copies of 2 publications, and a short (1-3 pages) description of past research accomplishments and future research plans. Applicants should include names and e-mail addresses for two potential referees. All application materials must be submitted as PDF(s) in a single email to: Elizabeth Rentzelos (chairsec.eeb@utoronto.ca) by the closing date.

Supervisor: member(s) of the EEB faculty (St. George campus) who has/have agreed to contribute to the salary of this postdoctoral fellow and to cover her/his research expenses. Expected start date: As early as Feb 1, 2017 and no later than Sept 1, 2017. Term: 12 months with the potential for a second, renewed term, assuming suitable progress. FTE: 100%

The University of Toronto is a leading academic institution in Canada with over 60 faculty members specializing in ecology and evolution. Strong links exist between the Department of Ecology and Evolutionary Biology and the Royal Ontario Museum, the Centre for Global Change, and the School of the Environment. The University owns a nearby field station dedicated to ecological and evolutionary research (the Koffler Scientific Reserve, www.ksr.utoronto.ca). The department also has a partnership with the Ontario Ministry of Natural Resources that helps provide access to infrastructure, including lab facilities in Algonquin Provincial Park (www.harkness.ca), funding, and long-term data sets. Genomic analyses are supported by a number of high-performance computing resources, multi-lab bioinformaticians, as well as staff at the Centre for the Analysis of Genome Evolution and Function.

Employment as a Postdoctoral Fellow at the University of Toronto is covered by the terms of the CUPE 3902 Unit 5 Collective Agreement. Please note that should the minimum rates stipulated in the collective agreement be higher than rates stated in this posting, the minimum rates stated in the collective agreement shall prevail. This job is posted in accordance with the CUPE 3902 Unit 5 Collective Agreement. The University of Toronto is strongly committed to diversity within its community and especially welcomes applications from visible minority group members, women, Aboriginal persons, persons with disabilities, members of sexual minority groups, and others who may contribute to the further diversification of ideas.

"luke.mahler@utoronto.ca" <luke.mahler@utoronto.ca>

WorkshopsCourses

Berlin DataManipulationVisualizationWithPython Mar13-17

Data manipulation and visualization with Python

13-17 March 2017, Berlin (Germany)

http://www.physalia-courses.org/courses/course10/ Instructor: Dr. Martin Jones

http://www.physalia-courses.org/instructors/t1/
Course overview:

One of the strengths of the Python language is the availability of mature, high-quality libraries for working with scientific data. Integration between the most popular libraries has led to the concept of a "scientific Python stack": a collection of packages which are designed to work well together. In this workshop we will see how to leverage these libraries to efficiently work with and visualize large volumes of data.

Workshop format:

The workshop is delivered over ten half-day sessions. Each session consists of roughly a one hour lecture followed by two hours of practical exercises, with breaks at the organizer's discretion. Each session uses examples and exercises that build on material from the previous one, so it's important that students attend all sessions. The last two sessions will be kept free for students to work on their own datasets with the assistance of the instructor. A description of the sessions can be found at the bottom of this page.

Who should attend:

This workshop is aimed at researchers and technical workers with a background in biology and a

basic knowledge of Python (if you've taken the Introductory Python course then you have the Python knowledge; if you're not sure whether you know enough Python to benefit from this course then just drop us an email).

Requirements:

Students should have enough biological/bioinformatics background to appreciate the example datasets. They should also have some basic Python experience (the Introduction to Python course will fulfill these requirements). Students should be familiar with the use of lists, loops, functions and conditions in Python and have written at least a few small programs from scratch. Students will require the scientific Python stack to be installed on their laptops before attending; instructions for this will be sent out prior to the course.

Curriculum

Monday 13th - Classes from 09:30 to 17:30

Session 1 - Introduction and datasets

Jupyter (formerly iPython) is a programming environment that is rapidly becoming the de facto standard for scientific data analysis. In this session we'll learn why Jupyter is so useful, covering its ability to mix notes and code, to render inline plots, charts and tables, to use custom styles and to create polished web pages. We'll also take a look at the datasets that we'll be investigating during the course and discuss the different types of data we encounter in bioinformatics work.

Session 2 - Introduction to pandas

In this session we introduce the first part of the scientific Python stack: the pandas data manipulation package. We'll learn about Dataframes the core data structure that much of the rest of the course will rely on and how they allow us to quickly select, sort, filter and summarize large datasets. We'll also see how to extend existing Dataframes by writing functions to create new columns, as well as how to deal with common problems like missing or inconsistent values in datasets. We'll get our first look at data visualization by using pandas' built in plotting ability to investigate basic properties of our datasets.

Tuesday 14th - Classes from 09:30 to 17:30

Session 3- Grouping and pivoting with pandas

This session continues our look at pandas with advanced uses of Dataframes that allow us to answer more complicated questions. We'll look two very powerful tools: grouping, which allows us to aggregate information in datasets, and pivoting/stacking, which allows us to flexibly rearrange data (a key step in preparing datasets for visualization). In this session we'll also go into more detail about pandas indexing system.

Session 4- Advanced manipulation with pandas

In this final session on the pandas library we'll look at a few common types of data manipulation binning data (very useful for working with time series), carrying out principal component analysis, and creating networks. We'll also cover some features of pandas designed for working with specific types of data like timestamps and ordered categories.

Wednesday 15th - Classes from 09:30 to 17:30

Session 5-Introduction to seaborn

This session introduces the seaborn charting library by showing how we can use it to investigate relationships between different variables in our datasets. Initially we concentrate on showing distributions with histograms, scatter plots and regressions, as well as a few more exotic chart types like hexbins and KDE plots. We also cover heatmaps, in particular looking at how they lend themselves to displaying the type of aggregate data that we can generate with pandas.

Session 6-Categories in seaborn

— / —

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

Berlin EukaryoticMetabarcoding Feb20-24 2

Dear all,

we still have a few places available on our next Eukaryotic-metabarcoding workshop: http://www.physalia-courses.org/courses/course4/ http://www.physalia-courses.org/courses/course4/ This course is being delivered by Dr. Owen S. Wangensteen, an expert in the application of molecular techniques to the study of marine ecological issues and biodiversity assessment of marine benthic ecosystems, including high-throughput sequencing and bioinformatics. He is currently working at the University of Salford (UK), actively participating on the development of new metabarcoding techniques for the assessment of biodiversity in the marine realm (both in benthic and seawater samples), as a member of Project SeaDNA (NERC, UK). The course will run from Monday 20th to Friday 24th February 2017 in Berlin, Germany.

