EvolDir

October 1, 2017

Month in Review

Foreword

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

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

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

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Conferences

ASAB LondonZoo SexualSelection Dec7-8

REMINDER: ABSTRACT DEADLINE 1st OCTOBER

The 2017 ASAB Winter meeting (Thursday 7th and Friday 8th December 2017):

Sexual selection: do we still need to test the alternatives?

Organised by Professor Nina Wedell and Dr David Shuker

ABSTRACT SUBMISSION NOW OPEN: DEADLINE 1st OCTOBER

The 30 years since the publication of Bradbury and Andersson's landmark "Sexual selection: testing the alternatives" has seen a wealth of new empirical data on the mechanisms and patterns of sexual selection, alongside major theoretical advances. However, some key concerns remain, including what drives the evolution of mate choice and how sexual selection and natural selection interact. Moreover, the very definition of sexual selection remains contested. In this meeting, we will explore the latest findings in sexual selection, in terms of both theory and experiment, to chart our progress in understanding this most beguiling of evolutionary mechanisms, and to map the way forward for the next generation of sexual selection researchers.

Our invited speakers are Suzanne Alonzo, David Hosken, and Hope Klug, and we are also delighted that Christine Nicol will be presenting the 2017 Tinbergen Lecture during the meeting. We invite spoken and poster presentations encompassing the widest range of current work on sexual selection. Please note that due to space constraints, poster space will unfortunately be limited.

The meeting will be held at the Zoological Society of London, Huxley Lecture Theatre, London Zoo. As is traditional for the ASAB winter meeting, there is no registration and delegates need to organise their own accommodation and main meals. Tea and coffee will be provided both days, along with a wine reception on the evening of the 7th. We welcome those wishing to indicate their likely attendance however, and we are very pleased to announce that abstract submissions for spoken and poster presentations is now open (deadline 1st October 2017). An abstract submission form is available on our website: http://asabwinter2017.weebly.com/ and only submissions using this form will be accepted. Presentations will be chosen blind to author(s) and host institution(s).

For further details, please visit our website (http://asabwinter2017.weebly.com/) or contact us on our dedicated conference email: asab2017@st-andrews.ac.uk

We very much look forward to seeing you in December,

Nina Wedell and Dave Shuker

David Shuker <dms14@st-andrews.ac.uk>

Assam India BacterialEvolution Dec14-16

WHERE: Kaziranga National Park, Assam, India

WHAT: SMBE satellite meeting on Bacterial Evolution

WHEN: 14-16 December 2017

Travel awards available for PhDs and post-docs.

see: http://www.smbe.org/smbe/HOME/TabId/37/ArtMID/1395/ArticleID/55/SM BE-Satellite-Meeting-in-India-This-December.aspx

Edward Feil <E.Feil@bath.ac.uk>

Bangalore India ButterflyEvolution Jul11-15

8th International Conference on the Biology of Butterflies

Dates: 11-14 June 2018

Place: Bangalore, India

The 8th International Conference on the Biology of Butterflies conference will be held in Bangalore, India, from 11-14 June 2018. The International Conferences on the Biology of Butterflies are international gatherings, organized every four years, of primarily professional biologists who study evolutionary biology, behaviour, ecology, systematics, biogeography, genetics, developmental biology, and biodiversity conservation, with butterflies and moths as their focal study organisms. This is an excellent academic and professional forum for latest discoveries and to exchange news in these research areas.

Website: www.biologyofbutterflies.org Organisers: Krushnamegh Kunte (krushnamegh@ncbs.res.in) Ullasa Kodandaramaiah (ullasa@iisertvm.ac.in)

Ullasa Kodandaramaiah

Indian Institute of Science Education and Research (IISER) Thiruvananthapuram < http://iisertvm.ac.in > Maruthamala P.O. Vithura Kerala, India. 695 551.

ullasa@iisertvm.ac.in

Harvard YoungInvestigator Oct11

Young Investigator Symposium

Date:

Wednesday, October 11, 2017: 9:00 am - 1:00 pm

Location: Robinson Hall Lower Library, 35 Quincy Street (Harvard Yard), Cambridge, MA, USA

The Max Planck-Harvard Research Center for the Archaeoscience of the Ancient Mediterranean (MHAAM), a collaboration between The Initiative for the Science of the Human Past at Harvard (SoHP) and the Max Planck Institute for the Science of Human History in Jena, Germany (MPISHH) announces an opportunity for recent and graduating seniors and Master's students to participate in a Symposium scheduled at Harvard University on Wednesday, October 11th, 2017. Students will have an opportunity to present cross-disciplinary research which utilizes modern scientific tools and knowledge to illuminate the history of humanity, and to network with other students and faculty members similarly engaged, including Prof. Michael McCormick (Harvard University, Department of History), Prof. Dr. Johannes Krause (MPISHH), David Reich (Harvard Medical School, Department of Genetics), Prof. Dr. Philipp Stockhammer (Ludwig-Maximilians-Universität München), and other leaders in the field. An interest in the Ancient Mediterranean is desirable but not indispensable.

For students coming from outside the Boston/Cambridge area for the October 11th Symposium, a limited number of awards of up to $500 to defray lodging and travel costs are available. Students interested in applying for the Symposium should arrange to send a letter of application, along with an abstract of research to be presented, a CV, an academic transcript, and a letter of recommendation, to be submitted by September 27th at the latest to sohpchair@fas.harvard.edu

New MHAAM PhD Fellowship Opportunity

The Symposium will also present a new PhD Fellowship opportunity for the 2018-2019 academic year and beyond. MHAAM is expecting to offer up to three 5-year fully-funded PhD fellowships for study and research on the science of the human past. PhD degrees have been or will be awarded through Harvard University, notably in the following departments: §The Archaeology Program within the Anthropology Department §History §Human Evolutionary Biology §Organismic and Evolutionary Biology §Additional Departments Forthcoming

Candidates for the Fellowship will apply for admission to one of these Harvard University PhD Programs to be considered eligible for this full funding opportunity through the Max Planck-Harvard collaboration. Applicants must specify their interest in the MHAAM Fellowship Program at the top of the application, and must additionally send a copy of the application to sohpchair@fas.harvard.edu, or via mail to:

Lisa Ransom Lubarr Harvard University Robinson Hall M-03 35 Quincy Street Cambridge, MA 02138

Inquiries can be sent to: sohpchair@fas.harvard.edu

"Lubarr, Lisa R." <llubarr@fas.harvard.edu>

Lisbon MathBiol Jul23-27

The *11**th** European Conference on Mathematical and Theoretical Biology (ECMTB 2018)* will be held in *Lisbon, Portugal*, from *23 to 27 July, 2018*. The venue is the Faculty of Sciences of the University of Lisbon and its research centre CMAF-CIO will host the event. This will be a main event of the *YEAR OF MATHEMATICAL BIOLOGY (YMB; * *http://euro-math-soc.eu/year-mathematical-biology-2018* set up by European Society for Mathematical and Theoretical Biology (ESMTB) and the European Mathematical Society (EMS). For that reason, ECMTB 2018 will, for the first time, be a joint ESMTB-EMS conference and will be co-organized by SPM (Portuguese Mathematical Society).

We invite all researchers and students interested in Mathematical and Theoretical Biology and its applications to join us on this exciting conference! Registrations are now open on the Conference webpage *http://www.ecmtb2018.org*. Applications to Minisymposia, Contributed Talks and Posters are also opened and the corresponding abstract templates are available on the webpage.

Paula Patrício <pcpr@fct.unl.pt>

Marseilles 22ndEvolutionaryBiol Sep25-28

Dear all the dates of the 22nd evolutionary biology meeting "at" Marseilles are September 25-28 2018 followed by 2 days of visit of Marseilles

note the the 21st Meeting will run next week (see the program aeeb.fr and follow the evolutionary biology meeting link)

It is still possible to register : contact marie-helene.rome@univ-amu.fr

best regards Pierre

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

NHNM London YoungSystematists Dec1

19th YOUNG SYSTEMATISTS' FORUM

Friday, 1 December 2017, 9:30 am

Venue: Flett Lecture Theatre,

Natural History Museum, London, UK

The annual Young Systematists' Forum represents an exciting setting for Masters, PhD and young postdoctoral researchers to present their data, often for the first time, to a scientific audience interested in taxonomy, systematics and phylogenetics. This well-established event provides an important opportunity for budding systematists to discuss their research in front of their peers within a supportive environment. Supervisors and other established systematists are also encouraged to attend.

Prizes will be awarded for the most promising oral and poster presentation as judged by a small panel on the day.

Registration is FREE.

Send applications by e-mail to YSF.SystematicsAssociation@gmail.com , supplying your name, contact address and stating whether or not you wish to give an oral or poster presentation. Please also tell us your academic stage - e.g., Masters, PhD or postdoc. Space will be allocated subject to availability and for a balanced programme of animal, plant, algal, microbial, molecular and other research. Non-presenting attendees are also very welcome - please register as above.

Again the YSF will be held the day after the Molluscan Forum (http://www.malacsoc.org.uk/-MolluscanForum.htm) also at the Natural History Museum. This has been arranged so both meetings can be attended, although if attending both you will have to register for both meetings separately.

Abstracts must be submitted by e-mail in English and in Word format no later than Friday 3 November 2017. The body text should not exceed 150 words in length. Title, authors, and their professional affiliations should be included with the abstracts. If the presentation is co-authored, the actual speaker (oral) or presenter (poster) must be clearly indicated in BOLD text.

If you have presented a talk at the YSF before, we ask that you submit only for a poster presentation, as speaker slots are limited and we want to give as many people a chance as possible. Similarly, if you are presenting at both the YSF and MF, we ask that you not apply for speaking slots in both (or let us know so we can assess).

All registered attendants will receive further information about the meeting, including abstracts, by e-mail one week in advance. This information will also be displayed on the Systematics Association website (www.systass.org).

Ellinor Michel <e.michel@nhm.ac.uk>

Salzburg Austria Conservation Nov2-3

—– 6th International Symposium for Research in Protected Areas 2017 —–

REGISTER NOW!

National Parks Austria (nationalparksaustria.at) and Hohe Tauern National Park (hohetauern.at) take great pleasure in inviting you to the 6th International Symposium for Research in Protected Areas taking place on 2-3 November 2017 in Salzburg, Austria. The symposium will be held at the Faculty of Natural Sciences at the University of Salzburg.

DEADLINE for registration: 4th October 2017!

For registration and further information, please visit www.nationalparksaustria.at/symposium2017 The conference will cover topical research and concepts e.g. on wilderness, biodiversity, species protection, ecology and the function of running waters, the effects of climate change and the role of long-term monitoring. In addition, issues of applied conservation research, protected area management and sustainable development will be debated.

The symposium provides a perfect opportunity for encounters across disciplinary and protected area boundaries, where participants can share and exchange views and findings and intensify the dialogue between researchers and practitioners.

Fringe events include a public talk on Thursday evening on “Whatsalp Vienna - Nice 2017. A trip by foot through the Alps and their large protected areas” and the “Nationalparks Austria Science Award 2017” gala on Friday evening.

We look forward to welcoming you in Salzburg!

We apologize for any cross-postings and associated inconveniences.

Kind regards,

Dipl.-Ing. Wolfgang Urban, MBA Director, Hohe Tauern National Park, Salzburg (on behalf of the organizers and the conference team)

Conference Office Hohe Tauern National Park Salzburg Gerlos Straße 18/2 5730 Mittersill Email: symposium2017@salzburg.gv.at

Dr. Anja Hörger University of Salzburg Department of Ecology and Evolution Hellbrunnerstr. 34 5020 Salzburg Austria

email: anja.hoerger@sbg.ac.at Tel: +43 662 8044-5501

Hörger Anja <anja.hoerger@sbg.ac.at>

SanDiego AvianGenomicsPAG January2018

Dear colleagues,

There will be an "Avian Genomics" workshop at the international PAG conference in January in San Diego http://www.intlpag.org/. I will host it for the 3rd time: "Avian Genomics - Gone Wild!". PAG 2018 will be from Jan 13th to Jan 17th.

To get an overview of the last session of 2017 here is the link:

https://pag.confex.com/pag/xxv/meetingapp.cgi/-Session/4169 And this was the first edition in 2016:

https://pag.confex.com/pag/xxiv/meetingapp.cgi/-Session/3531 If your work falls within the area of avian genomics, especially of birds in the wild, please send your abstract (200-300 words, no special format) to me by October 15th. Do not hesitate to ask any questions.

Best wishes, Robert

rkraus@orn.mpg.de

Shenzhen Evolution Apr18-20 CallForAbstracts

Dear Colleagues:

We would like to invite you to submit abstract for contributed talks and posters now for the 1st Asian Evolution Conference to be held on April 18th-20th, 2018 at Shenzhen, China. We have now planned a total of 42 symposiums spanning various topics of evolution studies, with invited speakers from all over the world. Each symposium will allocate one hour for 2-3 confirmed invited speakers, and one hour for contributed talks. 10 travel fellowships will be awarded to students or postdocs to encourage them to attend the conference.

You can find the full program information here: http://-asianevo.org/ programme/program_schedule.html. The deadline for early registration is February 1st, 2018: http://asianevo.org/registration/index.html

Thanks Regards, Qi Zhou zhouqi1982@zju.edu.cn www.qizhoulab.org Qi <muntjaczhou@gmail.com>

Toronto Barrettfest August10-12

Dear Colleagues,

2018 will mark Spencer Barrett's 70th birthday and 40th year at the University of Toronto. We will celebrate this occasion and Spencer's career so far with a symposium entitled 'Evolution of Plant Reproductive Systems: From Muddy Boots to Genomics'.

The symposium, to be held at the University of Toronto August 10-12, will be an opportunity to explore the latest cutting edge research in this field. The tentative schedule of speakers includes:

Aneil Agrawal (U Toronto) Tia-Lynn Ashman (U Pittsburgh)

Andrea Case (Kent State) Deborah Charlesworth (U Edinburgh)

Lynda Delph (Indiana U) Chris Eckert (Queens U)

David Field (U Vienna) Jannice Friedman (U Syracuse)

Emma Goldberg (U Minnesota) Sean Graham (UBC)

Lawrence Harder (U Calgary) Brian Husband (U Guelph)

Michael Lenhard (Max Planck) Sally Otto (UBC)

John Pannell (U Lausanne) Daniel Schoen (U McGill)

James Thomson (U Toronto) Stephen Wright (U Toronto)

Many thanks to the University of Toronto's EEB department and the faculty of Arts & Science for co-sponsoring the event. More details and registration will follow in late 2017. Please contact us if you have any questions.

Stephen Wright, Daniel Schoen, and Marc Johnson co-organizers

Stephen I. Wright Professor and Canada Research Chair in Population Genomics Department of Ecology and Evolutionary Biology University of Toronto 25 Willcocks St. Toronto ON M5S 3B2 http://wright.eeb.utoronto.ca/ Stephen Wright <stephen.wright@utoronto.ca>

Torun Poland EvoLang Apr16-19 ExtDeadline

EVOLANG XII - 16-19 April 2018, Torun, Poland — submission deadline extended (15 September 2017)

The 12th International Conference on the Evolution of Language invites substantive contributions relating to the evolution of human language. Please note the relevance of "general evolutionary" topics, such as signalling theory, population genetics, ancient DNA genomics, evolution of cooperation, cultural evolution, or extended synthesis.

Submissions may be in any relevant discipline, including, but not limited to: anthropology, archeology, artificial life, biology, cognitive science, genetics, linguistics, modeling, paleontology, physiology, primatology, philosophy, semiotics, and psychology. Please see the Call for Papers for details:

https://www.facebook.com/EvoLang2018/ http://evolang.cles.umk.pl/ A number of official workshops as well as additional special thematic sessions will be held, including a special session sponsored by Human Behavior and Evolution Society.

Slawomir Wacewicz Nicolaus Copernicus University, Torun http://www.cles.umk.pl http://www.maius.umk.pl/ang/?pid=1&spid=123

Slawomir Wacewicz <wacewicz@umk.pl>

Trondheim HoleNestingBirds Oct30-Nov2 DeadlineSep25

— Eighth International Hole-Nesting Birds Conference — The Centre for Biodiversity Dynamics (CBD) at the Norwegian University of Science and Technology (NTNU) is pleased to announce that the Eighth International Hole-Nesting Birds Conference will be held from October 30 to November 2, 2017 in Trondheim, Norway. The conference aims to bring together leading academic scientists, researchers, research scholars and citizen scientists to exchange and share their experiences in research involving all aspects of hole-nesting birds.

The scientific program will consist of eight sessions for keynote speakers and contributed speakers to present their latest research results, ideas and challenges within the fields of population dynamics, behaviour, physiology, life-history strategies, speciation, genetics, dispersal and movement, and climate change.

In addition, there will be poster session, and a discussion session that will allow attendees to discuss research plans and challenges in parallel group sessions. A central focus will be to improve communication and interactions between different groups working on hole-nesting birds across Europe.

— Deadlines — Deadline for registration and submission of abstracts for talks and posters is September 25, 2017. The CBD will offer some grants that provide financial support for some of those who may wish to attend the conference. Those with financial need for travel and/or accommodation may apply at the registration.

— Genomics satellite meeting — A satellite meeting on hole-nesting birds genomics will be held on Friday 3 November (from 9:00 to ca. 15:00). The satellite meeting will take place at NTNU Gløshaugen campus (ca. 500 m northeast of the conference venue), and will consist of short presentations and discussions on topics suggested by the participants. Registration and suggestion of topics can be done by sending an e-mail to Alina Niskanen (alinan@ntnu.no), who will also answer any questions related to the satellite meeting. The satellite meeting is free of charge.

— Website and social media — For more information, please visit the conference website: https://www.ntnu.edu/hnb-conference Follow us on Twitter: https://twitter.com/HNBirds2017 And join the Facebook event: Eighth International Hole-Nesting Birds Conference 2017 < https://t.co/fOtwFKjghW >

We are looking forward to seeing you all at the conference!

The Eighth International Hole-Nesting Birds Conference organizing committee: Bernt-Erik SÃther Marcel E. Visser Ben C. Sheldon Stefan J.G. Vriend

stefan.vriend@ntnu.no

UGothenburg Sweden MarineEvolution May15-18

Dear friends,

Session proposals for Marine Evolution 2018 (http://cemeb.science.gu.se/activities/marine-evolution-2018), organized by the Linnaeus Centre of Marine Evolutionary Biology, which will take place the 15th through 17th of May 2018 in Strömstad on the West Coast of Sweden, can now be submitted. Deadline for session proposals is October 1st.

Marine Evolution 2018 invites session proposals broadly within the field of Marine Evolutionary Biology. Plenary presentations by six renowned speakers have been confirmed, and are listed on the conference website. Session topics can be developed in relation to these, or in any other relevant discipline within Marine Evolutionary Biology.

The conference will take place over three days in the beautiful Bohuslän region, listed as one of the "ten last great wildernesses in the world" by CNN. It is situated on the Swedish West Coast, strategically located between major international airports in Oslo, Norway and Gothenburg, Sweden. It will host nine sessions, as well as excursion events, evening performances and time for discussions and relaxation. The venue is the Strömstad Spa (http://stromstadspa.se/english), a modern conference infrastructure with pool and gym facilities. The conference fee will be 3600 SEK (1600 SEK for PhD students), excl. VAT.

Session proposals should include: A short but descriptive title of the topic, a list of chairs of the session with contact information, a brief abstract (max 200 words), and a tentative list of proposed speakers to invite. Session chairs are expected to actively invite peers to register and submit abstracts for presentations. Once registration opens (November 1st 2017) participants will suggest which session they would like to fit into, and these registrations will be forwarded to the session chairs for consideration. Session chairs are free to organize sessions in the manner they see fit, with possibilities for keynote talks, speed talks, oral presentations of posters, etc. All session chairs will have the opportunity to designate poster presentations to applicants who cannot be fitted into the oral presentation timeframe. Session chairs are also free to organize publication of presented materials in scientific journals, if deemed of interest by the participants. Sessions will be run three in parallel each day, from 11:00 - 14:45 with a 75-minute break for lunch.

Session proposals are due on October 1st, 2017, and should be submitted through the web portal at (http://cemeb.science.gu.se/activities/marine-evolution-2018/sessions).

If you have questions about the scientific program, including content questions relative to the sessions, or any questions regarding logistics, please contact the organizing committee at infomare@marine.gu.se.

Sincerely, the Marine Evolution 2018 Organizing Committee Kerstin Johannesson Anders Blomberg Pierre De Wit Eva Marie Rödström Samuel Perini

Pierre de Wit <pierre.de_wit@marine.gu.se>

ULisbon HumanEvolution Dec13-14

Call for Abstracts Conference Human Enhancement and Evolution Scientific, Technological, Policy & ELS Considerations Lisbon 13- 14th December 2017 Host Institution: Centre for Philosophy of Science of the University of Lisbon (CFCUL) [http://cfcul.fc.ul.pt/] The Conference will have two parts:

1. Evolution and the Sciences and Technologies of Human Enhancement

Organismal dynamics are such that organisms incontrovertibly affect the very evolutionary pressures that shape them, even if only indirectly. But seemingly, amongst all organisms and perhaps owing to their cognitive evolution, humans became exceptionally fine controllers of both theirs and other organisms' evolutionary processes. In virtue of the sciences and technologies of human enhancement, more effective exertion of control over evolution is nowadays becoming evident, and this is shown among others by the rise of new technics such as genetic editing tools. However, human enhancement and its broad evolutionary effects are still understudied.

We invite contributions to the effort of understanding the plethora of ways in which evolution relates to human enhancement. As such, topics of interest may include, but are not limited to:

* The human evolutionary possibilities: predictive models, challenges and limitations; * Directed evolution, both gene driven (e.g. genetic engineering, induced

mutagenesis, and reprogenetics) or non-germline based; * Evolutionary trade-offs of assisted modes of human reproduction, immunity engineering, medical and health technologies, and of longevity enhancements (interferences in senescence and lifespan), their demographics and population dynamics; * Natural and artificially induced reticulate evolution (e.g. human-non- human transgenesis); * Present & future human evolution (e.g. k-selection and speciation); * The impact of technological evolution qua niche construction on human evolution and ecology (e.g. geoengineering; non-Earth- bounded evolution); * Non-carbon-based evolution (including AIs of all kinds & alien); * The evolution of 4E and scaffolded cognition; * The relation between fitness and human enhancement (e.g. does human enhancement enhance fitness?); * Working definitions of "human enhancement" for Evolutionary Theories; * Is there actual control over evolution? How could we understand it? * Human evolution in relation to Technology evolution (e.g. human- machine interfaces);

Keynote Speaker(s): Professor John Harris; TBA. Invited Speaker(s): TBA.

Local Organizing Committee: Joāo Pinheiro [CFCUL]; Dr. Alexander Gerner [CFCUL]

2. Policy & ELSA of Genome Editing and Human Enhancement

Genome editing is a technology with the potential to promote and enhance health, and understand disease. However, as many other disruptive advances in science, it also brings challenges at an ethical, legal, social, and political level, particularly regarding the treatment of hereditary diseases and the integrity of the human germline. The possibilities of genome-editing and its limits and consequences, specifically to therapeutic applications and targeted interventions in ecosystems are being broadly discussed by many. It will be important to contribute to the debate in a critical and transparent way with the participation of scientists, society and policy-makers. This will provide a platform to better assess the benefits and potential risks of the technology to help support the development of sound policies in the future.

We invite reflections upon the following themes (including but not limited to):

Ethical, legal, political and social challenges associated with genome-editing;

* Genetic editing: evolution of technology and medicine and its implications for human health, and the natural environment; * Socio-ethical and policy-related questions about the acceptability of germline modification; * Challenges on defining "Genetic identity", parenthood and respective responsibilities: limits and consequences; * "Human enhancement" potential of genetic editing: Implications and scientific- technological feasibility thereof; * Responses to the challenge of established norms.

Keynote Speaker(s): Professor Bartha Maria Knoppers; TBA.

Invited Speakers: Professor Alexandre Quintanilha; TBA.

Local Organizing Committee: Dr. Alexander Gerner [CFCUL]; Dr. Mara Almeida [CFCUL]

Scientific Committee: Professor Philip Kitcher; Professor Gregory Stock; Professor Susan Kelly; Professor Kevin M. Esvelt; Professor Rita Zilhāo; Dr. Nathalie Gontier; Professor Maria Fernanda Palma.

Abstract submission

For your submission please make sure to provide two separate documents: (1) Information Document with all authors' names and affiliations,

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

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UNorthCarolina ChapelHill SEPEEG Oct20-22

The 43rd Annual Southeastern Population Ecology & Evolutionary Genetics Meeting (a.k.a. SEPEEG 2017 and "sepage") will be held October 20-22, 2017, and is hosted by the Department of Biology at the University of North Carolina at Chapel Hill. It will be at the Camp Monroe Retreat Center in Laurel Hill, NC.

Website: http://sepeeg.web.unc.edu/ Corbin D. Jones, Ph.D. Professor Department of Biology iBGS - Integrative Program for Biological & Genome Sciences Campus Box 3280, Genome Science Building UNC-Chapel Hill Chapel Hill, NC 27599-3280

"Jones, Corbin D" <cdjones@email.unc.edu>

Waimea Hawaii AdaptiveRadiation Jul22-25

AGA2018, the AGA President's Symposium, will take place next July in the beautiful rolling hills of Waimea, Hawai'i. The meeting will open with a pupu reception on July 22, encompass 2 days of invited talks and poster sessions, and end with a luau banquet featuring local entertainment. A half-day applied workshop will follow on July 25.

AGA symposia are small, friendly gatherings, and provide wonderful opportunities for researchers and students to engage with one another and share their science. The 2018 meeting will focus on processes at the early stages of adaptive radiation, such as admixture, priority effects, and repeated evolution. Invited speakers confirmed thus far include:

* The AGA Key Distinguished Lecturer: Ole Seehausen, EAWAG (The Swiss Federal Institute of Aquatic Science and Technology) * Jonathan Losos, Harvard * Kerry Shaw, Cornell * Christine Parent, Univ of Idaho * Jim Mallett, Harvard * Scott Hodges, UC Santa Barbara

The AGA keeps registration costs low to encourage participation. Awards will be available to help support students.

Watch for more details soon on the AGA website: http://www.theaga.org and AGA Facebook page: https://www.facebook.com/theAGA.org/ Best wishes,

Rosemary Gillespie AGA President 2018 theaga@theaga.org

theaga@theaga.org

WashingtonDC CrustaceanAdaptations May22-25

Dear Colleagues,

We would like to announce a special session on "Adaptations to Life in the Deep Sea and Caves" to be held during the 9th International Crustacean Congress (ICC9) in Washington, D.C. from May 22-25, 2018. Through this session we aim to bring together a diverse set of researchers studying common evolutionary themes in extreme environments such as deep sea, polar regions, and caves. Talks on adaptations related to the "Darkness Syndrome" (Danielopol et al., 1996) or any other aspects of life in these extreme environments are welcome, including physiological, morphological, neurological, behavioral and ecological mechanisms related to crustacean survival.

For more information regarding the conference, please check the conference website at http://www.birenheide.com/ICC2018/index.php Abstract submissions are due 1 March 2018. If you have any questions about the session, please feel free to contact any of the session organizers.

Megan Porter mlporter@hawaii.edu Karen Osborn osbornk@si.edu Tammy Frank tfrank1@nova.edu

We hope to see you next year in Washington, D.C. Tammy, Megan, and Karen

Karen Osborn Research Zoologist/Curator of Polychaetes, Peracarids and Plankton Department of Invertebrate Zoology w 202.633.3668 osbornk@si.edu http://invertebrates.si.edu/osborn/ http://orcid.org/0000-0002-4226-9257 SMITHSONIAN INSTITUTION NATIONAL MUSEUM OF NATURAL HISTORY Facebook < https://www.facebook.com/nmnh.fanpage/ > | Twitter < https://twitter.com/NMNH > | Instagram < https://www.instagram.com/smithsoniannmnh/ >

Mail: Department of Invertebrate Zoology, Smithsonian National Museum of Natural History, MRC-163 P.O. Box 37012, Washington, D.C. 20013-7012 USA

Courier Address: Smithsonian Institution, MR 0163, Natural History, West Loading Dock, 10th and Constitution Ave NW, Washington, D.C. 20560

"Osborn, Karen" <OsbornK@si.edu>

WashingtonDC CrustaceanEvolution May22-25

Dear colleagues,

My co-organizer, Joanna "Jo" Wolfe, and I would like to invite you to present your research in the session "Molecular Insights: The Genomic Revolution in Crustacean Biology" at the upcoming International Crustacean Congress IX to be held May 22-25th 2018 in Washington DC. This conference is hosted by the Smithsonian Institution and Renaissance Hotel. We hope this session will provide a platform to share and discuss studies incorporating crustacean genetics and/or genomics. We encourage submissions that cover any crustacean taxa and we are particularly interested in phylogenetics/omics, transcriptomics, gene expression studies, tree of life studies, and population genomics. Graduate Students, Postdoctoral Scholars and Professors (at all levels) are encouraged to participate!

If you are interested in participating please reach out to Heather Bracken-Grissom at hbracken@fiu.edu as we expect the session spots to fill quickly.

The deadline for abstract submissions is *March 1st 2018.*

More information on the conference can be found here detailing registration and abstract due dates and logistics: http://www.birenheide.com/ICC2018/index.php *Session details*:

*Molecular Insights: The Genomic Revolution in Crustacean Biology *

Co-Coordinators:

Heather Bracken-Grissom, Florida International University, hbracken@fiu.edu

Joanna Wolfe, Massachusetts Institute of Technology, jowolfe@mit.edu

The field of crustacean genetics has undergone an exciting revolution in recent years. The advancement of sequencing technologies and methods has transformed the way carcinologists ask questions and collect data, especially for non-model organisms that lack genomic references. For several groups within Crustacea, this "genomic revolution" is still in its infancy. The potential to capitalize on recent technology is great, and findings from these studies will lead to unprecedented insights into the fields of evolutionary biology and molecular ecology.

For this session, we would like to invite researchers working in the field of crustacean genetics/genomics. We welcome contributions from phylogenetics/omics, population genomics, transcriptomics, among others. In addition to the abovementioned, theoretical and methodological talks will be considered.

We hope to highlight a diverse group of organisms that span various fields of crustacean biology. Please indicate that you would like to be included in the "Molecular Insights" session.

We do not plan to publish a special issue.

We do not plan to apply for funding to recruit specific speakers.

The session will accept as many talk proposals as appropriate based on submitted abstracts.

We look forward to seeing you in DC!

Kind regards,

Heather Bracken-Grissom and Jo Wolfe

– 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 www.fiu.edu/~marine Heather Bracken-Grissom <heather.bracken@gmail.com>

GradStudentPositions

BarIlanU Israel SexualSelection

We are looking for an enthusiastic and fit graduate student (MSc or PhD) for a multidisciplinary project on sperm competition and sexual selection in rock hyrax. The project involves extensive fieldwork in the Ein Gedi Nature Reserve, near the Dead Sea, Israel. The ideal applicant has a strong background in behavioural ecology, field experience handling wildlife, and an ability to work both independently, and as part of a team. The project starts in January 2018, and is open for domestic and international students, who will receive a scholarship from Bar Ilan University. For more information, please contact Dr. Lee Koren (Lee.Koren@biu.ac.il). Please include a CV and a cover letter with field experience and interests.

Thanks and best wishes,

Lee

Lee Koren, PhD The Mina and Everard Goodman Faculty of Life Sciences Bar-Ilan University Ramat Gan, 5290002 Israel Institute of Nanotechnology and Advanced Materials (Building 206) Office B-940; Lab B-935 (9th floor) Telephones: office +972-3-7384371 lab +972-3-7384372 Skype: leezik Lee.Koren@biu.ac.il http://faculty.biu.ac.il/~korenle1/ Lee Koren Lab (Facebook page)

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

Bialowieza Poland BisonDiseaseEvolution 2

Mammal Research Institute of the Polish Academy of Sciences in Bialowieza announces the competition for a doctoral scholarship within the project:

“ Genetic background of a lethal posthitis disease in the European bison males”

Project Leader: Malgorzata Tokarska, PhD. Eng.

Requirements:

1. MSc degree in biology, molecular biology or related fields

2. expertise in standard molecular biology techniques

3. experience in biostatistical analyzes using either Genome Studio, Plink, R or Golden Helix SVS (or others, if valid)

4. team cooperation skills

5. fluent spoken and written English;

6. enjoyment from conducting the scientific studies and presenting the results;

Required documents:

1. CV

2. Information on the candidate's scientific experience (specialization, research techniques, and achievements (including list of publications and reports) (max. 500 words)

3. An opinion from the academic tutor or/and previous scientific employer

Conditions of employment: PhD student scholarship of 3000 PLN / month

The summary and objectives of the project

Posthitis (necrotic inflamation of the prepuce) is a severe disease of the European bison, which affects approx. 6 % of males a year. The disease is incurable and the affected animals are usually eliminated or otherwise the disease leads to penis autoamputation and death. The etiology of posthitis is unknown but recent studies on European bison using cattle tools indicated significant associations between certain cattle markers and the occurence of the disease. A study by Olenski et al. (2015) has shown the existence of genetic background of posthitis in the European bison but the cross - species character of their study did not allow to either indicate the genes and their variants involved in the disease or explain the mechanism if its inheritance.

Sequence - Based Genotyping (SBG) technique will allow to achieve an extensive amount of species-specific data from the whole genome. European bison specific markers will undergo genome wide association analysis (GWAS) to identify markers, regions of chromosomes and genes and their variants affecting susceptibility bison on posthitis. The results will enable to design simple genetic tests of the 20 - 30 most informative SNP markers detected. These tests will allow rapid and reliable genotyping of bison susceptibility to posthitis and the carriers of unfavourable genetic variants.

The aims of the project are:

1. identification of the species specific SNPs (single nucleotide polymorphisms markers) associated with postithis in the European bison

2. indication the genes and their variants, underlying the development of posthitis in the European bison,

3. developing the model of the disease inheritance,

4. verification of the potential role of the Y chromosome in the pathogenic process,

5.designing informative and cost-effective SNP -chip based genetic test that allows verification of susceptibility to posthitis as well as carriers of unfavorable variants

We provide:

1. participation in an interesting scientific project;

2. work in a friendly research team, in a well-equipped and organized biological laboratory with a support and supervision of competent colleagues;

3. the possibility of effective scientific development through cooperation with the best world research centres in the world;

4. possibility of extension the scholarship for subsequent 2 years;

5. possibility of additional funding through participation in other research projects;

6. the possibility to apply for accommodation in MRI PAS flats - at least temporal stay in Bialowieza during the project is required.

Candidates will be evaluated by a commission at the Mammal Research Institute Polish Academy of Sciences in Bialowieza. After a preliminary assessment of the submitted documents, the candidates will be invited for an interview.

Applications should be sent directly to the Project Leader by letter or electronically by September 20th 2017. The candidates will be invited to an interview and the decision will be announced by September 21th 2017.

Contact: - Malgorzata Tokarska PhD - posthitis project leader

Mammal Research Institute Polish Academy of Sciences

ul.Waszkiewicza 1

17-230 Bialowieza, Poland

e-mail: tokarska@ibs.bialowieza.pl; phone +48 85 682-77-61

Link: Preview Link: themeData Link: colorSchemeMapping

Malgorzata Tokarska Instytut Biologii Ssakow Polskiej Akademii Nauk Zakład Genetyki i Ewolucji Mammal Research Institute Polish Academy of Sciences Genetics and Evolution Department Waszkiewicza 1 17-230 Bialowieza Poland tel.4885 6827761

tokarska <tokarska@ibs.bialowieza.pl>

BrighamYoungU PlantEvoDevo

Graduate Position in Evolution of Plant Development Brigham Young University Fall 2018

A PhD graduate student position is available beginning Fall 2018 in the Whipple lab, Department of Biology, Brigham Young University. Research interests in the Whipple lab center on the genetic basis of morphological diversity in plants, employing both model and nonmodel systems (see whipplelab.byu.edu). Students will employ molecular, morphological and genetic approaches to address basic questions in the evolution of plant development. Specific research projects include an analysis of gene networks that jointly regulate leaf growth and inflorescence architecture in maize (Poaceae), as well genetic mechanisms underlying a dramatic shift in floral and inflorescence morphology in Gilia (Polemoniaceae).

The successful applicant will be highly motivated with a strong interest in plant development, and demonstrated experience with basic molecular biology techniques (PCR, cloning, sequence analysis, etc.).

Funding for this position is guaranteed through a combination of Teaching Assistantships from the Department of Biology, and Research Assistantships from external NSF research funds and will cover tuition and benefits in addition to a competitive yearly stipend.

BYU is located in Provo, UT, centrally situated in a state renowned for its spectacular outdoor recreational offerings. For the more urban-oriented, diverse cultural and social opportunities abound in both Provo and nearby Salt Lake City.

Interested applicants should send a CV, transcripts, GRE scores (if available) and a statement of research interests to Clinton Whipple (whipple@byu.edu). Applications will be screened starting immediately and continue until to Jan 1st 2014. International students with strong credentials are welcome and encouraged to apply.

All application materials and any questions should be directed to:

Clinton Whipple Associate Professor Department of Biology Brigham Young University 4102 LSB Provo UT, 84602 USA

Email: whipple@byu.edu

Email correspondence is preferred

Clinton Whipple <whipple@byu.edu>

Budapest HostParasiteCoevolution

Young researcher position is offered for 2 years at Plant Protection Institute, Centre for Agricultural Research, Budapest, Hungary. Applicants must have MSc degree. We consider fresh graduates, as well as those at the final stage of their PhD or postdocs, as long as they can devote themselves to this task. Wage according to standard Hungarian academic wage table. We expect Hungarian candidates who finished their studies abroad and wish to return, but any EU citizen could equally apply. Outside EU we have no experience, but might investigate possibilities. Within the lab/institute you get along with English, outside also, but maybe with some difficulties.

Topic: Our group studies a multitrophic model system that consists of a predator (spider), sap feeding herbivore that is also a vector of plant disease (leafhopper), plant disease (a virus) and plant (cereal crop). We are interested in trait mediated cascading effects and the binary relationship between the actors, including coevolution between the parasite (virus) and its host and vector and the possibility/consequences of host/vector manipulation. We have multiple approaches (behavioural observations, electrophysiological and chemical ecological studies, as well as semi-field and field work). In the topic we also offer the possibility to start PhD at a Hungarian university (concrete topic, possibilities to be discussed). See project and publications posted on Researchgate.

Task: The researcher should conduct molecular work (PCR) to analyse spider gut contents and follow the route of virus infection within the system during the experiments, develop own PhD/postdoc topic on parasite-host evolution.

Send enquiries to Dr. Ferenc Samu at samu.ferenc@agrar.mta.hu

Ferenc Samu <feri.samu@gmail.com>

CNAG-CRG PopulationGeneticsBioinformatics

The Centro Nacional de Análisis Genómico (CNAG-CRG) is seeking:

Population genetics/Genetic epidemiology/Bioinformatics PhD

The CNAG-CRG is one of the major Genome Sequencing Centers in Europe. It is integrated in the Centre for Genomic Regulation (CRG), an international biomedical research institute of excellence classified in the 9th position (Q1 indicator, Health sector) by the SCImago Institution Rankings (SIR) World Report 2014. — The CNAG-CRG is actively involved in collaborative research projects on a number of specific topics: Disease Gene Identification, Cancer Genomics, Genomics of Infectious Diseases, Model Organism Genomics and Synthetic Biology Genomics of Model Organisms. Researchers at CNAG-CRG actively participate in several H2020 consortia, lead one ERC Synergy grant and are involved in major international initiatives in Genomics (ICGC, IRDiRC, iHEC, GA4GH).

We offer a PhD position to work at the CNAG-CRG on the analysis of whole-exome sequencing and GWAS data to evaluate the role of common and rare genetic variants as possible contributors to dimensional scores of ADHD and their evolutionary consequences, led by the team leader of Population Genomics Dr Oscar Lao.

The position requires a candidate with good knowledge in bioinformatics/population genetics and next generation sequencing/exome sequencing. The duration of the contract is for three years.

Requirements: A BSc or MSc degree in Biology, Biomedical Sciences, Bioinformatics or a related field. An advanced knowledge of at least a high-performance language for numerical computation (C, C++, JAVA, Phyton or Perl), as well as a good working knowledge of statistical packages such as R. A good working knowledge of Unix systems, in particular large Unix clusters. Good spoken and written English. May not have resided or carried out her/his main activity (work, study, etc) for more than 12 months in the last 3 years in Spain at the moment the candidate signs her/his contract. The candidate should be within the first four years (full-time equivalent) after obtaining her/his BSc or MSc degree. - The candidate must be eligible for a national PhD fellowship.

Application procedure: Interested candidates should submit a CV and a brief statement of experience and interests before October 30st to the recruitment portal through the following link: http://www.crg.eu/en/content/jobs/cnag-jobs Pearl Sue van Embricqs <pearl.vanembricqs@crg.eu>

ColoradoStateU Evolution

Colorado State University is seeking outstanding graduate students in the field of evolutionary biology. CSU is home to a strong and diverse group of evolution-focused labs, many of which are accepting grad students this year. Interested students are highly encouraged to explore the research pages of CSU faculty and contact professors before applying to a CSU graduate program. The university is home to a number of departmental and interdisciplinary graduate programs, and prospective faculty mentors can assist in selecting the program that would be the best match for a student's interests. CSU faculty members currently accepting graduate students include:

Mike Antolin Department of Biology http://www.biology.colostate.edu/people/antolin/ Chris Funk Department of Biology http://wp.natsci.colostate.edu/funklab/ Cameron Ghalambor Department of Biology http://sites.biology.colostate.edu/ghalamborlab/Ghalambor_Lab/Welcome.html Kim Hoke Department of Biology http://hokelab.weebly.com/ Ruth Hufbauer Bioagricultural Sciences and Pest Management http://www.hufbauerlab.org/ John McKay Bioagricultural Sciences and Pest Management http://www.mckaylab.colostate.edu/ Rachel Mueller Department of Biology http://wp.natsci.colostate.edu/muellerlab/ Dhruba Naug Department of Biology http://rydberg.biology.colostate.edu/dhruba/ Paul Ode Bioagricultural Sciences and Pest Management http://paulode.agsci.colostate.edu/ Mark Simmons Department of Biology http://sites.biology.colostate.edu/simmonslab/ Dan Sloan Department of Biology https://sites.google.com/site/danielbsloan/ Colleen Webb Department of Biology http://webblabb.github.io/ CSU is a world-class research university located in Fort Collins, CO, about an hour north of Denver and right at the foothills of the Rocky Mountains. Fort Collins is widely regarded as having a great quality of life at a reasonable cost of living. It has excellent opportunities for outdoor recreation, an active music scene, a strong biking culture, and numerous great restaurants and breweries.

dbsloan@rams.colostate.edu

CWilliamMary London 2 PlantButterflyGenomics

Graduate Position: Monarch Butterfly and Milkweed Conservation The Puzey lab at the College of William and Mary is recruiting graduate students (M.S) interested understanding the evolutionary history of Monarch-Milkweed interactions. More information about my lab can be found here: http://puzeylab.weebly.com . Positions for MS program start Fall 2018. Please contact Josh Puzey (jrpuzey@wm.edu) for more information.

The successful applicant will be passionate about evolution, interested in plant and insect interactions, and keen to use genomic techniques to address their research questions. Students working the Puzey lab get exposure to a wide range of analyses and techniques including next-generation sequencing (DNA, RNA, smRNA), population genomic analyses, and molecular ecology.

Graduate position: Plant Evolutionary Genomics The Puzey lab at the College of William and Mary is recruiting graduate students (M.S) interested exploring the evolutionary and genomic consequences of whole genome duplication in plants (http://puzeylab.weebly.com). Positions for MS program start Fall 2018. Please contact Josh Puzey (jrpuzey@wm.edu) for more information.

The successful applicant will be passionate about evolution, interested in plants, and keen to use genomic techniques to address their research questions. Students working the Puzey lab get exposure to a wide range of analyses and techniques including next-generation sequencing (DNA, RNA, smRNA), population genomic analyses, and molecular ecology.

Details about the M.S. program in Biology at W&M can be found here (http://www.wm.edu/as/biology/graduate/). Full-time students are supported by teaching assistantships and full tuition waivers.

Most students complete their master's degree in two years and go on to pursue either a Ph.D. or M.D. degree. Our program also provides the training required to enter technical positions in industry and government. Recent grads are pursuing Ph.D.s at Duke, UC Davis, Johns Hopkins, and University of Toronto; others are following career paths in academia, biotech, pharmaceuticals, resource management, and environmental consulting.

Joshua Puzey <jrpuzey@gmail.com>

DTU Denmark PopGenomicsArchivedSharks

A PhD Scholarship in Population Genomics of archived shark samples is available at the National Institute of Aquatic Resources (DTU Aqua) with starting time December 2017. DTU Aqua is an institute at the Technical University of Denmark. The project will be carried out in affiliation to the Section for Marine Living Resources' population genetics research group in Silkeborg, Denmark and in collaboration with the Molecular Fisheries Laboratory at the University of Queensland, Australia. The Application deadline is October 15th 2017. Online application at: http://www.dtu.dk/job/job?id=6f14e3e8-e45e-4aa9-88ab-264a8c4d412f For further information about the project, please contact Professor Einar Eg Nielsen, een@aqua.dtu.dk

Einar Eg Nielsen <een@aqua.dtu.dk>

EastCarolinaU EvolutionMimicry

Ph.D. Position in the Department of Biology at East Carolina University.

I am searching for a doctoral student to carry out research associated with an NSF-supported project focused on the genetic underpinnings of mimicry and color pattern evolution in a mimetic radiation of poison frogs in Peru (see description below), starting in the fall semester of 2018. Desirable qualifications for this position include an interest in the evolutionary biology and genetics of tropical amphibians, and some combination of 1) background in molecular evolutionary genetics, 2) experience working in a molecular genetic laboratory, 3) previous work with amphibians and captive breeding, 4) fieldwork on amphibians (especially in Latin America), 5) programming experience in R, Python and/or UNIX, 6) research experience in genomics. PhD trainees receive full stipends, tuition, and health insurance. Direct support through research assistantships is available for 3 years, followed by support through teaching assistantships (at least 5 years of support in total). The successful applicant will pursue their degree through an interdisciplinary program in the biological sciences (IDPBS: www.ecu.edu/-IDPBS). More information about our faculty and program offerings in the Department of Biology is available at (www.ecu.edu/biology) < http://www.ecu.edu/-biology%29 >. The department is large and multidisciplinary, with strong research groups in evolution, ecology, behavior and genomics. East Carolina University is located in Greenville, North Carolina, centrally located between Raleigh and the Atlantic Coast. I encourage applications from minorities and members of underrepresented groups. Please send a letter detailing your research interests and experience, as well as a current CV (including coursework and grades), and GRE scores (if available) to Kyle Summers (summersk@ecu.edu). Please feel free to contact me with questions if you would like further information.

The evolution of color pattern diversity in the context of mimicry has been a focus of theoretical and empirical attention, yet knowledge of the genetic basis of this diversity remains limited, especially in vertebrates. This project involves three research groups with complementary skills and realms of expertise in an investigation of the genetic basis and population genomic processes underlying color pattern divergence in the context of mimicry in the Peruvian mimic poison frog, *Ranitomeya imitator*: Dr. Kyle Summers (East Carolina University), Dr. Rasmus Nielsen (UC Berkeley) and Dr. Matthew MacManes (University of New Hampshire). The project focuses on identifying genetic factors involved in color pattern development and divergence between populations in *R. imitator. *Several approaches will be used, including investigations of differential gene expression across developmental stages and color pattern morphs using transcriptomics (RNAseq), and the use of genome-wide marker arrays (exome capture sequences) to screen samples collected in the field and enable admixture mapping. We have identified three admixture zones in the mimetic radiation that are appropriate for these analyses. We will also test the association of specific loci putatively affecting color pattern using pedigree analyses of candidate genes, using multigenerational pedigrees from frogs raised in captivity. Molecular probes will be used to investigate the role of candidate genes in the development of color pattern. Finally, we will test specific hypotheses regarding selection and demographic processes in the transition zones and between mimics and models. Together these complementary, mutually reinforcing approaches will begin to reveal the genetic underpinnings and population genomics of color pattern diversity in this mimetic radiation of poison frogs.

For more information on recent research on these frogs, please see:

Twomey, E., Vestergaard, J.S., Venegas, P., Summers, K. 2016. Mimetic divergence and the speciation continuum in the mimic poison frog *Ranitomeya imitator*. *Am. Nat*. 187:205-224.

Vestergaard, J.S., Twomey, E., Summers, K., Larsen, R., Nielsen, R. 2015. Number of genes controlling a quantitative trait in a hybrid zone. *Proc. Roy. Soc. Lond. B* 282:20141950.

Twomey, E., Vestergaard, J.S., Summers, K. 2014. Reproductive isolation related to mimetic divergence in the poison frog *Ranitomeya imitator*. *Nature Comm*. 5:4749.

Stuckert, A., Saporito, R., Venegas, P., Summers, K. 2014. The toxicity of co-mimics in a putatively Müllerian mimetic radiation. *BMC Evol. Biol.* 14:76.

Kyle Summers Dept. of Biology East Carolina University Greenville, NC 27858 252-328-6304 summersk@ecu.edu

Kyle Summers <summers.kyle8@gmail.com>

EPFL Switzerland SexualConflict

A Ph.D. student position is available at the Ecole Polytechnique Federale de Lausanne (EPFL) to study the evolutionary genetics of sexual conflict. The position is based in Lausanne, Switzerland, in the group of Dr. Brian Hollis. The project will combine experimental work in Drosophila melanogaster with molecular genetic and bioinformatic approaches (e.g. population genomics, genome-wide association, expression profiling). There is considerable scope for the Ph.D. student to shape the project and develop his or her own research questions.

Highly motivated candidates with a Masters degree (or a Bachelors degree for applicants from the U.S.) in biology, computational science, or related disciplines are encouraged to apply. Previous experience with Drosophila is a plus, but not strictly necessary. A background and interest in quantitative biology is essential, along with excellent writing and communication skills.

The EPFL is a dynamic university ranked among the top research institutions in Europe and offers a rich international environment with English as the working language. The university's core facilities provide state of the art sequencing and computational resources. Lausanne is located on Lake Geneva, a short ride from the Alps, with an attractive climate and standard of living.

For informal inquiries, feel free to send me a message at brian.hollis@epfl.ch.

Dr. Brian Hollis

School of Life Sciences

Ecole Polytechnique Federale de Lausanne

Lausanne, Switzerland

brian.hollis@epfl.ch

Brian Hollis <brian.hollis@epfl.ch>

GeorgetownU EvolutionaryBiol

The Department of Biology at Georgetown University has multiple opportunities for doctoral study in ecology, evolution and behavior (EEB).

Georgetown faculty are dedicated to the development of doctoral candidates into insightful and skilled scientists, scholars and teachers. Funding for graduate study is supported by a combination of assistantships, teaching fellowships and research grant support. Our program and institution welcomes students of all racial, ethnic and religious backgrounds. Students interested in any of the opportunities listed below are strongly encouraged to contact the relevant faculty member(s) via email. The Department of Biology graduate program is described at http://biology.georgetown.edu/graduate/applicants/. Information about graduate school application procedures and deadlines can be found at http://grad.georgetown.edu/pages/admissions.cfm . Molecular basis of adaptation: Dr. Peter Armbruster seeks a highly motivated PhD student to join his laboratory's research program on the molecular basis of adaptation in natural populations. The Armbruster lab is currently focusing on the invasive and medically important mosquito Aedes albopictus. This mosquito invaded the US in 1985 and spread rapidly over approximately 15 degrees of latitude. A major focus of work in the Armbruster lab is the use of transcriptome sequencing and genomics approaches to elucidate the genetic basis and molecular physiology of photoperiodic diapause in Ae. albopictus. Interested students should contact Dr. Peter Armbruster (paa9@georgetown.edu). For further information on the Armbruster lab see: http://faculty.georgetown.edu/paa9/ Ecological interactions, behavior & learning: Research in Dr. Martha Weiss' lab focuses on ecological interactions (between plants and animals, as well as predator and prey), with an emphasis on behavior and learning. Ongoing or recent projects include investigations of the ecological factors supporting shifts in host plant usage, butterfly and caterpillar learning, retention of memory across complete metamorphosis, and the ecological context of defecation behavior. We are also working on development of hands-on science curricular materials, mostly related to plants and insects, for use in K-12 classrooms. We seek an outstanding graduate student interested in these or related projects. For more information see the Weiss Lab website: http://www.weisslab.org/ Butterfly responses to climate change: Dr. Leslie Ries is seeking a PhD student interested in field, laboratory and data-intensive approaches to ecology to join her lab's research program on butterfly responses to climate change. The Ries lab uses both experimental approaches, measuring thermal tolerances of caterpillars in the lab and data-intensive approaches, exploring large-scale spatiotemporal patterns using data sets mostly derived from citizen science monitoring programs. Students with previous independent research experience and/or excellent quantitative or computational skills will be given precedence. In addition, the ability to start work during the summer of 2018 would be highly advantageous. Interested students should contact Dr. Leslie Ries (Leslie.Ries@georgetown.edu). For further information on the Ries lab see: http://www.butterflyinformatics.org/ Disease ecology and network epidemiology: Dr. Shweta Bansal is seeking outstanding PhD students to collaborate on mathematical modeling projects for infectious disease dynamics. The Bansal Lab (http://bansallab.com) focuses on the feedback between host behavior and disease transmission using tools from network theory, statistical modeling, and computer science. Current study systems include influenza in humans, pathogen spread in ant colonies, and foot and mouth disease in cattle, with support from the NIH and NSF. Interested students should contact Dr. Bansal (shweta.bansal@georgetown.edu) with a description of their research interests.

Population genetics and molecular evolution: Dr. Matthew B. Hamilton is seeking students interested in using DNA sequence or genetic marker data to test fundamental hypotheses in population genetics and molecular evolution. On-going empirical projects include using genomic or transcriptome sequence data to infer possible causes of molecular clock variation in plants or in arthropods, estimating genetic effective population size, and testing for ecological-evolutionary coupling through genetic variation and effective population size in a salt marsh community of a foundation plant and insect herbivores and predators. The lab also develops software for estimation of

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IGB Berlin FunctionalGenomics extended

Extended deadline for applications: October, 31, 2017 PhD position in Functional genomics for aquaculture - growth, sex determination and disease resistance at the Leibniz-Institute of Freshwater Ecology and Inland Fisheries (www.igb-berlin.de) Since 1996, the IGB has been committed to research on sturgeon aquaculture, remediation and restoration, including several national and international projects and programmes.

Within EU ERA-Net, the COFASP project STURGEoNOMICS involves France, Romania, and Germany (here subject to final approval of the Federal Office for Agriculture and Food, BLE).

At the IGB, the Research Group Applied Fish Physiology and Aquaculture, led by Dr. Sven Wurtz, is looking for a hard-working, enthusiastic PhD student: Functional genomics for aquaculture - growth, sex determination and disease resistance, from now on for a 3 year period Within STURGEoNOMICS, whole genome-based approaches will be explored to improve sturgeon aquaculture, working on two species of sturgeon. The PhD candidate will experimentally extract candidate genes related to target traits (growth, disease resistance, sex determination) for an optimization of management strategies as well as breeding. During the project the candidate will be able to work collaboratively on high quality genome information and transcriptomics to determine the genetic basis of variability in disease resistance and growth during early development as well as sex determination and early sex differentiation.

This work is an essential prerequisite for future selective breeding in order to improve rearing in aquaculture (aiming at maximized growth and disease resistance, as well as early determination of sex and subsequent selection of females for caviar production). The candidate will spend up to 6 months in the facilities of the other partners, which will enhance multidisciplinary training of the student, and give him/her important experience of both academic and non-academic sectors (sturgeon farming).

Applicants should have a 2.1 degree or equivalent in a relevant life science (bioinformatics, molecular biology, fisheries sciences, aquaculture). Excellent communication skills in English are required. Experience with molecular techniques (e.g. genome and transcriptome analysis, next generation sequencing) and fish rearing is highly preferred.

Salary will be according to TVoD (50%). In keeping with the IGB's policy regarding gender equity, female applicants are particularly encouraged. Among candidates of equal aptitude and qualifications, a person with disabilities will be given preference.

This position is subject to approval of the responsible funding body (Federal Office for Agriculture and Food, BLE).

Review of applications meeting the required standards will start immediately and continue until a candidate is appointed.

Please send your application and further inquiries to work leader Dr.

Sven Wurtz (wuertz@igb-berlin.de),— and project coordinator Dr.

Matthias Stock (matthias.stoeck@igb-berlin.de).

Extended deadline for applications: October, 31, 2017 Leibniz-Institut fur Gewasserokologie und Binnenfischerei im Forschungsverbund Berlin e.V., Muggelseedamm 301 D-12587 Berlin The Leibniz-Institute of Freshwater Ecology and Inland Fisheries (www.igb-berlin.de) is the largest research institute for freshwater research in Germany. It is member of the Leibniz Association and the Forschungsverbund Berlin e.V. IGB has close links to all three universities in the German capital and currently hosts about 50 doctoral students from approximately 15 different nations.

Matthias Stoeck <matthias.stoeck@igb-berlin.de>

LaurentianU MooseEvolution

M.Sc. Opportunity-Incorporating Traditional Indigenous Knowledge and Climate Change in the

Evolution of Moose Ecology-Dr. Jesse N. Popp (jpopp@laurentian.ca)

Frank Mallory <fmallory@laurentian.ca>

MaxPlanck Cologne PopulationGenetics

PhD position in population genetics

A PhD position is available for 3 years in the new group of Dr. Stefan Laurent at the Department of Comparative Genetics and Development MPI for Plant Breeding Research in Cologne, Germany (www.laurentlab.org). We are seeking a candidate with a strong interest in population genetics, bioinformatics, and statistical inference to join our group starting in October 2017. The successful candidate will have a M.Sc. in a related discipline (ecology and evolution, population or statistical genetics). Students with solid skills in R or other programming languages are especially encouraged to apply.

Our group will be focused on studying demographic and adaptive processes using modeling and statistical inference approaches (Duchen et al 2013, Laurent and Pfeifer et al. 2016, Pfeifer, Laurent and Sousa et al. submitted). The successful candidate will work on the development of new statistical methods and tools to address the following problems:

1) The joint estimation of demographic and selective parameters using genome-wide polymorphism datasets

2) The inference of demographic parameters in the presence of skewed offspring distributions (Irwin et al 2016).

3) The relevance of chromosomal inversions and mating system on population genetic inference

[INS: :INS]

Potential for applications and collaboration exist with our colleagues from the group of Prof. Miltos Tsiantis, the Director of the Department who recently sequenced full genomes of the selfing plant Cardamine hirsuta.

Applications should be sent to Stefan Laurent (laurent@mpipz.mpg.de) together with details of two academic referees. Deadline for applications is 06-10-2017.

Salary and working hours are in accordance with the funding guidelines of the Max Planck Society for junior scientists. Working hours are fulltime; salary is 50 % of E13 TVoD-Bund. The Max-Planck society is committed to increasing the number of individuals with disabilities in its workforce and therefore encourages applications from such qualified individuals. Furthermore, 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.

Bibliography

Duchen et al 2013:

http://www.ncbi.nlm.nih.gov/pubmed/23150605

Laurent and Pfeifer et al. 2016: http://www.ncbi.nlm.nih.gov/pubmed/26363411 Irwin et al. 2016:

http://www.ncbi.nlm.nih.gov/pubmed/27649621 Pfeifer, Laurent, Sousa, Linnen et al. (bioarxiv):

http://www.biorxiv.org/content/biorxiv/early/2017/06/20/152694.full.pdf Stefan Laurent <laurent@mpipz.mpg.de>

MemorialU Canada FishSexualSelection

PhD student opportunities

At least one graduate student position is available with Dr. Craig Purchase at Memorial University, in St. John's, Newfoundland, Canada.

A Ph.D. student is preferred but I will consider taking M.Sc. students with highly relevant backgrounds. I am unlikely to make decisions about M.Sc. students until the new year.

We conduct research on a variety of marine and freshwater fishes. Lab research includes life history variation, phenotypic plasticity, local adaptation, sperm & egg quality, habitat selection and conservation biology. The current focus is on gamete interactions/ecology in external fertilizers, including the roles of natural (water chemistry/temperature) and post-copulatory sexual selection (female chemical cues) on sperm.

I will take a student who's research project would address evolutionary ecology questions related to fish reproduction, and will likely focus on aspects of sperm biology. It is not an aquaculture-oriented project, nor ecological monitoring. I may take other students for other ecological projects. Most of the work will focus on wild Atlantic salmon, but other species may be involved. The research is lab experimental based, with some collection of parent fish from the field. I am most interested in students that have backgrounds in sexual selection or sperm biology (any taxa), with the next most desirable being fish reproduction or salmon biology.

For more information on my research program visit www.ucs.mun.ca/~cfpurchase A PhD student will receive a financial package of at least $80,000 (strong students are likely to obtain significantly more). Start date should be January or May 2018.

Interested students should send a cover letter, CV, and unofficial copy of transcripts to cfpurchase@mun.ca.

Review of applications will continue until the position is filled.

Cheers

Craig

Dr. Craig F. Purchase Associate Professor, Biology Department Cross appointed to the Dept. of Ocean Sciences Cross appointed to the School of Fisheries Memorial University St. John's, Newfoundland & Labrador, Canada, A1B 3X9 Science Building 232 Elizabeth Avenue Office: Room 4103, T: (709)864-4452 Lab: Room 4105, T: (709)864-2454 Fax: (709)864-3018 Twitter: @CraigPurchase Website: ucs.mun.ca/~cfpurchase Email: craig.purchase@mun.ca

Craig Purchase <cfpurchase@mun.ca>

MemorialU PlantConservation

Ph.D. position in Plant Conservation and Phylogeography at Memorial University of Newfoundland, Canada

I am seeking a motivated Ph.D. student to conduct a project with two main objectives. The first is to characterize a trans-Andean migration route for rainforest taxa. This project will use palm taxa (Arecaceae) as case studies to elucidate a pattern of trans-Andean migration across a region of low elevation in the Andes of Loja, Ecuador. There are numerous taxa in the palm family with a disjunct distribution on the pacific side of Ecuador and Colombia (Choco region) and the eastern side of the Andes in Peru and Bolivia (Western Amazonia). Diversification times for taxa on either side of this barrier and a potential directionality of the migration will be inferred through a phylogeographic approach. A second goal is to conduct a conservation genetics study of the palm genus Parajubaea hypothesized to have colonized the Andes from the Atlantic forest of Brazil <22 million years ago. This genus contains only 3 species (did not radiate much), two of which are IUCN threatened with wild populations restricted to Bolivia, where it is economically important. Its reproductive biology and specialized habitat could explain its limited diversification and colonization to the rest of the Andes. Other research questions of interest to the student are welcome within the framework of Neotropical plant evolution. The Ph.D. student will work under the mentorship of Dr. Julissa Roncal and will interact with other graduate and undergraduate students in the team, as well as with collaborators in Ecuador (Dr. Nora Oleas), Colombia (Dr. Maria Jose Sanin) and Bolivia (Dr. Monica Moraes).

Student's qualifications:

A MSc degree in a related discipline (e.g. biology, botany, ecology, molecular biology, bioinformatics). Experience in organismic botany, phylogenetics and/or population genetics analyses, and bioinformatics is highly desirable.

Excellent writing, analytical, organization and communication skills. Attention to detail.

Written and oral proficiency in English is mandatory for international students. TOEFL test required for admission to the university, but not the GRE tests.

Position characteristics:

Project start date is January 5, 2018. The PhD program comprises four years with an annual stipend of $19,500. The student is expected to teach on average 10 hr/wk during the fall and winter semesters but not in the spring. The department of Biology at Memorial University has 29 faculty members and over 100 graduate students. Memorial University is Atlantic Canada's largest university offering a multicultural environment. Screening will begin immediately and will continue until the position is filled.

How to apply:

Interested applicants should send their CV, a one-page statement of research interests and career goals, transcripts, and contact information of 3 references (who have agreed to be contacted) in a single pdf or word file to Dr. Julissa Roncal at Email: jroncal@mun.ca.

For instructions on how to apply to Memorial's graduate program visit: http://www.mun.ca/become/graduate/-apply/index.php – Julissa Roncal, Ph.D. Assistant Professor and curator of the Ayre Herbarium Department of Biology Memorial University of Newfoundland 232 Elizabeth Avenue St. John's, NL, A1B 3X9, Canada Office SN4102, phone (709) 864 2241 Laboratory SN4096-4097, phone (709) 864 2093 Ayre herbarium (709) 864 6233 Mobile: (709) 351 6771 http://-

julissaroncal.wordpress.com/ View our newest article on phenolics and antioxidant capacity on Vaccinium vitis-idaea at: http://www.nrcresearchpress.com/eprint/-qgaHNDzMEJ3iY8YSScec/full "jroncal@mun.ca" <jroncal@mun.ca>

Netherlands ParentalEffectsEvolution

PhD position available at Groningen Institute for Evolutionary Life Sciences, University of Groningen, The Netherlands

Project title:

Environmental predictability and the evolution of parental effects: integrating ecology, phylogeny, modelling and genetics

Project summary:

To predict how species will adapt in a rapidly changing world requires evolutionary models based on knowledge of developmental plasticity to various forms of environmental fluctuations. A hotly debated pathway of such plasticity is based on the transfer of non-genetic information from parents to offspring - known as parental effects. According to recent theoretical models, if parental and offspring environments are sufficiently alike, then the parental phenotype can be used as a source of information for offspring to adaptively match their environment. Thus, parental effects may play a crucial role in adaptation to changing environments. We will use a comparative approach to test this prediction in multiple Drosophila species, sampled globally from populations with different levels of similarity in ambient temperature between parental and offspring environments. We recently demonstrated adaptive parental effects in Drosophila melanogaster: the eggs of parents who reproduced at low or high temperatures survived better to adulthood when parental and offspring thermal conditions matched (both low or both high). Using similar experiments, we will quantify how parental effects affect adaptation in the sampled Drosophila populations. To test the theory, we will develop quantitative evolutionary models, taking into account observed population-specific demography and temperature fluctuations, and predict the relative importance of parental effects. Using genes discovered in our ongoing experimental evolution study on parental effects in D. melanogaster, we will compare sequence and structure of candidate genes underlying parental effects from the sampled populations. By thus integrating theory, ecology and genetics we will critically advance our understanding of transgenerational adaptive plasticity and quantify its importance for adaptation in a world with increasingly rapid changes in temperature.

Requirements of candidates:

We are looking for a highly motivated candidate with a relevant M.Sc. who can work in a multidisciplinary team combining evolutionary studies with mathematical modelling.

For more information or applying (incl. letter of motivation + CV) please contact:

Prof. Ido Pen (Theoretical Research in Evolutionary Life Sciences, GELIFES, i.r.pen@rug.nl)

Prof. Jean-Christophe Billeter (Evolutionary Genetics, Development & Behavior, GELIFES, j.c.billeter@rug.nl)

Prof. Ton Groothuis (Evolutionary Genetics, Development & Behavior, GELIFES, a.g.g.groothuis@rug.nl)

"Pen, I.R." <i.r.pen@rug.nl>

NorthDakotaStateU ConservationGenomics

Graduate Position: Conservation Genomics of the rare Californian endemic, Torrey Pine (Pinus torreyana)

An MS or PhD graduate position in conservation genomics is available to study fine-scale population genomic structure of the rare Californian endemic, Torrey Pine with Jill Hamilton at North Dakota State University, Fargo, North Dakota in collaboration with Sean Hoban (The Morton Arboretum, Lisle, IL) starting January 2017.

Torrey pine (Pinus torreyana Parry) in one of the rarest pines in the world, restricted to two populations, a mainland grove of approximately 3400 trees just north of San Diego and an island population of approximately 2000 trees on Santa Rosa Island, one of the Channel Islands (nearly 300 km away). This project will evaluate the fine-scale genomic structure of natural populations using RAD-seq, comparing mainland and island population and assess the status of genetic variation captured within an ex situ seed collection. There is plenty of room to pursue particular questions of interest depending on the interest and experience of the candidate. This interdisciplinary research will combine genomic, spatial and environmental datasets to ground-truth an ex situ seed collection and investigate genetic connectivity at a fine-scale. This project will involve substantial collaboration with tree scientists at the Morton Arboretum in Lisle, IL (outside of Chicago) and is part of a lar ge collaborative network to conserve Torrey pine between the US Forest Service, National Park Service, California State Parks, San Diego Zoo, and North Dakota State University.

The ideal graduate student will be independent, organized and a problem solver. Ideally the student will have some experience in lab bench work, molecular ecology/population genetics, and/or bioinformatics for genomic data analyses, and be prepared to conduct some field-based research in a collaborative environment.

For more information on the Hamilton Lab please visit the lab website at: http://www.jillahamilton.com and more information on the Department of Biological Sciences at NDSU at https://www.ndsu.edu/biology/- . Fargo is the largest city in the northern Midwest and as the 'Gateway to the West' is a vibrant, growing community that has access to numerous outdoor opportunities for all seasons. Short visits (one week to one month) will be hosted at the Morton Arboretum (http:/- /www.mortonarb.org/) in Lisle, Illinios, with Dr. Sean Hoban as primary host (http://www.mortonarb.org/- science-conservation/scientists-and-staff/sean-hoban).

Interested students are encouraged to contact Dr. Hamilton (jill.hamilton@ndsu.edu). Please include a brief description of your research interests, a writing sample and a CV in your email. This position is fully-funded and includes an annual salary, a tuition waiver and is open to US students or international students.

jillahamilton@gmail.com

Norway CarpEvolution

PhD position in Applied Ecology: Evolutionary history and predator inducted morphology in cruican carp

A 100% position as a PhD candidate in applied ecology is available at Inland Norway University of Applied Sciences, Faculty of Applied Ecology and Agricultural Sciences at Campus Evenstad from 01.01.2018 until 31.12.2020.

This position is a part of an ongoing research project targeting the phylogeny, life-history evolution and body morphology in the crucian carp (Carassius carassius). One of the main objectives of the project is to describe the phylogeny of the crucian carp in Northern Europe with regard to natural and human induced distribution of the species. Another objective is to clarify the life history evolution and body morphology in the species, and particularly elucidate the contrast between lakes with or without piscivorus predators. We will search for body morphology traits, behavior and stress in crossing experiments with crucian carps the two categories of lakes. We will also look at the gene expression patterns, growth trajectories and energetic consequences in crucian carp experimentally exposed to predators in different ways. In such, the position will include responsibility for fieldwork, laboratory experiments, data management and analysis. The PhD-student is expected to be a part of the freshwater ecology group and assist in advising bachelor and master students.

The candidate will be supervised by associated professor Antonio B.S. Poléo at Campus Evenstad, Inland Norway University of Applied Sciences. The PhD candidate will also have a supervisor group consisting of associated professor Kim PrÃbel from the University of Tromsø, Norway, Professor Kimmo Kahilainen and Professor Kjartan Ãstbye at Campus Evenstad, Inland Norway University of Applied Sciences. At least two research stays at labs outside Evenstad is to be expected. The candidate should develop the details of the PhD-plan together with the advisors once the position has been accepted.

Qualifications A master degree in ecology or equivalent education is required to be qualified for admission to the PhD study in Applied Ecology at Inland Norway University of Applied sciences. Candidates with a strong background or documented experience in population genetics and/or fish physiology may be prioritized.

Previous experience from relevant fieldwork or experimental work, and peer-reviewed publications is considered as important merits. We expect the candidate to be passionate about doing research, and that the candidate is willing to develop the skills to communicate this passion with other scientists and the general public. The candidate should welcome the opportunity to conduct research abroad and work within a multidisciplinary team. We are searching for reliable candidates who can work independently, but who will also function well in our large team. We emphasize personal qualifications when appointing personnel to the faculty.

Salary Salary follows the State salary scale for scholarship holders, position code 1017, salary framework 20, alternative 8, starting in salary step 50 which currently constitutes NOK 436 900 gross per year. For particularly well qualified applicants, code 1378 can be used.

Life insurance and occupational injuries insurance are included. Pension contributions to Statens pensjonskasse will be deducted. Questions about the position or work environment can be directed to associated professor Antonio B.S. Poléo, cell phone +47 91660075; e-mail: antonio.poleo@inn.no,

Other conditions The national workforce should, to the greatest possible extent, reflect the diversity of the population. There is therefore a personnel policy goal to achieve a balanced age and sex composition and recruit from ethnic minority groups.

Application Applications should be made to Inland Norway University of Applied sciences. The application and CV should be marked 2017/04399 and submitted electronically on the college website: www.hihm.no/job-opportunities . Do not send certificates and references with the application, we may ask for them later.

Kjartan Ãstbye <kjartan.ostbye@inn.no>

OhioStateU InsectEvolutionaryPhysiology

Graduate Research Assistantship

The Evolution of Seasonal Responses in Insects

The Meuti Laboratory

Department of Entomology

The Ohio State University, Columbus Ohio

Position description: A graduate assistantship for a MS or PhD candidate is available starting Fall 2018 in the Entomology Department at the Ohio State University within the Meuti Laboratory. The successful applicant will conduct research on the evolution of seasonal responses in mosquitoes and/or brown marmorated stink bugs. These studies will include conducting gene expression studies (qRT-PCR and RNAseq), measuring seasonal phenotypes, performing bioinformatics analyses and performing germline transformations using CRISPR/Cas9 genome editing. Candidates will be encouraged to develop their own experiments, particularly those with an evolutionary focus, within the context of the overall project. This competitive assistantship will cover tuition, stipend, and health insurance.

Deadline for applications: Although this position is open until a suitable candidate is found, for full consideration applicants should have all of their materials submitted to The Ohio State University Graduate School no later than December 1, 2017.

Qualifications: The successful candidate will have a bachelor's degree in Biological Sciences or a related discipline. A Master's Degree or previous research experience in evolutionary biology, molecular biology and/or physiology is preferred.

Application materials: Interested candidates are encouraged to email Dr. Megan Meuti (meuti.1@osu.edu) to discuss the position in detail. Your email message should include: (1) a short statement of intent, (2) contact information for three references, and (3) a concise, current CV complete with (a) degrees earned and relevant coursework, (b) GPA, (c) GRE scores and percentiles, (d) publications, (e) research presentations, (f) awards/scholarships/grants, and (g) other relevant skills/qualifications. Students from non-English speaking countries should also provide TOFEL scores.

Additional information: To learn more about members of the Meuti lab and our work please visit the laboratory website < http://u.osu.edu/meutilab/ >.

[image: The Ohio State University] Megan E. Meuti Assistant Professor College of Food, Agriculture and Environmental Sciences Department of Entomology

Room 400A Aronoff Lab 318 W. 12th Ave Columbus, OH 43210 Office: 614-688-2829 E-mail: meuti.1@osu.edu Website: u.osu.edu/meutilab/

Megan Meuti <meuti.1@osu.edu>

OhioStateU SquirrelEvolution

PhD Position

Adaptive Divergence and Reproductive Isolation in Tree Squirrels

The Chavez Lab

Department of Evolution, Ecology, and Organismal Biology

The Ohio State University, Columbus, Ohio

Position description: The Chavez lab is seeking two PhD students to start Fall 2018 in the EEOB (Evolution, Ecology, and Organismal Biology) Department at the Ohio State University. We are interested in both the ecological and molecular bases of reproductive barriers and are seeking students that will conduct speciation and adaptation research on tree squirrels in their hybrid zones in the Pacific Northwest. We have both field AND molecular studies that are ongoing with this system and successful applicants will conduct research that investigates EITHER (or BOTH) the ecological/behavioral, and/or genomic mechanisms of speciation and divergent adaptations. For applicants interested in the molecular studies, research methods will include collecting genomic data and using bioinformatics/population genetic analyses to study hybridization, introgression, and adaptive evolution. For applicants interested in the field studies, research will include collecting ecological and behavioral data as they pertain to divergent adaptations and reproductive barriers (assortative mating, hybrid viability, life history evolution, etc). Candidates will be encouraged to develop independent research topics within the context of the overall project.

Deadline for applications: Application materials should be submitted to The Ohio State University Graduate School no later than December 1, 2017.

Qualifications: The successful candidate will have a bachelor's degree (Master's degree is preferred) in Biological Sciences or a related discipline with previous research experience. Ideal applicant for the genomics position will have strong research interests in population genetics, molecular laboratory skills, strong quantitative skills, and some proficiency in basic bioinformatics. Ideal applicant for the ecological/behavioral position will have strong research interest in animal behavior, evolutionary ecology, and strong quantitative skills.

Application materials: Interested candidates are encouraged to email Dr. Andreas Chavez (chavez.102@osu.edu) to discuss the position in detail. Your email message should include: (1) a short statement of intent that includes why you are interested in our lab and your previous research experience, (2) contact information for three references (preferably those associated with your research experience), and (3) a concise, current CV complete with (a) degrees earned and relevant coursework, (b) GPA, (c) GRE scores and percentiles, (d) publications, (e) research presentations, (f) awards/scholarships/grants, and (g) other relevant skills/qualifications. Students from non-English speaking countries should also provide TOFEL scores. PLEASE INDICATE "Graduate position - Fall 2018" in your subject line.