Overview:

Metabarcoding techniques are a set of novel genetic tools for qualitatively and quantitatively assessing biodiversity of natural communities. Their potential applications include (but are not limited to) accurate water quality, soil diversity assessment, trophic analyses of digestive contents, diagnosis of health status of fisheries, early detection of non-indigenous species, studies of global ecological patterns and biomonitoring of anthropogenic impacts. This workshop gives an overview of metabarcoding procedures with an emphasis on practical problem-solving and hands-on work using analysis pipelines on real datasets. After completing the workshop, students should be in a position to (1) understand the potential and capabilities of metabarcoding, (2) run complete analyses of metabarcoding pipelines and obtain diversity inventories and ecologically interpretable data from raw next-generation sequence data and (3) design their own metabarcoding projects, using bespoke primer sets and custom reference databases. All course materials (including copies of presentations, practical exercises, data files, and example scripts prepared by the instructing team) will be provided electronically to participants.

Intended audience:

This workshop is mainly aimed at researchers and technical workers with a background in ecology, biodiversity or community biology who want to use molecular tools for biodiversity research and at researchers in other areas of bioinformatics who want to learn ecological applications for biodiversity-assessment. In general, it is suitable for every researcher who wants to join the growing community of metabarcoders worldwide. This workshop will review mostly techniques and software useful for eukaryotic metabarcoding. Another workshop focused on procedures currently used in microbial metabarcoding will be available from Physalia-courses.

Teaching format:

The workshop is delivered over ten half-day sessions (see the detailed curriculum below). Each session consists of roughly a one hour lecture followed by two hours of practical exercises, with breaks at the organizer's discretion.

Assumed background:

No programming or scripting experience is necessary, but some previous expertise using the Linux console and/or R will be most welcome. All examples will be run in a Linux environment. Thus, either a Linux PC or a virtual box running Linux under Windows or Mac environment will be needed. MacOSX systems might be OK, although installation of some additional Python packages might be needed in that case. The syllabus has been planned for people which have some previous experience running simple commands in Linux and using the R environment (preferently RStudio) for performing basic plots and statistical procedures. You will need to have a laptop with Python 2.7 installed for running OBITools, the main metabarcoding software package we will be using during the course, but no experience with Python is necessary. If in doubt, take a look at the detailed session content below or contact Dr. Owen S. Wangensteen (owenwangensteen@gmail.com mailto:owenwangensteen@gmail.com).

Course programme:

Monday 20th - Classes from 09:30 to 17:30

Session 1. Introduction to metabarcoding procedures. The metabarcoding pipeline.

In this session students will be introduced to the key concepts of metabarcoding and the different next-generation sequencing platforms currently available for implementing this technology. The kind of results that we may obtain from metabarcoding projects is explained using examples from real life. I will outline the different steps of a typical metabarcoding pipeline which will be further reviewed along the course. I will also explain the format of the course. In this session, we will check that the computing infrastructure for the rest of the course is in place and all the needed software is installed. Core concepts introduced: next-generation sequencer, multiplexing, NGS library,

— / —

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

---

Berlin PopulationGenomics May8-12

Workshop: Introductory Population Genomics: from Data to Inference

Monday 8th to Friday 12th May 2017, Berlin (Germany)

http://www.physalia-courses.org/courses/course9/ Instructor: Dr. Martin Taylor (http://www.physalia-courses.org/instructors/t9/)

Dr. Lewis Spurgin (http://www.physalia-courses.org/instructors/t8/)

Overview:

Next generation sequencing has revolutionized evolutionary biology allowing unprecedented resolution and insight into evolutionary questions that appeared intractable only a few years ago. The course will cover the basics of population genomic analysis from SNP data onwards and will cover the key analyses that may be required to successfully analyze a population genetic data set. The course will NOT cover steps prior to generation of a .vcf file or SNP data set such as NGS data demultiplexing, clustering and SNP calling (This is covered in detail in the Introduction to RADseq course). This course will introduce Linux and the command line environment, basic perl and python usage, file conversions and manipulation, population structure and differentiation in R, outlier analysis, landscape / seascape genomics and introgression. Having completed the course, students should have a good understanding of the software and methods available for population genomic analysis and be competent in population genomic analysis.

Intended audience & assumed background:

This workshop is aimed at postgraduate students and early career researchers who are interested in using population genomic tools in their research. No previous experience of bioinformatics is required, but an underpinning in evolutionary biology and basic population genetics concepts such as Hardy Weinberg Equilibrium and FST are desirable. The course will use a range of software including the Linux operating system and R.

Teaching format:

The workshop is delivered over ten half-day sessions (see the detailed curriculum below). Each session consists of a combination of lectures and practical exercises, with breaks at the organisers' discretion. There will also be time for students to discuss their own problems and data.

Curriculum:

Monday 8th-Classes from 9:30 to 17:30

Session 1- Introduction to Linux and the command line (Dr. Martin Taylor)

- Installation of required software
- Introduction to linux operating system
- Working on the command line. Basic bash shell commands and navigation.
- Introduction to Perl and Python

Session 2 - Understanding genomic data formats (Dr. Martin Taylor)

- Understanding and working with VCF files using VCF tools

- Data conversion and manipulation using Plink

- Text editors

Tuesday 9th-Classes from 9:30 to 17:30

Session 3- Introduction to genetic analysis in R (Dr. Lewis Spurgin)

- Introduction to R

- Reading data into R

- Data manipulation in R

- Introduction to Adegenet and other genetics packages

Session 4- Genomic diversity estimation (Dr. Lewis Spurgin)

- Estimating heterozygosity and nucleotide diversity

- Hardy Weinberg

- Linkage disequilibrium

- Introduction to ggplot2

Wednesday 10th-Classes from 9:30 to 17:30

Session 5- Population structure and differentiation (Dr. Martin Taylor & Dr. Lewis Spurgin)

- Estimating and understanding FST

- Visualising genetic structure using MDS and PCA

- STRUCTURE and related software

- Estimating migration

Session 6- Identifying selection within populations (Dr Lewis Spurgin)

- Marker-based genetic diversity

- Introduction to sliding windows

- Tajima's D and related statistics

- Introduction to GO analyses

Thursday 11th-Classes from 9:30 to 17:30

Session 7-Identifying selection among populations (Dr. Lewis Spurgin)

- FST outlier analysis

- EigenGWAS

Session 8-Incorporating landscape and seascape into population genomics (Dr. Martin Taylor)

- Seascape / landscape genetics

- Environmental / genomic correlation

Friday 12th-Classes from 9:30 to 17:30

Session 9-Hybridisation and introgression (Dr. Martin Taylor)

- Identifying hybrids and introgression using genotype data

Session 10-Summary data troubleshooting session (Dr Martin Taylor & Dr Lewis Spurgin)

- Time to answer questions on any areas covered during week.