Additional information: To learn more about members of the Chavez lab and our work please visit the lab website <www.aschavez.com or https://eeob.osu.edu/-people/chavez.102> . Andreas S. Chavez, PhD Assistant Professor Department of Evolution, Ecology, and Organismal Biology The Ohio State University 318 W. 12th Ave., 300 Aronoff Laboratory, Columbus OH, 43210 614-292-2204 chavez.102@osu.edu www.aschavez.com chavez.102@osu.edu

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Paris-Sud AdaptationDomestication

Title: Origin, spread and demographic history of the major apple aphid pest in Eurasia.

Summary

Ever since Darwin's time, domestication has been used as a model for investigating adaptation. Studies of the mechanisms of adaptation in the context of domestication are particularly relevant related to crop parasites, with frequent host shifts involving adaptation to new hosts following anthropic environmental changes. Our project aims at understanding the impact of apple domestication on the adaptation of a major apple aphid pest Dysaphis plantaginea (the rosy apple aphid), to its apple hosts in Eurasia, the cultivated (Malus domestica) and wild apples (Malus sylvestris, Malus sieversii and Malus orientalis).

A crucial first step in this project is to determine the worldwide spread routes, the genetic diversity and genetic structure of the Rosy apple aphid using population genetic approaches. The student will use newly developed microsatellite markers for the genetic characterization of collection of D. plantaginea accessions sampled from different hosts in Eurasia. It will make it possible to reconstruct the history of D. plantaginea populations in the context of the domestication of its apple host. In addition to understanding the adaptation of insect pests to recent anthropocene changes, this project will develop technical innovations aimed at biological sustainable agriculture to control parasitic aphids in apple production.

Methodology : population genetic analyses (genetic diversity, population structure and demographic inferences using Approximate Bayesian Computation).

Profile preferred for the candidate : Ideally, the candidate will have skills in genetics/genomics and evolution and at least will show strong interest in these fields. He/she will not necessarily be familiar with aphid models. The Master project will be proposed to the Doctoral School Science du Vegetal (Paris-Sud Doctoral School) for a PhD project on the genomic basis of aphid adaptation to their host in the context of domestication in june 2018.

Supervision: Amandine CORNILLE - Chargee de Recherche CNRS CR2 Genetique Quantitative et Evolution - Le Moulon Ferme du Moulon 91190, Gif.sur.Yvette, France mail??: amandine.cornille[at]gmail.com Google Scholar profile : https://scholar.google.com/citations?user=EqIE2h8AAAAJ&hl=fr Personal page : http://moulon.inra.fr/index.php/fr/equipes/dygap/355 Duration : 6 months, january 2018 ?? june 2018 or february 2018 ?? july 2018, starting dates are flexible, contact Amandine CORNILLE for further discussions.

Fixed indemnisation: 3500 euros for 6 months (˜580 euros/month).

References

Beaumont MA, Zhang W, Balding DJ (2002) Approximate Bayesian computation in population genetics. Genetics, 162, 2025-2035.

Cornille A, Gladieux P, Smulders MJ. et al. (2012) New insight into the history of domesticated apple: secondary contribution of the European wild apple to the genome of cultivated varieties. PLoS Genet, 8, e1002703.

Guillemaud T, Beaumont MA, Ciosi M, Cornuet JM, Estoup A (2009) Inferring introduction routes of invasive species using approximate Bayesian computation on microsatellite data. Heredity, 104, 88??99.

Amandine Cornille <amandine.cornille@gmail.com>

PurdueU PlantEvolutionaryGenet

Graduate assistantships in plant ecological and evolutionary genetics at Purdue University.

I'm recruiting 1-2 Ph.D. (or highly motiviated and independent M.S.) students to join my lab in Autumn 2018. I am broadly interested in plant ecological and evolutionary genetics, with a main focus understanding the genetic basis of local adaptation and fitness tradeoffs across environments. I am also interested in using heterosis as a tool to study the consequences of genetic drift for genetic variation with adaptive signficance. I also maintain an interest in the evolutionary maintenance of outcrossing in highly selfing species. I encourage students to develop independent projects within these main research areas.

More information about my lab, the positions, and the graduate program at Purdue can be found here: http://web.ics.purdue.edu/˜oakleyc/join-us.html Chris Oakley oakleyc@purdue.edu

"Oakley, Christopher G" <oakleyc@purdue.edu>

QueenMaryU UK HostSymbiontEvolution

*** PhD position available***

The genomic basis of host-symbiont dependency

*Background *

Organisms across the tree of life form partnerships with microbes for protection, metabolic and nutrition. In some cases, host and symbiont become so tightly associated that dependency evolves and the two organisms integrate both physically and genomically. Dependency on microbes is particularly prevalent among insects. These acquisitions have led many groups of insect to great success by allowing them to use otherwise unavailable resources and invade inaccessible habitats. Here we explore how dependency on microbes evolves, and how genomes combine to produce the novel functions that have allowed insects to dominate so many habitats.

In this project you will use the symbionts of ants and aphids to rigorously test hypotheses on the evolution of symbiotic dependency. This may include: exploring the early stages of genome integration in hosts that have recently evolved dependency on microbes; revealing the functional role of symbionts through shared metabolic pathways with hosts; and determining how host ecology influences gains and losses of symbionts.

o You will have access to large genetic databases, insect collections, in-house live organisms and cutting-edge research facilitates to fuel your investigation.

o You will gain experience of molecular/experimental biology, comparative/metagenomics, bioinformatics, and statistics (e.g. comparative phylogenetics).

o You will be encouraged to develop your own ideas and hypotheses.

Skills preferred In a multidisciplinary project such as this, candidates are unlikely to have a background in all disciplines involved. The most important qualification is motivation and that the project appeals to you. We can envisage strong candidates coming through various routes including: - bioinformatics - practical molecular biology - evolutionary theory

For informal requests, do not hesitate to contact me at l.henry@qmul.ac.uk

****Deadline for application: Sept 27, 2017****

Supervisor Information Dr. Lee Henry Email: l.henry@qmul.ac.uk Website: http://www.sbcs.qmul.ac.uk/staff/leehenry.html *Funding Notes*

The studentship is fully funded and available to EU, UK and International citizens. It will cover tuition fees as well as provide an annual tax-free maintenance allowance for 3 years at Research Councils UK rates (pounds 16,553 in 2017-18).

Applicants must have an excellent academic track record, with a bachelorâ euro s degree (1st or high 2.1) in a relevant degree. An MSc in bioinformatics, evolutionary biology, or ecology is also highly desirable.

References

Fisher RM, Henry LM, Cornwallis CK, Kiers ET and SA West (2017). The evolution of host-symbiont dependence. Nature Communications vol. 8

Henry LM, Maiden MJC, Ferrari J and HCJ Godfray (2015). Insect life history and the evolution of bacterial mutualism. Ecology Letters 18:516-25

Lee Henry Senior Lecturer Queen Mary University of London School of Biological and Chemical sciences Mile End Rd London E1 4NS

lee henry <leehenrym@gmail.com>

SyracuseU NY EvolutionSpeciesInteractions

Ph.D. Opportunity in Species Interactions

Althoff lab, Dept of Biology, Syracuse University

We are seeking exceptional students interested in studying the evolutionary ecology of species interactions. The lab focuses on studies of coevolution, specialization, and speciation, and we use a combination of diverse tools including field studies, molecular phylogenetics, and population genetics. Although we primarily examine plant-insect and parasitoid-host coevolution, students interested in other taxonomic groups are strongly encouraged to apply. There are currently two funded projects, one on the role of mutualism and antagonism in yucca and yucca moth speciation and another using a synthetic yeast mutualism to study the ecology and evolution of multi-mutualist species communities. Research is question-driven rather than taxon-driven. Please visit the lab webpage at althofflab.syr.edu for more information.

Funding is guaranteed via teaching assistantships for 5 years and potentially research assistantships. Syracuse University offers excellent benefits, a full tuition waiver, and a generous stipend (~$25K for 2016). Furthermore, the close proximity of S.U. to the SUNY-Environmental Science and Forestry campus and Cornell makes this a strong and vibrant community that facilitates an exciting graduate experience.

Prospective students are encouraged to contact Dr. David Althoff (dmalthof@syr.edu).

David M Althoff <dmalthof@syr.edu>

TrinityC Dublin NeuroGenomics

PhD Student Position, Trinity Translational Medicine Institute

Would you like to develop skills in a key biomedical research area? Do you have a background in genetics, statistics or computing? Are you curious about the molecular basis of the brain? Would you like to contribute to international neurogenomics research with cutting-edge technology?

If so, please join our group. We have a PhD position available.

You will be part of the Neuropsychiatric Group in the Trinity Translational Medicine Institute, supervised by Dr Lorna Lopez and Professor Louise Gallagher and undertake a project using whole genome sequencing to understand the molecular basis of neurodevelopmental disorders. International training and travelling opportunities will be provided.

We would like to invite outstanding graduates with a strong background in either molecular biology (particularly genetics) or maths (including statistics, computing, bioinformatics or psychology) to apply. An enthusiasm for understanding and communicating neuropsychiatric genetics is essential. This is a three-year position, starting before 1^st March 2018, and comes with a tax-free stipend of euro18,000 and covers fees up to EU level (non-EU students may apply, but fees are only covered up to EU rates). Please apply with a cover letter including a short summary of scientific interests, your CV, and contact details for two referees to Lorna (lorna.lopez@tcd.ie) by October 31^st 2017. Informal discussions to Lorna prior to application are very welcome.

Previous research by Dr Lopez can be found on google scholar

(https://scholar.google.com/citations?user=-2iFCgFoAAAAJ&hl=en)

Lorna Lopez <Lorna.Lopez@tcd.ie>

UAdelaide AboriginalHeritageProject

Aboriginal Heritage Project - winner of the prestigious 2017 Australian Eureka Prize for Interdisciplinary Research

Several PhD project opportunities starting immediately in bioinformatics, genomics, and statistical genetics.

We are seeking highly motivated students to fill three (3) PhD positions and join the landmark Aboriginal Heritage Project (www.adelaide.edu.au/acad/ahp/), which is reconstructing Indigenous Australian history from a remarkable collection of hair samples and ethnographic data. The project cuts across traditional research boundaries, incorporating cutting-edge statistical and population genetic analyses with anthropological, archaeological and archival research, whilst maintaining long-term engagement with Indigenous communities throughout Australia. The first results from the project revealed a remarkably deep and abiding population structure across Australia tracing back to the peopling of the continent 50kya (Tobler et al. Nature 2017;544:180-184).

The candidates must have, as a minimum, an excellent undergraduate academic record and meet the English Language Proficiency (ELP) requirement. The call is open to international and domestic students with backgrounds in bioinformatics, mathematics, statistics, computer science, population/quantitative genetics, or a related field. While a background in biology is desirable, it is not a prerequisite for success, as training opportunities in genetics, human evolution, molecular biology, or other related areas can be provided during the PhD. Successful candidates will be involved in the analyzing genomic datasets from Indigenous populations across Australia, New Guinea and Indonesia, with special emphasis on adoption and expansion of statistical tools to reconstruct the genetic history of the original human migrants into Australia.

Good computational and analytical skills are of high importance and a successful candidate would be competent in one or more of the following: - Statistical analysis of large datasets and/or mathematical modelling - Fluency in using Linux systems, with a prior hands-on experience with Bash scripting - Programming in a scripting language such as Python and/or R

The PhD will be situated in the Australian Centre for Ancient DNA (ACAD; www.adelaide.edu.au/acad/), a highly dynamic group based at the University of Adelaide, with world leading researchers in ancient DNA, human evolution, epigenetics, microbiomics, and megafaunal extinction.

Interested applicants are encouraged to send a CV (including names and contact details of three references) and a cover letter to Dr Ray Tobler (raymond.tobler@adelaide.edu.au) or Dr Yassine Souilmi (yassine.souilmi@adelaide.edu.au). The positions will remain open until filled.

raymond.tobler@adelaide.edu.au

UAuckland NZ EvolBirdSong

PhD, MSc and Honours positions available for new project on the evolutionary origins of song learning in birds. This project is a collaboration between Dr. Kristal Cain (kecain.weebly.com) at the University of Auckland in New Zealand, and Dr. Michelle Hall (michellehall.wordpress.com) at The University of Melbourne in Australia. Both domestic and international applications are encouraged.

Vocal learning in birds is of great interdisciplinary importance and an excellent model for human language. This research relies on a clear understanding of the evolutionary origins of vocal learning, but recent reports have undermined previous assumptions, leading to a hotly contested debate about the evolution of vocal learning. Vocal development in one group of birds, the New Zealand wrens (Acanthisitti), is critical for resolving this debate, but is currently unknown and unstudied. The project will focus on tiÌtipounamu/rifleman and combine in-depth behavioural analyses with new acoustic tools to determine whether vocalisations are learned or innate in these endemic birds. We are also interested in sex differences in vocal acquisition patterns.

This project is strongly field-oriented and will require substantial time in remote areas. There is flexibility for keen students to guide the direction of the research within the framework of the overall project. The PhD project is anticipated to start mid-2018, with fieldwork commencing in August. Informal inquiries are welcome.

Preferred selection criteria

- Strong previous academic record

- Enthusiasm and interest in the broad concepts and questions motivating the research

- Interest in undertaking field-based avian research, especially acoustic data

- Enjoyment of outdoor fieldwork and confidence in working in remote locations that can experience extreme weather.

- Excellent interpersonal, oral and written communication skills

- Ability to learn/use R (statistical programming language), new packages for analysis (e.g. warbleR), and new software (e.g. Sound Analysis Pro)

- Experience with bird banding/ringing, nest searching, and acoustic techniques is helpful, but not required

To apply, please send an e-mail briefly explaining your research interests and career goals, a CV, a copy of academic transcripts, and contact information for two references to Dr. KE Cain (k.cain@auckland.ac.nz). Informal enquires are also welcome.

Application and funding details: This project is currently under review and may be offered as a fellowship, supported by the Marsden Fund of The Royal Society of New Zealand (broadly equivalent to US NSF). If not funded students will need to qualify for a U Auckland scholarship. Funded fellowships and scholarships provide a tax-free living stipend and cover student fees for all postgraduates on the project (PhD, MSc, or honours); PhD candidates also receive additional research funds and we will provide opportunities and support to apply for further funding. All positions require the applicant to be eligible for admission at the University of Auckland (see https://www.auckland.ac.nz/en/for/-future-postgraduates). Please note the English language proficiency requirements.

We encourage all qualified applicants to apply. Auckland is a diverse and welcoming city and we are committed to increasing diversity in biology. We particularly encourage Maori/Pacifica students to apply; tiÌtipounamu are endemic songbirds and taonga, adding special significance and kaitiakitanga to our proposed research. Our project celebrates their unique status - the phylogeny/whakapapa of this species is critical to our project and for understanding the true origins of vocal learning worldwide.

k.cain@auckland.ac.nz k.cain@auckland.ac.nz

UBern ConservationBiology

1 PhD position for a conservation biologist/restoration ecologist at the University of Bern, Switzerland.

within our new research programme funded by the Swiss National Science Foundation:

Restoring grassland biodiversity: from degraded, species-poor to integral stable-state ecosystems

Farmland of the Swiss Lowlands is devoted to high-intensity, modern agriculture that has generated precarious conditions for biodiversity, as typically encountered in most Western and Central Europe. Agri-environment schemes have tried to remedy to these dramatic situation, but have had limited success so far. We shall experimentally - full-block design with random allocation of treatment to field - evaluate the effectiveness of pro-active reseeding methods for restoring flora-rich hay meadows. The restoration methods tested consist of 1) simple hay transfer from biodiversity-rich, donor meadows; 2) sawing locally collected or commercialised seed mixtures. The overarching objective is to push degraded plant and invertebrate assemblages towards species-richer, stable-state grasslands.

The PhD candidate will collect baseline data (before interventions) and monitor subsequent biotic and abiotic environmental changes (following experimental manipulation) using a series of metrics for biodiversity (plant and invertebrate species richness, diversity indices, functional traits, community analyses, etc.), as well as for hay productivity and quality. The reliance on a full block design will enable avoiding the caveats and biases typically encountered in mere observational studies, notably those caused by unavoidable confounding environmental factors such landscape naturalness. The ultimate objective of this research is to provide end-users, notably farmers and authorities, with easily implementable, evidence-based recommendations for future grassland restoration strategies that maximize the return on investment of the agricultural subsidies targeting biodiversity. The experiment will start in 2018 and is foreseen to run 4-8 years, with the PhD candidate engaged in its first phase.

The candidate holds a MSc degree, shows a strong interest in agro-ecology and masters modern analytical techniques and statistical software. Knowledge of grassland indicator taxa would be advantageous though not prerequisite. English literacy is important, while knowledge of German and French would represent a real asset, notably for dealing with farmers. Start: January 2018. Salary according to SNSF rules. The PhD student will have to contribute to teaching and some minor administrative duties.

Email a letter of motivation with CV, list of publications, summary of MSc thesis, as well as two references (name, institutional address, email and phone number) to jean-yves.humbert@iee.unibe.ch.

Application deadline: 12 November 2017. Interviews in Bern on 4 December 2017.

Prof. Dr. Raphael Arlettaz

Head of the Division Conservation Biology

University of Bern

Jean-Yves Humbert, PhD University of Bern

Institute of Ecology and Evolution

Office: Erlachstrasse 9a Trakt 2

Mail: Baltzerstrasse 6, CH-3012 Bern Tel. +41 31 631 31 73

jean-yves.humbert@iee.unibe.ch

http://www.cb.iee.unibe.ch/about_us/-dr_humbert_jean_yves/index_eng.html
“jean-yves.humbert@iee.unibe.ch” <jean-yves.humbert@iee.unibe.ch>

UBritishColumbia FoodWebPhylogenies

PhD opportunity: The phylogenetic ecology and biogeography of food webs

We are seeking an enthusiastic student for a PhD centered on the phylogenetic ecology of invertebrates in food webs. This PhD project will combine phylogeny, biogeography and community ecology to test mechanisms of food web change across geographic and environmental gradients. The large geographic scale of this project is made possible by an existing network of researchers, the Bromeliad Working Group, which has already documented aquatic invertebrate food webs from 2000 bromeliads in 16 sites across Central and South America. In this project, the PhD student will use sequencing to construct phylogenies of invertebrates from these sites, and then combine the phylogenies with the existing food web information. This creates a unique opportunity to reconcile the importance of evolution, dispersal and environmental filtering on food web structure.

The successful applicant will have a strong background in evolution and ecology, excellent grades, and above all a passion for biology. Ideally, the applicant will have independent research experience or a MSc. in evolution, molecular biology or ecology. The applicant should be competitive for national scholarships, such as NSERC or NSF, and will be expected to apply for such grants. The PhD student will spend time at both the University of British Columbia (Vancouver, Canada) and at Rutgers University (New Jersey, USA). Prof. Diane Srivastava (UBC) will supervise the food web aspects of the project, whereas Prof. Jessica Ware (Rutgers) will supervise the molecular and phylogenetic aspects. The student will be registered in the PhD program at UBC, and become part of the Biodiversity Research Centre - a leading research hub in ecology and evolution.

Send application with cv and transcripts to:

Diane Srivastava (srivast@zoology.ubc.ca)

Jessica Ware <jware42@newark.rutgers.edu>

U Hamburg Systematics gastropods

Universität Hamburg, Center of Natural History, invites applications for a Research Associate (PhD student) for the project

“Exploring genomic methods for delimiting species in radiations of terrestrial snails”

in accordance with Section 28 subsection 3 of the Hamburg Higher Education Act (Hamburgisches Hochschulgesetz, HmbHG). The position commences earliest on 1.12.2017.

It is remunerated at the salary level TV-L 13 and calls for 65 % of standard work hours per week*.

The fixed-term nature of this contract is based upon Section 2 of the Academic Fixed-Term Labor Contract Act (Wissenschaftszeitvertragsgesetz, WissZeitVG). The term is fixed for a period of 3 years.

The metropolis Hamburg is one of the most popular cities in Europe and harbors one of the largest universities in Germany. The University aims to increase the number of women in research and teaching and explicitly encourages qualified women to apply. Equally qualified female applicants will receive preference in accordance with the Hamburg Equality Act (Hamburgisches Gleichstellungsgesetz, HmbGleiG).

Responsibilities: Duties include academic services in the project named above. Research associates can also pursue independent research and further academic qualifications.

Specific Duties: The doctoral student will study the evolutionary history of land snail radiations and evaluate and optimize different genomic approaches for delimiting closely related species, both with regard to laboratory and analytical methods, within the framework of the DFG SPP 1991 Taxon-OMICS. Field work and the conservation of material also pertains to the duties.

Requirements: A university degree in a relevant field. The candidate should be experienced with molecular biological methods and preferentially also with "next generation sequencing" techniques and data analyses or a programming language (Perl, Python, R, etc.). The project requires analytical thinking and good English skills (German language skills are not absolutely necessary, the working language is English).

Severely disabled applicants will receive preference over equally qualified non-disabled applicants.

For further information, please contact Prof. Bernhard Hausdorf.

Applications should include a cover letter detailing your research interests and experience, curriculum vitae, and copies of degree certificates. The application deadline is October 15, 2017. Please send applications as a single pdf file to: Prof. Bernhard Hausdorf, hausdorf@zoologie.uni-hamburg.de.

Prof. Dr. Bernhard Hausdorf Center of Natural History University of Hamburg - Zoological Museum Martin-Luther-King-Platz 3 20146 Hamburg - Germany

"fb5a071@uni-hamburg.de" <fb5a071@uni-hamburg.de>

UIB Spain CrustaceanEvolution

The Universitat de les Illes Balears (UIB) and Institut Mediterrani d'Estudis Avançats (IMEDEA, CSIC-UIB, Spain) is seeking a candidate for a Spanish FPI PhD grant associated to our project "The Hyalella (Amphipoda: Crustacea) species-flock in the ancient endangered Lake Titicaca, High Andes: morphological and genetic biodiversity". The PhD project will explore species delimitation -based on molecular mitochondrial and nuclear data-, phylogeny -based on whole mitochondrial genomes- and the historical biogeography of the Titicaca Basin amphipods.

The PhD thesis (2017-2021) will be developed at the campus in Palma (Mallorca, Balearic Islands, Spain) and at the IMEDEA institute in Esporles (Mallorca, 5 km from campus).

The research team has considerable experience in arthropod evolution and phylogenetics (see https://www.nature.com/articles/s41598-017-03107-y for a recent publication and http://www.researcherid.com/rid/C-9856-2011 for a list of publications of the IP-1).

The position requires a highly-motivated candidate seeking to develop a research career in Evolutionary Biology. Ideally, he/she should be interested and in population biology/phylogenetics and bioinformatics/next generation sequencing. The duration of the contract is for four years.

Requirements:

The candidate must be eligible for a Spanish FPI PhD fellowship (see http://www.idi.mineco.gob.es/portal/site/MICINN/menuitem.dbc68b34d11ccbd5d52ffeb801432ea0/?vgnextoid=b96552ab45a7e510VgnVCM1000001d04140aRCRD&vgnex 11f35656ecfee310VgnVCM1000001d04140aRCRD for more information). A recent BSc or MSc degree is required, preferably in Biology, Biochemistry, Bioinformatics or related fields. The fellowships are open to European Union (EU) and non-EU citizens. Individuals with no residency in Spain may be also eligible.

Previous experience in Molecular Phylogenetics and/or Next Generation Sequencing data analyses/bioinformatics is preferred.

Application procedure:

Before the online formal application procedure (during the period October 3rd - 18th) interested candidates are invited to submit a CV, a brief statement of experience and unofficial transcripts to:

Carlos Juan <cjuan@uib.es>

UKonstanz EvolutionOfSelfing

University of Konstanz, PhD position, Evolutionary Ecology, Evolution of selfing

The Ecology Group in Department of Biology at the University of Konstanz invites applications for a Doctoral Research Position (salary scale 65 % of 13 TVL)

We are seeking to fill a 3-year PhD position, part of a DFG-funded project on reproductive isolation and drift load in the North American plant species Arabidopsis lyrata, which was recently granted to Dr.

Marc Stift (https://sites.google.com/site/marcstift/). Arabidopsis lyrata has become a model for the evolution of selfing. It is normally self-incompatible and thus obligately outcrossing, but in some North American populations self-incompatibility has broken down and led to high selfing rates. This offers unique opportunities to study the ecological processes that drive the evolution of new selfing lineages, which forms the core of the project.

The PhD student will be based at the Ecology lab at the University of Konstanz (led by Prof. Mark van Kleunen), but the project involves common-garden experiments in the speciesÂ native range in Canada. The student will thus stay in Canada during the field seasons (collaboration with Prof. Marcel Dorken, Trent University, Canada).

Applicants should have a keen interest in evolutionary ecology and hold a Master degree (or equivalent) in the relevant research fields (e.g.

plant ecology, evolution). Applicants should possess a driving license, and ideally have relevant experience with large and complex experiments in the field and/or the greenhouse. Knowledge of insects (pollinator identification in the field) is a plus. This full-time position requires strong writing and statistical skills (preferably in R). The salary will be at 65% of scale 13 TV-L (the standard PhD-position salary in Germany). The starting date is negotiable, but we intend to fill the position as soon as possible.

The University of Konstanz is one of the Universities of Excellence in the Federal Republic of Germany, and is located on a small campus just outside the beautiful university town of Konstanz at the shore of Lake Constance. The Ecology group is young and very international, and works on a diverse set of topics, including life-history evolution, plant responses to global change and determinants of plant invasiveness.

The University of Konstanz encourages applications from people with a disability. They will be given preference if appropriately qualified (contact +49 7531 / 88 - 4016). The University of Konstanz is an equal opportunity employer that tries to increase the number of women in research and teaching, and is committed to further the compatibility of work and family life. The University of Konstanz offers a "Dual Career Couples Program". Information can be obtained from: http://www.uni-konstanz.de/dcc . For more information, please do not hesitate to contact marc.stift@uni-konstanz.de. To apply, please send a letter of motivation of no more than two pages, your CV, a writing sample (for example part of your MSc or Bachelor thesis or a paper), and the contact details of two references to marc.stift@uni-konstanz.de. Merge these documents into a single PDF file, and include your name in the file name. We will start reviewing applications on 1 October 2017, and will accept applications until the position is filled.

– Mit freundlichen Grußen, with kind regards, Marc Stift.

Email: marc.stift@uni-konstanz.de = marcstift@gmail.com Accounts are automatically synchronised, so it does not matter to which address you send your message.

Dr. Marc Stift Ecology (AG van Kleunen) Department of Biology University of Konstanz 78457 Konstanz Germany Office M802: +49 (0)7531 88-2116 (email contact preferred) http://sites.google.com/site/-marcstift/ http://cms.uni-konstanz.de/vkleunen/the-team/marc-stift/ Marc Stift <marcstift@gmail.com>

ULausanne EvolutionaryEcol

PhD fellowships at the University of Lausanne (Switzerland)

Each year the University of Lausanne offers competitive PhD fellowships in broadly defined biological sciences, including evolution and ecology. The winners can choose a supervisor among those participating in the program, including many group leaders at the Department of Ecology of Evolution (www.unil.ch/dee). The Department of Ecology and Evolution is among the strongest research centers in evolutionary biology in Europe. The Department consists of over 20 research groups including about 50 postocs and 70 PhD students; several of those PhD students are winners of the fellowship in previous years. The fellowships are for three years plus a fourth year funded by grants of the supervisor. A Master or an equivalent degree is a prerequisite of being admitted into a PhD program in Switzerland (but the candidates do not yet have to hold a master at the time of application).

Information about the fellowships, requirements and the application procedure can be found under www.unil.ch/fbm-phd. The next application deadline is 16 October 2017; the successful applicants will be able to start their PhD between May 2017 and May 2018.— For questions, please follow the link on the website (and do not respond to this email).

Lausanne is a medium-sized city on the shores of Lake Geneva, surrounded by a wine growing region (recognized as one of UNESCO Heritage sites) and within one hour of the Alps. It offers a great variety of cultural, recreational and outdoor opportunities.

"tadeusz.kawecki@unil.ch" <tadeusz.kawecki@unil.ch>

ULondonQMUL EvolutionaryModelsCancer

Evolutionary Biologists into modelling, and Quants in general, are welcome to apply for a PhD applying evolutionary theory to understand drug resistance in cancer.

This collaboration of Evolutionary Biology and Cancer Biology departments.

Details here: https://sites.google.com/site/nottrevorgraham/lsi-phd The application deadline is 15 Oct 2017, but you you are strongly recommended to contact r.a.nichols@QMUL with questions ASAP.

richard.alan.nichols@googlemail.com

UMaryland EcologicalEvolutionaryGenomics

The Gugger Lab < http://research.al.umces.edu/pgugger > at the University of Maryland Center for Environmental Science (UMCES) is seeking a motivated Ph.D. or M.S. student to develop a thesis project on ecological, evolutionary, or conservation genomics of trees. The lab uses next-generation sequencing approaches to understand how populations of long-lived trees respond evolutionarily to environmental change, the molecular basis of local adaptation, the factors influencing population genetic variation, the role of hybridization in adaptation and speciation, and implications for conservation under global change.

The ideal applicant will have prior research experience in population genetics or plant ecology/evolution, molecular laboratory skills, strong quantitative skills, and proficiency in or interest in learning basic bioinformatics.

The graduate student will matriculate through the Marine, Estuarine, and Environmental Sciences (MEES) Graduate Program (http://mees.umd.edu/) at the University of Maryland, College Park but will reside at the Appalachian Laboratory in scenic Frostburg (western MD, http://www.umces.edu/al) for the duration of the degree. Three years of support are available through research assistantships, with additional support possible through teaching assistantships and fellowships (e.g., http://www.umces.edu/education/graduate/fellowships < http://www.umces.edu/fellowship-opportunities >). Starting date can be as soon as January 2018 and no later than Fall 2018.

To apply, please first email Paul Gugger (pgugger@umces.edu) a single PDF containing (1) a statement of interest, (2) a CV, and (3) contact information for three references. Please indicate "Genomics graduate position" in your subject line.

UMCES is an affirmative action, EOE. Individuals with disabilities, veterans, women and minorities are encouraged to apply.

– Assistant Professor University of Maryland Center for Environmental Science Appalachian Laboratory (301) 689-7161 <callto:301-689-7161> research.al.umces.edu/pgugger/

"pgugger@umces.edu" <pgugger@umces.edu>

UMelbourne HumanEvolutionaryGenomics

The Gallego Romero lab (http://blogs.unimelb.edu.au/-igr-lab) at the University of Melbourne is looking for one to two creative and enthusiastic PhD students to join our group, working in the fields of functional and evolutionary genomics. Our lab combines the flexibility of induced pluripotent stem cells (iPSCs) with genomic approaches to address questions about the mechanisms of evolutionary adaptation in humans and the great apes that are intractable by any other means, with a special interest in the role of gene regulation in human evolution. We also have a burgeoning interest in robust methods for comparative genomics.

We are part of the Centre for Systems Genomics (http:/-/sysgen.unimelb.edu.au) at the University, as well as a member of the School of BioSciences and of Stem Cells Australia. We also enjoy a very close association with the Centre for Stem Cell Systems (with whom we share a lab space).

All projects in the lab incorporate aspects of iPSC culture and experimental manipulation, genomics, and bioinformatics to varying degrees. Students will have the opportunity to be involved in both the tissue culture and data analysis aspects, and to contribute intellectually to the development of the project at all stages.

The University is located in the research precint of Parkville, and we are within walking distance of the Walter and Eliza Hall Institute (WEHI), the Murdoch's Children Research Institute (MCRI) or the Victorian Comprehensive Cancer Centre (VCCC). Beyond that, Melbourne is a thriving multicultural city and consistently tops rankings of the world's most liveable cities.

How to apply: Interested candidates should email a CV (including names and contact details of three references) and a one-page cover letter to Irene Gallego Romero (irene.gallego@unimelb.edu.au) with the subject line "PhD application" in the first instance.

Funding: PhD scholarships, including 3.5 years of stipend and a one-off relocation allowance, are available for both domestic and overseas students through multiple University of Melbourne schemes (see here for more information: https:/-/studenteforms.app.unimelb.edu.au/apex/f?p=-153:2:0:::2:P2_ID:641). Applicants *will* have to submit a formal application for admission to the School of BioSciences and obtain a scholarship for successful admission.

Start date: Flexible, late 2017-early 2018.

"irene.gallego@unimelb.edu.au"
<irene.gallego@unimelb.edu.au>

UMemphis FungalMicrobialEvolutionaryEcol

PhD assistantship in fungal and microbial ecology at the University of Memphis (Memphis, TN, USA).

I am looking for a PhD student(s) to start Fall 2018 to join the Brown Lab (http://-www.microbialmemphis.com) in the Department of Biological Sciences at the University of Memphis. In the Brown Lab, we use a cross-domain approach (Fungi, Bacteria, Archaea, Algae, etc.) to ask questions about how communities are structured, how microbe-microbe or microbe-host interactions influence assembly, and how these communities play a role in ecosystem processes.

Research questions are open, but may include: snowborne and alpine fungal and microbial community ecology, evolution of psychrophilic syntrophic associations, or urban microbial ecology.

Preferences given to candidates who have a strong background or interest in the following: next-generation sequence generation and analysis - including command line based analyses, familiarity with Fungi (as well as bacteria), and a strong sense of curiosity.

If interested, please contact me (Shawn Brown) at spbrown2@memphis.edu with "Memphis PhD position" in the subject line. Include in the email (in PDF or .docx format) a short description of your interests, preferred study system, experience, and career goals that includes undergraduate (and graduate if applicable) GPA. Also include a CV/resume, GRE scores and unofficial transcripts. Applicants will be screened as interest is expressed and a Skype interview may be invited soon thereafter. Official U of M graduate application deadline is February 1, 2018 but materials should be in sooner.

This is an equal opportunity position and I welcome applications from all suitably qualified persons regardless of their race, sex, disability, religion/belief, sexual orientation or age.

"Shawn Paul Brown (spbrown2)" <spbrown2@memphis.edu>

UMontana UNebraska EvolGenomics

Program announcement: Genome-to-phenome connections in wild populations

We are pleased to announce the establishment of a new collaborative research and training network created to advance evolutionary and ecological genomics in natural populations. The UNVEIL network (Using Natural Variation to Educate, Innovate, and Lead) is funded by a recent NSF EPSCoR award, and brings together researchers from the University of Montana and the University of Nebraska. The network seeks to advance our understanding of the genetic basis of fitness-related traits in wild populations and to train the next generation of integrative biologists to solve pressing societal challenges in ecological and conservation genomics.

https://www.nsf.gov/awardsearch/-showAward?AWD_ID=3D3D1736249 The research and training activities of the UNVEIL network will center around three core projects, which are united by their conceptual focus on adaptation to spatiotemporal environmental variation - high altitude adaptation and hypoxia resistance in deer mice, adaptation to climate change in snowshoe hares and other species that undergo seasonal phenotypic changes, and thermal adaptation in yellow monkeyflowers. Network members and trainees will work collaboratively on these projects to meet the following goals:

1. Advance the science of genome-to-phenome connections through the development of novel approaches for the integration of functional and genomic data.

2. Develop ethical guidelines for the application of genomic interventions for wildlife conservation.

3. Create a unique interdisciplinary training environment to broaden participation in the STEM workforce, and to train integrative biologists that are both technically and ethically equipped to leverage genomic approaches to solve ecological and conservation challenges.

In the coming years, the network will provide a variety of opportunities that may be of interest to the community:

Postdoctoral Fellowships: Over the next four years, we will fund four postdoctoral fellowships within the network. We anticipate filling two of these positions this year. In addition to a competitive salary and benefits package, fellows will be provided generous research funds ($50,000; $25,000/year over two years) to allow them the freedom to creatively extend the core projects in novel directions or to work on complementary questions in independent experimental systems with active mentorship from one or more members of the UNVEIL network.

Graduate Student Research Assistantships: We will also fund graduate student research assistantships on both campuses. Two UNVEIL Diversity Fellowships will be available in the Fall of 2018 and will support one graduate fellow on each campus for a three-year tenure. Additional research assistantships will be available for students to work on aspects of the core projects outlined above.

Annual symposia: Finally, to aid in the exchange of ideas and to advance research and training activities both within and beyond the network, we will hold yearly UNVEIL conferences. These conferences will feature 1.) a scientific program focused on evolutionary and ecological genomics in wild populations, 2.) technical and analytical workshops, and 3.) working group sessions to develop ethical frameworks for the application of genomic interventions for wildlife conservation. We anticipate broad participation from biologists, philosophers, and land managers in the ethics working groups and these sessions will serve as catalysis meetings to formulate policy position white papers, synthesis papers for academic audiences, and ethics training materials.

Specific announcements of all of these activities will be disseminated periodically as deadlines approach, but interested postdoctoral and graduate fellowship candidates are strongly encouraged to contact one or more of the following UNVEIL PIs to discuss these opportunities further:

Zac Cheviron (Ecophysiology and Evolutionary Genomics, www.chevironlab.org)

Lila Fishman (Evolutionary Genetics and Genomics; http://hs.umt.edu/dbs/labs/fishman/)

Jeff Good (Ecological and Evolutionary Genomics, www.thegoodlab.org)

L. Scott Mills (Population Ecology and Global Change Biology, www.umt.edu/research/millslab/)

Kristi Montooth (Evolutionary and Physiological Genetics, http://montoothlab.unl.edu)

Colin Meiklejohn (Evolutionary and Speciation Genomics, http://biosci.unl.edu/colin-meiklejohn)

Dane Scott (Environmental Ethics, www.cfc.umt.edu/-

personnel/details.php?ID45)

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UMunich 2 EvolutionaryBotany

Two Ph.D. positions (three years) in evolutionary botany are available at the University of Munich (LMU) to work on Climate change and plant functional traits

Susanne Renner and Constantin Zohner are looking for two students to work within our long-term project on climate change and the ecology, evolution, and function of plant traits. For details of our research see Google Scholar or Research Gate.

Skills that will be acquired within this project include field work (especially controlled experiments), physiological measurements (photosynthetic activity, chlorophyll breakdown, chemistry of colour change), programming in R, statistical analysis and models, phylogenetic-comparative analyses; modern research communication.

The department of biology at the University of Munich has implemented a structured Ph.D. program that includes a thesis advisory committee and that supports the conclusion of a doctoral thesis within (normally) three years. The university of Munich is among the World's best (see the online Times Higher Education Ranking), and the city and its environs have much to offer.

A Master's degree or its equivalent, preferably in ecology or evolutionary biology, is required.

Please email your letter of application, CV, university transcripts (where applicable), and the names of two people who could write a letter of support to Professor Susanne Renner (renner@lmu.de). Evaluation of applicants will begin immediately and continue until the position is filled.

Expected duration: 36 Months Payment: TV-L 13 / 50%

Susanne Renner <renner@lmu.de>

UNotreDame EvolutionEcology

Graduate Program in Ecology, Evolution, and the Environment at the University of Notre Dame

The Department of Biological Sciences at the University of Notre Dame offers a wide range of research opportunities and graduate coursework in ecology and evolutionary biology, allowing students to excel in field, laboratory, and mathematical biology. Strengths of the program include: studies on the dynamics and divergence of populations, evolutionary and ecological genomics, terrestrial and aquatic community and ecosystem ecology, epidemiology and disease ecology, experimental biology, and the impacts of global changes, including climate change, invasive species, and land use change. Our close-knit faculty provides interdisciplinary research opportunities and excellent research mentorship.