Talk to us about your own data

Further information:

The cost is 480 euros (VAT included) including refreshments and course materials. We also offer an all-inclusive package at 745 euros (VAT included), including course material, refreshments, accommodation and food.

Application deadline: April 14th 2017.

For any further information, please feel free to email me.

–

Carlo Pecoraro, Ph.D

— / —

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

---

Berlin PYTHONforBIOLOGISTS December5-9

Introduction to Python for biologists 5-9 December 2016 in Berlin, GermanyInstructor: Dr Martin Jones Application deadline is: November 21st , 2016.

Overview: Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. This workshop is aimed at complete beginners and assumes no prior programming experience. It gives an overview of the language with an emphasis on practical problem-solving, using examples and exercises drawn from various aspects of bioinformatics work. After completing the workshop, students should be in a position to (1) apply the skills they have learned to tackling problems in their own research and (2) continue their Python education in a self-directed way. All course materials (including copies of presentations, practical exercises, data files, and example scripts prepared by the instructing team) will be provided electronically to participants.

Intended audience: This workshop is aimed at all researchers and technical workers with a background in biology who want to learn programming. The syllabus has been planned with complete beginners in mind; people with previous programming experience are welcome to attend as a refresher but may find the pace a bit slow. If in doubt, take a look at the detailed session content below or drop Martin Jones (martin@pythonforbiologists.com) an email.

Teaching format: The workshop is delivered over ten half-day sessions (see the detailed curriculum below). Each session consists of roughly a one hour lecture followed by two hours of practical exercises, with breaks at the organizer's discretion. There will also be plenty of time for students to discuss their own problems and data.

Assumed background: Students should have enough biological background to appreciate the examples and exercise problems (i.e. they should know about DNA and protein sequences, what translation is, and what introns and exons are). No previous programming experience or computer skills (beyond the ability to use a text editor) are necessary, but you'll need to have a laptop with Python installed.

Course programme: Monday 5th - Classes from 09:30 to 17:30 Session 1-. Introduction Session 2-Output and text manipulation

Tuesday 6th - Classes from 09:30 to 17:30 Session 3-File IO and user interfaces Session 4. Flow control 1 : loops

Wednesday 7th - Classes from 09:30 to 17:30 Session 5-Flow control 2 : conditionals Session6- Organizing and structuring code

Thursday 17th - Classes from 09:30 to 17:30 Session-7. Regular expressions Session 8-Dictionaries

Friday 18th - Classes from 09:30 to 17:30 Session 9-Interaction with the filesystem Session-10-Optional free afternoon to cover previous modules and discuss data

Further information: The cost is 555 euros (VAT included) including refreshments and course materials. We also offer an all-inclusive package at 795 euros(VAT included), including breakfast, lunch, dinner, refreshments, accommodation, course and transfer from/to the main city's airports.

Please feel free to contact us if you need any further information: info@physalia-courses.org

_

Carlo Pecoraro, Ph.D

Physalia-courses Coordinator

info@physalia-courses.org

http://www.physalia-courses.org/ Twitter: @physacourses

mobile: +49 15771084054

Carlo Pecoraro <info@physalia-courses.org> Carlo Pecoraro <info@physalia-courses.org>

Berlin QGISforBiologists February6-10

GIS analysis with QGIS for biologists From Monday 6th to Friday 10th February 2017 in Berlin, Germany http://www.physalia-courses.org/courses/course5/ Instructors: Dr Paolo Cavallini and Matteo Ghetta

Overview QGIS is the most popular and reliable Open Source GIS in the world. QGIS is currently used in Universities, Public Facilities and private offices. Born in 2002 as a simple layer viewer in the last 5 year more than 200 developers all over the world contributes to the source code making QGIS the standard of the GIS. The course is intended for biologists with no experience of GIS but also for those who want to switch from another GIS software to QGIS. The course will be focused on practical examples so that the students will be able to load and process their own data and perform both simple and complex spatial analysis.

Course materials (example data, presentations, additional files) will be provided to participants.

Intended audience Students and researchers with absolutely no GIS experience will learn the basic GIS system concepts and will be able to work alone with QGIS. However, people with both GIS concept and QGIS experience will enjoy the course. Furthermore, the course is useful to all of those people who want to migrate from another GIS software (ArcMap, gvSIG, GRASS, etc..) to QGIS.

Teaching format The course is 5 full-day long. The first day a small presentation of GIS concept will be shown. The other days practical examples and guided exercises will be provided.

Assumed Background Biologists can have absolutely no GIS (or QGIS) experience. GIS experts that want refresh some GIS concept or want to discover hidden features of QGIS are welcome!

Outline Introduction and installation

Introduction to Free and Open Source GISQGIS installation or upgrading QGIS overview

The work environmentWork environment configurationProjection managementProjectsPlugins management

GIS data

Vector data

Properties, import/export, conversion between formatsVector theming and labelsTables of attributes and actions. Turn a table into a geographic layer Raster data

Properties and themingCoordinate reference systems management and mosaicsGeoreferencing

First data analysis

Creation of animated maps3D visualizationAdanced layouts/printing; serial printing (mapbooks) Vector and Raster analysis

Vector analyses

dissolve, merge, overlay, attribute management, etc.Correction of topological errors and vector generalization

Raster analysisgeomorphology analyses: digital terrain modules, contour, slope, aspect, shaded mapsInterpolationsdistance analysisreclassification of rasters, map algebrazonal statisticsexamples: intervisibility, multicriteria analyses; priority and risk maps

Other GIS data type

How to use GPS units in QGISVector digitizing. CAD toolsThe geographic databases PostGIS and Spatialite and QGISAdd layers from map servers: WMS, WFS, WFS-T, CSW, WPS, OpenLayers, Google MapsImporting photos as pointsExporting data directly to Google Earth

Further information: The cost is 395 euros (VAT included) including refreshments and course materials. We also offer an all-inclusive package at 635 euros (VAT included), including breakfast, lunch, dinner, refreshments, accommodation, course and transfer from/to the main city's airports.