Our students take advantage of many resources at Notre Dame, including excellent laboratory facilities in the Hank Family Center for Environmental Studies and state-of-the-art instrumentation in our Center for Environmental Science and Technology (CEST; https://cest.nd.edu), the Genomics & Bioinformatics Core Facility (http://genomics.nd.edu), and the Notre Dame Linked Experimental Ecosystem Facility (ND-LEEF). Other hubs of EEE research include the University of Notre Dame Environmental Research Center (UNDERC; http://underc.nd.edu/) with sites located in the Upper Peninsula of Michigan and western Montana and the Notre Dame Environmental Change Initiative (http://environmentalchange.nd.edu/). Numerous opportunities for interdisciplinary interactions among research areas are available, including our GLOBES graduate training program (http://reilly.nd.edu/globes/)

The following faculty members are currently training graduate students in diverse areas of ecology and evolution:

Beth Archie - behavioral ecology, disease ecology, and population biology

Gary Belovsky - terrestrial ecology and modeling, conservation biology

Sunny Boyd - behavorial ecology, neuroendocrinology and behavioral neuroscience

Jeff Feder - ecological and evolutionary genetics, speciation

Mike Ferdig - systems genetics of malaria parasite drug resistance

Hope Hollocher - population genetics, speciation, evo-devo, and landscape epidemiology

Stuart Jones - aquatic microbial and ecosystem ecology

Gary Lamberti - stream and wetland ecology, ecotoxicology, and plant-animal interactions

Jason McLachlan - ecology and evolution of plant populations, statistical modeling, paleoecology

David Medvigy - terrestrial ecosystem modeling, ecosystem-climate interactions

Alex Perkins - modeling, disease ecology, population biology of disease vectors

Mike Pfrender - ecological and evolutionary genomics, adaptation, phenotypic plasticity

Matt Ravosa - evolution and pathobiology of the mammalian skull and musculoskeletal system

Adrian Rocha - arctic terrestrial ecology

Jeanne Romero-Severson - genomics of adaptive variation in natural populations of forest trees

Jennifer Tank - stream ecosystem ecology and biogeochemistry

All graduate students are funded with competitive stipends. A variety of fellowship opportunities are open to top applicants. For more information regarding the Biology Graduate Program see http://biology.nd.edu/ and http://graduateschool.nd.edu/. The deadline for receipt of all application materials for the Ph.D. program is December 1st, 2017, although earlier submission is encouraged to ensure full consideration for available fellowships. Please begin your application by directly contacting faculty of interest.

Elizabeth Archie <Elizabeth.A.Archie.2@nd.edu>

UNotreDame RapidEvolution

ECOSYSTEM RESPONSE TO RAPID EVOLUTION, PHD OPPORTUNITY AT THE UNIVERSITY OF NOTRE DAME

We are recruiting a PhD student to work on an NSF sponsored project studying the impact of rapid evolution on the productivity and stability of coastal salt marshes. Our study system relies on individuals of a foundational plant in this system (Schoenoplectus americanus) revived from seed banks dating back over 100 years. Our approach involves: measuring changes in plant physiology and growth in controlled experiments; paleoecological analysis of marsh sediments; synthesis of extensive field data; and Bayesian approaches to link evolutionary and ecosystem processes. We welcome applicants with strengths in any of these disciplines. For more information, see the lab web page (https://sites.nd.edu/paleolab), or submit a letter detailing your interest and relevant background to Jason McLachlan (jmclachl@nd.edu). Please CC the project manager, Jody Peters (peters.63@nd.edu). Applications to Notre Dame Biological Sciences are due December 1.

Jody Peters

PalEON Program Manager

University of Notre Dame

Galvin 294

574-631-1852

Notre Dame IN 46556

paleonproject.org

@Pal_EON

Jody Peters <peters.63@nd.edu>

UNotreDame SocialBehaviorFitnessPrimates

The Archie Lab at the University of Notre Dame is seeking exceptional students interested in studying a diverse evolutionary topics, including: the health and fitness consequences of social relationships, the evolution of life histories, evolutionary medicine, microbiome dynamics, and the connections between host behavior and microbial composition. We address these topics in the Amboseli Baboon Population in Kenya. Founded in 1971, the Amboseli Baboon Project is one of the longest-running studies of a wild primate in the world. This population offers exceptional longitudinal data on baboon behavior, demography, ecology, diets, genetics, ranging patterns, endocrine physiology, and microbiome dynamics in hundreds of subjects over 4 decades. Please visit the lab webpage for more information http://sites.nd.edu/archielab/ . Interested applicants should email the PI, Beth Archie, at earchie@nd.edu. Top applicants will have prior experience in research and strong quantitative skills.

Funding is guaranteed via teaching assistantships for 5 years and potentially via research assistantships. The University of Notre Dame offers excellent benefits, a full tuition waiver, and a generous stipend (~$29K for 2017). A variety of fellowship opportunities are open to top applicants. For more information regarding the Biology Graduate Program see http://biology.nd.edu/ and http://graduateschool.nd.edu/. The deadline for receipt of all application materials for the Ph.D. program is December 1st, 2017.

Elizabeth Archie Associate Professor Department of Biological Sciences University of Notre Dame Notre Dame, IN Tel. (574) 631-0178 Office. 179 Galvin http://blogs.nd.edu/archielab/ "earchie@nd.edu" <earchie@nd.edu>

UOtagoNZ 2 Bioinformatic

Positions available for a Postdoctoral Fellow and a PhD Student to develop computational tools for tuning protein expression

http://www.ucbioinformatics.org/opportunities.html The Gardner Lab is seeking two fantastic researchers with strong programming skills to design new software tools for tuning protein expression. One of the determinants of protein expression level is the rate of translation. The rate is highly sequence-dependent and is highly variable across the vast number of synonymous messenger RNAs that encode a single protein.

The candidates will integrate the discoveries made in this recent eLife paper (https://elifesciences.org/articles/13479), and will extend the work into more complex biological systems. The successful candidates will be collaborating with an international research team that includes Sinan Umu and Eivind Valen (Norway), Ivo Hofacker (Vienna) and Gregorsz Kudla (Edinburgh).

For further enquiries please contact: Paul Gardner (paul.gardner@otago.ac.nz).

Required background: A degree or equivalent with a strong computational modelling component (e.g. computer science, physics, ...). Experience in bioinformatics, computational biology, probabilistic modelling and/or machine learning would be considered an advantage.

Please email a CV and cover letter to Paul Gardner (paul.gardner@otago.ac.nz). If short-listed, we will request further details from you.

Closing date 1 November, 2017.

A salary/stipend of up to $75,000 NZD/$28,000 NZD will be provided by funding from MBIE Smart Ideas (Building bioinformatic software for controlling protein expression) for the Postdoc/PhD.

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PhD position in developing bioinformatic methods for probing bacterial CRISPR-Cas regulation, University of Otago, NZ

http://www.ucbioinformatics.org/opportunities.html CRISPR-Cas systems may be regulated by RNA-binding proteins. The candidate will use computational and genomics approaches to identify targets of RNA binding proteins, and predict their impact on CRISPR-Cas regulation. Bioinformatics work will mainly consist of analysing data generated by new high-throughput sequencing technologies such as Tn-Seq (a.k.a. TraDIS) and RNA-seq, as well as comparative genomics. The successful candidate will join a research group that has a broad range of interests including the application of bioinformatic methods to analyse comparative genomic, transcriptomic and proteomic datasets. In particular we are interested in RNA biology and the consequences of prokaryotic genome variation. You will join the Gardner research group who has recently joined the University of Otago. We will work in close collaboration with A/Prof. Peter Fineran. Our groups are diverse, and we collaborate widely, including with groups in the UK, Denmark, US, Sweden, Germany and Australia. We work towards the free and rapid dissemination of research discoveries. For further enquiries please contact: Paul Gardner (paul.gardner@otago.ac.nz)

Required background: A honours or masters degree in a biological or mathematical discipline such as biochemistry, genetics, molecular biology, maths, statistics, physics, computer science or equivalent, and a demonstrated interest in developing bioinformatic skills.

Please email a CV with references and cover letter to Paul Gardner (paul.gardner@otago.ac.nz). If short-listed, we will request further details from you. Closing date 30th October, 2017.

A PhD stipend of up to $28,000 NZD including fees will be provided by the Bio-Protection Research Centre.

ppgardner@gmail.com

UTexas EvolutionaryGenomics

The Havird Lab at the University of Texas at Austin is looking for enthusiastic and motivated PhD students beginning in the Fall 2018 semester. Students will have the opportunity to develop independent dissertation projects that complement research themes in the lab on molecular evolution, mitonuclear interactions, or environmental adaptation. Ongoing projects in the lab examine coevolution between mitochondrial and nuclear genomes, the roles of cytoplasmic genomes at species boundaries, and ecophysiology/environmental adaptation (http://jchavird.wixsite.com/jchavird/currentresearch). Multiple organismal systems are used in the lab, including plants and animals, as well as making use of existing publicly available genomic datasets.

The Havird Lab is part of the growing Ecology, Evolution, and Behavior (EEB) group in the Integrative Biology Department at the University of Texas. Interested students should contact Justin Havird (justin.havird@colostate.edu) and provide a brief description of your research interests along with a current CV. Applicants are encouraged to consider applying for an NSF GRFP or NIH Predoctoral fellowship and should make contact early to discuss possible project ideas. Applicants can apply through the EEB, Plant Biology, or Cell and Molecular Biology (via rotations) Graduate Programs at UT following the links below.

Applications received before December 1st, 2017 will be given full consideration.

Additional information:

Havird Lab: http://jchavird.wixsite.com/jchavird/ Integrative Biology Dept. at UT: https://integrativebio.utexas.edu/ EEB Graduate Program at UT: https://cns.utexas.edu/eeb-graduate-program CMB Graduate Program at UT: https://icmb.utexas.edu/cmb Plant Biology Graduate Program at UT: https://cns.utexas.edu/plantbio-graduate-program Justin C. Havird Email: Justin.Havird@colostate.edu Justin's Research Website: http://jchavird.wix.com/jchavird Sloan Lab Website: https://sites.google.com/site/danielbsloan/ "Justin.Havird@colostate.edu" <Justin.Havird@colostate.edu>

UToronto AvianGenomics

PHD POSITIONS IN AVIAN GENOMICS, SPECIATION, AND COMPARATIVE PHYLOGEOGRAPHY AT THE UNIVERSITY OF TORONTO.

Multiple Ph.D. positions are available in the Weir Lab (http://www.utsc.utoronto.ca/ ˜ jweir/) for students with bioinformatic, genomic, or field skills. Our lab uses genomic and comparative methods to address broad scale questions related to speciation and the pace of evolution in tropical versus temperate faunas.

Ph.D. student positions are available for:

1) Genomic analyses of avian hybrid zones in Amazonian or Canadian birds.

2) Genomic analysis of reproductive isolation in a recently discovered avian hybrid species from the Amazon.

3) Conservation genomics and phylogeography of New Zealand kiwi.

4) Comparative phylogeography and population genomics across multiple co-distributed avian species complexes to better understand biogeographic drivers of diversification in boreal or Amazonian regions.

The positions would begin in September 2018 and could involve field work (collecting genetic samples in the Amazon of Peru or Brazil), lab work (generating genetic data sets using next generation sequencing methods that sample broadly across the genome), and bioinformatic analyses (mining genomic data).

In addition, students can pursue graduate projects in any of the key research areas of the lab and exceptional students may wish to pursue their own projects.

Students would be enrolled in the Graduate program of the Department of Ecology and Evolutionary Biology. If interested, please send Dr. Jason Weir (jason.weir at utoronto.ca) a statement of interest, a CV and an electronic copy of your transcripts. External sources of funding (e.g. fellowships) are generally required for international students (many Latin American countries as well as the EU and USA offer these).

Jason Weir <jason.weir@utoronto.ca>

UValencia ViralEvolution

A PhD contract is available at the laboratory of Rafael Sanjuán (University of Valencia, Spain).

Starting date: end 2017.

Place: recently created Institute for Integrative Systems Biology (I2SysBio), Valencia, Spain.

Project title: Collective Infectious Units and the Social Evolution of Viruses.

Funding: ERC Consolidator Grant, 2017-2022.

Goal: understand how multi-virion infectious units determine social-like interactions in viruses (cooperation versus conflict). We will baculoviruses as model systems.

Candidates should have a background in molecular/cell biology and virology (preferably with baculoviruses).

ERC project summary:

A widely accepted view in virology is that virions function as independent infectious units. However, recent work by us and others indicates that viruses are often transmitted as more complex structures, such as virion aggregates, lipid vesicles or protein matrices harbouring multiple infectious particles. This demonstrates that viruses can be transmitted as "collective infectious units", in contrast with the current paradigm. Critically, these recent discoveries now set the stage for the evolution of social interactions, a previously unappreciated facet of viruses. We propose to investigate how collective infectious units drive virus social evolution using state-of-the-art tools from the fields of virology, genetics, structural biology, and nanotechnology. The effects of collective infectivity on viral fitness will be tested directly using experimental evolution and genetic engineering, and confirmed in vivo. Three widely different viruses will be used to achieve generality: human enteroviruses, a vector-borne rhabdovirus, and a baculovirus. Furthermore, the implications of virus social interactions for the maintenance of genetic diversity, evolvability, virulence evolution, and the emergence of drug resistance will be investigated. New processes such as the putative extracellular fusion of viral particles will be also explored. We expect that infectious units constituted by viruses from different species will be uncovered as well, with far-reaching implications for epidemiology. It is becoming increasingly recognized that parasite sociality is a disease determinant, and our results may therefore inspire new antiviral strategies. Beyond their practical importance viruses will also provide a simple and tractable system that will help us to establish more general principles of social evolution.

Relevant literature: Sanjuán R. 2017. Collective Infectious Units in Viruses. Trends Microbiol., in press. https://www.ncbi.nlm.nih.gov/pubmed/28262512 Contact: rafael.sanjuan@uv.es; +34 96 354 32 70.

Rafael Sanjuan <rafael.sanjuan@uv.es>

UVienna EcologicalGenomics

The Research Group of Plant Ecological Genomics (http://plantgenomics.univie.ac.at) of the Department for Botany and Biodiversity Research at the University of Vienna, Austria is recruiting a

PhD student in Plant Evolutionary Biology (m/f)

Whole genome doubling and hybridization profoundly shaped plant genome evolution. However, to be successful, first generations allopolyploids must quickly adjust their genome and function, thereby altering their ecological properties and adaptive success, as a function of their environment. The duplicated nature of polyploids buffers more effectively deleterious alleles and provides genome-wide opportunities for adaptive evolution. Recurrent origins of polyploids are widespread and provide natural replicates to study the links between whole genome doubling and rapid adaptation to divergent environments.

A 3-years PhD position funded by the Austrian Science Fund (FWF) is immediately available in our group, focusing of a fairly young polyploid group in Dactylorhiza, comprising sibling European orchids with divergent ecological preferences. Specifically, to complement ongoing analyses of the nature of the extant molecular diversity in the Dactylorhiza allopolyploids, we will interrogate the adaptive value of this diversity within reciprocal transplant experiments in the Alps and Scandinavia. We will shed light on the links between genotype, epigenotype and environmental conditions, by focusing on the environmental sensitivity of gene expression (with RNAseq) and of post-transcriptional regulation by small RNAs (with smRNAseq), exploring also in detail the link between DNA methylation patterns, TE activity and expression of duplicated genes.

The candidate should have - a background in experimental or computational fields, such as experimental population genetics, evolutionary/functional genetics, molecular ecology, bioinformatics or similar; - high motivation, enthusiasm and interest in new developments in the field; - an excellent academic past record; - a demonstrated computer literacy, including R knowledge or Unix; - preferred: experience with NGS methodology (wet lab and/or bioinformatics); - excellent organization and communication skills; - fluency in English (NB German knowledge is not essential); - driving license class B (for field work).

We are an international team with English as the working language. The successful candidate will highly benefit from the advantages of being integrated in the Vienna Graduate School of Population Genetics (http://www.popgen-vienna.at). The position offers in addition a competitive salary (according to experience min. euro 28,500 per year before tax, including social and health insurance), the opportunity to attend at least one workshop/summer school and two international conferences, and to shortly visit one of the labs of our international collaborators. Field work across large Western European areas will be undertaken for ca one month every year.

To be considered please send your application as a single pdf file to ovidiu.paun@univie.ac.at, including a motivation letter with a statement of research interests (max. 2 pages), your CV and, if applicable, publication list, university certificates including grades, and the names and contacts of three referees. Please note: Incomplete applications will not be considered.

AssProf Dr Ovidiu Paun Department for Botany and Biodiversity Research University of Vienna Rennweg 14, A - 1030 Vienna http://plantgenomics.univie.ac.at ovidiu.paun@univie.ac.at

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UWesternAustralia DolphinPopulations

The Dolphin Alliance Project (www.sharkbaydolphins.org) is seeking high calibre students for two PhD projects to start in 2018. The first project will use acoustic, behavioural and genetic data to investigate the ontogeny of alliance formation in the Shark Bay dolphin population, focussing on juvenile and adult dolphins. The second project will explore how ecology, particularly the acoustic properties of the environment, contributes to variation in alliance behaviour and mating success in this remarkable population.

The students will be based at the University of Western Australia (UWA) under the supervision of Dr Stephanie King (UWA), and will be co-supervised by Professor Michael Krützen (University of Zürich), Professor Richard Connor (UMass Dartmouth) and Dr Simon Allen (UWA). Students will work in a dynamic research environment with access to a behavioural and demographic database spanning 30+ years, biopsy samples from 700+ individuals, and acoustic data from 15 well-documented alliances.

Applications are open to both domestic and international students, who need to be eligible for an RTP scholarship: http://www.science.uwa.edu.au/future-students/scholarships . Exceptional students are encouraged to apply for the Dean's Excellence in Science PhD Scholarships: http://www.science.uwa.edu.au/future-students/scholarships/deans-excellence, as well as the Keiran McNamara World Heritage PhD Top-Up Scholarship: http://www.scholarships.uwa.edu.au/search?sc_view=1&id=5521&all=1&page=27 . General requirements include a background in evolutionary and behavioural biology, a BSc (Hons) or MSc degree (first class) in a relevant discipline, and fieldwork experience (preferably with marine mammals and/or primates). Knowledge or experience in bio-acoustics and/or small boat handling skills would be advantageous.

Ideal candidates will have strong oral and written communication skills and the ability to work and share ideas in a highly collaborative setting. International students, in particular, should have at least one peer-reviewed publication.

Applicants should send an expression of interest and CV, including the contact details of two academic referees, to Dr Stephanie King (stephanie.king@uwa.edu.au) by 7th October 2017.

Successful candidates will be informed prior to the 21st October to ensure scholarship applications are submitted prior to the 31st October deadline.

Michael Krützen <michael.kruetzen@aim.uzh.ch>

UWollongong EvolutionFishSociality

We are seeking a highly motivated PhD student to join an on-going research project on the evolution of sociality in coral reef fishes, based at the University of Wollongong, NSW, Australia.

Overview: This is an exciting opportunity to join an interdisciplinary team of researchers to understand the causes and consequences of sociality in reef fishes. The project will combine field experimental investigations at multiple sites along the Great Barrier Reef with laboratory genetic analysis based at the University of Wollongong. Research funding for this project is secured, and we currently seek a motivated and talented student to undertake this project.

The project supervisors are: University of Wollongong: Dr. Marian Wong and Prof. Mark Dowton University of Technology Sydney: Dr. Selma Klanten Project Outline: Sociality is a common and taxonomically widespread phenomenon in tropical marine fishes. In spite of this, comparative analyses of sociality to date have been focused on birds, mammals and insects. Coral-reef fishes are an ideal group with which to test the generality of hypotheses for social evolution because: i) they exhibit considerable inter-specific variation in social organization, ii) species-level phylogenetic relationships have already been resolved for some key groups of coral-reef fishes, and iii) they inhabit shallow coral reefs facilitating field observations, experiments and collections (for summary see: https://academic.oup.com/bioscience/article/63/6/453/226119/Social-Systems-in-Habitat-Specialist-Reef). As the ecology and life-history of fish differ in major respects to birds, mammals and insects, this comparative analysis of sociality will likely yield novel and transformative results that will significantly advance the field of social evolution (see: DOI: 10.3389/fevo.2017.00100). This PhD project will investigate the causes and consequences of sociality in one particular group of coral-reef fishes known as “habitat-specialists”. These species reside permanently within discrete patches of reef habitat, including corals and anemones.

Mentorship: This project is supervised by Dr. Marian Wong, a behavioural ecologist and Senior Lecturer (http://smah.uow.edu.au/biol/contacts/UOW135217.html; http://marianwong.wixsite.com/thefishlabuow), Prof. Mark Dowton, molecular ecologist and Head of Students at the University of Wollongong (http://smah.uow.edu.au/biol/contacts/UOW043319.html) and Dr. Selma Klanten, a molecular biologist based at the University of Technology Sydney (http://www.selmaklanten.com/). The University of Wollongong offers excellent scholarship, career development and supervisory support for post-graduate students in a friendly and collegiate setting.

Applicant Requirements: The applicant is expected to have completed a recognised undergraduate degree in Biological Sciences with an Honours degree (or equivalent) in marine biology and/or ecology, and possess a demonstrated interest in animal behaviour. The successful applicant must also be SCUBA qualified. Boating skills are desirable but not essential. Domestic and international applicants are encouraged to apply - domestic students would need to apply for an AGRTP (http://www.uow.edu.au/research/grs/prospective/UOW070387.html) and international students would need to apply for a UPA (http://www.uow.edu.au/research/grs/prospective/UOW070389.html) to cover stipend costs.

Applications: Please send a CV to Dr. Marian Wong (marianw@uow.edu.au) and Prof. Mark Dowton (mdowton@uow.edu.au) no later than Friday 6th October.

Deadlines: 17th October (for scholarship applications for commencement of degree in February 2018).

O. Selma Klanten, PhD Research Scientist Fish Ecology Group School of Life Sciences Bldg 7 Level 6 University of Technology Sydney PO Box 123, Broadway NSW 2007, Australia Email: Oya.Klanten@uts.edu.au Alternate email: osklanten@me.com Fish Ecology Lab: http://www.fishecologylab.com selmaklanten.weebly.com Mob: +61-417341941 Secretary, Australian Coral Reef Society (ACRS) http://www.australiancoralreefsociety.org/ Oya.Klanten@uts.edu.au

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UZaragoza Spain GrassEvolution

We seek candidates for a Spanish FPI PhD grant associated to our project “Evolution of biological traits and speciation processes in the model genus Brachypodium (Poaceae) through comparative and functional genomic” (CGL2016-79790-P). The PhD thesis will investigate the origins and evolutionary changes of pereniality/annuality switches and the pangenomic diversity and phylogeography of model grass species of Brachypodium.

The PhD thesis (2018-2021) will be developed at the High Polytechnic School of Huesca (University of Zaragoza, Spain) with research stays at CSIC (EEAD, IAS) and international institutes and participation in CSP Joint Genome Institute projects. The PhD thesis will include field and greenhouse work, genomic and transcriptomic data generation and processing, and comparative and functional genomic and phylogenomic analyses of perennial and annual species of Brachypodium.

The research team has a large experience in evolutionary genomics (www.bifi.es/bioflora), computational biology (www.eead.csic.es/compbio) and translational genomics (www.ias.csic.es) studies of grasses.

Interested applicants should comply with the requirements to apply for a Spanish PhD contract (Open to European Community and other countries citizens, see information here). Experience in plant evolutionary biology, genomics and bioinformatics will be highly valued.

Interested applicants please contact Prof. Pilar Catalan (pcatalan@unizar.es) before October 3 2017.

Prof. Pilar Catalan Escuela Politecnica Superior de Huesca Universidad de Zaragoza Ctra. Cuarte km 1 22071 Huesca (Spain) phone +34 974232465/+34 974239301 fax +34 974239302 International Brachypodium Steering Committee

Pilar Catalan <pilar.catalan09@gmail.com>

UZurich MarineAdaptation

PhD Position in Evolutionary Ecology

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On: Demographic and evolutionary modelling of local adaptation to the tidal environment in /Clunio marinus/

**

at the University of Zurich, Switzerland

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A PhD position in evolutionary ecology, of 48 months duration, is available at the University of Zurich working with Prof Hanna Kokko and her international team www.kokkonuts.org . /Clunio marinus/is a marine midge that has a unique life history, living in the intertidal zone of the European Atlantic coast. Local adaptation is important, as the timing of low tides differs across coastal locations. Populations indeed differ in their lunar and diurnal rhythms of adult emergence, and the differences are genetic (as known from past crossing experiments and through genomic work by Dr. Tobias Kaiser).

This project, which forms a collaboration between Dr. Kaiser's group at the Max Planck Institute for Evolutionary Biology in Plön and Prof. Kokko's group at the University of Zurich, aims to fill in a knowledge gap considering the evolutionary demography of the species: how is local adaptation maintained, given the different dispersal options leading to different genotypes mating, potentially producing maladapted emergence times with respect to seasonal phenology and/or lunar cycles?

The ideal candidate has a grasp of demographic and/or evolutionary modelling, and a willingness to develop his/her skills further in this regard. The PhD will be awarded by the University of Zurich, which is also the main location of the student's work, but the project also involves visits to Plön and the potentially many coastal field sites.

The working language in the group is English (German skills are not essential). The position is available as soon as the candidate has been found. The evaluation of applications begins on October 10, 2017, and will continue until a suitable candidate has been found.

Applicants should send a cover letter with a

-Statement of their research interests

-C.V., and

-The names and contact details of at least one referee.

Applications should form a single pdf file and this should be sent to: hanna.kokko@ieu.uzh.ch

Petra Zehetmaier Administrative Assistant Prof. Dr. Hanna Kokko

Department of Evolutionary Biology and Environmental Studies University of Zurich Winterthurerstr. 190 8057 Zurich

Tel.: +41 (0) 44 635 47 61 Email: petra.zehetmaier@ieu.uzh.ch Office: Y13-H-81

Petra Zehetmaier <petra.zehetmaier@ieu.uzh.ch>

VirginiaTech EvolutionaryGenetics

The McGlothlin lab at Virginia Tech is looking for enthusiastic and motivated Ph.D. students beginning in fall 2018. Students will develop independent dissertation projects in evolutionary genetics or evolutionary ecology that complement work in the lab. Ongoing projects in the lab examine molecular evolution of toxin resistance genes in snakes, lizards, and birds, evolutionary quantitative genetics of Anolis lizards, and social evolution theory (http://www.mcglothlin.biol.vt.edu/research/).

The McGlothlin lab is part of the growing Ecology, Evolution, and Behavior and Integrative Organismal Biology groups in Virginia Tech's Department of Biological Sciences. Interested students should contact Joel McGlothlin (joelmcg@vt.edu), providing a description of your research interests and experience and a CV or resume that includes GPA, GRE scores, and contact information for three references. Applicants interested in applying for a NSF GRFP are encouraged to get in touch as soon as possible to discuss project ideas. For full consideration, applications to the department should be received by December 1, 2017.

Additional information: McGlothlin lab: http://www.mcglothlin.biol.vt.edu/ Graduate program: https://www.biol.vt.edu/Graduates.html Grad app: https://www.biol.vt.edu/Graduates/how_to_apply.html Biological Sciences at VT: https://www.biol.vt.edu/ Ecology, Evolution, and Behavior at VT: https://www.biol.vt.edu/research/Ecology_Evolution_and_Behavior.html

Joel W. McGlothlin Virginia Tech, Dept. of Biological Sciences Derring Hall 2125, 1405 Perry St. Blacksburg, VA 24061 http://www.mcglothlin.biol.vt.edu Email: joelmcg@vt.edu Phone: (540) 231-0046 Office: Derring Hall 4002

Graduate Program in Ecology, Evolution, and Behavior Virginia Tech Department of Biological Sciences Blacksburg, VA

Faculty studying Ecology, Evolution, and Behavior in the Department of Biological Sciences at Virginia Tech are seeking graduate students for fall 2018. As a collaborative group of faculty and students, we offer training in interdisciplinary research and prioritize mentorship. We value diversity and seek to support students from all backgrounds.

Our students take advantage of many resources at Virginia Tech, including the Genomics Sequencing Center (https://www.bi.vt.edu/services/genomics-sequencing-center), the Fralin Life Science Institute (https://fralin.vt.edu/), and the Global Change Center (http://www.globalchange.vt.edu/).

Although students are encouraged to pursue extramural funding opportunities, accepted Ph.D. students are guaranteed 5 years of funding (including summers) through a combination of teaching assistantships and graduate research assistantships. Our students have received fellowships through the Interfaces of Global Change program (http://www.globalchange.vt.edu/igc/), Institute for Critical Technology and Applied Science program (http://www.ictas.vt.edu/education/docScholars.php), and NIH funded IMSD program (https://imsd.apsc.vt.edu/).

The following faculty members are currently recruiting graduate students:

Frank Aylward: microbial ecology, bioinformatics, and genomic sciences http://www.aylwardlab.com Lisa Belden: community ecology, disease and the microbiome http://www.belden.biol.vt.edu Cayelan Carey: freshwater ecosystem ecology and limnology http://www.carey.biol.vt.edu Dana Hawley: wildlife disease ecology https://www.biol.vt.edu/faculty/hawley/ Erin Hotchkiss: freshwater ecosystem ecology and biogeochemistry https://sites.google.com/site/ehotchkiss/ Kate Langwig: disease ecology and evolution, conservation and disease https://scholar.harvard.edu/klangwig/home Joel McGlothlin: evolutionary genetics and evolutionary ecology http://www.mcglothlin.biol.vt.edu Meryl Mims: population, community, and conservation ecology of freshwater systems http://www.mimslab.org

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WageningenU PlancentalEvolution

PhD position

Comparative genomics of placenta development in livebearing fish

Job description

One of the fundamental questions in biology is: “how do complex traits evolve?” Our ability to discern how complex traits evolved is limited because their origin occurred in the distant past and details of their evolution have been lost due to the extinction of species with intermediate stages of complexity. In this project you aim to unravel the molecular pathways that underlie the evolution of the placenta in the livebearing fish family Poeciliidae (which includes the guppy). This family evolved placentas multiple times independently and contains closely-related species as well as populations within species that vary markedly in placental complexity. The presence of this variation in placental complexity at such shallow taxonomic levels is truly unparalleled in nature and offers a unique opportunity to study the evolution of complexity. In the project you will apply a comparative genomics approach, studying multiple independent evolutionary origins of the placenta aiming to uncover the commonalities in genome architecture that underlie its evolution. The project will involve whole genome sequencing of selected species across the phylogeny, as well as the de-novo assembly and annotation of the genomes of a number of key species to fill in taxonomic gaps. You will aim to infer the evolution of genes and the modification of developmental and metabolic pathways during the evolution of the placenta. The project is for a period of 4 years.

Requirements

For this interdisciplinary project, we look for an enthusiastic, result-driven person with an MSc degree in biology, bioinformatics, or related field. The candidate should have affinity with evolutionary biology. Affinity with computational biology or bioinformatics is required, proficiency in a programming language (e.g. Python, R), and experience in working with Linux are highly valued. Excellent research skills are required and excellent communication skills and proficiency in English (both oral and written) are prerequisite.

Conditions of employment

The PhD student will work at the Experimental Zoology (EZO) and Animal Breeding and Genomics (ABG) groups of Wageningen University (the Netherlands). The PhD student will be supervised by Dr. Pollux, an expert on placenta evolution in livebearing fish, and Dr. Megens, who is an expert on evolutionary genomics and bioinformatics. The PhD project is part of a larger research programme at Wageningen University led by Dr. Pollux that focuses on the causes, mechanisms and consequences of placenta evolution using cutting-edge interdisciplinary research, including field-based research, biomechanics, life history evolution, quantitative genetics, functional genomics and bioinformatics. Employment basis: temporary for a 4 year period, maximum hours per week: 38. Continuation of the appointment will be based on a performance evaluation after 18 months. Gross salary will increase from euro 2222,- in the first year up to euro 2840,- per month in the last year based on a full-time appointment (38 hours per week).

Additional information

Applications should include a letter of motivation, CV and names of three references. You can apply for this position until September 25, 2017.

* Online (preferred): http://www.wur.nl/en/Jobs/-Vacancies/Show/PhD-position-Comparative-genom ics-of-placenta-development-in-livebearing-fish-.htm

* Or send your application directly via email to Dr. Pollux and Dr. Megens: Dr. Hendrik-Jan Megens, Animal Breeding and Genomics, phone: +31(0)317 482469, email: hendrik-jan.megens@wur.nl or Dr. Bart Pollux, Experimental Zoology, phone: +31.(0)317 486083, email: bart.pollux@wur.nl, website: www.bartpollux.nl Acquisition regarding this vacancy is not appreciated.

“Pollux, Bart” <bart.pollux@wur.nl>

Jobs

ArizonaStateU CenterForMechanismsOfEvolution

ARIZONA STATE UNIVERSITY An Equal Opportunity/Affirmative Action Employer

Rank Open (Job #12113) Arizona State University School of Mathematical and Statistical Sciences and Biodesign Center for Mechanisms of Evolution

The School of Mathematical and Statistical Sciences (SoMSS) and the Biodesign Center for Mechanisms of Evolution (CME) at Arizona State University invite applications for one tenure-eligible position in statistics. Rank and tenure status will be commensurate with experience. Anticipated start date is Fall 2018. This position is jointly funded by SoMSS and CME with tenure home in SoMSS.

The Statistics program within SoMSS currently contains eight faculty members and the University intends to increase the size and scope of this program significantly within the next few years. The expanded statistics group will be expected to increase its interdisciplinary, applied and core research productivity, foster growth in its teaching programs, and provide consulting services to the university and business community.

The CME is part of a growing community of evolutionary biologists at ASU (https://sols.asu.edu/evolutionary-biology-faculty and http://asupopgen.org/). The research focus of the Center will primarily be at the cellular level, with the group being populated by scientists from the areas of cell biology, microbiology, biophysics, biochemistry, and population genetics. The field of population genetics and its applications is particularly germane to this search.

The essential duties of this position will be to conduct research on statistical theory, methodology, and applications in areas germane to the mechanistic processes underlying evolutionary change; publish in appropriate high-quality journals, develop proposals for extramural funding, both independently and collaboratively with the CME. The teaching load is anticipated to be one to two classes per year in advanced undergraduate or graduate statistics classes along with mentoring graduate students. In addition, appropriate professional service is expected.

Applicants are required to have a Ph.D. in statistics or a closely related area by August 10, 2018. Candidates must also have knowledge and experience in statistical applications to evolutionary and/or population-genetic mechanisms; strong research and teaching potential; desire and ability to work collaboratively in an interdisciplinary environment.

The desired qualifications include at least two years of postdoctoral experience; a documented record of published research in statistics with applications to evolutionary mechanisms; a documented history of grant support; a strong record of instruction and student mentoring, and demonstrated success working collaboratively with diverse student and/or faculty populations.

SoMSS currently has 53 full-time tenured or tenure-track faculty members and approximately 85 supported Ph.D. students (including 15 statistics students), along with 40 Masters students. The School offers bachelors, masters, and Ph.D. programs in statistics, applied mathematics, mathematics, mathematics education as well as an undergraduate program in actuarial science. SoMSS has excellent computing resources that include individual faculty workstations, several high-performance servers and a small cluster, as well as access to the University's central computing facilities and the High Performance Computing Initiative.

SoMSS has a strongly interdisciplinary research profile that includes numerous collaborations inside and outside the university, such as in the biological, environmental, medical, physical and social sciences, education, and multiple areas of engineering. In addition to the Biodesign Institute, there are numerous opportunities for collaboration with other interdisciplinary centers and institutes, such as the Translational Genomics Research Institute (TGen), the Institute for Social Science Research, the new College of Health Solutions, the Global Institute of Sustainability, and the nearby Mayo Clinic.

The Tempe campus of Arizona State University has approximately 60,000 students. It is located in the rapidly growing metropolitan Phoenix area, which provides a wide variety of recreational and cultural opportunities. The surrounding countryside is very attractive to outdoor enthusiasts who enjoy hiking, biking, skiing, and other activities in the exquisite Arizona canyon lands and mountainous terrain.

To apply, please submit the following through https://-www.mathjobs.org/jobs/jobs/10819: 1. a cover letter that briefly explains the candidate's interest in, and fit with, the position 2. a curriculum vitae 3. a personal statement addressing the candidate's research program

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

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Arlington Virginia Head BFA NFS

Dear Colleague:

We have initiated a national search for the National Science Foundation's Head of the Office of Budget, Finance and Award Management (BFA). The Office Head also serves as the NSF's Chief Financial Officer (CFO).

BFA oversees NSF's budget, financial management, grants and agreements, and contracts functions and provides business, financial and analytical services to diverse stakeholders and customers, including NSF staff, members of Congress and their staffs, the executive branch, Governors and other state officials, colleges and universities, professional societies, business leaders, and the public. The Office Head/CFO is a member of the NSF leadership team and the principal advisor to the NSF Director and Deputy Director/Chief Operating Officer, and other senior managers on issues related to financial and grants management. The Office Head leads a diverse staff of over 150 contract, grants and agreements and policy specialists, accountants, systems analysts, cost analysts, program and budget analysts, large facilities advisors, and administration support staff. Attached is a signed, PDF version of this letter, which includes an information sheet summarizing the activities and the responsibilities of the position.

Members of the search advisory committee can be found at https://www.nsf.gov/od/searches/bfa-170901/-bfa_search_cmte.jsp. I appreciate that each of these very busy, very accomplished individuals is willing to lend their time and expertise to help us fill this vital position.

We seek your help in disseminating this opportunity and encouraging qualified people to apply for this crucial post. Ideal candidates must demonstrate outstanding leadership; a deep appreciation for the role that science, technology, engineering, and mathematics play in our society; a grasp of the issues and challenges involved; and the ability to serve effectively as a key member of the NSF leadership team. We are especially interested in identifying women, members of minority groups, and persons with disabilities for this vital post. Individuals from any sector – academic or government – are welcome to apply.

Please see https://www.usajobs.gov/GetJob/-ViewDetails/478845200 for a full position description, and instructions on submitting an application. Applications can only be made through the USAJobs Web site, and must be submitted by October 5, 2017.

Your assistance in this very important task is appreciated.

Sincerely, /// signed /// France A. Cordova Director National Science Foundation 4201 Wilson Boulevard, Suite 1205N Arlington, VA 22230

France C??rdova <director@nsf.gov>

CIBIOInBIO Portugal EnvironmentalMetagenomics

ERA Chair in Environmental Metagenomics

Reference: ICETA 2017-32

Link to the call http://www.eracareers.pt/-opportunities/index.aspx?task=global&jobId=931 02

Main research field: Biological sciences

Applications are open for a Chair in Environmental Metagenomics (Reference ICETA 2017-32) to be hosted by CIBIO-InBIO - Research Network in Biodiversity and Evolutionary Biology, University of Porto (Portugal). The Chair position will be contracted in the scope of the project "EnvMetaGen - Capacity Building at InBIO for Research and Innovation Using Environmental Metagenomics" (Reference No 668981), funded by the European Commission under the call H2020-WIDESPREAD-2014-2, and that will run until August 31st 2020. The project aims to expand the research and innovation potential of InBIO, supporting emerging research lines in environmental metagenomics for applications in biodiversity surveys, invasive species control, ecosystem services assessment, and environmental (bio)monitoring. The ERA Chair holder will have a leading role in the development of the project, coordinating the research and support team selected in the early stages of the project, as well as the scientific, networking and capacity building actions of the project along the lines established in the grant agreement.

CIBIO-InBIO is a young and highly dynamic research centre located near Porto, in Northern Portugal, which conducts world-class research in the fields of biodiversity and evolution. It is an inclusive, equal opportunity employer offering attractive conditions and benefits. The Centre offers great opportunities for multidisciplinary research and hosts 20 research groups, which include over 160 PhD level researchers, and over 100 MSc and PhD students, from across the world. The Centre has state of the art ecology and molecular laboratories and conducts research projects at a global scale. The working language of the institute is English, and it offers a vibrant, multicultural and enthusiastic working atmosphere. In addition, the Northern region of Portugal provides rich cultural and outdoor activities and Porto is a UNESCO world-heritage city and the capital of Port wine.

Requirements:

- Internationally Leading or Established Researcher in environmental metagenomics or closely related fields of research - preference will be given to senior researchers (with > 10 years of post-doctoral research experience); less experienced candidates may also be considered in light of her/his contributions to the research field;

- Proven experience in: managing research teams; supervising graduate students; and in operating with key international funding agencies allowing securing research funding.

- With an established international and cross-disciplinary collaborative network;

- Preference will be given to applicants with experience in the use of metagenomic approaches to address research questions in one or more of the following areas: (i) Biodiversity surveys and assessment; (ii) Environmental biomonitoring; and (iii) Assembling and analysing food webs.

Benefits:

Exceptional research and technical conditions will be offered to the appointed Chair, including:

- Initial appointment for up to three years;

- Internationally competitive salary commensurate with qualifications and experience;

- A team of researchers and technical support staff, including a project manager, a knowledge transfer and dissemination officer, three post-doc researchers and two lab technicians;

- Substantial travel budget for training, conference attendance and networking;

- Access to fully equipped genetics and genomic labs, at the CIBIO-InBIO facilities.

Application:

Applicants should submit:

- Detailed Curriculum Vitae;

- The three most important research papers;
- A brief (2-pages) statement of research interests.

Applications should be submitted by mail to bolsas@iceta.up.pt with the reference ICETA 2017-32. The call for applications is open between 01/09/2017 to 01/10/2017.

The EnvMetaGen project is available upon request to the same mail address.

Evaluation:

Candidates will be evaluated by an international selection panel. Short-listed candidates will be invited for an interview.

Employer:

ICETA - Instituto de Ciencias, Tecnologias e Agroambiente da Universidade do Porto (ICETA-UP), on behalf of CIBIO-InBIO.

Websites:

http://inbio.pt/ http://cibio.up.pt/ Location:

CIBIO-InBIO, Campus Agrario de Vairao, Rua Padre Armando Quintas, 4485-661 Vairao, Portugal (Coordinates: N41.328940, W8.672635).

Sem vÃrus. www.avast.com CIBIO-InBIO Divulgaç̧ão

Concepcion Chile 6 Biodiversity

CALL FOR APPLICATIONS: 6 TENURE-TRACK (FULL-TIME) POSITIONS, FACULTY OF SCIENCES, Universidad Catolica de la Santisima Concepcion (UCSC) Concepcion, CHILE

To download full call in Spanish and English: http://ciencias.ucsc.cl/concurso2017/ ABOUT THE FACULTY The Faculty of Sciences, located at the main campus of the UCSC (http://ciencias.ucsc.cl/) in the city of Concepción, central Chile, is committed to (i) basic and applied research in the fields of biology and chemistry, and (ii) the education of new scientists and professionals through two undergraduate programs (Marine Biology and Environmental Chemistry) and three graduate programs (Master of Marine Ecology, Master of Environment, and -since 2018- Doctorate in Biodiversity and Bioresources).

The Faculty of Sciences is made up of two departments: (i) Department of Ecology, with research lines in Biodiversity, Ecology and evolution of aquatic organisms, and Sustainability of coastal and aquatic ecosystems; (ii) Department of Environmental Chemistry, with research lines in Dynamics of chemical substances in the environment, Environmental remediation, and Technology of bioresources (see http://ciencias.ucsc.cl/depto/). All full-time faculty members are engaged in research and teaching, and provide institutional service related with academic administration and outreach.

In such a context, the Faculty of Sciences SSC welcomes applications for six tenure-track (full-time) faculty positions appointed at the minimum rank of Assistant Professor*.

* Assistant Professor is the third academic rank in the university, below the tenured ranks of Associate Professor and Full Professor. The rank will be determined by a formal Faculty Committee, which might recommend a higher rank depending on the academic biography of the selected applicants.

REQUIRED ACADEMIC PROFILES

POSITION 1 - CODE: CIE-01 (appointed to the Department of Ecology) Researcher with experience in management and/or conservation of biodiversity in coastal marine systems, either in intertidal, subtidal or coastal-terrestrial habitats, or their interphases.

POSITION 2 - CODE: CIE-02 (appointed to the Department of Environmental Chemistry) Researcher with prior background in geology, chemistry or related areas of engineering. Proven experience in soil chemistry (organic and/or inorganic chemistry) with particular regard to its application in either urban, agricultural or industrial areas. His/her research should focus on one or more of the following areas: - Study of the origin and composition of soils, as well as the behavior, bioavailability and transport of inorganic and organic chemicals (e.g., trace metals, nutrients, pollutants, stable isotopes, etc.) from soil to atmosphere and aquatic systems. - Remediation and restoration of degraded soils in contaminated areas. - Regional/national monitoring programs of soil pollution and management of natural resources.

POSITION 3 - CODE: CIE-03 (appointed to the Department of Environmental Chemistry) Researcher with prior background in chemistry or related areas of engineering, with proven experience in atmospheric chemistry (organic and/or inorganic). His/her research should focus on one or more of the following areas: - Implementation of analytical techniques for separation, detection and quantification of organic and inorganic chemical substances in air. - Study of the spatiotemporal dynamics of organic and inorganic pollutants in the atmosphere. - Regional/national monitoring programs of air quality and air pollution.

POSITIONS 4, 5 and 6 - COMMON CODE: CIE-04 (Department chosen by the selected applicants) In accordance with Faculty-wide objectives, positions 3, 4 and 5 all have the same profile: Researcher with prior undergraduate or graduate background in some of the following areas: biology, chemistry or biochemistry, or engineering disciplines related with the above areas. Experience in scientific or technological research related with biodiversity (as defined by the Convention on Biological Diversity), oriented to the analysis and utilization of bioresources in coastal environments (either in marine, terrestrial or freshwater habitats, or their interphases).

GENERAL APPLICATION REQUIREMENTS (FOR ALL POSITIONS) - Doctorate or PhD degree (postdoctoral experience is desirable). - Capability to develop basic and/or applied scientific research, demonstrated through scholarly publications (and/or patents) and research projects granted in competitive calls from national or international agencies. - Minimum productivity in the last five years: 8 publications (WOS), and 1 research grant as principal investigator. - Experience desirable in undergraduate and graduate teaching. - Advanced level in written and spoken English. Non-native Spanish

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

Conference Manager

Conference Manager

The Society for the Study of Evolution (SSE), on behalf of the Joint ASN/SSB/SSE council, seeks an individual to help plan and run their annual scientific conference.

Duties will include, but are not limited to:

with faculty conference organizers for the planning of each conference and choosing locations for future conferences.

and maintaining the conference web site and compiling the program and other conference related materials.

with conference preparations, including conference center and hotel contract negotiations.

in pre-conference site visits to finalize plans for oral presentation sessions, poster and exhibitor space, and social events.

on-site conference activities including working with convention center, AV support, catering staff, and with student volunteers to ensure that talk sessions and social events run smoothly.

Skills & Qualifications:

training in conference organization/management preferred

with the planning of conferences, workshops, or other events required; experience with large events preferred

planning scientific meetings and working with non-profit societies an asset

written and verbal communication skills and interpersonal skills required

to detail and competence with budgets and financial accounting required

be able to meet deadlines and multitask in an organized way

be able to respond promptly to queries and requests

designing and updating websites preferred

travel required for planning visits, to attend the meeting, and possibly future meeting site selection

Compensation will be commensurate with duties and will be issued as lump sums once or twice annually. The Conference Manager may use these payments for hire additional staff if required. In addition to compensation payments, the Conference Manager and associated staff will be reimbursed for all travel expenses required for site visits and conference management.

Additional details: http://www.evolutionmeetings.org/conference-manager.html How to Apply:

Please send a cover letter and a CV or resume to Dr. Andrea Case: execvp@evolutionsociety.org

Application deadline:

31 October, 2017

About the SSE:

The Society for the Study of Evolution was founded in March, 1946. The objectives of the Society are the promotion of the study of organic evolution and the integration of the various fields of science concerned with evolution. The Society publishes the scientific journal /Evolution/ and co-publishes /Evolution Letters/ along with the European Society of Evolutionary Biology. SSE also holds an annual conference, in conjunction with the

American Society of Naturalists (ASN) and the Society of Systematic Biologists (SSB), at which scientific findings on evolutionary biology are presented and discussed. More information is available at the society web site (http://www.evolutionsociety.org/).

About the annual conference:

Evolution is the joint conference of the American Society of Naturalists, the Society for the Study of Evolution, and the Society of Systematic Biologists. The Evolution conference is held in a different location every year. Recent and future locations include Austin, TX, Portland, OR, Providence, RI, and Cleveland, OH. This meeting is the premier opportunity for sharing research on evolutionary biology. The conference attracts between 1700-2400 attendees and includes more than 1,000 oral presentations, 400-500 posters, and social events such as luncheons and evening mixers. It runs for approximately 5 days (depending on satellite events) in mid-late June. More information is available on the conference web site: http://www.evolutionmeetings.org/, including complete programs from recent meetings. Conferences are run on a break-even basis with careful attention given to minimizing registration costs for attendees.

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

CornellU 2 EvolutionBehavior

There are two independent searches currently underway at Cornell for assistant professors working on the evolution of behavior in the Department of Neurobiology and Behavior and Department of Psychology respectively.

(1) Assistant Professor of Animal Behavior (NBB)

The Department of Neurobiology and Behavior (NBB) invites applications for a tenure-track position as Assistant Professor of Behavior. We seek broad thinkers with a strong understanding of evolutionary biology who can show how their research helps answer major questions in animal behavior and why they are particularly suited to tackle these questions. We encourage candidates whose aim is to discover general principles of animal behavior that link to other areas of biology. The successful candidate is expected to establish a vigorous, externally funded, internationally recognized research program, and to teach at the graduate and undergraduate levels.

Apply: https://academicjobsonline.org/ajo/jobs/9512 . Questions can be directed to Prof. Kern Reeve, Search Committee Chair, NBB, Cornell University, Ithaca, NY 14853, tmn3@cornell.edu. Application deadline, including 3 letters of recommendation: 1 November 2017.

Diversity and Inclusion are a part of Cornell University's heritage. We are a recognized employer and educator valuing AA/EEO, Protected Veterans, and Individuals with Disabilities.

(2) Assistant Professor - Behavioral and Evolutionary Neuroscience (Psychology)

The Department of Psychology at Cornell University invites applications for a full-time, tenure-track faculty position in systems and behavioral neuroscience, at the Assistant Professor level. Candidates must have a PhD or equivalent degree, relevant postdoctoral experience, and a strong record of published research.

We are seeking innovative, independently-minded investigators with research interests that integrate central nervous system function and behavior. Research areas of interest include, but are not limited to, sensory or motor systems, learning and memory, cognition and decision-making, evolution and development, genetics and genomics, social behavior and communication, theory and computation, and the mechanisms of attentional, affective/emotional, or hormonal regulation of neural systems.

Successful candidates may employ a variety of research techniques and will seek to leverage the technological resources and collaborative environment of Cornell University to enhance their research program. Candidates who pursue integrative research questions that embrace the complexities of natural environments are particularly encouraged. Candidates are expected to establish a vigorous, externally funded, and internationally recognized research program, and to teach at the graduate and undergraduate levels.

Review of applications will begin October 15 and continue until the position is filled. Diversity and inclusion are fundamental to Cornell University's heritage of "any person, any study." Applications from women and minority candidates are especially welcome. Diversity and Inclusion are parts of Cornell University's heritage. Cornell is an employer and educator recognized for valuing AA/EEO, Protected Veterans, and Individuals with Disabilities.

Please apply at:

https://academicjobsonline.org/ajo/jobs/9653 Michael J Sheehan Assistant Professor Nancy and Peter Meinig Investigator in the Life Sciences Neurobiology and Behavior Cornell University W303 Mudd Hall 215 Tower Rd Ithaca NY, 14853

(607) 254-4302

msheehan@cornell.edu

Michael Sheehan <msheehan@cornell.edu>

Denver Museum CollectionsDirector

Integrative Collections Director

Denver Museum of Nature & Science

Description:

The Denver Museum of Nature & Science (DMNS, www.dmns.org) seeks a motivated individual with a background and passion for natural history and the management of collections to fill a new and exciting position, Director of Integrative Collections. The Museum's research, education, archives, and library collections have been consolidated under one functional area, and we are in search of a leader to guide this new branch. The successful individual will help craft a vision to raise the profile and accessibility of DMNS' collections, while leading a highly skilled team that provides professional collections management, and support for research, education, and Museum programming. The ability to do collections outreach and communicate the value of our collections is an important component of this position.

The Museum has committed significant resources towards caring for its growing collections including opening of the 63,000 sq. ft. state-of-the-art Avenir Collections Center in 2014. The museum has also committed to supporting the research collections by establishing new collections support positions within the Research and Collections Division.

This position will report directly to the Vice President of Research & Collections/Chief Curator. It will be key to work closely with the division's other directors, directly supervise collections managers, archives, and education collections staff, and manage a budget focused on collections care.

The world-class collections at DMNS include 4.1 million objects and specimens in Anthropology, Archives, Earth Sciences, Education, Health Sciences, Library, and Zoology. Collections span seven continents, deep time to the present, with a major focus on the American West. A large portion of the collections are databased and publicly accessible, including access through other portals (e.g., iDigBio, GBIF). The Research and Collections Division is supported by 35 staff members, multiple-grant-funded positions, and approximately 700 volunteers.

Information about the Museum's collections can be found here: https://www.dmns.org/science/integrative-collections/ Essential duties: * Provides strategic leadership for collections staff by providing opportunities for career growth and continuing education by building networks with museums for training in collections management. * Awareness of pan-Museum strategy and initiatives and ability to communicate that vision to the staff and integrate into the department. * Inspires staff to excellence, by providing timely feedback and rewarding exceptional performance. * Provides vision for team collaboration within the department and across the museum. * Works with curators to ensure strategic growth of the collections, deaccessions, and repatriation are within parameters of DMNS collection policies. * Evaluates, develops, updates and oversees the implementation of collections management policies and the long-term collections plan and submits for approval through the appropriate channels. * Ensures proper utilization and methodology of collection databases. * Assists with logistics of collection acquisitions that are relevant to the mission of the museum. * Oversees grant administration, budgets, and projects in accordance with museum procedures to improve the care, growth, access, and use of collections.

* Oversees implementation of innovative approaches for increasing accessibility and use of the collections. * Serves as a Museum public spokesperson for the collections, and provides professional expertise as needed to other areas of the museum and the media in a timely and professional manner.

Requirements: * Master's degree in earth sciences, life sciences or social sciences is required; PhD preferred. * 7 years' experience in managing natural history collections. * 5 years' experience utilizing a collection database. * 5 years' experience managing professional level staff required. * 5 years' experience securing and administering grants and budget management required. * Some travel will be required. * Some evening and weekend work required. * Intermediate proficiency with Microsoft Office suite required.

Ideal candidate will: * Have a PhD preferred in earth sciences, life sciences, or social sciences. * Be a leader that can inspire their team. * Be a visionary that can increase community and research exposure to our collections. * Have public speaking and experience working with media.

Core values: * We love science.

* We are curious, creative and playful. * We cultivate relationships with each other, diverse communities, the environment and for our future. * We think critically and act with empathy.

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

Denver MuseumNatureSci Preparator

The Zoology department at the Denver Museum of Nature & Science seeks a talented and experienced individual to supervise and manage specimen preparation in a new Biosafety Level 2 (BSL2) Laboratory. The Zoology collections are growing rapidly and we are seeking a vertebrate preparator to ensure that the new specimens prepared and incorporated into our collections are of the highest standard for future scientific research. All vertebrate specimens are prepared in the BSL2 lab, as well as, some fluid preparation of invertebrate specimens.

The successful applicant will report to the Curator of Ornithology, work closely with the other Zoology curators and collections managers, and supervise and manage volunteers, interns and other part-time staff. They will be passionate about museum collections and be able to articulate that the scientific merit of natural history specimens stems from proper preparation and preservation. They will also work with colleagues to execute the Museum's mission and vision and uphold its values.

The world class zoology collections at DMNS house approximately 1.2 million specimens, vials, or specimen lots in multiple collections: Arachnology (~60,000); Marine Invertebrates (~37,235); Entomology (~985,100); Botany (~4,512); Herpetology (~540); Mammalogy (~20,200); Parasites (~1,200); and Ornithology (~58,460).

Essential duties: * Provides direct supervision of volunteers, interns, and part-time staff. * Practices and teaches professional preparation as directed by the Curators. * Oversees the work of lab volunteers, provides additional trainings as required and mentors/supervises volunteers, students, and interns. * Provides support to Curators through preparation and in research projects as requested. * Oversees and manages a high-quality Zoology preparation laboratory. * Prepares vertebrate skins, skeletons, frozen tissues, parasites, and all other specimen associated materials. * Provides preparation expertise as needed to other areas of the museum.

Requirements: * Bachelor's degree required, Biology/Zoology major preferred. * 2 years' experience in aspects of specimen preparation required. * Basic proficiency with Microsoft Office suite required.

Ideal candidate will have: * Experience preparing mammal and bird specimens, including skins, skeletons and their associated parasites. Willingness to learn invertebrate specimen preparation.

Core values: * We love science. * We are curious, creative and playful. * We cultivate relationships with each other, diverse communities, the environment and for our future. * We think critically and act with empathy.

Application Instructions:

Please submit your cover letter and resume by October 4, 2017. Resumes will not be accepted after this time.

Applications may only be accepted electronically via the Museum's website www.dmns.org . Garth M. Spellman Curator of Ornithology Zoology Department

garth.spellman@dmns.org W 303.370.6469 2001 Colorado Blvd. Denver, CO 80205

Garth Spellman <Garth.Spellman@dmns.org>

EarlhamC Indiana PlantEvolution

Earlham College: Tenure-Track Assistant Professor of Plant Biology

The Department of Biology at Earlham College invites applications for a tenure-track Assistant Professor of plant biology with teaching and research interests in field-based ecology and evolutionary biology. The position begins in July 2018.

The Department seeks an individual who is first and foremost excited about teaching in lecture, laboratory, and research venues to bright and motivated undergraduates in a nationally ranked department at a small liberal arts college.

Responsibilities

Teaching responsibilities will include contributing to introductory team-taught and upper-level courses in ecological/evolutionary/organismal biology. Applicants who have an expertise in one or more of the following areas are especially attractive: population, community, or landscape ecology of plants; quantitative methods; plant systematics; natural history; conservation; land management. There are opportunities for student-faculty collaborative research, and the college owns a natural history museum, greenhouse, herbarium, student-run farm, and hundreds of acres of natural properties managed by the Biology department.

Qualifications

A Ph.D. or equivalent is required; post-doctoral research and/or teaching experience is desirable.

For an expanded description about Earlham College and the Department of Biology please visit: http://-www.earlham.edu/biology To Apply: Arrange for three letters of reference to be emailed (willski@earlham.edu), and please send, as a *single* *pdf*, a cover letter, curriculum vitae, statement of teaching philosophy, a research plan, and an explicit plan detailing how you plan to interact with and teach a diverse community to: willski@earlham.edu. Direct questions about the position to Dr. Chris R. Smith (smithch@earlham.edu).

Review of applications will begin on Oct. 15 and continue until the position is filled.

Earlham College continues to build a community that reflects the gender and racial diversity of the society at large, and, therefore, we are particularly interested in inviting and encouraging applications from African Americans, other ethnic minorities, and women. Earlham also is eager to solicit applications from members of the Religious Society of Friends (Quakers).

Earlham College is an Equal Opportunity Employer. Earlham utilizes E-Verify < http://www.dhs.gov/e-verify > to confirm employment eligibility for all newly hired employees within the United States.

– Chris R. Smith Associate Professor Department of Biology Earlham College 801 National Road West Richmond, IN 47374 USA tel: 765-983-1377 Link to GoogleScholar < https://scholar.google.com/-citations?user=3Fdnq2sAAAAJ&hl=en > Profile Link to Website < https://sites.google.com/site/ecantlab/-home >

Chris Smith <crsmith.ant@gmail.com>

HowardU VertAnat AnimPhysio

Assistant Professor of Animal Physiology (tenure track) and Assistant Professor of Anatomy (tenure track)

The Department of Biology in the College of Arts and Sciences at Howard University invites applications for two tenure-track positions at the rank of Assistant Professor, one with specialization in Comparative Vertebrate Anatomy and the other in Animal Physiology with an emphasis in Neurobiology. We seek outstanding applicants with a demonstrated track record of excellence in research and teaching. In addition to teaching and developing courses in their areas of specialization, candidates are expected to teach in the Introductory Biology courses (Biology 101 and Biology 102).

Qualifications: Successful candidates are expected to develop vigorous, extramurally funded research programs in their areas of expertise, actively participate in the Department's teaching and curriculum development at the undergraduate and graduate levels, and mentor undergraduate and graduate students.

Candidates must have: Earned doctorate in Biology or related field from an accredited institution, with specialization in neurobiology or comparative vertebrate anatomy from an accredited institution, Record of scholarship, teaching, and professional service commensurate with the rank of assistant professor, Effective communication and organizational skills, and Postdoctoral and grant-writing experience preferred.

Overview Howard University, founded in 1867, is a private, comprehensive research university, and a Historically Black College/University (HBCU) comprising 13 schools and colleges. It is a residential campus of approximately 10,000 students located in the heart of the nationâ euro s capital, Washington, DC. Students pursue studies in more than 120 areas leading to undergraduate, graduate and professional degrees. Howard also produces more on campus African-American Ph.D. recipients than any other university in the United States. In keeping with the legacy of Howard University, the department is committed to the education and preparation of academicians and professionals to assume positions of leadership and responsibility both nationally and internationally. The candidate must demonstrate understanding of and support for the mission of the Howard University.

The Department of Biology consists of 21 faculty and 4 staff members. It offers BS, MS, and PhD degrees in Biology with foci in cell and molecular biology and ecology and evolution, and is a leading unit in the Environmental Studies Interdisciplinary major. Faculty members are professionally active, conducting research in diverse areas of contemporary biology. Application Process Complete applications consist of a single PDF file containing

1) a cover letter addressing qualifications listed above,

2) a current curriculum vitae,

3) a two-page statement of research accomplishments, interests and future plans,

4) a two-page statement of teaching experience and philosophy, and

5) the names and contact information for at least three references who will provide letters upon request from the search committee.

Completed applications should be addressed to the Chair of the search committee Dr. Franklin Ampy and emailed to either:

hubio.neuro@gmail.com for the animal physiology position

hubio.anat@gmail.com for the comparative anatomy position.

Only complete applications submitted electronically will be considered. Other documentation may be requested. All application materials should be received by September 30, 2017 when screening will begin and continue until the positions are filled.

The starting date for both positions is August 15, 2018.

Howard University is an Equal Opportunity/Equal Access/Affirmative Action employer fully committed to achieving a diverse workforce. All individuals, including minorities, women, individuals with disabilities, and protected veterans are encouraged to apply.

Additional details and information can be found at http://hubiosearch.wixsite.com/2017 . Kenneth A. Hayes Assistant Professor Howard University Department of Biology Web: http://hayeslab.weebly.com/ Ken Hayes <hayes.ken@gmail.com>

INHS UIllinois BiodiversityDirector

INHS_University of Illinois.PrincipalResearchScientist/Director

The Prairie Research Institute at the University of Illinois at Urbana-Champaign, centrally located between Chicago, St. Louis, and Indianapolis, is seeking a Principal Research Scientist/Director of the Illinois Natural History Survey < http://www.inhs.illinois.edu/ >. The successful individual will serve as the lead scientist and chief executive officer for INHS, will provide leadership, direction, and overall administration for the development, coordination, and implementation of scientific programs undertaken by INHS, which includes >260 employees working on diverse taxa in Illinois, nationally, and internationally. Requires a Ph.D. in a scientific discipline relevant to the mission of PRI and INHS, significant experience in academic or government research environments, administrative experience in a university or state, federal, or non-government organization, and an established record of scholarship and obtaining sponsored funding from state and federal agencies and/or the private sector. To ensure full consideration, applications should be submitted by October 20, 2017; however, the search will remain open until a successful candidate is identified. For additional information, including instructions on how to apply, please visit https://jobs.illinois.edu/academic-job-board .You may also contact Lori Walston-Vonderharr, Human Resources, Prairie Research Institute at lwalston@illinois.edu.

The University of Illinois conducts criminal background checks on all job candidates upon acceptance of a contingent offer. The U of I is an EEO Employer/Vet/Disabled http://www.inclusiveillinois.illinois.edu . "Johnson, Kevin P" <kpjohnso@illinois.edu>

LiverpoolJohnMooresU Epigenetics

Apologies for the late notice, but we have a vacancy for a faculty member working broadly in the area of epigenetics, closing on 26th September.

Lecturer or Senior Lecturer in Epigenetics Liverpool John Moores University - School of Natural Sciences and Psychology

The School of Natural Sciences and Psychology seeks to appoint a Lecturer or Senior Lecturer in Epigenetics to contribute to our successful undergraduate programmes in Biology, Animal Behaviour, Wildlife Conservation and Zoology. We would welcome applications from persons whose research has an applied focus such as the application of epigenetics to the study of health and disease. Further details: http://www.jobs.ac.uk/job/BDW775/lecturer-or-senior-lecturer-in-epigenetics/ Working in the School of Natural Sciences and Psychology you will have a track record of conducting and publishing high quality research or be able to demonstrate outstanding research promise. The School has thriving research programmes and outstanding facilities. We encourage collaboration between researchers within the School and elsewhere in the Faculty as well as with other universities and research organisations. This appointment is part of a strategic investment in the research and teaching of Biosciences at LJMU.

Informal enquiries may be made to Dr Alan Gunn (Subject Leader, Biological Sciences, School of Natural Sciences and Psychology), email: a.gunn@ljmu.ac.uk

School website: http://www.ljmu.ac.uk/nsp/ "W.T.Swaney@ljmu.ac.uk" <W.T.Swaney@ljmu.ac.uk>

Luxembourg Museum Zoologist

The National Natural History Museum of Luxembourg is recruiting a full-time invertebrate zoologist on a permanent basis.

The job is open to all EU nationals, but the successful candidate must be fluent in German, French, English and (yes) Luxembourgeois.

If you yourself fit the above criteria, or you know somebody that does, please get in touch / get them to get in touch with me.

I also encourage multi-lingual vertebrate zoologists to get in touch.

Best wishes

Alain Frantz <afrantz@mnhn.lu>

MBL WoodsHole MA MicrobialAdaptation

https://mbl.simplehire.com/postings/3790 Assistant/Associate Scientist, Marine Biological Laboratory

The Marine Biological Laboratory (MBL) invites applications for faculty positions at the Assistant/Associate level. The MBL is engaged in a major expansion in the areas of (1) microbial diversity and ecology across environments; (2) adaptation and resilience to rapidly changing environments; (3) cutting edge imaging and computational image analysis; and (4) the biology of aquatic organisms. A successful candidate will establish an independent research program that bridges these areas and intersects with one or more of the MBL's three year-round research centers. Research in the Bay Paul Center employs comparative genomic approaches to understand the complex patterns and mechanisms that make possible the persistence and diversity of life on earth. Research in the Bell Center broadly focuses on cell, tissue and organismal biology with particular interests in integrative and comparative approaches to key questions in developmental and regenerative biology, neurobiology, and sensory physiology and behavior. The Ecosystems Center investigates the structure and function of ecological systems to understand and predict their response to changing environmental conditions. For more information, go to: http://www.mbl.edu/research/research-centers/ The MBL fosters a rich intellectual environment that includes affiliations with the University of Chicago and Argonne National Laboratory, as well as a strong community of more than 100 affiliated scientists from academic institutions around the world. The collaborative research community enables the extension of highly simplified experimental systems to the greater complexities of evolutionary innovation and ecological function among diverse organisms and ecosystems.

Applicants should submit a full CV, cover letter, and statement of research interests and goals, and the names and contact information of at least four references. Submit all materials electronically at https://mbl.simplehire.com. Priority will be given to applications received before November 1. Inquiries may be made to search committee chair David Mark Welch at dmarkwelch@mbl.edu.

*The MBL is an Equal Opportunity/Affirmative Action

Employer*

B. Duygu Ã-zpolat, Ph.D.

Hibbitt Fellow Eugene Bell Center for Regenerative Biology and Tissue Engineering Marine Biological Laboratory 7 MBL Street Woods Hole, MA 02543 508 289-7245 (office) dozpolat@mbl.edu

http://bduyguozpolat.org/ "Duygu" is pronounced "doee-goo < https://forvo.com/word/tr/duygu/ >"

"B. Duygu Ozpolat" <dozpolat@gmail.com>

Melbourne ComputationalBiology

Dear All,

We are seeking a motivated and experienced scientist for an exciting role in our Computational Biology team at Agriculture Victoria utilising "big data" and the implementation of computing, analysis and software innovations which are essential to meet the challenges arising from rapid growth in scale and complexity of Life Sciences research.

The successful applicant will be required to provide a substantial individual science contribution in AgriBio, Centre for AgriBioscience - a state-of-the-art biosciences research centre and joint venture between the Agriculture Victoria and La Trobe University - by leading research and computational capability for projects in the areas of statistical genomics and quantitative genetics applied to dairy cattle and crops in the Computational Biology group. The Computational Biology team of approximately 40 staff and students have expertise in quantitative genetics, statistical genomics, bioinformatics, statistics, biology, and high performance computing. The group works across livestock, crops, forages, and microbial systems.

We are looking for an experienced researcher with excellent organisational skills and a strong foundation in computer programming as well as expertise in predictive statistical models. A background in the use of genomic and phenomic data in general, and specifically for genomic prediction, is preferred. A critical component of this position is to foster computational capability development within the Computational Biology team in Agriculture Victoria.

For more detail on the key selection criteria and to apply please visit https://jobs.careers.vic.gov.au/jobs/-VG-020076 This is a level D position with a salary range of $113,156 - $151,426 (Plus Superannuation). Applications close on 19th September. Location: Bundoora (Melbourne, Australia), AgriBio, Centre for AgriBioscience, La Trobe University Campus

Please feel free to contact me for more information.

Best wishes,

Hans

Dr. Hans Daetwyler | Research Leader Computational Biology Agriculture Research Division | Agriculture Victoria | DEDJTR Senior Research Fellow | Applied Systems Biology | La Trobe University AgriBio Centre, 5 Ring Rd., Bundoora 3083, Victoria T: 03 9032 7037 | E: hans.daetwyler@ecodev.vic.gov.au

Department of Economic Development, Jobs, Transport and Resources, Government of Victoria, Victoria, Australia.

hans.daetwyler@ecodev.vic.gov.au

MonashU EvolutionaryGenetics

The School of Biological Sciences is seeking to appoint a dynamic individual wishing to pursue an academic career in genetics/genomics and/or developmental biology as a Senior Lecturer (Level C, equivalent to Assistant Professor), Associate Professor (Level D) or Professor (Level E).

Genetics/genomics and developmental biology should be interpreted broadly and may for example, include animal, plant or microbial biology and may encompass specific areas including, but not limited to, epigenetics/gene regulation, bioinformatics, cellular and developmental genetics, functional genomics, evolutionary developmental biology, molecular pathology, and reproductive biology.

The School of Biological Sciences, and Monash University as a whole, is a world leader in research and teaching and committed to providing a better future for the globe. The successful applicant will be housed in high-quality research facilities, provided with an attractive recruitment package and employment conditions, and given access to world class research infrastructure including: genomics and bioinformatics support, a broad range of high end microscopy, green houses, state of the art model organism facilities, antibody and recombinant protein production and histological services.

The School of Biological Sciences is committed to the provision of an equitable and supportive work place. The successful applicant will be activity mentored so as to ease the transition into the Australian research system.

The applicant should have: * an outstanding track record of excellence in research relative to opportunity * a demonstrated ability (or strong potential) to obtain external research funds * developed and delivered teaching materials or have the potential to develop such materials * excellent written and verbal communication skills * experience with supervision of higher degree by research students.

Applicants will: * be innovative in and develop/lead successful research programs * be proactive in building funded research collaborations internally and with appropriate external partners * have the clear potential to excel in teaching activities at the undergraduate level and in postgraduate supervision.

This role is a full-time position; however, flexible working arrangements may be negotiated.

Senior Lecturer http://careers.pageuppeople.com/513/-cw/en/ job/567393/senior-lecturer-school-of-biological-sciences

Associate Professor or Professor http://careers .pageuppeople.com/513/cw/en/job/567280/associate-professor-or-professor-school-of-biological-sciences

Tim Connallon <tim.connallon@monash.edu>

NHM LosAngelesCounty OrnithologyCurator

Curator, Ornithology

The Natural History Museum of Los Angeles County (NHM) seeks a Curator to lead its research on birds, oversee the growth and care of the ornithology collection, and to provide content for a variety of public programs. These activities will support NHM's new strategic goals of understanding and promoting urban biodiversity and strengthening and activating its research and collections departments.

NHM, the largest natural history museum in the western United States, holds one of the world's best collections of extant birds. This includes over 120,000 specimens-primarily study skins and skeletons-representing more than 5,200 species. The collection is strongest for the Americas and Africa, and it is also important for the Pacific region. NHM also holds extensive collections of fossil birds, including the renowned collection of the La Brea Tar Pits. These, together with other important ornithological collections in Southern California (e.g., the Moore Laboratory of Zoology, UCLA-Dickey Bird and Mammal Collection, and Western Foundation of Vertebrate Zoology), make Los Angeles an unparalleled place for collections-based, ornithological research. Moreover, the region is home to over 500 extant bird species and comprises a diversity of habitats that offer many potential sites for field research.

The successful candidate will have a record of outstanding research, excellent communication skills, and a demonstrated ability to engage the public and stakeholders. A Ph.D. and a strong track record of peer-reviewed publications that focus on evolutionary biology and/or ecology (e.g., taxonomy, systematics, biogeography, global change, urban nature, and/or biodiversity science) are required. He/she will be expected to build an active and publically appealing research program, to oversee all NHM's programs on living birds, and to supervise the staff and volunteers of the Department of Ornithology. Additionally, the successful candidate is expected to develop working relationships with local universities, mentor students and postdoctoral fellows, strengthen NHM's presence in key professional and governmental networks, and maintain research through competitive grants and/or other funding from external sources. The successful candidate will also be expected to participate actively in a broad range of museum activities, including exhibits, education, citizen science programs, training of educators and volunteers, public communications and media interactions, and fundraising activities. A vision and capability to build a research program that can be integrated within the NHM's ongoing efforts to understand urban biodiversity-particularly in Southern California-and to shape the collections and research in ways that activate both its scientific and public appeal is paramount.

NHM is seeking applicants who have demonstrated experience and commitment working with a diverse community. This is a full-time position with a salary and title commensurate with experience, plus excellent benefits.

Application deadline is November 15th, 2017. The starting date is July 1st, 2018. Applicants should send a cover letter and vision statement, curriculum vitae, salary history, and the full contact information of at least three professional references to thayden@nhm.org - Tyler Hayden, Research & Collections, Natural History Museum of Los Angeles County, 900 Exposition Blvd., Los Angeles, CA 90007, USA.

The Natural History Museum of Los Angeles County is an Equal Opportunity Employer. Please, No Phone Calls, No Fax.

Tyler Hayden <thayden@nhm.org>

OhioStateU PlantDiseaseEvolution

The Department of Plant Pathology at The Ohio State University (OSU) seeks applicants to fill a tenure-track, assistant/associate professor position. The position is part of a University-wide Discovery Theme Initiative in Infectious Diseases, with emphasis on Emerging and Re-Emerging Diseases. The successful candidate is expected to develop a strong, interdisciplinary, internationally recognized, and extramurally-funded research program focusing on emerging infectious diseases of plants. Research topics of interest include, but are not limited to, (1) the ecology, epidemiology and ecological genomics of emerging plant diseases, (2) the emergence and evolution of invasive traits (e.g. modeling virulence/antimicrobial resistance) in plant pathogens, (3) the role of climatic and/or phytobiome changes in disease emergence.

Review of applications begins September 15, 2017 and continues until a suitable candidate is found.

For full posting, including instructions for application package, go to:

https://discovery.osu.edu/career-opportunities/open-positions/emerging- infectious-disease-ecology.html

Jason C. Slot Assistant Professor The Ohio State University College of Food, Agricultural, and Environmental Sciences Department of Plant Pathology 481C Kottman Hall, 2021 Coffey Rd., Columbus, OH 43210 614-688-2122 (office) 614-292-3390 (lab) 614 292-4455 (fax) slot.1@osu.edu - plantpath.osu.edu/slot

"Slot, Jason C." <slot.1@osu.edu>

OntarioInstCancerRes ComputationalBiol

The Ontario Institute for Cancer Research (OICR) is seeking a Principal Investigator (PI) in Computational Biology to undertake world-class computational research. We seek to strengthen and complement our existing expertise in genomics and cancer genomics, machine-learning, statistical genetics, analysis of next-generation sequencing, knowledge-bases and pathway/network analysis. We welcome applications from computational biologists of all types, but a career focus on cancer research is critical going forward.