Application deadline is: December 22nd, 2016. Please feel free to contact us for any further information.

–

Carlo Pecoraro, Ph.D

Physalia-courses Coordinator

info@physalia-courses.org

http://www.physalia-courses.org/ Twitter: @physacourses

mobile: +49 15771084054

Skype: carlo_pecoraro

Carlo Pecoraro <info@physalia-courses.org>

England
AdvancedPythonForBiologists
Feb6-10

We still have a few places available on our next Advanced Python for biologists workshop - full details below

http://www.prstatistics.com/course/advanced-python-biologists-apyb01/ This course is being delivered by Dr Martin Jones, an expert in Python and author of two text books,

Python for Biologists [http://www.amazon.com/-Python-Biologists-complete- programming-beginners/dp/1492346136/]

Advanced Python for Biologists [http://-www.amazon.com/Advanced-Python- Biologists-Martin-Jones/dp/1495244377/].

This course will run from 6th 10th February 2017 at Flatford Mill field centre, Suffolk, England

This workshop is aimed at researchers and technical workers with a background in biology and a basic knowledge of Python.

The workshop is delivered over ten half-day sessions. Each session consists of roughly a one hour lecture followed by two hours of practical exercises, with breaks at the organizers discretion. Each session uses examples and exercises that build on material from the previous one, so its important that students attend all sessions. A description of the sessions can be found under programme.

Students should have enough biological/bioinformatics background to appreciate the examples and exercise problems (i.e. they should know what a protein accession number, BLAST report, and FASTA sequence is).

Curriculum:

Day 1:

Session 1 Data structures in Python In this session we will briefly recap Pythons basic data structures, before looking at a couple of new data types tuples and sets and discussing where each should be used. We will then see how we can combine these basic types to make more complex data structures for solving specific problems. Well finish our discussion by looking at specialized data types that are found in the Python core library. This session will also be our first introduction to benchmarking as we talk about the relative performance of different data types. In the practical session well learn how to parse an input file into a complex data structure which we can then use to rapidly query the data. Core concepts introduced: tuples, sets, higher-order data structures, default dicts, Counters, big-O notation.

Session 2 Recursion and trees In this session we will cover two very closely related concepts: trees (i.e. the various ways that we can store hierarchical data) and recursive functions (the best way to operate on treelike data). As recursion is inherently confusing, well start with a gentle introduction using biological examples before moving on to consider a number of core tree algorithms concerning parents, children, and common ancestors. In the practical session well look in detail at one particular way of identifying the last common ancestor of a group of nodes, which will give us an opportunity to explore the role of recursion. Core concepts introduced: nested lists, storing hierarchical data, recursive functions, relationship between recursion and iteration.

Day 2:

Session 3 Classes and objects In this session we will introduce the core concepts of object-oriented programming, and see how the data types that we use all the time in Python are actually examples of classes. Well take a very simple example and use it to examine how we can construct our own classes, moving from an imperative style of programming to an object-oriented style. As we do so, well discuss where and when object-orientation is a good idea. In the practical we will practise writing classes to solve simple biological problems and familiarize ourselves with the division of code into library and client that object-oriented programming demands. Core concepts introduced: classes, instances, methods vs. functions, self, constructors, magic methods.

Session 4 Object-oriented programming Following on from the previous session, we will go over some advanced ideas that are common to most object-oriented programming languages. For each idea well discuss the basic concept, the scenarios in which its useful, and the details of how it works in Python. This overview will also allow us to consider the challenges involved in designing object-oriented code. In the practical we will work on a simulation which will involve multiple classes working together. Core concepts introduced: inheritance and class hierarchies, method overriding, superclasses and subclasses, polymorphism, composition, multiple inheritance.

Day 3:

Session 5 Functional programming in Python This session will start with a look at a few different concepts that are important in functional programming, culminating in a discussion of the idea of state and its role in program design. We will see how functional programming is, in many ways, the complement of object-oriented

— / —

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

---

Faro Portugal Phylogenetics Apr24-29

**** REGISTRATION DEADLINE APPROACHING - 30th November ****

EMBO Practical Course: http://events.embo.org/17-phylogenetics Tree building: Advanced concepts and practice of phylogenetic analysis

24 - 29 April 2017, Faro, Portugal

About the practical course

The use of phylogenetic methods to reconstruct the evolutionary history of molecular sequences is a vital part of biological research. These methods underpin studies on the evolution and epidemiology of plant and animal parasites and disease-causing organisms, and more generally they allow an objective analysis of the patterns and processes generating biological diversity. To carry out phylogenetic analysis properly, it is necessary to have a good understanding of the strengths and weaknesses of the key methods and approaches. This EMBO Practical Course has been designed to provide the theoretical and practical skills needed to carry out state-of-the-art phylogenetic analyses.

The past few years have seen have an explosion in new methods of analysis including the application of Bayesian analysis methods in phylogeny reconstruction, the development of improved non-homogeneous models that much better represent the dynamics of sequence evolution, and the development of methods for high-throughput genome-wide analyses. This EMBO Practical Course has been designed to cater for these newest of methods and for understanding how they relate to the more traditional methods. Our goal is to teach technical sophistication without losing sight of the need for a critical attitude to data and analyses.

Speakers

Martin Embley - University of Newcastle, UK Tal Dagan- University of Kiel, Germany Tom Williams - University of Bristol, UK Peter Foster - Natural History Museum (London), UK Naiara Rodriguez-Ezpeleta - AZTI Tecnalia, Spain Mark Wilkinson - Natural History Museum (London), UK

Selection criteria

Participants will be early-career postdoctoral researchers and advanced PhD students who will be chosen on merit, as judged from a motivational letter and a CV. The selection procedure will also consider the need to balance numbers of participants representing different nationalities, to avoid over-representation from the host country (Portugal), to include a majority of participants resident in EMBC countries, and to maintain a reasonable gender balance.