The PI will be expected to mentor trainees, and to build collaborations both within and outside the OICR community. In addition to base funds provided by the Institute to support the PI's salary and personnel, the PI is expected to raise additional research funds from external competitive granting agencies. The OICR will assist the PI in obtaining faculty appointments at the University of Toronto or another affiliated academic institution. Faculty appointments (Assistant, Associate and Full) at the University of Toronto of current OICR Scientists have Departmental affiliations at Molecular Genetics, Medical Biophysics, Pharmacology, Computer Science and the School of Public Health.

OICR's Computational Biology Program is the home of the International Cancer Genome Consortium (ICGC) Data Coordination Centre, leads analysis for two ICGC projects (PanCuRx and CPC-GENE), the Genome Canada Canadian Data Integration Centre (CDIC), the Ontario Health Study and numerous other large-scale studies. It is the home of multiple international projects (e.g. Pan-cancer Analysis of Whole Genomes, Reactome, ICGC-TCGA DREAM Somatic Mutation Calling Challenge) and provides a robust intellectual environment for computational biology. A ~10,000-CPU institutional cluster is available to support analysis by the Program.

OICR is a multi-disciplinary, team-science-driven translational research institute. It has research programs in Diagnostic Development, Drug Discovery, Genomics, Imaging and Informatics. These support major national and international initiatives, including a multi-site targeted somatic sequencing study (OCTANE) and the International Cancer Genome Consortium (ICGC). Please visit https://oicr.on.ca/research-portfolio/ for details on our research portfolio.

QUALIFICATIONS

* An MD or PhD with a proven track record in computational biology, bioinformatics, or biostatistics * For new PIs, a record of independent research and either first- author or senior-authored peer reviewed publications or the publication of software, databases or other significant community resources. * For senior and intermediate-level PIs, international recognition and a strong publication record of relevance, proven leadership and management experience including the building of strong research teams, as well as a strong record of grant-

funding and mentorship. * Excellent communication and presentation skills.

Please attach the following to your application: - A covering letter, including the names of 3 potential referees; - A complete academic CV in PDF format; - A 2-4 page proposed research document, including a section highlighting relevance of the proposed studies to cancer.

OICR is an innovative cancer research institute located in the MaRS Centre in the Discovery District in downtown Toronto. OICR is addressing significant challenges in cancer research with multi-disciplinary, multi-institutional teams. New discoveries to prevent, detect and treat cancer will be moved from the bench to practical applications in patients. The OICR team is growing quickly. We are innovative, dedicated professionals who bring expertise to each of our roles. We are looking for individuals interested in being part of a culture of excellence that will result in Ontario being recognized internationally as a leading jurisdiction for cancer research.

Launched in December 2005, OICR is an independent institute funded by the Government of Ontario through the Ministry of Research, Innovation and Science.

For more information about OICR, please visit the website at www.oicr.on.ca . POSTED DATE: August 30, 2017 CLOSING DATE: Until Filled

OICR is an inclusive employer dedicated to building a diverse workforce. We encourage applications from all qualified candidates and will accommodate applicants' needs throughout all stages of the recruitment and selection process. Please advise the Recruiter to ensure your accessibility needs are accommodated throughout this process. Information received relating to accommodation will be addressed confidentially.

The Ontario Institute for Cancer Research thanks all applicants. However, only those under consideration will be contacted.

Apply at https://oicr.on.ca/careers/

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OxfordEmory Georgia BiologyEvolution

ASSISTANT PROFESSOR of BIOLOGY - tenure-track. Evolutionary biologists are encouraged to apply.

To apply for this position, follow this link: http://apply.interfolio.com/43879 Located 36 miles east of Atlanta on Emory's original campus in Oxford, Georgia, Oxford College invites applications for: Assistant Professor of Biology, Tenure- track, to begin August 2018. Responsibilities include teaching lecture and laboratory courses in introductory Biology for majors and non-majors, and developing an upper-level Biology course. The successful candidate will work with Biology faculty in using recommendations of Vision and Change and PULSE as guiding principles in department practices. Oxford has a new, state-of-the-art science facility (opened 2016) designed to promote student-faculty collaboration, scholarship, and innovative teaching in STEM.

Preferred Qualifications A PhD in Biology or a subdiscipline with experience or advanced training in cellular and molecular biology is required. Candidates with background in evolutionary Biology and experience in inquiry-based teaching and student-centered learning are particularly encouraged to apply.

Additional Job Details

APPLICATION INSTRUCTIONS Interested candidates should submit a cover letter, CV, statement of teaching philosophy, transcripts, and three letters of recommendation to this link: http://apply.interfolio.com/43879. The cover letter should address the candidate's qualifications for the position as well as their interest in working at a liberal arts college. Evaluation of candidates will begin October 2, 2017.

One of Emory University's four schools partnering in undergraduate education, Oxford College provides 950 first- and second-year students of high academic profile an intensive liberal-arts program for the first two years of their Emory bachelor's degree. We are interested in candidates with a commitment to working with a remarkably diverse student body in an inclusive learning community. Applications from women and historically underrepresented minorities are particularly welcome.

For more information about Oxford College and for a full listing of open positions, visit http://oxford.emory.edu/-hiring EEO/AA/Individuals with Disabilities/Veteran Employer

M. Eloise Brown Carter Professor of Biology Oxford College of Emory University Oxford, Georgia 30054 ecarter@emory.edu

"Carter, Eloise B" <ecarter@emory.edu>

QueenMaryU London BehaviourEvolution

QueenMaryULondon. AcademicPosition. Biological/ Experimental Psychology. Applications are invited for a new academic position at the level of either Lecturer or Senior Lecturer/Reader (Associate Professor) in Biological or Experimental Psychology, in the School of Biological and Chemical Sciences. We seek an outstanding and ambitious candidate, and particularly welcome applicants whose research complements our existing strengths in comparative psychology, animal behaviour and cognition, as well as biological psychology (human or animal). The successful candidate will be involved in teaching on our biology and psychology courses. Successful candidates will have an internationally-recognised research profile, with demonstrable success in gaining research funding and a strong track record of publishing high quality papers as a significant author. Applicants must also have the ability to teach in relevant areas at undergraduate level. Queen Mary is one of the largest colleges in the University of London, and one of the UK's leading research-intensive institutions. The College joined the Russell Group in 2012, was ranked 9th in the National 2014 Research Excellence Framework, and has made a strategic commitment to world-class research and teaching across all its disciplines. Within Queen Mary, the School of Biological and Chemical Sciences is a large and expanding academic unit, which provides a supportive and friendly environment and encourages interdisciplinary research. Our environment offers rich opportunities for collaborative research with strong links to other Schools within the Faculty, and Barts and the London School of Medicine and Dentistry, and to research centres and facilities including the Centre for Psychiatry, the Life Sciences Institute, the Centre for Mind and Society, and the Centre for Cognitive Science.

The School is strongly committed to promoting diversity, including gender equality. We are also happy to consider applications from individuals with their own fellowship funding who wish to explore proleptic positions in the School.

The post is full time and permanent with a start date as soon as possible. The salary will be in the range of 40,865 - 50,881 (Lecturer) or 53,777 - 60,109 for Senior Lecturer/Reader) and in accordance with experience and qualifications. Benefits include 30 days annual leave, childcare vouchers scheme, defined benefit pension scheme and interest-free season ticket loan. A competitive remuneration package and start-up funds are negotiable.

Non-UK/EU citizens may apply, but must be able to demonstrate their eligibility to work in the UK in accordance with the Immigration, Asylum and Nationality Act 2006. Where required this may include entry clearance or continued leave to remain under the Points Based Immigration Scheme. The deadline for applications is the 20 September 2017, and applicants shortlisted for interview will be notified soon after. We thank other applicants for their interest but regret that we are unable to contact all applicants individually.

To apply, please visit the Human Resources website on http://www.jobs.qmul.ac.uk/ and search for reference number QMUL12448

Application enquiries should be directed to recruitment@qmul.ac.uk

Applicants must submit their CV as well as a two page summary of their current research and future research plans at Queen Mary London.

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

RBG Kew 2 MycologyResearchLeaders

Senior Research Leader & Research Leader in Mycology Royal Botanic Gardens, Kew

An opportunity has arisen for two new research positions in fungal biology at the Royal Botanic Gardens, Kew. One position will be hired at a Senior Research Leader level, the other at Research Leader level.

The posts will be tailored according to qualifications and experience and located within Kew's Comparative Plant and Fungal Biology department and Identification and Naming department. We are seeking two highly motivated and enthusiastic individuals to build a strong research group, with the aim of delivering high-quality science in an area of fungal biology that is relevant to Kew's mission, as outlined in the Science Strategy available on Kew's website, and the priorities of the two departments.

The SRL will manage a small team of fungi researchers and build a Mycology strategy group at Kew that will develop and consolidate Kew's position as a world leader in mycological research.

These are permanent, full-time positions. Indicative salary will 36,000 - 43,000 per annum for the Research Leader, and 50,000 - 57,000 per annum for the Senior Research Leader.

Closing Date:22/10/2017

Further information: https://careers.kew.org/vacancy/-senior-research-leader-research-leader-in-mycology-327316.html The Royal Botanic Gardens, Kew is a non-departmental public body with exempt charitable status, whose principal place of business is at Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AE, United Kingdom.

William Baker <W.Baker@kew.org>

SanDiegoStateU QuantEvolutionaryBiology

Assistant Professor: Quantitative Integrative Biology

San Diego State University THE DEPARTMENT OF BIOLOGY AT SAN DIEGO STATE UNIVERSITY invites applications for a tenure-track faculty position in QUANTITATIVE INTEGRATIVE BIOLOGY at the Assistant Professor level. We encourage applications from candidates using current quantitative and statistical methods to understand complex biological and ecological systems. Specific research areas that would complement existing strengths in the department include landscape ecology, disease ecology/epidemiology, population biology, microbial evolution, global change science, phylogenetic inference, and population/conservation genetics. We are particularly interested in candidates with expertise in statistical approaches that can be applied broadly across our department, such as complex multivariate analyses, spatial analyses and geostatistics, Bayesian statistics, and analysis of big data.

Candidates should have a PhD and post-doctoral experience in a relevant field of biology, a strong history of research accomplishments and funding, and a record of collaborating across traditional disciplinary boundaries. Teaching responsibilities will include participating in and developing undergraduate and graduate biostatistics courses using "R" statistical packages, and additional advanced courses in the candidate's areas of expertise. The successful candidate will participate in MS and PhD programs in Ecology, Evolutionary Biology, and/or Cell and Molecular Biology. Preference will be given to candidates who will mentor students in more than one of these graduate programs. Many of our faculty also participate in graduate programs such as Computational Sciences, and Biomedical and Medical Informatics.

SDSU is a large, diverse, urban university and Hispanic-Serving Institution with a commitment to diversity, equity, and inclusive excellence. Our campus community is diverse in many ways, including race, religion, color, sex, age, disability, marital status, sexual orientation, gender identity and expression, national origin, pregnancy, medical condition, and covered veteran status. We strive to build and sustain a welcoming environment for all. SDSU is seeking applicants with demonstrated experience in and/or commitment to teaching and working effectively with individuals from diverse backgrounds and members of underrepresented groups. The College of Sciences is host to a large number of federally-funded minority training programs (described at http://www.sci.sdsu.edu/casa/).

This position may also be eligible for the SDSU Building on Inclusive Excellence (BIE) hiring program that creates additional faculty lines for candidates who meet two or more of the criteria listed in http://sdsu-bie.weebly.com/. Candidates who meet two or more of these criteria should explain in their cover letter how they meet the identified criteria.

Apply via Interfolio at http://apply.interfolio.com/-45538. Review of applications will begin 23 October 2017, and will continue until the position is filled. Incomplete applications are not guaranteed full consideration.

Rulon Clark <rclark@mail.sdsu.edu>

TexasAM ResAssist ParasitePopGenetics

Texas A&M University in College Station: Research Assistant The lab of Charles Criscione (http://www.bio.tamu.edu/index.php/faculty/criscione/) is searching for a research assistant. The employee will participate in various population genetic studies of parasitic helminths including a NSF-funded study that will test the role parasite mating systems have in impacting the evolution of parasite life cycle complexity (example of previous work see Kasl et al. Evolution 69:3156). The position is for up to 3 years, subject to annual renewal based on performance. The salary range is $30,000-$35,000 (depending on experience), with benefits.

Job duties: Under direction of the PI and graduate students, the research assistant will be involved in molecular lab work (e.g., DNA extractions, PCR) and extensive field work. Main duties will include obtaining microsatellite genotype data, dissecting host species (catfish, crayfish, leeches and other inverts) for helminth parasites, field-collection of host species (including backpack electrofishing, trapping, and netting), driving to remote field sites, and assisting in maintaining a stocked and organized laboratory. Occasional duties include assisting with animal husbandry, and interacting with private landowners and various state officials.

Education and Experience: Appropriate bachelor's degree in biology or related field or equivalent combination of education and experience. Preferred education is a master's degree in biology or related field. Experience in one or more of the following areas: molecular genetics research, parasitology, or aquatic field-based ecological research. Must have a valid driver's license. Must be able to conduct field work for extensive periods away from College Station, TX (e.g., up to a month at a time). Must be able to backpack or carry 50lbs of field gear while hiking distances of 1-3 miles. Previous experience in field-based ecological research on fishes or aquatic invertebrates, or working with helminth parasites will be heavily weighted. It is imperative that the research assistant have a strong attention to detail, the ability to collect data under strenuous field conditions, and the character to maintain a positive attitude after working long hours in hot, humid, and buggy conditions.

Applicants need to do an electronic application through http://jobpath.tamu.edu/postings/112753. In addition to filling out the information on the jobpath link, the application must include a single pdf file containing the following, in order 1) 1-page cover letter that includes summary of research experience and career goals, 2) C.V., and 3) List of three references with contact information (email, telephone, and mailing address). After identifying top candidates, we will request letters from these references. The position will begin as soon as possible. For questions about this position, please email ccriscione@bio.tamu.edu.

Charles D. Criscione, Associate Professor Department of Biology Texas A&M University 3258 TAMU College Station, TX 77843-3258

phone: (office: 979-845-0917, lab:979-845-0925, fax:979-845-2891) email: (ccriscione@bio.tamu.edu) faculty web page: http://www.bio.tamu.edu/FACMENU/FACULTY/CriscioneC.php Charles Criscione <ccriscione@bio.tamu.edu>

TexasStateU MicrobialGenomics

Assistant Professor Functional Microbial Genomics

The Department of Biology at Texas State University (www.bio.txstate.edu) invites applications for a tenure-track, Assistant Professor specializing in functional microbial genomics. The successful candidate will be expected to teach both graduate and undergraduate microbiology courses in the Department of Biology and develop an externally funded research program involving graduate students that complements the strengths of our 50-member faculty.

Required qualifications are an earned Ph.D. in microbiology, virology, or related areas, and a record of peer-reviewed publications in genome-scale research and analyses. Preferred qualifications include postdoctoral experience, a record of grant funding to support research, strong bioinformatics skills, and research experience in microbiology complementing the research strengths of the Department. Salary and start-up package are negotiable. For full consideration, all application materials must be received by October 15, 2017.

Interested applicants should submit the following materials: 1. A letter of application with statements on research plans and teaching philosophy, 2. CV, 3. pdfs of up to five publications, and 4. contact information of five people willing to serve as references.

Only applications submitted through the Texas State

University website will be accepted and considered, https://jobs.hr.txstate.edu/postings/20542. Questions about this position should be addressed to Michael Forstner, MF@txstate.edu, (512) 245-3362, Texas State University, 601 University Drive, San Marcos, TX 78666.

Texas State University is an Affirmative Action/Equal Opportunity Employer. Texas State University is a member of the Texas State University System.

"Rodriguez, David" <drdz@txstate.edu>

UBath MathStatsBiology

The Department of Mathematical Sciences at the University of Bath is currently advertising multiple positions that may be of interest to people working on problems in evolutionary biology.

Two positions as a Professor (Chair) in Statistics, with research in evolution and data science included as areas of interest:

https://www.bath.ac.uk/jobs/Vacancy.aspx?ref=-SF5136 One position as either a Lecturer (Assistant Prof) or Senior Lecturer/Reader (Associate Prof) in Statistics, again with research in evolution and data science included as areas of interest:

https://www.bath.ac.uk/jobs/Vacancy.aspx?ref=-SF5137 One position as a Lecturer (Assistant Professor) in Applied Mathematics, which explicitly mentions mathematical biology as one of the areas of interest:

https://www.bath.ac.uk/jobs/Vacancy.aspx?ref=-SF5138 In addition to the interactions and resources available through the Department of Mathematical Sciences (see the adverts for more information), these positions offer the opportunity to join the Milner Centre for Evolution (http://www.bath.ac.uk/groups/milner-centre-for-evolution/) and the Centre for Mathematical Biology (http://www.bath.ac.uk/cmb/)

Jason Wolf <jason@evolutionarygenetics.org>

UBergen SystematicInvertebrateZoology

Associate Prof in Systematic Invertebrate Zoology University Museum of Bergen University of Bergen, Norway

The Department of Natural History, University Museum of Bergen, has a vacancy for a permanent position as associate professor in biosystematics from 1.9.2017. The position is linked to the ForBio Research School in Biosystematics, externally funded by The Research Council of Norway and The Norwegian Biodiversity Information Centre

Work tasks and duties:

The successful candidate will dedicate 50% of his/her working time on research on systematic invertebrate zoology and 50% on continuing and developing the Nordic Research School in Biosystematics in collaboration with the ForBio leader in Oslo and coordinator colleagues in Trondheim and Tromsø. Tasks will include initiating, organizing and administrating research courses and other events, mostly aimed at PhD students affiliated with Nordic universities. The ForBio coordinator in Bergen will have an important role in shaping the University Museum's contribution towards the research school, as well as coordinating these activities with the educational activities at the Institute of Biology, University of Bergen. The museum retains the right to impose changes in the content of the required duties in case of future changes in the funding base for the position, for example including tasks related to curation of museum collections.

The University Museum of Bergen aims to strengthen its research on systematics of marine invertebrates. We are therefore looking for an active researcher with an interest in marine biodiversity and high competence in systematic zoology and taxonomic research. The invertebrate collections have several ongoing projects as well as national and international collaborations. The University Museum owns facilities for morphological (microscopy, SEM) and molecular studies (Sanger sequencing and IonTorrent), in addition to having access to shared infrastructure including the University of Bergen Genomics Core Facility (GFC), research vessels and field stations. The successful candidate will be expected to actively participate in the research group, as well as contribute to securing additional external funds both for his/her own research as well as research school activities.

Required qualifications:

We are looking for an active researcher with excellent qualifications in systematic zoology, preferably with international research experience. The applicants must have obtained a doctoral degree on biosystematics of marine invertebrates or comparable qualifications. They should have a strong professional network in marine biology and systematics. Familiarity with taxonomic research, a good knowledge of marine faunistics, and experience from scientific cruises and museum work are desirable. Candidates will be evaluated based on their scientific competence, in particular pertaining to taxonomical research utilizing both molecular and morphological methods.

The applicants must have a genuine interest for teaching and doctoral education, a sound understanding of the Norwegian/Nordic higher education system, and knowledge on the relevant institutions involved in education, research and management. Prior experience in developing and organizing research courses or other similar activities will be useful. Within ForBio, the Bergen node is intended to have an emphasis on zoology and marine biology, and we hope to find a person with solid professional networks internationally and an overview of relevant higher education programs in the Nordic countries.

The successful candidate must have good collaboration and communication skills. Candidates should also have experience writing grant applications for external funding.

Basic pedagogical training is a requirement for the position. The successful applicant will be offered training if this requirement is not met prior to employment.

Working language at the department is Norwegian, but candidates must be fluent in both written and spoken English.

We can offer: - A good and professionally challenging working environment - Salary at pay grade 58 - 62 (code 1011, pay range 24) in the state salary scale. This currently amounts to an annual salary of NOK 494.800 - 537.700 before taxes. Further increase in salary will depend on seniority. A higher salary may be considered for a particularly well qualified applicant. - Enrolment in the Norwegian Public Service Pension Fund - A position in an inclusive workplace (IA enterprise) - Good welfare benefits

Your application must include: The application is to be written in English and must include: - CV - Diplomas - References - Complete list of publications - List of academic work that the applicant believes should be taken into consideration in the assessment, maximum 10, including information where this work was published - List with appendices that document your pedagogical qualifications

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UCalifornia Berkeley HostMicrobe

Recruitment Period Open August 31st, 2017 through October 16th, 2017 If you apply to this recruitment by October 16th, 2017, you will have until October 31st, 2017 to complete your application.

Description

The Department of Molecular and Cell Biology at the University of California, Berkeley, is soliciting applications for a faculty position in the area of Host/Microbe Interactions at the level of Assistant Professor (tenure track). We seek applicants who are studying how interactions with microbes shape the biology (at all levels) of animals and other eukaryotes. The expected start date is July 1, 2018.

A Ph.D. and/or M.D. or equivalent degree in Molecular and Cell Biology or a related field is required at the time of application. Our preference is for applicants who would use molecular, cell biological, genomic, and/or systems biology methods to study how microbes associate with and affect the physiology, development, behavior or function of the host. We seek candidates who have demonstrated excellence, originality and productivity in research.

Preferred qualifications (by start date): Interest and experience in undergraduate and graduate teaching in molecular and cell biology, including microbiology.

Applications must be received by October 31, 2017. To apply, please go to the following link: http://apptrkr.com/1078012. Please direct questions to MCB-Search.committee@berkeley.edu, with a note indicating this Search # JPF01440.

Applicants should include: - Cover Letter - Summarize your interest and qualifications for this position. - Curriculum Vitae - Your most recently updated C.V.

- Summary of Major Research Accomplishments - A summary of major research accomplishments of approximately 250 words - Publication List - A complete list of publications. - Ongoing and Planned Research Program - A summary of approximately 1,500 words of the applicant's ongoing and planned research program, plus up to one page of figures and a list of essential publication citations. - Significant Publication #1 - In addition to your publication, provide a statement that begins with the manuscript title and author list and then summarizes, in approximately 300 words, the significance of the selected publication. - Significant Publication #2 - In addition to your publication, provide a statement that begins with the manuscript title and author list and then summarizes, in approximately 300 words, the significance of the selected publication. - Significant Publication #3 - In addition to your publication, provide a statement that begins with the manuscript title and author list and then summarizes, in approximately 300 words, the significance of the selected publication. - Statement of Teaching - Summary of teaching interests, as well as any prior teaching and mentoring experience, of approximately 500 words. - Statement of Contributions to Diversity - Statement addressing past and/or potential contributions to diversity through research, teaching and/or service.

Applicants should arrange to have three letters of reference submitted online. All letters will be treated as confidential per University of California policy and California state law. Please refer potential referees, including when letters are produced via a third party (i.e. dossier service or career center), to the UC Berkeley statement of confidentiality (http://apo.berkeley.edu/evalltr.html) prior to submitting their letters.

The Department of Molecular and Cell Biology, UC Berkeley, is committed to addressing the family needs of faculty, including dual career couples and single parents. The Department is interested in candidates who will contribute to diversity and equal opportunity in higher education through their teaching, research, and service. For information about potential relocation to Berkeley, or career needs of accompanying partners and spouses, please visit: http://ofew.berkeley.edu/new-faculty . The department seeks candidates whose research, teaching, or service has prepared them to contribute to our commitment to diversity and inclusion in higher education.

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age or protected veteran status. The department is also interested in individuals who may have had nonâcareer paths or who may have taken time off for family reasons (e.g., children, disabled, or elderly), or who have achieved excellence in careers outside academe (e.g., in professional or industry service). The University is responsive to the needs of dual career couples." For the complete University

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UCalifornia Berkeley VertebrateEvolution

Assistant Professor/Curator, Vertebrate Evolutionary Biology Department of Integrative Biology & Museum of Vertebrate Zoology University of California, Berkeley

The Department of Integrative Biology and the Museum of Vertebrate Zoology at the University of California, Berkeley invite applications for a full time (50% IB, 50% MVZ) tenure-track position in vertebrate evolutionary biology at the Assistant Professor/Assistant Curator level. Potential start date is July 1, 2018. The Museum of Vertebrate Zoology is a world-renowned institution dedicated to understanding the ecology, evolution, and organismal biology of vertebrates using field studies, museum collections, and laboratory research. We seek exceptional candidates working in any area of vertebrate biology, and on any vertebrate group, whose work emphasizes collection or field based studies within a comparative context. Possible research areas include (but are not limited to) phylogenetics, biogeography, adaptation, speciation, ecological and evolutionary genetics, genomics, behavior, population dynamics, physiology, comparative morphology, and developmental biology. Candidates will be expected to maintain an active field program and to contribute to building and utilizing museum collections, facilitating ongoing MVZ programs of research and education. Candidates will also be expected to contribute to teaching in the undergraduate and graduate curriculum of the Department of Integrative Biology.

Required Minimum Basic Qualifications: Applicants with an exceptional research record in any area of vertebrate biology are encouraged to apply. The Museum and Department are interested in candidates who will contribute to diversity and equal opportunity in higher education through their teaching, research, and service. Applicants must have completed all Ph.D. or equivalent degree requirements except the dissertation at the time of application.

Additional Qualifications: Demonstrated excellence, originality, and productivity in research, and interest in undergraduate and graduate teaching as well as public outreach. Applicants must have a Ph.D. or equivalent degree by the start date of the position.

Preferred qualifications: Expertise in collections-based research and field studies.

Applications must be received by December 1, 2017. To apply, please go to the following link: http://apptrkr.com/1078573 Please direct all questions to Integrative Biology Academic Personnel ib_recruit@berkeley.edu.

Applicants should include the following required documents: - Cover Letter - Curriculum Vitae - Brief Description of Research Accomplishments - Statement of Research Objectives - Statement of Curatorial Experience and Interest in Museum-Based Research - Statement of Teaching Interests - Statement of Contributions to Diversity Statement addressing past and/or potential contributions to diversity through research, teaching, and/or service.

- List of Publications - Significant Publication #1 - Significant Publication #2 - Significant Publication #3 - Large Publication File (Optional) In case file needs to be split - Large Publication File (Optional) In case file needs to be split - Large Publication File (Optional) In case file needs to be split Applicants should arrange to have three letters of reference submitted online. All letters will be treated as confidential per University of California policy and California state law. Please refer potential referees, including when letters are produced via a third party (i.e.

dossier service or career center), to the UC Berkeley statement of confidentiality (http://apo.berkeley.edu/-evalltr.html) prior to submitting their letters.

The Department of Integrative Biology and the Museum of Vertebrate Zoology, UC Berkeley, are committed to addressing the family needs of faculty, including dual career couples and single parents. For information about potential relocation to Berkeley, or career needs of accompanying partners and spouses, please visit: http://ofew.berkeley.edu/new-faculty . The University of California is an Affirmative Action/Equal Opportunity Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy see: http://-/policy.ucop.edu/doc/4000376/NondiscrimAffirmAct Thank you,

Vanessa Phanouvong vanessa@jobelephant.com 5443 Fremontia Lane San Diego, CA 92115 Tel: 619.795.0837 Fax: 619.243.1484 Toll-Free Direct: 800.311.0563

Vanessa Phanouvong <vanessa@jobelephant.com>

UCalifornia Davis PlantGenomics

POSITION ANNOUNCEMENT Assistant Professor of Climate Adaptation: Plant Genomics Department of Plant Sciences, University of California, Davis Title: Assistant Professor of Climate Adaptation: Plant Genomics. The Department of Plant Sciences in the College of Agricultural and Environmental Sciences at the University of California, Davis is recruiting an Assistant Professor of Climate Change Adaptation with an emphasis on using genomic approaches to understand plant adaptation to changing climates so as to inform breeding, restoration and/or management strategies in agricultural or natural systems. This is an academic year (9-month), Assistant Professor tenure-track position with teaching, research, outreach/engagement and service responsibilities and includes the expectation that the appointee will conduct mission-oriented research and outreach/engagement of relevance to the California Agricultural Experiment Station (http://-www.caes.ucdavis.edu/research/aes).

Responsibilities: The Department of Plant Sciences is seeking applicants that focus on plant adaptation to changing climates. The appointee is expected to establish a competitively funded research program to address critical or emerging issues in climate adaptation and plant genomics. The appointee will be responsible for teaching undergraduate and graduate classes which, depending on expertise, could include classes such as Landscape Conservation Genetics, Population Genetics in a Changing Environment. Agriculture and the Environment, Genes and Gene Expression, Taxonomy and Ecology of Environmental Plant Families, or Genetics and Plant Conservation. The typical teaching expectation is 2 courses per year. Participation in departmental and university service is expected.

Qualifications: Ph.D. or equivalent degree in plant science, genetics, genomics, ecology, evolution, or a related field. Post-doctoral experience is preferred. Evidence of research excellence is expected. The candidate should have the ability to develop and instruct undergraduate and graduate courses and the ability to develop and conduct extramurally funded research using genomic approaches to understand plant adaptation to changing climates so as to inform breeding, restoration and/or management strategies in agricultural or natural systems. Candidates with a willingness to build relationships with relevant State of California and federal agencies, farmers, land and resource managers, plant breeding companies and other stakeholders are desired.

Salary: Commensurate with qualifications and experience.

Applications: Application materials must be submitted via the following website: http://apptrkr.com/1076303. The position will remain open until filled.

To ensure consideration, applications should be received by October 15, 2017.

Required application materials include: 1) curriculum vitae including publication list, 2) up to three publications, 3) transcripts if the applicant is within five years of Ph.D. degree, 4) statement of research accomplishments, 5) statement of teaching accomplishments and philosophy, 6) statement of future research plans relevant to the position 7) Statement of Contributions to Diversity, and 8) the names, addresses, including e-mail, of four professional references.

Additional inquiries should be directed to the search committee chair, Mary L. Cadenasso (mlcadenasso@ucdavis.edu).

UC Davis is an affirmative action/equal employment opportunity employer and is dedicated to recruiting a diverse faculty community. We welcome all qualified applicants to apply, including women, minorities, veterans, and individuals with disabilities. Applicants with disabilities can contact University of California, Davis, Accessibility Services with questions at http://-accessibility.ucdavis.edu/index.html Thank you,

Vanessa Phanouvong vanessa@jobelephant.com 5443 Fremontia Lane San Diego, CA 92115 Tel: 619.795.0837 Fax: 619.243.1484 Toll-Free Direct: 800.311.0563

Vanessa Phanouvong <vanessa@jobelephant.com>

UCalifornia LosAngeles EvolutionOfMicrobes

Tenure track Assistant Professor position in Quantitative Ecology or Evolution of Microbes

The Department of Ecology and Evolutionary Biology and the new Institute for Quantitative and Computational Biosciences (QCBio) at the University of California, Los Angeles are searching for a joint faculty appointment at the level of Assistant Professor.

We seek quantitative and computational biologists who study the ecology or evolution of microbes, at the level of populations or communities, including microbiomes, free-living microbes, microbial symbionts and pathogens. The competitive applicant will apply fundamental principles of ecology or evolutionary biology, in conjunction with quantitative approaches, to understand the dynamics of microbial systems. Research on naturally-occurring (terrestrial, aquatic or marine) or laboratory systems will be considered, and research with implications for health is welcome but not essential. Quantitative empirical approaches (including experiments) and use of cutting edge technologies are encouraged, as is potential to synergize with UCLA's strong biomedical research community via connections across disciplines and spatial scales.

UCLA boasts thriving research communities in ecology and evolutionary biology, as well as in genomics, bioinformatics, mathematical modeling and computational systems biology. There is a strong and growing community of microbiology and microbiome researchers on campus (http://www.microbiome.ucla.edu/), and excellent opportunities to interface with biomedical or environmental science programs. UCLA has outstanding resources, including the UC Natural Reserve System, the NSF Institute of Pure and Applied Mathematics, the Institute of the Environment and Sustainability, the Molecular Biology Institute, the David Geffen School of Medicine and the Fielding School of Public Health. This joint position will support the new faculty member to contribute to educational programs at the undergraduate and graduate level associated with the missions of QCBio and the Department of Ecology and Evolutionary Biology.

Review of applications will begin on October 30, 2017 and continue until the position is filled. Applicants should submit materials online through https://-

recruit.apo.ucla.edu/apply/JPF03251 Please include (1) a cover letter, (2) CV, (3) research statement covering both past accomplishments and future plans, (4) teaching statement, (5) statement on contributions to equity, diversity, and inclusion, (6) 2-3 significant and relevant publications, and (7) names and contact information for at least three references. Candidates must have a PhD within the field of Biology, Microbiology, Computational Sciences or other relevant discipline and an established track record of productivity and innovative research in microbial ecology and/or evolution, and should convey their commitment to excellence in research, teaching, mentoring, and contributions to diversity.

Questions regarding the position should be sent to Jamie Lloyd-Smith (jlloydsmith@ucla.edu).

As a campus with a diverse student body, we encourage applications from women, minorities, and individuals with a history of mentoring under-represented minorities in the sciences. UCLA has programs to assist in partner employment, childcare, schooling and other family concerns. For additional information, visit the UCLA Academic Personnel Office website (https://-www.apo.ucla.edu/) or the UC Office of the President's website (http://www.ucop.edu/).

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy, see: UC Nondiscrimination & Affirmative Action Policy (http://policy.ucop.edu/doc/4000376/-NondiscrimAffirmAct).

Jamie Lloyd-Smith <jlloydsmith@ucla.edu>

UCalifornia SanDiego EvolutionaryBiology

Academic Personnel Manager | Division of Biological Sciences

1730 Urey Hall, MC 0346 | Phone: (858) 534-6387 | Fax: (858) 534-6341

UCSanDiego-BioSci-Blue_Gold-RGB2

Assistant, Associate, or Full Professor: Evolutionary Biology

The Section of Ecology, Behavior and Evolution in the Division of Biological Sciences (www.biology.ucsd.edu) invites applications for a faculty position in Evolutionary Biology at the tenure-track Assistant, or tenured Associate or Full Professor level. We are broadly searching for an evolutionary biologist. Research topics could include, but are not limited to, vertebrate biology, evolutionary ecology, or comparative or population genomics.

All candidates must have earned a Ph.D. or equivalent degree, and be committed to teaching at the undergraduate and graduate levels. In addition to excellence and creativity in research and scholarship, successful candidates must also demonstrate a commitment to equity and inclusion in higher education. We are especially interested in candidates who have created or contributed to programs that aim to increase access and success of underrepresented students and/or faculty in the sciences, and/or have detailed plans to accomplish such goals.

The Division of Biological Sciences at UCSD is a vibrant center of scientific discovery, innovation, and collaboration. Our large research base spans many areas of biology and has one of the most celebrated graduate programs in the country. We are committed to academic excellence and diversity within the faculty, staff, and student body.

Salary is commensurate with qualifications and based on University of California pay scales.

Initial review of applications will commence on October 23, 2017 and will continue until position is filled.

Interested applicants must submit a cover letter, curriculum vitae, statement of research, statement of teaching, a statement describing their past experience and leadership in fostering equity and diversity and/or their potential to make future contributions, and 3-5 publications. For information on preparing diversity statements and divisional initiatives to promote diversity, see: http://facultyequity.ucsd.edu/Faculty-Applicant-C2D-Info.asp and http://biology.ucsd.edu/diversity/-index.html. Applicants at the Assistant Professor level need to submit 3-5 references, and applicants at the Associate or Full Professor level need to provide contact information for 3-5 references.

Applications must be submitted through the University of California San Diego's Academic Personnel RECRUIT System:

Assistant Professor: https://apol-recruit.ucsd.edu/-apply/JPF01535 Associate or Full Professor: https://-apol-recruit.ucsd.edu/apply/JPF01537 Further details about the required application material can be found at: http://biology.ucsd.edu/jobs/apply-lrf-lsoe.html UCSD is an Affirmative Action/Equal Opportunity Employer with a strong institutional commitment to excellence through diversity (http://diversity.ucsd.edu/). All qualified applicants will receive consideration for employment without regard to gender, race, color, religion, sex, sexual orientation, national origin, disability, age or protected veteran status.

“Ta, Laura” <lta@ucsd.edu>

UCLondon Tech MultivariateYeastAdaptation

Research Technician Grade 5 at University College London

The effects of genetics, mutation and selection on Evolutionary Rescue in complex environments

We are looking for a research technician to work alongside a postdoctoral research associate under the supervision of Max Reuter and Jürg Bähler at University College London. The position is available for three years and funded by a grant from the BBSRC. The aim of the project is to understand how the interplay between genetics and evolutionary forces (mutation, selection) shapes the capacity of populations to show rapid adaptive responses. The results will be relevant in a variety of applied contexts, including climate change, antibiotic treatments or agricultural pest control. Practically, the project will use high-throughput phenotyping, genomics and quantitative genetics in the fission yeast Schizosaccharomyces pombe and day-to day activities will involve techniques from micro- and molecular biology.

The research technician will work as part of a dedicated team and interact with both the groups of Max Reuter, working on evolutionary constraints on phenotypic adaptation (http://www.homepages.ucl.ac.uk/~ucbtmre/Labsite), and Jürg Bähler, working on genome regulation (http://www.bahlerlab.info/home/). The post will be based in UCL’s Research Department of Genetics, Evolution and Environment, which offers a stimulating and interactive environment across the fields of evolutionary and human genetics to biodiversity research. Further afield, UCL offers a great diversity of world-class research right in the centre of London.

The position is an opportunity for a highly motivated and ambitious individual who enjoys working in a team. The candidate will have (or be about to obtain) an undergraduate degree in a relevant discipline, proven research skills and relevant experience (molecular and/or microbiology, high-throughput techniques) and excellent verbal and written communication skills.

The post is available from 1st November 2017 (negotiable) for up to 30 months, with a starting salary between 23,604 (20,624 plus 2,980 London Allowance) and 26,859 per annum (23,879 plus 2,980 London Allowance), depending on experience.

For more information on the application process and to submit applications, search reference 1674895 on the UCL Jobs database or follow this link: https://atsv7.wcn.co.uk/search_engine/jobs.cgi?SID=amNvZGU9MTY3NDg5NSZ2dF90ZW1wbGF0ZT05NjUmb3duZXI9N In case you have difficulties with the online system, please email biosciences.staffing@ucl.ac.uk. For informal enquiries or more information on the project, email Max Reuter (m.reuter@ucl.ac.uk).

The closing date for applications is 5 October 2017.

Max Reuter

Research Department of Genetics, Evolution and Environment Faculty of Life Sciences University College London Darwin Building Gower Street, London WC1E 6BT, UK

Phone: +44-20-76792201 (internal 32201)

Lab: http://www.homepages.ucl.ac.uk/~ucbtmre/Labsite/ Department: http://www.ucl.ac.uk/gee m.reuter@ucl.ac.uk

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UFlorida Gainesville ConservationTeachingQuantBiol

The Department of Wildlife Ecology and Conservation at the University of Florida in Gainesville is announcing a new tenure track position at the rank of Assistant Professor.

This position announcement is part of the Provosts university-wide initiative to create tenure-track faculty positions emphasizing teaching-scholarship (http://news.ufl.edu/articles/2017/06/uf-to-hire-500-new-faculty-in-major-initiative.php). Our department (Wildlife Ecology and Conservation) recognizes the need for enhancing our student learning in quantitative approaches to studying wildlife ecology. Quantitative expertise for decision making in natural resources is a critical need at the state, regional, national, and international arenas. This hire is expected to further cement our department as a national leader in ecology and conservation of wildlife and its contribution to UFs reputation as a leading institution in natural resources education.

This position is a 12-month tenure-accruing appointment available in the Department of Wildlife Ecology and Conservation, Institute of Food and Agricultural Sciences (IFAS), at the University of Florida (UF). The appointment will be 60% teaching (College of Agricultural and Life Sciences) and 40% research (Florida Agricultural Experiment Station).

Duties and Responsibilities: Assigned responsibilities will include: (1) Teaching undergraduate courses (one semester each) in the Wildlife Ecology undergraduate curriculum i) WIS 4501 Wildlife Population Ecology and ii) WIS 4601 Quantitative Wildlife Ecology. (2) Developing and teaching a quantitative course for graduate students in wildlife population estimation to be taught annually. 3) Developing an internationally recognized scholarly research program that incorporates quantitative approaches in the study of wildlife populations. Possible areas of specialty include capture-recapture modeling and design, parameter estimation, occupancy modeling, decision science, and adaptive management.

The successful candidate will engage in activities related to instruction, including scholarship on teaching, mentoring of, and supervising undergraduate and graduate students in research and creative work, curriculum revision and enhancement; and engaging in professional teaching development activities, for which there are many resources available to UF faculty. The position will be 60% teaching and 40% research. Because of the IFAS land-grant mission, all faculty are expected to be supportive of and engaged in all three mission areasResearch, Teaching and Extensionregardless of the assignment split specified in the position description.

Required Qualifications: A doctorate (PhD or DPhil) (foreign equivalent acceptable) with an emphasis on wildlife biology, ecology, biomath, or a related biological sciences or natural resources discipline is required. Candidates must have a demonstrated commitment to teaching, experience mentoring students, and promotion of a diverse educational and professional environment. Applicants will also be expected to illustrate evidence of scholarship and depth of knowledge in wildlife ecology and conservation; and willingness to work with natural resource agencies, NGOs, and stakeholders. Candidates will demonstrate their skills in verbal and written communication, interpersonal relationships across cultures, and commitment to grantsmanship. Candidates also must have a commitment to values of excellence, diversity, global involvement, and accountability.

Preferred Qualifications: Preferred qualifications/attributes: 1) Candidates with a well-developed teaching portfolio and/or postdoctoral teaching experience (experience in quantitative ecology, such as courses listed above, will be ranked favorably). 2) Demonstrated commitment to developing a productive research program, commensurate with a 40% research appointment at an R1 academic institution is expected from candidates. 3) Candidates with a primary interest in research programs focusing on wildlife populations. Although the preference is for a research program emphasizing terrestrial vertebrates or marine mammals, other study systems will be considered. Topical expertise can be demonstrated by activities such as publication in peer-reviewed journals, demonstrated graduate student mentoring experience and/or philosophy, development of management or recovery plans for species and habitats of conservation importance, and securing research funding.

Employment Conditions: This position is available 1 April 2018, and will be filled as soon thereafter as an acceptable applicant is available; specific start date is negotiable; however, the expectation is that the candidate will begin by the start of Fall term 2018. Compensation is commensurate with the education, experience, and qualifications of the selected applicant.

Background Information:

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UGeorgia EvolutionaryEcol

Dear colleagues,

The Odum School of Ecology at the University of Georgia (http://www.ecology.uga.edu/) invites applications for a tenure-track, academic year (9-month) position at the Assistant Professor level. We seek candidates whose research is at the organismal scale of organization, and that integrates ecophysiology, behavioral ecology, evolutionary ecology or functional morphology. The ideal candidate will use innovative approaches to address fundamental questions in their field, and be able to collaborate effectively with other members of the school. We are interested in candidates whose research program has a strong empirical focus, and applicants can focus on any taxonomic group or study system (terrestrial, marine or freshwater). The successful candidate will be expected to have demonstrated excellence and productivity in research, to maintain a rigorous, externally funded research program, and to participate in undergraduate and graduate teaching. Primary teaching responsibilities will include contributing to a large-enrollment introductory course in ecology, and upper-level courses in the successful candidate's area of expertise. Applicants with an interest in utilizing one or more of our field stations and facilities (http://www.ecology.uga.edu/-facilitiesList.php) are especially encouraged to apply. The ideal candidate would establish bridges with other units at UGA such as Genetics, Forestry and Natural Resources, Veterinary Medicine, Plant Biology, Marine Sciences, Microbiology orEntomology.

To apply, candidates must have a Ph.D. or terminal degree in ecology, biology, or a related field. Candidates should submit applications electronically at

https://facultyjobs.uga.edu/postings/2765. Applicants should be prepared to upload the following items in PDF format: (a) a cover letter, (b) curriculum vitae, (c) a statement of research goals (2 pages max.), (d) a statement of teaching philosophy (2 pages max.), (e) 3 representative peer-reviewed journal articles, and (f) names and contact information (email, address and phone) for three referees. Applications should be received by 23 October 2017 to ensure full consideration. The anticipated start date for the position is August 2018.

The University of Georgia is located in Athens, Georgia. Georgia is well known for its quality of life with both outdoor and urban activities (www.georgia.gov). UGA (www.uga.edu) is a land grant/sea grant institution located approximately 60 miles northeast of Atlanta. It is within an hour driving distance from the North Georgia Mountains and four hours from the Atlantic coast. Athens enjoys a mild climate and yet still sees the benefits of the changing seasons, and is well known for its vibrant music scene.

The University of Georgia is an Equal Opportunity/Affirmative Action employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability, gender identity, sexual orientation or protected veteran status.

Jill T Anderson <jta24@uga.edu>

UGlasgow 2 Bioinformatics

MRC-University of Glasgow Centre for Virus Research, Glasgow, Scotland

We've two positions to offer to join our expanding bioinformatics team and enhance the research activities of the MRC-University of Glasgow Centre for Virus Research (CVR) (http://www.cvr.ac.uk/). CVR Bioinformatics comprises a large team of MRC-funded researchers embedded in the Centre (http://-www.bioinformatics.cvr.ac.uk/). They have extensive expertise in analysing next generation sequencing data, metagenomics, transcriptomics, proteomics, molecular phylogenetics, software design and database development.

The CVR has invested significantly in bioinformatics and efforts are currently focussed on the development of novel computational strategies that can be used to answer questions of importance to our understanding of viral biology, evolution, emergence, transmission and diagnostics. The CVR brings together virologists with computer-based researchers, and has advanced IT infrastructure and the facilities to handle viruses at various biosafety containment levels. Uniquely, the bioinformaticians are solely dedicated to virology and are experts in viral genomics, systems virology and evolution. The CVR is an OIE Collaborating Centre for Viral Genomics and Bioinformatics.

The post holder will work with the bioinformatics team and other CVR researchers, contributing to the support and research output of the Centre and she/he will be encouraged to develop independent research interests in the area of viral bioinformatics. The postholder will help in the development of pipelines for the analysis of data arising from virus and virus-host research, visualization of results, and perform data analysis as appropriate. Candidates with a background in bioinformatics, omics research, computer science, evolutionary, computational and/or systems biology, biostatistics and/or machine learning are encouraged to apply.

You will be located at the Garscube Campus in the recently completed Sir Michael Stoker Research Building. The University of Glasgow was established in 1451 and is one of oldest and most successful research and teaching organisations in the world. Glasgow itself is Scotland's largest city, third largest in the UK, and offers a vibrant and friendly place to live. We are close to the Scottish Highlands, and Glasgow international Airport is very well connected and only eight miles from the city centre. International applicants are welcome.

The position is funded until 31 March 2021 in the first instance. Please email informal enquires to Prof David Robertson (david.l.robertson@glasgow.ac.uk).

Salary will be on the University's Research and Teaching Grade, level 6/7 depending on experience, 28,098 - 31,604/34,520 - 38,833 per annum.

Interested applicants should apply on-line at http://www.gla.ac.uk/explore/jobs/ and seek vacancy reference 018901 by 8 October 2017.

It is the University of Glasgow's mission to foster an inclusive climate, which ensures equality in our working, learning, research and teaching environment.

We strongly endorse the principles of Athena SWAN, including a supportive and flexible working environment, with commitment from all levels of the organisation in promoting gender equity.

The University of Glasgow, charity number SC004401.

– David Robertson

David.L.Robertson@glasgow.ac.uk

UIllinoisChicago Adaptation

ASSISTANT PROFESSOR BIOLOGY POSITION, GENE-ENVIRONMENT INTERACTIONS - University of Illinois at Chicago

The Department of Biological Sciences in the College of Liberal Arts & Sciences at the University of Illinois at Chicago (UIC) invites applications for a tenure-track position at the assistant professor level. Located in the heart of Chicago, UIC is one of the nation's leading research universities. Numerous opportunities exist for collaborative research in biological sciences across disciplines at UIC and with colleagues and institutions throughout the Chicago region. Final authorization of the position is subject to availability of funding.

We seek to hire a rising star who investigates the genetic mechanisms underlying short-term ecological and/or long-term evolutionary responses of organisms to their environment. The ideal candidate will study evolutionary, ecological, and/or community processes using bioinformatic or genomic approaches, which might include, but are not limited to, metagenomics, transcriptomics, or comparative genomics. Research expertise might encompass any level of biological hierarchy, ecological scale, or organismal group. Successful candidates will be expected to establish a vigorous, externally funded research program. Commitment to teaching excellence in the graduate and undergraduate programs is expected.

The successful candidate will join an interdisciplinary scientific community on the UIC campus and the Chicago area, as a member of a diverse department investigating a broad range of areas in biology, supported by excellent facilities and resources. Resources include outstanding core facilities for high performance computing, high-throughput DNA/RNA sequencing, imaging, mass spectrometry, flow cytometry, structural analyses, and automated screening.

Candidates must have a Ph.D. degree, with postdoctoral experience and a demonstrated record of research accomplishments. Ability to teach microbiology is preferred.

To receive full consideration, candidates must complete an on-line application, including the names and email addresses of three references, and submit a CV and statements of research and teaching interests, at https://jobs.uic.edu/job-board/job-details?jobID=86338&job=assistant-pr ofessor-gene-environment-interactions-biological-sciences by October 20, 2017. Questions should be directed to Jacquelyn DeLaurentis at jdelaur@uic.edu.

The University of Illinois at Chicago is an affirmative action, equal opportunity employer, dedicated to the goal of building a culturally diverse and pluralistic faculty and staff committed to teaching and working in a multicultural environment. We strongly encourage applications from women, minorities, individuals with disabilities and covered veterans. The University of Illinois may conduct background checks on all job candidates upon acceptance of a contingent offer. Background checks will be performed in compliance with the Fair Credit Reporting Act.

Thank you,

Jacquelyn DeLaurentis

Human Resource Associate

University of Illinois at Chicago

Department of Biological Sciences

845 W Taylor St, Room 3238 (M/C 066)

Chicago, IL 60607

(312) 996-2213| Fax:(312)413-3277

jdelaur@uic.edu

"DeLaurentis, Jacquelyn Marie" <jdelaur@uic.edu>

UKansas ComputationalEvolutionaryBiology

The Center for Computational Biology (Computational Biology Program) and the Department of Ecology and Evolutionary Biology invite applications for an assistant professor, tenure-track faculty position to begin as early as August 18, 2018. The interdisciplinary Center for Computational Biology (http://compbio.ku.edu) seeks to leverage and complement existing strengths in the Department of Ecology and Evolutionary Biology (http://eeb.ku.edu) by recruiting in the area of computational evolutionary biology. The Center fosters international activities in Computational Biology and combines outstanding research and a Ph.D. program. The Department of Ecology and Evolutionary Biology has research foci in Ecology and Global Change Biology, Evolutionary Mechanisms, and Biodiversity and Macroevolution. Its graduate program includes students seeking Masters or Ph.D. degrees.

The University of Kansas is especially interested in hiring faculty members who can contribute to the climate of diversity in the College of Liberal Arts and Sciences and four key campus-wide strategic initiatives: (1) Sustaining the Planet, Powering the World; (2) Promoting Well-Being, Finding Cures; (3) Building Communities, Expanding Opportunities; and (4) Harnessing Information, Multiplying Knowledge. For more information, see http://www.provost.ku.edu/planning/themes/ .

Required Qualifications: Ph.D. in a discipline related to Computational Evolutionary Biology is expected by the start date of the appointment; potential for excellence in research in Computational Evolutionary Biology; demonstrated commitment to teaching life sciences courses; and a strong record of research accomplishments in the area of computational evolutionary biology, broadly construed, including but not limited to molecular evolution, evolution of interaction networks, microbial evolution, and the evolution of protein structure and/or function. To apply online, go to https://employment.ku.edu/-academic/10107BR . A complete online application includes the following materials: curriculum vitae; letter of application, statement of teaching interests, research plan, and the names, e-mail, and contact information for three professional references. Initial review of applications will begin November 14, 2017 and will continue as long as needed to identify a qualified pool. Direct inquiries to Drs. Mark Holder (mtholder@ku.edu) or Christian Ray (jjray@ku.edu). The successful candidate for the position must be eligible to work in the U.S. prior to the start of the position.

The University of Kansas prohibits discrimination on the basis of race, color, ethnicity, religion, sex, national origin, age, ancestry, disability, status as a veteran, sexual orientation, marital status, parental status, retaliation, gender identity, gender expression and genetic information in the University's programs and activities. The following person has been designated to handle inquiries regarding the non-discrimination policies and is the University's Title IX Coordinator: the Executive Director of the Office of Institutional Opportunity and Access, IOA@ku.edu, 1246 W. Campus Road, Room 153A, Lawrence, KS, 66045, (785)864-6414 <(785)%20864-6414>, 711 TTY.

Sincerely, Mark Holder

– Mark T. Holder

mtholder@ku.edu http://phylo.bio.ku.edu/mark-holder Associate Professor Dept. Ecology and Evolutionary Biology and the Biodiversity Institute Univ. Kansas

"Mark T. Holder" <mtholder@ku.edu>

UKansas ResAssist EvolutionaryGenentics

The Department of Molecular Biosciences, University of Kansas, seeks an assistant researcher with interests and experience in molecular biology and Drosophila husbandry. The successful candidate will work with a research group that addresses the broad themes of host-pathogen interaction and genetic conflict using Drosophila. This position consists of an initial 2-yr appointment beginning in early-November 2017. The applicant should be extremely organized, work well with others, have a willingness to learn, and be able to participate at many levels in the laboratory. Required qualifications include a B.S. in Biology or closely related field and experience with molecular biological techniques as evidenced by application material.

For a complete announcement and to apply online, go to https://employment.ku.edu/staff/9969BR. A complete online application includes the following materials: CV, Cover letter, contact information for two reference letters. Initial review of applications begins 10/01/17 and will continue as long as required to identify a qualified pool.

The University of Kansas prohibits discrimination on the basis of race, color, ethnicity, religion, sex, national origin, age, ancestry, disability status as a veteran, sexual orientation, marital status, parental status, 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

ULouisiana Lafayette EvoDevo

University of Louisiana at Lafayette

Assistant Professor in Developmental Biology

The Department of Biology (*http://biology.louisiana.edu* < http://biology.louisiana.edu/ >) at the University of Louisiana at Lafayette seeks to fill a tenure-track position at the *Assistant Professor *level. We are searching for an outstanding scientist who studies the genetic regulation or evolution of developmental processes.

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: *Development.search@louisiana.edu <Development.search@louisiana.edu>*. To ensure full consideration, applications should be received by October 20, 2017.

The University of Louisiana at Lafayette is a public research university with High Research Activity and accreditation from the Southern Association of Colleges and Schools Commission on Colleges. With an enrollment of over 18,000 students and more than 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 masterâ euro s degree in 28 disciplines, and the doctorate in 10 disciplines. UL Lafayette was ranked in the top 20% for total R&D expenditures in the biological sciences in the United States by the National Science Foundation (2015 Herd Data Report). The Brookings Institution recently ranked UL Lafayette 9th for promoting social mobility among four-year public universities in the United States. Further information about UL Lafayette is available on the University's webpage at http://louisiana.edu . The UL Lafayette Department of Biology is one of the largest biology programs on the Gulf Coast, with about 30 faculty members, 70 graduate students, and 900 undergraduate students. Support for research includes a mouse vivarium, aquatics labs, departmental vehicles, green houses, DNA sequencers and other shared instrumentation, the Ecology Center < http://ecology.louisiana.edu/ >, Microscopy Center < http://microscope.louisiana.edu/index.shtml >, and New Iberia Research Center < http://nirc.louisiana.edu/about-us > (a primate facility), and Louisiana Universities Marine Consortium (LUMCON < https://lumcon.edu/ >) marine lab. Opportunities for collaboration are available within the Department, and with personnel at university affiliated centers and two federal research centers (the USGS Wetland and Aquatic Research Center < https://www.usgs.gov/centers/wetland-and-aquatic-research-center-warc > and the NOAA Estuarine Habitats and Coastal Fisheries Center < http://www.galvestonlab.sefsc.noaa.gov/research/fishery_ecology/wetlandrestoration/index.html >) located in the University's Research Park.

The University of Louisiana at Lafayette is an EEO/AA employer and is dedicated to the goal of building a diverse faculty committed to teaching and working in a multicultural environment. Women, minorities, and individuals with disabilities are strongly encouraged to apply.

Paul Leberg <Leberg@louisiana.edu>

ULouisiana Lafayette PopGenetics

University of Louisiana at Lafayette

Assistant Professor in Population Genetics

The Department of Biology (http://-biology.louisiana.edu) at the University of Louisiana at Lafayette seeks to fill a tenure-track position at the Assistant Professor level. We are searching for an outstanding scientist who studies population genetics. Although we are especially interested in applicants that have a record of utilizing genome-scale datasets in animal or plant systems, researchers studying all aspects of population genetics are 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 (particularly courses in population genetics and genetics) 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: Genetics.search@Louisiana.edu. To ensure full consideration, applications should be received by October 20, 2017.

The University of Louisiana at Lafayette is a public research university with High Research Activity and accreditation from the Southern Association of Colleges and Schools Commission on Colleges. With an enrollment of over 18,000 students and more than 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. UL Lafayette was ranked in the top 20% for total R&D expenditures in the biological sciences in the United States by the National Science Foundation (2015 Herd Data Report). The Brookings Institution recently ranked UL Lafayette 9th for promoting social mobility among four-year public universities in the United States. Further information about UL Lafayette is available on the University's webpage at http://louisiana.edu . The UL Lafayette Department of Biology is one of the largest biology programs on the Gulf Coast, with about 30 faculty members, 70 graduate students, and more than 900 undergraduate students. Support for research includes a mouse vivarium, aquatics labs, departmental vehicles, green houses, DNA sequencers and other shared instrumentation, the Ecology Center, Microscopy Center, and New Iberia Research Center (a primate facility), and Louisiana Universities Marine Consortium (LUMCON) marine lab. Opportunities for collaboration are available within the Department, and with personnel at university affiliated centers and two federal research centers (the USGS Wetland and Aquatic Research Center and the NOAA Estuarine Habitats and Coastal Fisheries Center) located in the University's Research Park.

The University of Louisiana at Lafayette is an EEO/AA employer and is dedicated to the goal of building a diverse faculty committed to teaching and working in a multicultural environment. Women, minorities, and individuals with disabilities are strongly encouraged to apply.

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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.

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Scott C France <france@louisiana.edu>

UMassachusetts Lowell EvolutionaryBiol

General Summary of Position:

The University of Massachusetts Lowell Department of Biological Sciences invites applications to fill a full-time tenure-track faculty position, at the Assistant or Associate Professor level, to start September 2018. We have recently built a state-of-the-art aquatics facility and are interested in candidates using zebrafish or small aquatic animals as a model organism in their research.

The ideal candidate's research focus should complement and leverage existing departmental and campus strengths. In addition to the broad range of research interests within the Biological Sciences Department, UMass Lowell has a diverse group of science and engineering faculty who use multiple model systems to evaluate new technologies (e.g. nanomedicine, biomaterials, robotics and tissue engineering) including an anticipated hire in the Chemistry department focusing on the biochemistry of muscle proteins. Candidates interested in establishing collaborations with faculty in these fields are therefore encouraged to apply.

The successful candidate will be expected to establish a vigorous, externally funded research program, and contribute to the department's teaching mission. Teaching responsibilities may include the development of undergraduate courses, in addition to upper-level and graduate courses.

The University of Massachusetts Lowell is located in the heart of the life sciences supercluster of the northeast region of Massachusetts, which is home to more than 100 life science companies. Together with its proximity to the Boston/Cambridge biotechnology and biomedical hub, there are ample opportunities for scientific interaction, exchange, and collaboration.

Minimum Qualifications (Required): - Earned doctorate and postdoctoral experience (required at the time of application) - The ability to work effectively with diverse groups

Additional Considerations: - Demonstrated teaching ability at the undergraduate and/or graduate levels - Potential to establish a sustainable externally funded research program - Demonstrated publication record in scholarly journals - Excellent communication and interpersonal skills - Demonstrated ability to work with diverse student and faculty populations - The ability to work effectively with diverse groups

Special Instructions to Applicants:

Please submit a CV, cover letter, teaching philosophy and research statement. * Names and email addresses of three references will also be required during the application process. The references will be notified and should upload recommendation letters. Only recommendation letters that are uploaded to the system by the referee will be accepted. Emailed or hardcopy letters will not be accepted.

For full consideration, please apply by 27th Sept. 2017. Add is at: https://www.higheredjobs.com/search/details.cfm?JobCode=176546130&Title=Assistant%2FAssociate%20Professor%20%2D%20Biological%20Sciences

Nicolai Konow <Nicolai_konow@uml.edu>

UNevada Reno EvolutionaryBiology

The Department of Biology at the Universty of Nevada Reno invites applications for a tenure-track Assistant Professor position in Evolutionary Biology. We seek an outstanding scientist who will enhance and complement existing strengths in evolutionary biology in our department. We welcome applications from all candidates working on cutting edge questions in evolutionary biology using animal (both vertebrate and invertebrate), plant, or microbial systems. Candidates working in any area of evolutionary biology will be given full consideration. Potential areas of interest include but are not limited to: (1) Population, functional, evolutionary, or phylo- genomics, (2) Evolutionary physiology, (3) Evolutionary developmental biology, (4) Experimental or theoretical evolution. Competitive start-up and outstanding compensation and benefits packages are offered. Candidates must have a Ph.D. and will be expected to establish an extramurally funded research program, train graduate students, and actively participate in undergraduate science education.

The Department of Biology is one of the premier teaching and research units on campus, spanning a wide range of life sciences. Departmental strengths include plant-animal interactions, community and physiological ecology, animal behavior and genomics as well as developmental neurobiology and neurogenetics. Excellent core facilities on campus include proteomics, genomics, microscopy, bioinformatics, flow cytometry, tissue culture, transgenic and animal care. The successful candidate will expand and complement departmental research and contribute to collaborations with other biological sciences faculty across campus.

The University of Nevada, Reno has a growing and increasingly diverse student population of approximately 21,000, including over 2,800 graduate students. The city of Reno offers an excellent quality of life, with entertainment and cultural opportunities in excess of most cities of similar size. The city lies one hour from Lake Tahoe and four hours east of San Francisco in the valley of the Truckee River on the eastern slope of the Sierra Nevada, and has a mild high desert climate. A highly rated location for living and outdoor recreation, the Reno area also enjoys a flourishing and diverse intellectual, artistic, and cultural community.

The University of Nevada, Reno recognizes that diversity promotes excellence in education and research. We are an inclusive and engaged community and recognize the added value that students, faculty, and staff from different backgrounds bring to the educational experience.

Required qualifications: - PhD degree in any area of biology or related field

Preferred qualifications: Candidates with postdoctoral research experience; a strong publication record; potential for strong teaching skills; expertise that complements and expands the research capacity of the department; and the potential to develop nationally-competitive research program are desirable.

Contact information for this position: Sharee Williams (775) 682-8795 shareew@unr.edu

The following materials must be submitted with your application: - Resume/CV - Cover letter - Statement of research and plans - Statement of teaching philopsohy - Contact information for three professional references

Application deadline: 10/31/2017

More information here: https://www.unrsearch.com/-postings/25915 – David Alvarez-Ponce, PhD Assistant Professor Department of Biology University of Nevada, Reno Max Fleischmann Agriculture Building, office 140B Tel.: (775) 682-5735 www.genomeevol.wordpress.com david.alvarez.ponce@gmail.com

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UNorthCarolina Charlotte ResAssoc MicrobialGenomics

University of North Carolina Charlotte Research Associate - Microbial Genomics

The Department of Bioinformatics and Genomics at University of North Carolina in Charlotte (bioinformatics.uncc.edu) invites applications for a one-year research associate in microbial genomics in the Sung Laboratory at UNCC.

The successful candidate will be expected to perform research study and conduct laboratory experiments on research projects within well-defined guidelines. The candidate is responsible for maintaining the efficient operation of the laboratory; assists the principal investigator with summation, analysis, and organization of data for publication; may assist with preparation of grant applications; assists and/or teaches graduate students and others rotating through the lab; and assists in supervision and training of junior research personnel. teach both graduate and undergraduate microbiology courses.

Required qualifications are an earned Ph.D. in Microbiology, Molecular Biology, Evolutionary, Computational Biology, Computer Science or related areas , and a record of peer-reviewed publications. Preferred qualifications include postdoctoral experience, strong bioinformatics skills, and research experience using third-generation PCR, microbiology, molecular and microbiological techniques, and BSL2/3 experience. Salary is dependent on experience. For full consideration, all application materials must be received by Sept. 30, 2017.

Interested applicants should submit the following materials: 1. CV, 2. Letter of interest, 3. unofficial transcripts, 4. contact information of five people willing to serve as references.

Only applications submitted through the UNCC University website will be accepted and considered, https://jobs.uncc.edu/postings/18016. Questions about this position should be addressed to Way Sung, wsung@uncc.edu, (704) 687-5155, UNC Charlotte, 9201 University City Blvd, Charlotte, NC, 28223.

The University of North Carolina Charlotte is an Equal Opportunity/Affirmative Action employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability, gender identity, sexual orientation or protected veteran status.

Way Sung <wsung@uncc.edu>

UOklahoma Proteomics

Title of Position: Tenure Track Assistant Professor

Start Date: Fall 2018

The University of Oklahoma invites applicants for a tenure-track faculty position at the Assistant Professor level, as part of a multi-departmental cluster-hire initiative. The successful candidate, will be expected to establish a leading-edge research program using proteomics methods to address wide-ranging basic and translational research problems that bridge biological and anthropological sciences. Areas of research focus may include ecological and evolutionary research, basic biomedical science, host-microbiome dynamics, diet and metabolism, ancient biomolecules, or human biology. Strong consideration will also be given to candidates who complement and contribute to OU's Biology of Behavior initiative (www.ou.edu/bb/) integrating evolutionary, developmental, physiological and genetic mechanisms of behavior from the social to molecular levels.

This strategic cluster hire initiative expands upon the success of our highly collaborative team of researchers who are addressing critical questions in biological and anthropological sciences from diverse perspectives. These studies, which span the range from extant to prehistoric cultures, are helping to shape perspectives about cultural and evolutionary drivers of human biology, health and disease, as well as human-enviroment interactions on many scales. The successful candidate is expected to lead teams applying modern proteomic technologies, especially mass spectrometry tools, to better understand the intersection of biological and anthropological science. Strong candidates will bring novel perspectives to partners in the University's Laboratories of Molecular Anthropology and Microbiome Research (http://lmamr.org/), facilitated by access to cutting-edge equipment, including top of the line spectrometric instruments for proteomics.

The primary appointment will be within either the Department of Biology or the Department of Anthropology, depending on expertise. The ideal candidate will demonstrate a commitment to proteomics approaches to basic biology and to excellence in teaching at the undergraduate and graduate levels (one course per semester in general courses and areas of expertise). Candidates must have earned a Ph.D. in biological science, anthropology or a closely related field (postdoctoral experience preferred) by the appointment start date. A review of applications will begin October 10, 2017 and continue until filled. The position will begin in August 2018.

The University of Oklahoma is a Carnegie-R1 comprehensive public research university known for excellence in teaching, research, and community engagement. The institution serves the educational, cultural, economic, and health-care needs of the state, region, and nation from three campuses: Norman, Health Sciences Center in Oklahoma City, and Tulsa Schusterman Center. The University of Oklahoma enrolls over 30,000 students and has more than 2,700 full-time faculty members in 21 colleges. The 277-acre Research Campus in Norman was named the number one research campus in the nation by the Association of Research Parks in 2013. Norman is a culturally rich and vibrant community located just outside of Oklahoma City. With outstanding schools, amenities, and a low cost of living, Norman is often cited in "best places to live" rankings. The greater Oklahoma City metropolitan area has a population of over 1.25 million residents and offers all of the culture, dining, entertainment, and amenities typical of a modern metropolis.

Interested individuals should post the following at http://apply.interfolio.com/44555 : 1) a cover letter describing their interest in this position, 2) a full curriculum vita, 3) a description of research accomplishments and future research plans as they relate to this focused search (6-page limit), and 4) a statement of teaching experience and interests. Candidates should request three letters of recommendation, to be uploaded to http://apply.interfolio.com/44555 The University of Oklahoma, in compliance with all applicable federal and state laws and regulations does not discriminate on the basis of race, color, national origin, sex, sexual orientation, genetic information, gender identity, gender expression, age, religion, disability, political beliefs, or status as a veteran in any of its policies, practices, or procedures. This includes, but is not limited to: admissions, employment, financial aid, and educational services. Women, minorities, protected veterans, and individuals with disabilities are strongly encouraged to apply.

"cmlewis@ou.edu" <cmlewis@ou.edu>

UOtago BioinformaticsTech

Bioinformatician

Department of Zoology, University of Otago, New Zealand

Job ID: 1701603

The Role

We are seeking a motivated person with advanced experience in bioinformatics to provide support for a range of research projects, including:

* Understanding the genomic basis of flight loss in New Zealand's alpine stoneflies.

* Inbreeding depression (hatching success and sperm abnormalities) in the Kakapo using whole genomes from all living birds.

* How parental challenges (hypoxia, toxins, social isolation) affect DNA methylation and offspring gene expression patterns in zebrafish.

* Using RNA-Seq to understand how gene expression corresponds to aggressive behaviour within and between colonies of social wasps.

* Community diversity metrics from amplicon sequencing data of bacterial nitrogenase genes (nifH) in different soil habitats.

This role will involve the use of existing bioinformatics software, analysis pipeline development, and training and supervising students and staff to promote bioinformatics capabilities within the departments of the Division of Sciences.

The person appointed to this position will be able to show initiative and have strong attention to detail whilst responding to a broad range of academic demands. The position requires a highly organised person who has a genuine interest in the application of bioinformatics to contemporary science and excellent communication and interpersonal skills, as well as being a team player and a problem-solver. Otago employs bioinformaticians in several departments, thus the successful candidate will also be expected to maintain relationships with bioinformaticians outside of the Division of Sciences departments.

Your Skills and Experience

* MSc degree minimum in Bioinformatics or a related discipline.

* Significant bioinformatic experience and a strong interest in Biological Sciences.

* Familiarity with Linux shell scripting and analysis pipeline development.

Further Details

This is a full-time, fixed term position for three years and is available from 1 October 2017.

For further information about the position, the Department, and to apply, see:

https://otago.taleo.net/careersection/2/-jobdetail.ftl?lang=en&job=1701603 ??

Specific enquiries may be directed to Associate Professor Bruce Robertson, Department of Zoology, bruce.robertson@otago.ac.nz

Applications quoting reference number 1701603 will close on Sunday, 24 September 2017.

sheri.johnson@otago.ac.nz

URhodeIsland Tech EvolutionMarinePlankton

Job opportunity in the Rynearson lab at the University of Rhode Island Graduate School of Oceanography (https://web.uri.edu/rynearson-lab/) to work on marine plankton and global change biology.

For full details on the position and application process please see: https://jobs.uri.edu/postings/2742 Tatiana Rynearson Professor Graduate School of Oceanography University of Rhode Island, Bay Campus South Ferry Road Narragansett, RI 02882-1197 Phone (401)874-6022 http://www.gso.uri.edu/rynearson-lab/ "T. Rynearson" <rynearson@uri.edu>

UTennessee 1yrTeacherEvolution

Institution: University of Tennessee, Knoxville Location: Knoxville, Tennessee Position: Botanical Education and Greenhouse Support The Division of Biology and Department of Ecology and Evolutionary Biology 12-month position

Description: The Division of Biology and the Department of Ecology and Evolutionary Biology (EEB) jointly seek a full-time Lecturer to support the Director of Biology Teaching and Learning and the EEB Greenhouse Manager. This position is a 50/50 split between these two units. The primary supervisor would be the Director of Teaching and Learning, currently Dr. Beth Schussler.

For the Division, this position will oversee the Introductory Botany lab course (Biology 115-offered in fall and spring). This includes preparing all materials for the labs, purchasing and maintaining course supplies, training and supporting the graduate student instructors of the labs, and revising the curriculum as needed. Growing and maintaining plants in the greenhouse for the botany lab is a necessary role.

This position will also assist with maintenance of the greenhouse facilities, plant collections, and outdoor gardens under EEB and Division care. This work will be done under the supervision of Greenhouse Manager Jeff

Martin. Duties include running the greenhouse equipment, watering, insect and disease scouting, and plant care. Supervising student workers is part of the required duties. This position will also grow and provide plant materials needed for instructional purposes in other Division courses.

Qualifications: Minimum of a Master's degree and 18 hours coursework in botany or plant sciences required. Introductory botany teaching experience (especially as a GTA), and prior work in a greenhouse preferred.

Interested individuals should send a cover letter and CV electronically to Dr. Beth Schussler (eschussl@utk.edu).

"Kalisz, Susan" <skalisz@utk.edu>

UTexas Arlington EvolutionEcol

The Department of Biology at the University of Texas at Arlington (http://www.uta.edu/biology/) invites applications for a tenure-track faculty position in Ecology (broadly defined) at the level of Assistant Professor. Research areas of interest include fundamental questions related to global change biology and/or ecological genomics. Candidates who use computational and/or genomic approaches to understand the ecological, developmental, physiological, genetic, and/or epigenetic mechanisms underlying responses to environmental changes are particularly attractive. Successful candidates will have a doctoral degree in a relevant field and will be expected to develop a nationally recognized, extramurally funded research program, as well as teach at the undergraduate and graduate (Master's and Ph.D.) levels. Start-up funds, salaries, and teaching loads are highly competitive. We are deeply committed to increasing diversity and especially encourage applications from women and minority scholars.

The Department and University have numerous resources including state-of-the-art labs, an Animal Care Facility, a Biology Genomics Core Facility, a Center for Human Genomics, and an Amphibian and Reptile Diversity Research Center housing specimen and tissue collections, and affiliations with the Botanical Research Institute of Texas (BRIT). The UT Arlington campus also houses the newly established North Texas Genome Center, and the Shimadzu Institute for Research Technologies (a major partnership between UT Arlington and Shimadzu Scientific Instruments) that offers extensive resources for advanced 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. Excellent opportunities exist at UT Arlington and in the Dallas-Fort Worth Metroplex for collaborations with researchers in ecology, evolution, genomics, biochemistry, and biomedical sciences.

The University of Texas at Arlington is a Carnegie Research-1 "highest research activity" institution. With a projected global enrollment of over 58,000 in AY 2016-17, UTA is rapidly becoming largest institution in The University of Texas System. Guided by its Strategic Plan Bold Solutions | Global Impact, UTA fosters interdisciplinary research and teaching to enable the sustainable megacity of the future within four broad themes: health and the human condition, sustainable urban communities, global environmental impact, and data-driven discovery. UTA was cited by U.S. News & World Report as having the second lowest average student debt among U.S. universities. U.S. News & World Report also ranks UTA fifth in the nation for undergraduate diversity. The University is a Hispanic-Serving Institution and is ranked as the top four-year college in Texas for veterans on Military Times' 2017 Best for Vets list.

Review of applications will begin immediately and continue until the position is filled. For full consideration, applications should be submitted by October 1. Applicants must apply online at http://uta.peopleadmin.com/postings/3777. Applicants should include in their application: 1) curriculum vitae, 2) summary of current and proposed research (three pages), 3) teaching interests, and 4) names and email addresses of four references. A criminal background check will be conducted on finalists.

As an equal employment opportunity and affirmative action employer, it is the policy of The University of Texas at Arlington to promote and ensure equal employment opportunity for all individuals without regard to race, color, religion, sex, national origin, age, sexual orientation, gender identity, disability, or veteran status.

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>

UTexas Austin 3 Biodiversity

UT Austin Cluster Hire in Integrative Biology

The Department of Integrative Biology at The University of Texas at Austin is initiating a cluster hire in support of our new Biodiversity Center. We are searching for three new faculty colleagues, two at the level of Assistant Professor and one at open rank.

Qualifications

Open Rank in Ecology: The University of Texas at Austin is expanding from our original search at (https://apply.interfolio.com/43206) to also include a search for a tenured or tenure-track faculty position at the open rank level in the Department of Integrative Biology, in the area of ecology, broadly defined. Candidates should have a record of research that demonstrates originality in addressing fundamental topics in ecology, such as interactions across trophic levels, plant interactions with symbionts, herbivores, or mutualists, and/or the impacts of global change drivers on ecological interactions.

*Assistant Professor in Integrative Biology: *The University of Texas at Austin invites applications for a tenure-track faculty position at the Assistant Professor level in the Department of Integrative Biology. We wish to hire an exceptional candidate whose research focuses broadly on working on fundamental topics in behavior, evolution, and/or ecology. We especially encourage applicants that take an integrative approach to animal behavior, and will consider excellent applicants in any area. Study systems can include species or communities of any group of organisms. A PhD or equivalent is required at the time of appointment.

We are a vibrant and inclusive community, and we seek candidates who are interested in contributing to diversity and equal opportunity within higher education.

*Application Instructions *

Open Rank in Ecology Apply: https://apply.interfolio.com/45062 Assistant Professor in Integrative Biology Apply: https://apply.interfolio.com/44983 Applicants should submit the following items via Interfolio: i) a cover letter with contact information (ii) a CV, (iii) a research statement, (iv) a teaching statement, (v) up to 5 reprints/preprints, and (vi) names of three individuals who will write letters of recommendation. Note that letters are not required for initial consideration; candidates will be notified if letters are needed. Applications received prior to October 31, 2017 will be assured of full consideration. For additional information about the department, see https://integrativebio.utexas.edu . *The University of Texas at Austin, as an Equal Opportunity/Affirmative Action Employer, complies with all applicable federal and state laws regarding nondiscrimination and affirmative action. The University is committed to a policy of equal opportunity for all persons and does not discriminate on the basis of race, color, national origin, age, marital status, sex, sexual orientation, gender identity, gender expression, disability, religion, or veteran status in employment, educational programs and activities, and admissions.*

“cfarrior@utexas.edu” <cfarrior@utexas.edu>

UTexas SanAntonio PrimateConservation

The University of Texas at San Antonio Department of Anthropology seeks to hire a Biological Anthropologist at the level of Assistant Professor. We seek a theoretically motivated scholar with a research focus on primate conservation who has a track record of external funding and publications and preferably an established field research site. Research interests could include, but are not limited to: biogeography, human-primate interaction, macroecology, ethnoprimatology, and conservation strategies and policies. We are interested in a scholar whose research complements existing faculty, will help build our BA, MA, and PhD programs, and demonstrates an openness to interdisciplinary collaboration and the ability to engage cross-campus linkages.