Abstract guidelines

Abstract for a 10 minute PowerPoint presentation that each student will present (200 words)

Registration fees

Student/postdocs 200 euros Academic 300 euros Industry 300 euros

Registration includes: Accommodation 23rd - 29th April 2017, inclusive (7 nights) Lunch and coffee each day Dinner each day, including Welcome Dinner and Gala Transport to and from UALG campus (Gambelas) Registration administration Course materials

(We will try to accommodate all participants in single rooms but due to availability we have ask for some participants to share.)

Payment

Payment of the registration fees will be made by interbank transfer after notification of acceptance.

Registration deadline

30 November 2016

Selected participants will be notified by

14 December 2016 http://events.embo.org/17-phylogenetics For informal enquires contact: ccmaratt@ualg.pt

Cymon J. Cox

FCT Investigador - Coordinating Researcher Plant Systematics and Bioinformatics Research Group (PSB) Centro de Ciencias do Mar (CCMAR) - CIMAR-Lab. Assoc.

ccmaratt@ualg.pt

Herrsching Germany SelectionTheory Mar25-Apr1

The Chair of Plant Breeding of the Technical University of Munich will organise a one week spring school on “Selection Theory I” with Bruce Walsh of the University of Arizona, one of the leading authorities in this field. The TUM Spring School 2017 will provide an introduction to selection theory and breeding methodology relevant for PhD students and postdoctoral researchers in animal and plant breeding. The course consists of lectures and practical components with hands-on exercises.

TUM Spring School 2017 on “Selection Theory I” Lecturer: Professor Bruce Walsh, University of Arizona Herrsching am Ammersee, Germany March 25 - April 1, 2017

Topics covered:

- Introduction to basic concepts in selection
- Changes in mean and variance under selection
- Family based selection
- Recurrent selection
- Multi-stage selection
- Index selection

More information and online registration: http://www.plantbreeding.wzw.tum.de/index.php?id- Contact: Chair of Plant Breeding TUM School of Life Sciences Weihenstephan Technische Universität München Ulrike Utans-Schneitz, Ute Wiegand Liesel-Beckmann-Str. 2 85354 Freising, Germany Tel +49.8161.71.5226 plantbreeding.wzw@tum.de

Dr. Ulrike Utans-Schneitz Technische Universität München Lehrstuhl für Pflanzenzüchtung

Liesel-Beckmann-Str. 2 85354 Freising

Tel. +49 8161 71-5226

utansschneitz@tum.de www.plantbreeding.wzw.tum.de
Ulrike Utans-Schneitz <utansschneitz@tum.de>

MaxPlanckInst EvolBio Zoonoses aDNA Feb15-17

The Max Planck Institute for Evolutionary Biology and the Robert Koch Institute are organizing the workshop

One Past Health

- Understanding past zoonotic events to predict future ones -

from February 15th to 17th, 2017, at the Max Planck Institute for Evolutionary Biology in Ploen/Germany.

http://web.evolbio.mpg.de/OnePastHealth This workshop aims to foster the interdisciplinary dialog between medical, veterinary and biological sciences, bringing together empirical and theoretical researchers interested in disease ecology, epidemiology, host-pathogen coevolution, paleogenomics, and more. The resulting interactions will promote interdisciplinary scientific progress and may ultimately help uncovering ways to prevent future zoonotic events.

Synopsis: Many infectious diseases that are of high public health relevance today find their roots in past zoonotic events, e.g. the HIV-1 pandemics. Similarly, for these infectious diseases involving recurrent transmission from zoonotic reservoirs, most transmission events lie in the past, e.g. the historical pandemics of Yersinia pestis. These past events are an immense, precious and underexplored record of the processes leading to zoonotic emergence.

We have some tools to indirectly frame the context of zoonotic events. Historical outbreak records are such a tool but unfortunately often reveal a very unclear source of information. Over the last 2 decades, we took advantage of major advances in molecular biology, statistics and computational sciences to leverage the power of a natural record of the evolutionary history: the genetic diversity of present-day pathogens. This information was used to determine the origin in time and space as well as the later spread of Ebola viruses or HIV-1. But what if we could travel back in time and observe what really happened? We could then directly test the hypotheses we derive from present-day genetic diversity and catch evolution red-handed at crucial steps of the emergence process. Ancient DNA (aDNA) approaches are now ripe to simultaneously investigate the evolution of many pathogens (including zoonotic ones) and the evolution of the immune system of their hosts. This maturity nicely coincides with the development of modeling frameworks that allow us to make the most of heterochronous data and to describe individual pathogen trajectories in the context of the microbial communities they belong to.

Confirmed keynote speakers are:

Charlie Nunn, Duke University, USA Christian Drosten, Uni Bonn, Germany Frank Kirchhoff, Uni Ulm, Germany Simone Sommer, Uni Ulm, Germany Philippe Lemey, KU Leuven, Belgium Johannes Krause, MPI-SHH, Germany

Registration: There will be some slots for contributed talks as well as a poster session. Registration is on a first-come-first-serve basis. Deadline for registration is December 21st 2016. Please see the registration page on the workshop website for more details:

http://web.evolbio.mpg.de/OnePastHealth
Organizers: Sebastien Calvignac, Robert Koch Institute, Berlin Tobias Lenz, MPI for Evolutionary Biology, Ploen

_

Dr. Tobias Lenz, Group Leader Emmy Noether Group for Evolutionary Immunogenomics Department of Evolutionary Ecology Max Planck Institute for Evolutionary Biology August-Thienemann-Str. 2 24306 Ploen, Germany Tel: +49 4522 763-228 Fax: +49 4522 763-310 Email: lenz@evolbio.mpg.de

http://www.evolbio.mpg.de/-EvolutionaryImmunogenomics "lenz@evolbio.mpg.de" <lenz@evolbio.mpg.de>

Nairobi TraitsPastPresentFuture Mar6-8

Please join us for a workshop titled, "Traits past, present, and future: Quantitative approaches to conservation and climate change biology in Africa" held on 6 - 8 March 2017 at the National Museums of Kenya in Nairobi, Kenya. This event will bring together paleontologists, ecologists, and quantitative biologists to discuss how data from paleontology, modern ecology, and conservation biology can be integrated to provide a comprehensive framework for monitoring and measuring 'the evolution of' ecosystem structure and function through space and time.

For complete information, visit iccbio.org < http://iccbio.org/resources/Ecometrics%20Training%20Workshop%20Info.pdf > Register now at iccb.eventsmart.com < http://iccb.eventsmart.com >

– A. Michelle Lawing, PhD Assistant Professor Ecosystem Science and Management Texas A&M University 2120 TAMU Centeq Building B, 223 College Station, TX 77843

"alawing@tamu.edu" <alawing@tamu.edu>

Naples PhylogeneticsComparativeMethods Dec5-7

Dear Colleagues,

we are happy to announce an upcoming intensive workshop on phylogenetic and comparative methods

Dates: December 5-7.

PLACE: Stazione Zoologica A. Dohrn, Naples (Italy)

The workshop will include lectures on the theoretical aspects of generating time-calibrated phylogenies, reconstructing trait evolution and investigating rates of lineage diversification, as well as practical tutorials. A brief description of the program is listed below. The number of participants will be limited to 25, and admission is on a first come, first served basis. No previous experience with R is necessary, but students will be expected to have a basic understanding of molecular evolution:

REGISTRATION: by email at sergio.stefanni@szn.it

FEES: 100€(fees include lunches); special price at 50€for students enrolled at the Universities of Naples (Federico II and Parthenope) with no lunch included

PARTICIPANTS: this workshop is preferentially addressed to PhD students, postdocs and researchers with basic knowledge of phylogeny (sequence alignments, nucleotide substitution models and basic tree building). Max number 25

PROGRAM:

Day 1 - Introduction to the use of phylogenies in comparative methods - Introduction to Likelihood and bayesian phylogenetic inference - Theory of molecular clocks - Tutorial on relaxed clock node-dating - Introduction to R

Day 2 - Tutorial on total-evidence dating - Introduction to the use of remote servers (Cipres) for phylogenetic analyses - Tutorial on comparative methods for exploring the evolution of discrete and continuous characters

Day 3 - Theory and approaches to the study of adaptive radiations - Tutorials on comparative methods for detecting and quantifying heterogeneity in evolutionary rates

with best regards, Sergio Stefanni, PhD

Research FellowDept. of Biology and Evolution of Marine Organisms (BEOM)Stazione Zoologica "Anton Dohrn"Villa Comunale80121 - NaplesItaly

email: sergio.stefanni@szn.it / sstefanni@gmail.com office: +39 081 5833228

Sergio Stefanni <sstefanni@gmail.com> Sergio Stefanni <sstefanni@gmail.com>

Scotland GeometricMorphometrics Jun5-9

Geometric Morphometrics Using R (GMMR01)

This course is being delivered by Prof. Dean Adams, Prof. Michael Collyer and Dr. Antigoni Kaliontzopoulou

This course will run from 5th - 9th June 2017 at Millport Field centre on the Isle of Cumbre, Scotland. Please note that although the course is held on an island it is extremely accessible and easy to reach using public transport.

The field of geometric morphometrics (GM) is concerned with the quantification and analysis of patterns of shape variation, and its covariation with other variables. Over the past several decades these approaches have become a mainstay in the field of ecology, evolutionary biology, and anthropology, and a panoply of analytical tools for addressing specific biological hypotheses concerning shape have been developed. The goal of this is to provide participants with a working knowledge of the theory of geometric morphometrics, as well as practical training in the application of these methods.

The course is organized in both theoretical and practical sessions. The theoretical sessions will provide a comprehensive introduction to the methods of landmark-based geometric morphometrics, which aims at providing the participants with a solid theoretical background for understanding the procedures used in shape data analysis. Practical sessions will include worked examples, giving the participants the opportunity to gain hands-on experience in the treatment of shape data using the R package geomorph. These sessions focus on the generation of shape variables from primary landmark data, the statistical treatment of shape variation with respect to biological hypotheses, and the visualization of patterns of shape variation and of the shapes themselves for interpretation of statistical findings, using the R language for statistical programming. While practice datasets will be available, it is strongly recommended that participants come with their own datasets.

Note: Because this is a geometric morphometrics workshop in R, it is required that participants have some working knowledge in R. The practical sessions of the course will focus on GM-based analyses, and not basic R user-interfacing. It is therefore strongly recommended that participants refresh their R skills prior to attending the workshop.

Course cost is 520 for students and academic staff and 630 for people working in industry. Accommodation package available for 275, includes all meals and refreshments.

Course Programme

Sunday 5th Meet at Millport field centre at approximately 18:30.

Monday 6th - Classes from 09:00 to 18:001: 1: Morphometrics: History, Introduction and Data Types 2: Review of matrix algebra and multivariate statistics 3: Superimposition 4: Software demonstration and lab practicum

Tuesday 7th - Classes from 09:00 to 18:00 1: Shape spaces, shape variables, PCA 2: GPA with semi-landmarks 3: Shape covariation 4: Software demonstration and lab practicum

Wednesday 8th - Classes from 09:00 to 18:00 1: Phylogenetic shape variation 2: Group Differences & Trajectory Analysis 3: Allometry 4: Software demonstration and lab practicum

Thursday 9th - Classes from 09:00 to 18:00 1: Assymetry 2: Missing Data 3: Integration and Modularity 4: Disparity 5: Software demonstration and lab practicum

Friday 10th - Classes from 09:00 to 16:00 1: Future Directions 2: Lab Pacticum 3: Student Presentations

Please send inquiries to oliverhooker@prstatistics.co.uk or visit the website www.prstatistics.com Please feel free to distribute this information anywhere you think suitable

Upcoming courses - email for details oliverhooker@prstatistics.com 1. ADVANCING IN STATISTICAL MODELLING USING R (December 2016, April 2017, December 2017 http://www.prstatistics.com/course/advancing-statistical-modelling-using-r-advr05/ 2. SPATIAL ANALYSIS OF ECOLOGICAL DATA USING R (November 2016, July 2017) http://www.prstatistics.com/course/spatial-analysis-ecological-data-using-r-spae04/ 3. STABLE ISOTOPE MIXING MODELS USING SIAR, SIBER AND MIXSIAR USING R (February 2017) http://www.prstatistics.com/course/stable-isotope-mixing-models-using-r-simm03/ 4. GENETIC DATA ANALYSIS USING R (TBC) 5. BIOINFORMAITCS FOR GENETICISTS AND BIOLOGISTS (July 2017) 6. APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS (November 2017) 7. INTRODUCTION TO R AND STATISTICS FOR BIOLOGISTS (April 2017) 8. INTRODUCTION TO PYTHON FOR BIOLOGISTS (TBC) 9. TIME SERIES MODELS FOR ECOLOGISTS AND CLIMATOLOGISTS (TBC) 10. ADVANCES IN MULTIVAIRAITE ANALYSIS OF SPATIAL ECOLOGICAL DATA (April 2017) 11. ADVANCES IN DNA TAXONOMY (TBC)

— / —

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

---

Switzerland WholeGenomeSeqAnalysis Jan15

Reminder: Registration for the Triple A Winter School on Whole Genome Sequence Assembly, Annotation and Analysis closes 30th November.

Where: Monte Verita, Switzerland When: 15-20th January 2017

Triple A Winter School is a intensive workshop on how to Assemble, Annotate and Analyse Whole Sequence Data - with a focus on de novo whole genome assembly and analysis of complex genomes. The Winter School will combine lectures with computer based practicals, and will be most valuable to those who have or will soon have whole genome sequence data.

Webpage: http://www.adaptation.ethz.ch/education/-triple-a-winterschool.html Instructors include:

Monica Munoz-Torres from Lawrence Berkeley National Laboratory, USA. http://www.berkeleybop.org/-people/monica-munoz-torres/ Robert Waterhouse from Universite de Geneve and the Swiss Institute of Bioinformatics, Switzerland. http://rmwaterhouse.org/ Emmanuelle Lerat from Charge de recherche CNRS, France. https://lbbe.univ-lyon1.fr/-Lerat-Emmanuelle-.html?lang=3Den Peter Fields from Universität Basel, Switzerland. http://www.peterdfields.com/ < http://rmwaterhouse.org/ >

TOTAL COST: 610 CHF + travel to Locarno (Switzerland) Covers tuition, accommodation (shared double room) and all meals (breakfast, lunch, dinner, and coffee breaks).

Spaces are limited to 40 participants. See our webpage for more details.

ORGANISERS Dr Jessica Stapley < http://-jessicastapley.com/ >, ETH Zurich; Dr Stuart Dennis < http://stuartdennis.com/ >, EAWAG < http://www.eawag.ch/en/ >; Dr Stefan Zoller, GDC < http://www.gdc.ethz.ch/ > ETH Zurich and Professor Alex Widmer < http://www.peg.ethz.ch/-people/person-detail.html?persid=46511 > ETH Zurich.

Jessica Stapley <jessica.stapley@env.ethz.ch>

UEdinburgh IntroductionPython Dec12-16

We still have a few places left on the following course:

INTRODUCTION TO PYTHON FOR BIOLOGISTS

DATE: Monday 12 - Friday 16 December 2016 VENUE: The King's Buildings, The University of Edinburgh, Edinburgh, Scotland, UK REGISTRATION DEADLINE: Monday 28 November 2016 noon CANCELLATION DEADLINE: Monday 5 December 2016 noon PLACES: 20 (first come, first served) REGISTRATION FEE: pounds 500 (includes coffee/tea, but no lunch) INFORMATION: Bert Overduin (bert.overduin@ed.ac.uk), Martin Jones (martin@pythonforbiologists.com)

TO REGISTER: http://genomics.ed.ac.uk/services/-introduction- python-biologists

Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. This workshop is aimed at complete beginners and assumes no prior programming experience. It gives an overview of the language with an emphasis on practical problem-solving, using examples and exercises drawn from various aspects of bioinformatics work. The workshop is structured so that the parts of the language most useful for bioinformatics are introduced as early as possible, and that students can start writing plausibly-useful programs after the first few sessions. After completing the workshop, students should be in a position to (1) apply the skills they have learned to tackling problems in their own research and (2) continue their Python education in a self-directed way.

"Great learning from someone with a biology background rather than computer science - meant we were on the same wavelength." (February 2016) "Brilliantly well-run. From the book; to the USB stick with all the files we need; to the topics covered; to the system of helping us one-on-one, I cannot fault this course." (February 2016)

INSTRUCTORS

Dr. Martin Jones (Founder, Python for Biologists) Dr. Bert Overduin (Training and Outreach Bioinformatician, Edinburgh Genomics)

WORKSHOP FORMAT

The workshop is delivered over ten half-day sessions. Each session consists of roughly a one hour lecture followed by two hours of practical exercises, with breaks at the organiser's discretion. Each session uses examples and exercises that build on material from the previous one, so it's important that students attend all sessions. A description of the sessions can be found at the bottom of this page.

WHO SHOULD ATTEND

This workshop is aimed at researchers and technical workers with a background in biology who want to learn programming. The syllabus has been planned with complete beginners in mind; people with previous programming experience are welcome to attend as a refresher but may find the pace a bit slow. If in doubt, take a look at the detailed session content below or drop Martin Jones or Bert Overduinan email.

REQUIREMENTS

Students should have enough biological/bioinformatics background to appreciate the examples and exercise problems (i.e. they should know what a protein accession number, BLAST report, and FASTA sequence is). No previous programming experience or computer skills (beyond the ability to use a text editor) are necessary.

SESSION CONTENT

1. Introduction

In this session I introduce the students to Python and explain what we expect them to get out of it and how learning to program can benefit their research. I explain the format of the course and take care of any housekeeping details (like coffee breaks and catering arrangements). I outline the edit-run-fix cycle of software development and talk about how to avoid common text editing errors. In this session, we also check that the computing infrastructure for the rest of the course is in place (e.g. making sure that everybody has an appropriate version of Python installed). Core concepts introduced: source code, text editors, whitespace, syntax and syntax errors, Python versions

2. Manipulating text

In this session students learn to write very simple programs that produce output to the terminal, and in doing so become comfortable with editing and running Python code. This session also introduces many of the technical terms that we'll rely on in future sessions. I run through some examples of tools for working with text and show how they work in the context of biological sequence manipulation. We also cover different types of errors and error messages, and learn how to go about fixing them methodically. Core concepts introduced: terminals, standard output, variables and naming, strings and characters, special characters, output formatting, statements, functions, methods, arguments, comments.

3. Working with files

I introduce this session by talking about the importance of files in bioinformatics pipelines and workflows, and we then explore the Python interfaces for reading from and writing to files. This involves introducing the idea of types and objects, and a bit of discussion about how Python

— / —

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

---

ULeipzig ProgrammingForEvolBiol Mar4-20

Course on Programming for Evolutionary Biology

When: March 4th - March 20th 2017

Location: Leipzig, Germany

Application deadline: December 31st 2016

Detailed information about the course content and how to apply: http://evop.bioinf.uni-leipzig.de/ In this intensive 17 days course, students will learn how to survive in a Linux environment, get hands-on experience in two widely used programming languages (Python and R), and statistical data analysis. The classes will be given by experts in the field and consist of lectures and exercises with the computer. The aim of the course is to provide the students with the necessary background and skills to perform computational analyses with a focus on solving research questions related to genomics and evolution. The philosophy of the course will be "learning by doing", which means that the computational skills will be taught using examples and real data from evolutionary biology for the exercises. During the course, students will also propose projects of their own interest and perform them as final projects in small groups under the supervision of a teaching assistant. This summer school is open for students from all countries and targeted toward PhD students and postdocs of evolutionary biology or related research fields with no or little programming experience who want to become proficient in computational evolutionary biology in a couple of weeks.

The course takes place at the University of Leipzig.

– Dr. Katja Nowick

Group Leader "TFome and Transcriptome Evolution" www.nowick-lab.info Universität Leipzig Härtelstrasse 16-18 04107 Leipzig Germany Phone 1: +49 341 97-16684 Phone 2: +49 341 97-16653 Fax: +49 341 97-16679

Katja Nowick <nowick@bioinf.uni-leipzig.de>

USheffield PopulationGenomics Jan16-18

POPULATION GENOMICS WORKSHOP

January 16th-18th 2017 University of Sheffield, UK

This course will be held at the NERC Biomolecular Analysis Facility at the University of Sheffield and introduce participants to a variety of population genomics analyses for large next generation sequencing (NGS) datasets. It will include discussion on single nucleotide polymorphism (SNP) calling and filtering options, an introduction to population genomics statistics using the PopGenome R package, examining genetic structure, Fst-based analyses such as outlier detection/genomic islands of divergence, and genome-wide association analysis (GWAS).

The majority of the course will comprise practical computer sessions, giving participants hands-on experience in these analyses. We will perform these on the high performance computing cluster at Sheffield and computers will be provided. Prior experience with the Linux environment and basic command line tools would be advantageous.

There is no charge for the course, and successful applicants will be provided with accommodation for two nights and up to 100 towards travel costs to Sheffield.

The application closing deadline is at 5pm on Monday 28th November.

Further details and how to apply can be found at: https://www.sheffield.ac.uk/nbaf-s/courses/popgen Dr Helen Hipperson

Data Analyst NERC Biomolecular Analysis Facility - Sheffield http://www.shef.ac.uk/nbaf-s/home https://www.facebook.com/nbafsheffield h.hipperson@sheffield.ac.uk

---

Weggis Switzerland AdaptationBioinformatics Feb5-11

Winter School - Bioinformatics for Adaptation Genomics (B@G3 2017)

DATE: February 5-11, 2017

Reminder for the Winter School of Bioinformatics for Adaptation Genomics. The registration deadline is approaching fast. Applications need to be submitted by November 20th 2016.

AIMS AND OBJECTIVES The application of next-generation sequencing (NGS) technologies to non-model organisms is now well-established and has unlocked new frontiers for research on adaptation genomics. Despite recent technological developments enabling an increasing number of projects to use genome-scale data, the analysis of such complex data sets still raises substantial hurdles for researchers with primarily a biological background. Bioinformatic pipelines offer an invaluable resource to process genomic data, but their underlying rationale often remains hard to understand, which poses significant challenges for their rigorous use and for the accurate interpretation of the results. The B@G Winter School provides an opportunity for researchers to penetrate the 'black box' behind the complex bioinformatics approaches available for investigating adaptation genomics throughout the analytical pipeline; from the programs and assumptions necessary to produce a high quality SNP dataset to the in-depth interpretation of methods designed to address key evolutionary questions. B@G teachers are established scientists with a primary role in the development of widely used bioinformatic software, and will provide insights into the foundations of the algorithms and suggest best practice in experimental design and analysis.

AUDIENCE The School is primarily aimed at evolutionary biologists and bioinformaticians who want to gain deeper knowledge on state-of-the-art methods used to detect evolutionary patterns from genome-wide nucleotide data. Applications from early career researchers (PhD and post-doctoral level), as well as faculty with a background in ecology, genetics, or bioinformatics, will be considered. The workshop is particularly aimed at candidates with experience of the Unix environment and with preliminary knowledge on analytical pipelines for genomic data.

VENUE The school will be hosted at the Alexander & Gerbi Hotel in Weggis, Switzerland (http://www.alexander-gerbi.ch).

COST Total fee for participants is 750.- CHF. This includes tuition and accommodation in double rooms with full board (Breakfast, Lunch, Dinner and coffee breaks) at the Alexander & Gerbi Hotel during the workshop. A limited number of single rooms may be available upon request at an additional fee of 300.- CHF.

REGISTRATION The workshop will be limited to 30 participants. We ask that all interested participants submit a cover letter (1 page max) detailing their research interests, their level of bioinformatics experience, and motivation for attending the workshop, as well as their CV (2 pages max) to BioinfAdapt@env.ethz.ch by November 20th 2016. Participants will be notified of the outcome of the selection process by December 5th 2016.

SCHOOL LECTURERS Dr. Jonathan Puritz - Marine Science Center, Northeastern University, USA Website: http://www.marineevoeco.com Mr. Erik Garrison - Wellcome Trust Sanger Institute, UK Website: http://hypervolu.me/ ˜ erik/erik_garrison.html Prof. Dr. Alex Buerkle - University of Wyoming, USA Website: http://www.uwyo.edu/buerkle/ Dr. Anders Albrechtsen - Bioinformatics Centre, Copenhagen University, Denmark Website: http://popgen.dk/-albrecht/web/WelcomePage.html Prof. Dr. Daniel Wegmann - University of Fribourg, Switzerland Website: http://www.unifr.ch/biochem/index.php?id=789 ORGANISERS Dr. Simone Fior, ETH Zurich (simone.fior@env.ethz.ch) Dr. Martin C. Fischer, ETH Zurich (martin.fischer@env.ethz.ch) Dr. Stefan Zoller, GDC-ETH Zurich (stefan.zoller@env.ethz.ch) Prof. Dr. Alex Widmer, ETH Zurich (alex.widmer@env.ethz.ch)

Funded by Adaptation to a Changing Environment (ACE) initiative, ETH Zürich, Switzerland

For more information: http://www.adaptation.ethz.ch/-education/winter-school-2017.html

---

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.