Required Qualifications: PhD in Anthropology or Human Evolutionary Biology in-hand by time of appointment; theoretically motivated research; desire and ability to contribute to growth and excellence of a PhD program broadly engaging ecology and environmental issues; desire and ability to educate and mentor students with either academic or applied career goals; and successful granting and publication records.

Preferred Qualifications: Excellence in teaching; strong record of external funding; fluency across a broad spectrum of theory in anthropology and biology; laboratory and/or field/laboratory integrated methods; strong quantitative background; commitment to multidisciplinary anthropology; interests that complement existing faculty; potential to contribute to interdisciplinary areas of collaborative excellence; and record of service appropriate to the rank of Assistant Professor.

Responsibilities include: Maintaining an active research program; teaching introductory courses in general anthropology and biological anthropology, elective undergraduate courses, and graduate courses in areas of specialization; mentoring graduate students in the department's MA and PhD programs; department and college service.

Applicants must submit: 1) Letter of application that includes research, teaching, and service goals; 2) a CV; 3) sample publications; 4) teaching evaluations if available; and 5) the names, addresses, emails, and phone numbers of three references. Materials must be submitted on-line via https://jobs.utsa.edu/ no later than October 16, 2017. Please reference posting TT20170004P.

The University of Texas at San Antonio is an affirmative action, equal opportunity employer. Minorities, women, veterans, and individuals with disabilities are encouraged to apply. Applicants who are selected to interview must be able to show proof that they are eligible and qualified to work in the United States.

Luca Pozzi, PhD

Assistant Professor Department of Anthropology University of Texas at San Antonio One UTSA Circle San Antonio, TX 78249

email: luca.pozzi@utsa.edu website: www.lucapozzi.me phone: 210.458.7558 follow me @LPozzi81

lucapozzi.ml@gmail.com

UToronto 2 EEB Professorships

ECOLOGY AND EVOLUTION - Two Assistant Professorships

The Department of Ecology and Evolutionary Biology at the University of Toronto invites applications for two tenure-stream appointments in ecology and evolution. These appointments will be at the rank of Assistant Professor, with an expected start date of July 1, 2018.

We seek candidates who conduct conceptually driven research in ecology and evolution, especially those with research programs in disease and/or theory. We seek applications from candidates whose research program complements the research programs of the highly collaborative faculty currently in the department.

The successful applicants must have a PhD in a related field by July 1, 2018 or soon thereafter, with a record of sustained publications in top-ranked, field-relevant journals. The appointees will be expected to build an active, externally funded and internationally recognized research program. The successful candidates will also demonstrate excellence in teaching and contributions to the education and training of undergraduate and graduate students. Evidence of demonstrated excellence in research and teaching should be documented through the applicant's CV, publications, research and teaching statements, strong letters of reference from referees of high standing and where appropriate, course evaluations.

The University of Toronto is a leading academic institution 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 Science, Dalla Lana School of Public Health, the School of the Environment, the University network of leading academic research hospitals (www.uhn.ca, sunnybrook.ca/) and research groups with provincial and federal government agencies. The University owns a nearby field station dedicated to ecological research (the Koffler Scientific Reserve; www.ksr.utoronto.ca). Toronto is a vibrant and cosmopolitan city, one of the most desirable in the world in which to work and live.

Salary to be commensurate with qualifications and experience.

All qualified candidates are invited to apply online.

https://utoronto.taleo.net/careersection/10050/-jobdetail.ftl?job=322321 Applications must include a CV and statements of research and teaching interests combined into a single PDF file, plus three representative publications. Applicants should arrange to have three confidential letters of recommendation (signed and on letterhead) sent directly to: Professor Donald Jackson, Chair of Search Committee, Department of Ecology and Evolutionary Biology, 25 Willcocks Street, University of Toronto, Toronto, Ontario, M5S 3B2 Canada. Letters of reference may be e-mailed to chairsec.eeb@utoronto.ca. Deadline for receipt of applications, including reference letters, is September 13, 2017.

For further information on the Department of Ecology and Evolutionary Biology, please visit our website at www.eeb.utoronto.ca. Questions regarding this position can be directed to Liz Rentzelos at chairsec.eeb@utoronto.ca or (416-946-3340).

The University of Toronto is strongly committed to diversity within its community and especially welcomes applications from racialized persons / persons of colour, women, Indigenous / Aboriginal People of North America, persons with disabilities, LGBTQ persons, and others who may contribute to the further diversification of ideas. As part of your application, you will be asked to complete a brief Diversity Survey. This survey is voluntary. Any information directly related to you is confidential and cannot be accessed by search committees or human resources staff. Results will be aggregated for institutional planning purposes. For more information, please see http://uoft.me/UP. All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority.

< http://mahlerlab.com/ >

Luke Mahler <luke.mahler@utoronto.ca>

UWisconsin Milwaukee ResAssist GeneticSelectionKelp

Research Assistant position

The Department of Biological Sciences at the University of Wisconsin-Milwaukee (UWM) is currently accepting application submissions for a research intern position in Dr. Filipe Alberto's laboratory, studying genetic improvement for aquaculture of the giant kelp Macrocystis pyrifera.

A research intern position to conduct the development of a germplasm collection of haploid strains of kelp (brown algae) is available in the Alberto lab at UW-Milwaukee, US. The collection will be the basis for a genetic improvement program aimed at faster growth and temperature and low nutrient tolerance in aquaculture. The project will require setting a large number of individual gametophyte cultures, medium preparation, environmental chamber work, excellent organizational skills and capacity to work under strict deadlines. Individual haploid cultures will have their biomass bulked up to provide sufficient biomass to extract DNA in quantity and quality required for genomic analysis and allow strain crossing. A post-doctoral researcher will work closely with the research intern and the PI to achieve the project goals. Experience in population genomics lab techniques is a plus. Microsatellite marker analysis will also be used to monitor strain identity and culture purity at different stages of growth. The germplasm collection will be at the basis of a Marker Assisted Selection program developed with partner institutions (UC Santa Barbara, U Southern California and JCVI) involving genome sequencing and annotation, phenotype typing of outplanted sporophytes in Southern California, capture sequencing of genetic variants (SNP) and the estimation of a predictive model linking genotype and phenotype for traits of interest.

Applicants are required to have a Bachelor of Sciences in Biological Sciences, or equivalent degree. Research experience in breeding experiments, seaweed biology and seaweed cultivation are preferred. Familiarity with population genetics software is a plus. Computer skills in data analysis and biostatistics are also important merits.

Other broad research interests in the Alberto lab are population genetics and evolutionary ecology of seaweeds and marine plants. Our focus is both on empirical research through the acquisition of population genetics data, using molecular marker techniques, and simulation based hypothesis testing.

Informal inquiries about the project are encouraged. Please apply by sending a single pdf document including 1) CV, 2) a declaration of research interests, 3) previous experience and fit for the position and 4) the email address and telephone number of potential contacts for reference letters.

Applications should be emailed to Dr. Filipe Alberto, alberto<mailto:albertof@uwm.edu>f(at) <mailto:albertof@uwm.edu>uwm.edu <mailto:albertof@uwm.edu>. Initial contract will be for one year with possible extension to three years. Benefits information can be found at: http://uwm.edu/hr/home/benefits/new-employee-benefits/ Review of applications starts on the 16th of September, 2017, and will continue until position is filled. The position is expected to start January 2018.

UWM is an AA/EEO employer.

For more information about the lab see: http://alberto-lab.blogspot.com/ . UWM has an active group of researchers studying evolutionary ecology and behavior:

https://uwm.edu/biology/research/ecology-evolution-and-behavior/ Filipe Alberto Associate Professor

Dept. of Biological Sciences University of Wisconsin - Milwaukee 3209 N. Maryland Ave. Milwaukee, WI 53211

URL: http://alberto-lab.blogspot.com/ Email: albertof@uwm.edu Tel: 414-229-6343

Filipe Aos Alberto <albertof@uwm.edu>

UWitwatersrand 5yr Palaeontology

Vacancy: Researcher/Senior Researcher - Palaeobotanist/Palynologist

Closing Date: 28 September 2017

Position: The Evolutionary Studies Institute invites suitably qualified and experienced applicants to apply for the position of Senior Researcher for a five-year contract, potentially renewable for an additional five years if funding is available.

Requirements: The Institute is looking for a dynamic candidate with a PhD in Palaeontology, Palaeobotany or similar with expertise in past environments, past climates, past vegetation, palynology or micropalaeontology, to complement the existing research strengths of the Institute. The successful candidate will have an excellent research track record, well established international collaborations, and publications in high impact journals. Teaching experience in palaeobotany, palynology, or palaeoenvironments; experience in fieldwork, postgraduate student supervision, media communication and outreach, and ability to raise research funding are important.

Key responsibilities: The incumbent is expected to establish an active field-based research programme, including supervision of postgraduate students, make regular contributions to scientific meetings and publish work in internationally accredited scientific journals. The incumbent will be required to teach specialist courses at undergraduate and Honours levels in palaeobotany, palynology and related fields, and to lead appropriate field excursions.

Remuneration and conditions of service: A competitive university package with excellent benefits offered, commensurate with the level of appointment.

To apply, please submit a covering letter explicitly addressing the above, as well as a detailed Curriculum Vitae with names, addresses, contact numbers and e-mail addresses of 3 referees, and certified copies of qualifications, as well as a South African ID (Passport if not South African).

Informal inquires may be directed to Ms Bronwyn Quinn Bronwyn.quinn@wits.ac.za Evolutionary Studies Institute, University of the Witwatersrand. Tel: 011 717 6682.

External applicants are invited to apply, by registering their profile on the Wits i-recruitment platform located at https://irec.wits.ac.za and submitting their application. Page 2 of 2

Internal employees are invited to apply directly on Oracle by following the path: iWits /Self Service application/" Apply for a job".

The University is committed to employment equity. Preference may be given to appointable applicants from the underrepresented designated groups in terms of the relevant employment equity plans and policies of the University. The University retains the right not to make an appointment, to re-advertise and to verify all information provided by candidates.

Please note that correspondence will only be entered into with shortlisted candidates.

Prof Jonah Choiniere Reader Evolutionary Studies Institute University of the Witwatersrand 079 906 3169

Jonah Choiniere <Jonah.Choiniere@wits.ac.za>

VirginiaTech ChairBiological Sciences

Virginia Tech Department of Biological Sciences: Professor and Head

The Department of Biological Sciences, in the College of Science at Virginia Tech, invites applications from visionary, creative, and energetic leaders for the position of Department Head. We combine an international reputation for excellence in research with a substantial teaching mission. The department currently includes 47 tenure-track faculty members, two professors of practice, eight instructors, 25 support staff, and 23 research scientists, as well as more than 80 graduate students and 1300 undergraduate students. We are a diverse department with research groups in (1) ecology, evolution and behavior, (2) microbiology and immunology, and (3) molecular, cellular, developmental, and computational biology (http://www.biol.vt.edu). We play a central role in interdisciplinary research on campus, which includes engagement in Centers and Institutes such as the Global Change Center and Fralin Life Sciences Institute, and nine out of Virginia Tech's 14 Interdisciplinary Graduate Education Programs. Several faculty are associated with the Virginia Tech Carilion Research Institute, located adjacent to the VTC School of Medicine in Roanoke, Virginia.

The successful applicant will advocate for the research, teaching and service missions of the department at the local, national, and international level, and will focus on achieving strategic goals within the department, college and university. She or he will foster the health and growth of the department, provide mentorship and professional guidance for existing faculty, and promote diversity and inclusion. Potential candidates must have a Ph.D. in Biological Sciences or closely related fields, demonstrated administrative and programmatic leadership experience, a broad understanding of the life sciences and interdisciplinary research, and exceptional professional achievements as evidenced by outstanding publications and sustained extramural funding. We seek a leader with vision, an open and inclusive management style, and the ability to communicate effectively across disciplines and at all levels within the university. The appointment will be at the level of tenured Full Professor.

Interested candidates should submit a current CV, a letter of interest (maximum 3 pages) that describes research interests, relevant experience and leadership style, and a list of three professional references upon applying through www.jobs.vt.edu posting number TR0170112 or via the link: https://listings.jobs.vt.edu/postings/79650. Review of applications will begin on October 31, 2017 and will continue until the position is filled. Please address inquiries to Professor Jeffrey Walters, Search Chair (jrwalt@vt.edu; Department of Biological Sciences, Virginia Tech, Blacksburg, VA 24061, USA; 540-231-3847). If you are an individual with a disability and desire an accommodation, please contact Ms. Dreama Price (dreama@vt.edu). Virginia Tech does not discriminate against employees, students, or applicants on the basis of age, color, disability, gender, national origin, political affiliation, race, religion, sexual orientation, genetic information, veteran status, or any other basis protected by law. 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.

– Valerie Sutherland Program Support Technician Department of Biological Sciences 2125 Derring Hall (MC 0406) Blacksburg, VA 24061 (540) 231-3447

Valerie Sutherland <vsutherl@vt.edu>

YalePeabodyMuseum HeadBiodiversityInformaticsData

The Yale Peabody Museum of Natural History (YPM) and Yale University invite applications for a data scientist to help develop and advance the innovative use of informatics tools for the synthesis and utilization of biodiversity information in research and education. The YPM is among the oldest, largest, and most active university natural history museums in the world. The museum has a strong track record in specimen digitization and database efforts and in contributing to national biodiversity informatics initiatives. The university hosts a range of activities in biodiversity data science and global change, including the Max Planck Yale Center of Biodiversity Movement and Global Change and digital infrastructure projects addressing global phylogenies, remote sensing, and species distributions (Map of Life).

The Head of Biodiversity Informatics and Data Science is expected to support the development of an expanded vision for biodiversity- and specimen-based informatics that links the YPM scientific divisions and other university activities with the goal of developing national and international leadership roles in this arena. Responsibilities include: advancing the innovative use of informatics tools for the synthesis and utilization of biodiversity information in research and education; setting priorities and developing plans and initiatives related to Biodiversity Informatics and Data Science; partnering in the development of grant proposals for funding of informatics and data science projects; facilitating interdisciplinary collaborations and research programs at the museum, University, and national and international levels; serving as a liaison and/or representative of YPM and its partner projects.

We seek an outstanding applicant working in any area of ecology, evolution, or paleobiology, and with demonstrated informatics expertise and a passion for contributing to this vision. A record of outstanding achievement and a promising research program are more important than the specific scientific area. While developer skills (below) are required, we seek candidates with active research programs and a strong record in obtaining funding in this area.

We expect candidates to bring a range of skills spanning software and database development, and to specifically have the following qualifications: - Experience in taxonomic integration, such as familiarity with concepts and tools addressing taxonomic harmonization. - Familiarity with taxonomic naming concept management and formal knowledge representation addressing ontologies and semantics. - Experience with Web GIS development. - Experience in relational database management and SQL, with Postgres/PostGIS experience particularly welcome. - Experience with API development. - Programming skills in Python and R required; JavaScript and Java a plus. - Experience in R package development. - Background in cloud architecture, cloud data flows and pipelines.

Preferred Education, Experience and Skills: Ph.D. in the natural sciences or computer sciences. Experience in planning, development, and implementation of biodiversity informatics projects or equivalent combination of education and experience. Competency in innovative approaches for data integration and data fusion. Previous experience with highly technical and collaborative projects.

Application: To apply, please go to http://bit.ly/2fGpt34. The review of applications will begin 2 October 2017; the search will remain open until the position is filled.

Yale University offers exciting opportunities for achievement and growth in New Haven, Connecticut. Conveniently located between Boston and New York, New Haven is the creative capital of Connecticut with cultural resources that include three major museums, a critically-acclaimed repertory theater, state-of-the-art concert hall, and world-renowned schools of Architecture, Art, Drama, Forestry & Environmental Studies and Music. We invite you to discover the excitement, diversity, rewards and excellence of a career at Yale University. One of the country's great workplaces, Yale University offers exciting opportunities for meaningful accomplishment and true growth. Our benefits package is among the best anywhere, with a wide variety of insurance choices, liberal paid time off, fantastic family and educational benefits, a variety of retirement benefits, extensive recreational facilities, and much more.

Yale University considers applicants for employment without regard to, and does not discriminate on the basis of an individual's sex, race, color, religion, age, disability, status as a veteran, or national or ethnic origin; nor does Yale discriminate on the basis of sexual orientation or gender identity or expression.

walter.jetz@yale.edu

Yale Singapore TeachingEvolution

FACULTY (OPEN RANK) LIFE SCIENCES

Yale-NUS College, a highly selective liberal arts and science college in Singapore, founded by Yale University and the National University of Singapore, seeks to appoint a scholar in the field of Life Sciences. Applicants should be active researchers with a commitment to creative and effective undergraduate teaching and mentoring. Research areas of special interest include computational biology, cellular and molecular biology, and microbial physiology, as well as any area that builds on connections to environmental or physical sciences. However, candidates from all areas of biology are strongly encouraged to apply. The successful candidate will maintain an active research programme that involves undergraduates and will teach in both the Life Science major and in the Yale-NUS Common Curriculum (http://www.yale- nus.edu.sg/curriculum/common-curriculum). The position is a tenure-track or tenured appointment, depending on qualifications, with an expectation of starting in the 2018-2019 academic year. Salary, benefits, and leave policies are competitive at an international level.

Applications should consist of the following: a cover letter explaining why the position at Yale-NUS is of interest; a full curriculum vitae, including a complete list of publications; statements on research interests, teaching experience, and teaching philosophy, including how these might fit with the College's particular mission and curriculum; and the names and contact information of three academic referees. These can be submitted via https://academicjobsonline.org/ajo/YaleNUS. Review of applications will begin on October 31st, 2017; early applications are encouraged. The interview process will include on-campus visits for the finalists. For more information about Yale-NUS College, please visit our web site at: http://www.yale- nus.edu.sg/.

The College values diversity and is committed to equality of opportunity. For more information about Yale- NUS College, please visit our web site at: http://www.yale-nus.edu.sg/ . Candidates should understand that by sharing information with Yale-NUS College, they authorise Yale-NUS College to use their personal data for the purposes of this application. Candidates may also understand that Yale-NUS College will not use their data for any purposes beyond those relevant to the application process, and that their data remains secure and confidential.

Vinod Kumar Saranathan <vinodkumar.saranathan@aya.yale.edu>

Other

B10K unpublished bird genomes

Dear Evoldir,

The B10K consortium has generated an assembled and annotated avian genome dataset of over 300 species, principally using Illumina technology. These represent at least one individual of almost all avian families. Our principal intended use of the genomes will be to undertake two major studies - (1) a pan-avian phylogenomic analysis and (2) a pan-avian comparative genome analysis, similar to papers we published previously on a smaller ordinal-level dataset (Zhang et al, Science, 2014; Jarvis et al, Science 2014). We intend to commence these analyses in November 2017.

The purpose of this email is to enquire whether any members of the evoldir community have other unpublished avian de novo sequenced genomes that they may wish to contribute to the project (by October 31st 2017), and in doing so join the consortium and its papers. In this regard, if the data is of suitable quality we would be very happy to assemble (or re-assemble) and (re-) annotate them with our pipelines to render them consistent with our dataset.

Should this be of potential interest please do not hesitate to contact Josefin Stiller: josefinstiller@gmail.com

Many thanks,

Guojie Zhang, Tom Gilbert & Erich Jarvis on behalf of the B10K Consortium

Josefin Stiller <josefinstiller@gmail.com>

Bird Colour Base

Dear EvolDir, @BirdColourBase is a database of bird plumage colour measured with spectrophotometry. Our database is predominantly comprised of samples collected from museum based collections and all of the data is standardised by Prof. John Endler. @BirdColourBase covers >2500 avian species across more than 50% of all avian families (e.g. Muir PNAS 2005; Dale et al. Nature 2015; Dunn et al. Sci. Adv. 2015). We would like to cover all avian families.

Initially, these data will be used for macroevolutionary questions about the shape and evolution of avian colour space. These projects will begin when all families are represented in the database. If any members of the EvolDir community have unpublished data on bird plumage colouration collected with spectrophotometry we encourage them to get in touch with a view to joining our group/projects/publications if they can provide new data.

Regards, @BirdColourBase: Dr. Thanh-Lan Gluckman (@tlgluckman), Prof. Peter Dunn, Dr. Kaspar Delhey, Prof. Kevin Burns (@SDSUbirds), Prof. James Dale, Dr. Goncalo Cardoso, Prof. Paulo Mota, Dr. Doris Gomez, Dr. Claire Doutrelant, Dr. Rafael Maia (@hylopsar), Dr. Muir Eaton and Prof. John Endler. Email: avian.colour@gmail.com

BirdColourBase <avian.colour@gmail.com>

Call ESEB HewittMobilityAward

Godfrey Hewitt Mobility Award 2018 - Call for Applications

Godfrey Hewitt (1940-2013) was President of the European Society for Evolutionary Biology (ESEB) from 1999-2001. He was exceptionally influential in evolutionary biology both through his research and through his mentoring of young scientists. He was also a great believer in seeing organisms in their environment first-hand and in exchanges of ideas between labs. Therefore, ESEB has decided to offer, annually, mobility grants for young scientists in his name.

Closing date: Monday 15 January 2018, 12.00 GMT.

*Eligibility: *

The award is open to PhD students or postdoctoral scientists who are, at the closing date for applications, both within 6 years of the start date of their PhD and ESEB members. In addition, applicants will be considered who are more than 6 years from the start of their PhD if they have had career breaks, worked part-time, or for other reasons have not worked continuously. The maximum single award will be 2000 Euros. It must be used to support fieldwork or a period of research at a lab that you have not previously visited. There is no restriction on the country of residence or nationality of the applicant. A report will be required by 30 April 2019, by which time the funds must have been used.

*Application procedure: *

Your application should be sent as a single PDF file to Ute Friedrich at the ESEB office, office@eseb.org. It should include your name, current status and institution, your PhD start date, your ESEB membership number, a description of the work to be carried out (maximum 500 words), an outline budget with brief justification (maximum 100 words) and a signed statement from your PhD supervisor or postdoctoral adviser (maximum 100 words) explaining why the work cannot be funded from your home institution or your proposed host institution.

Applications will be considered by a committee chaired by Roger Butlin. The aim will be to announce decisions before the end of March 2018. In previous rounds, success rates have been between 20 and 40%.

The committee will consider the following key criteria:

1.The value of the proposed mobility in terms of its expected output and impact on the applicant's career. The committee prefers projects that are: a. Not a core component of the applicant's existing PhD or postdoctoral project, but a new venture. b. Clearly based on the applicant's own initiative c. Likely to be completed and have definable output within the award period d. Have the potential to lead to larger future projects or to enhance the applicant's career in evolutionary biology

2. The need for the GHM award, i.e. the potential for the funding provided by ESEB to make a difference, in relation to resources already available through the home or host institution.

Please endeavour to address these points in your application.

Sincerely, Ute Friedrich ESEB Office Manager

– European Society for Evolutionary Biology Email: office@eseb.org Homepage:www.eseb.org office@eseb.org

Conservation Management Survey

The Conservation Genetics Working Group within the Society for Conservation Biology is working to bring conservation managers and academic researchers closer together to help create and implement genetic assessments that can inform conservation management. To do this we need to know more about the current use of genetic assessments in conservation management and how geneticists can collaborate with managers to achieve their conservation goals.

If you are a conservation/resource manager we would appreciate you taking the time to complete the conservation manager survey (https://docs.google.com/forms/d/e/1FAIpQLSfv9auU2Op87u2gqXbp4_yA37666FXcABGhU8pV56SihjgUA/viewform?usp=sf_link). Also please share the survey link with any conservation managers you know, we aim to distribute this as widely as possible.

If you have any questions please contact me, Dr. Heather Taft, at Heather.R.Taft@gmail.com.

Thank you for helping us out!

Joshua Miller <millerjm86@gmail.com>

DNA from formaldehyde

My collaborators and I have field work coming up to sample various tissues such as liver and spleen from a rodent species. Local requirements for the fieldwork entails storing the tissues in a 10% formaldehyde solution. Does anyone have experience extraction high quality DNA from such samples and could provide useful tips for how best to do it?

Kind regards, Pernille

"pernille.nilsson@ibv.uio.no"
<pernille.nilsson@ibv.uio.no>

ESEB OpportunitiesFund DeadlineOct31

** ESEB EQUAL OPPORTUNITIES FUND **

The European Society for Evolutionary Biology is pleased to announce the open call for proposals for activities that increase knowledge and awareness of unequal opportunities. Such proposals can include, but are not limited to, short workshops (for instance, on unconscious bias) and/or seminars (with invited speakers) at your home organization, data collection, publication activities and similar events. It must be clear from the proposal how the activity will improve knowledge and awareness of unequal opportunities, or how the activity will improve equal opportunities directly, in the ESEB specifically, or Evolutionary Biology as a field in general. There are two calls per year, with the next upcoming deadline being the *31st of October 2017*. More information about the Equal Opportunities (EO) Initiative is available at http://eseb.org/prizes-funding/equal-opportunities-initiative/equal-opportunities-initiative-fund/ . *ELIGIBILITY*

- The main applicant must be ESEB member (to become a member of ESEB, please visit http://eseb.org/society/membership/) - Applications can be submitted by scientists at any stage of a professional career (e.g., undergraduate, Masters and PhD students, postdocs, and lecturers). - Applicants must provide proof of support of the host institution where the activity should take place, if applicable (letter from head of department) - Applicants must explain explicitly how their activity will improve our knowledge, awareness of unequal opportunities, or how the activity will improve equal opportunities directly, in ESEB specifically, or Evolutionary Biology as a field in general. - Applicants must detail which group of people, and how many, will benefit from this activity (for instance, 50 undergraduates, 10 graduate students, 15 faculty members) - Budgets should be reasonable (usually not exceeding 1000 EUR, if more is required, please contact EO committee first), and, if applicable, detail costs per person (that benefit from this event).

HOW TO APPLY

The application should be no more than 3 pages long (excluding CV and support letter) and include: - Name of the applicant(s), please indicate the main applicant if appropriate. - A proposal of the activity - A justification of how the activity will improve our knowledge, awareness of unequal opportunities, or how the activity will improve equal opportunities directly, in ESEB specifically, or Evolutionary Biology as a field in general. - Which group of people will benefit (students, staff, general public), and how many - A detailed, justified budget (including cost per beneficiary) and a time schedule - A short summary to be published on the website (100-150 words) - CVs of the applicants (1-2 pages) - A letter of support of the host institution's head of the department

Please submit the application as a single PDF-file by email to Ute Friedrich (office@eseb.org; Subject: EO Fund) at the ESEB Office and take care to limit the size of attachments (total < 10 MB) in any one email.

*Deadline 31^st October, 2017

* Successful applications must hand in a report about the activity, including details of how funds were spent, within 3 months of the event.

On behalf of the ESEB EO committee, Ute Friedrich

Dr. Ute Friedrich | ESEB Office Manager Postfach 910225 | 90260 Nuernberg | Germany | office@eseb.org

European Society for Evolutionary Biology | www.eseb.org office@eseb.org

ESEB ProgressMeetings

****Progress meetings in evolutionary biology****

We are excited to announce a new initiative by the European Society of Evolutionary Biology (ESEB), in partnership with the Journal of Evolutionary Biology (JEB).

We invite applications for funding to support focussed conference or workshops on a topical issue where rapid progress is currently being made in understanding Evolutionary Biology. ESEB will supply funds up to euro 15,000 to assist with workshop planning (venue, travel or attendance support). We encourage proposals on any topic.

We expect these meetings to bring together a range of researchers focussed around a topic for a "state of the art" conference, ideally proposing a new synthesis, viewpoint or technical or analytical breakthrough facilitating new avenues of research. Attendees would represent researchers from all career stages and must accord with our Equal Opportunities guidelines. Attendance should be open to all, but ESEB members should be prioritised. Typically, meetings would last 2-3 days.

A condition of the funding is that the meeting has a clear objective to produce either a Special Issue or Target Review for JEB. Within 4 months of the meeting manuscripts arising from the meeting should be submitted to the journal, to be handled by the organisers as guest editors or the editorial board of JEB, as appropriate.

This is a new opportunity for a one-off topical meeting for ESEB members and the evolutionary community. There will be one round per year, with a deadline of *Dec 12h 2017*. Applicants should be members of ESEB or our sister society, the Society for the Study of Evolution.

There is no official application form. The application document should include

- The title of the conference and why this is suitable for a Progress Meeting.

-Names and addresses of the organisers, with short (1 page each) CVs

- List of keynote speakers, with justification (potentially key recent references). They should have agreed in principle to participate

- A 2-page description of the aims and potential scope of the conference

- Conference venue details

- Methods of selecting participants

- Publication plans

Applications should be submitted to office@eseb.org <mailto:office@eseb.org> by the deadline. The successful application will be chosen by an ESEB committee.

Mike Ritchie, former Editor in Chief, JEB Wolf Blanckenhorn, Editor in Chief, JEB Luke Holman, Reviews Editor, JEB Tanja Schwander, Deciding Editor and former Special Issue Editor, JEB

Ute Friedrich | ESEB Office Manager| office@eseb.org European Society for Evolutionary Biology | www.eseb.org office@eseb.org

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EvolutionaryPlantBiologists ApplyForTheTansleyMedal

Calling all early career plant scientists!

The New Phytologist Tansley Medal is awarded annually in recognition of an outstanding contribution to plant science by an individual in the early stages of their career (student and post-doctoral researchers with up to five years' experience since gaining / defending their PhD are eligible).

The winner will receive 2000 (GBP) and will author a short Tansley insight review to be published in New Phytologist, accompanied by an Editorial announcing the winner and finalists. The application deadline for this year's Tansley Medal is 1 November 2017. Apply at https://www.newphytologist.org/tansleymedal The Tansley Medal award is an opportunity to recognise outstanding scientists in the early stages of their careers, and supporting the next generation of plant scientists is one of the main activities of the New Phytologist Trust. Please support us in this endeavour by spreading the word to anyone you know who might be eligible to apply for the Tansley Medal award. If you have any queries, please get in touch. More details can be found at: https://www.newphytologist.org/tansleymedal . Apologies for any cross-posting.

With best wishes, Mike Whitfield

Dr Mike Whitfield Development Coordinator, New Phytologist

New Phytologist Central Office, Bailrigg House, Lancaster University, Lancaster, LA1 4YE, UK Tel: + 44 1524 592839; Fax: + 44 1524 594696 www.newphytologist.org Twitter: @NewPhyt Facebook: fb.com/NewPhytologist

The New Phytologist Trust, registered charity number 1154867

2016 Impact Factor 7.33

Calling early career scientists! Your CV needs a New Phytologist Tansley Medal. Apply now.

New Phyt blog | https://newphytologist.org/blog Read the latest stories behind the research!

m.whitfield@lancaster.ac.uk

GenomeBiol SpecialIssue EvolGenomics

The open access journal, Genome Biology is pleased to invite submissions to new special issue, Evolutionary Genomics (https://www.biomedcentral.com/collections/-evolutionarygenomics).

The special issue, which is planned for the first half of 2018, will be guest edited by Professor Sarah Tishkoff and Professor Hans Ellegren and will also include commissioned Reviews and Opinions on timely topics, written by leaders in the field.

The study of evolution is being transformed by the use and integration of 'big data' with other well-established approaches, to advance our understanding of evolutionary processes. Genome Biology will highlight these advances in evolutionary genomics with a special issue showcasing important work in this area. For more information visit our website (https://-genomebiology.biomedcentral.com)

The special issue will accept Research, Method, and Software manuscript submissions presenting outstanding contributions applying -omic methods and data to questions of evolutionary importance, including in the areas of:

Phylogenomics Comparative Genomics Molecular Evolution Genome Evolution Selection and Adaptation Speciation Evo Devo Human Evolution Population Genomics

Submission deadline: 12th January 2018

Please use the online submission system, and indicate in your covering letter that you would like the manuscript to be considered for the 'Evolutionary Genomics' special issue. If you would like to inquire about the suitability of a manuscript for consideration, please email a pre-submission inquiry to editorial@genomebiology.com.

Best wishes,

Tim Sands Special issue editor

Louisa Flintoft Chief Editor

Sarah Tishkoff Hans Ellegren Guest editors Hans Ellegren <hans.ellegren@ebc.uu.se> Hans Ellegren <hans.ellegren@ebc.uu.se>

Groningen VolFieldAssit ChilianBirds

PhD research project of the department of Behavioural Ecology at GELIFES (Groningen Institute for Evolutionary Life Science) Field work close to Santiago de Chile, in collaboration with Universidad de Chile

I am looking for a field assistent with experience bird catching and handling. Due to an accident, I can not perform these activities by myself and need help on very short notice. In september, I will study the incubation behaviour of the small passerine thorn-tailed rayadito, Aphrastura spinicauda. This bird breeds in nest boxes which makes it convenient to study.

The field assistent would catch the birds with mist nets during the nest building stage (cautious to prevent abandoning), ring them with PIT tags, to follow the incubation behaviour later on. Another responsibility would be the measuring and bleeding of the nestlings (mass, wing length, skull length, etc.).

Travel and housing will be paid for. Successful candidates should have experience in the above mentioned tasks and should be independent workers. As daily working hours can be long, the candidate should be highly motivated and have a hard-working mentality. Free hours and days depend fully on the bird behaviour and will be scheduled spontanously.

The candidate would work closely together with me, a newly started PhD researcher. I am a hard worker myself, however temporarily limited by my injury. I like to have a good atmosphere while working and having a good laugh. The working language in Chile is Spanish. Spanish skills would be a plus but no obligation.

Interested? Contact me through mlmbirker@gmail.com, so we can set a Skype meeting for further information.

Kind regards,

Martje Birker PhD candidate University of Groningen mlmbirker@gmail.com +31 63 411 57 33

Martje Birker <mlmbirker@gmail.com>

New Modeltest Software

Dear Community,

We just released the all new, completely re-designed version of Modeltest: it's much faster, better & more stable and available for download here https://github.com/-ddarriba/modeltest Alexis

– Alexandros (Alexis) Stamatakis

Research Group Leader, Heidelberg Institute for Theoretical Studies Full Professor, Dept. of Informatics, Karlsruhe Institute of Technology

www.exelixis-lab.org Alexandros Stamatakis <alexandros.stamatakis@gmail.com>

PCI Evol Biol submissions

Dear colleagues

We invite you to submit your future preprints (= articles not yet published and not under consideration for publication) to Peer Community in Evolutionary Biology (PCI Evol Biol, https://evolbiol.peercommunityin.org) in order to obtain a recommendation from this community after peer-reviewing.

PCI Evol Biol is a group of scientists who review and recommend preprints in evolutionary biology, free of charge and transparently. It is a research community working for researchers to create a new publication system that is completely free of charge and independent of private publishers. This community already includes 330 researchers (the full list can be found at https://evolbiol.peercommunityin.org/public/-recommenders) motivated to review and recommend preprints.

To understand what Peer Community in (PCI, https:/-/peercommunityin.org) is, you can watch this video https://youtu.be/4PZhpnc8wwo and to understand the value of submitting your preprints to these communities, you can watch it: https://www.youtube.com/watch?v=-3DjMhVl__gupg . Some important points:

- PCI Evol Biol is supported by the American Evolutionary Society (the SSE), the Spanish Evolutionary Society (the SESBE) and the French Ecological Society (the SFE); - PCI Evol Biol does not publish the preprints (they stay on the preprint server) but the associated reviews and recommendations; - PCI Evol Biol does not evaluate preprints already submitted for publication in a journal, in order to avoid parallel reviewings; - Although it is not our goal, authors can submit their preprints to traditional journals once they have been recommended by PCI Evol Biol. Reviews obtained before the recommendation can help improve the quality of the preprint; - Journals such as Ecology Letters, Evolutionary Applications, Evolutionary Ecology, Evolutionary Biology, Journal of Evolutionary Biology, BMC Evolutionary Biology, Oikos, Genetica, Journal of Biogeography and Molecular Ecology indicated that they will consider the preprints recommended by PCI Evol Biol and that they will take into account the reviews and recommendations of PCI Evol Biol in their own editorial process if adequate. - PCI Evol Biol is free for all users (readers AND authors); - PCI Evol Biol's recommendations are transparent (reviews and recommendations are published, recommendations are signed, reviewers can remain anonymous if they wish); - Only reviews leading to a recommendation are published; - A preprint recommended by PCI Evol Biol is scientifically validated and can therefore be cited (eg. Brisson 2017, recommended by Bravo 2017); - PCI Evol Biol's recommendations have a DOI, are referenced and can therefore also be cited; - Three new communities (PCI Ecology, PCI Computational Statistics and PCI Paleontology) are expected to be launched at the end of the year/early next year.

To submit your preprints, simply go to https://-evolbiol.peercommunityin.org and follow the instructions ('Request a recommendation for your preprint').

We hope to have aroused your interest,

The Managing Board of PCI Evol Biol https://evolbiol.peercommunityin.org contact@evolbiol.peercommunityin.org https://youtu.be/-4PZhpnc8wwo Guillaume Achaz (Paris, MNHN, ISyEB, France) Juan Arroyo (Sevilla, Univ. Sevilla, Spain) Denis Bourguet (Montpellier, CBGP, France) Marianne Elias (Paris, MNHN, ISEB, France) Benoit Facon (Reunion Island, PVBMT, France) Tatiana Giraud (Orsay, ESE, France) Thomas Guillemaud (Sophia Antipolis, ISA, France) Ruth Hufbauer (Fort Collins, Colorado S. Univ., USA) Gergely J Szollosi (Budapest, Eotvos Univ., Hungary)

"thomas.guillemaud@inra.fr" <thomas.guillemaud@inra.fr>

Phylogenomics PhD lab suggestions

Evoldir community,

One of my M.S. students is applying to PhD labs this fall (starting fall 2018) and he's looking for lab recommendations. He's interested broadly in evolutionary genomics, which could range from populations to higher-level phylogenetics. His background is in plants (amjbot.org/content/104/8/1254.short), but he's open to any organism. He has field, lab, and coding (mainly python) skills.

Please let me know of any labs that are potential fits-we're really casting the net wide. Also feel free to forward this to relevant colleagues.

Thanks!! James

James Beck Department of Biological Sciences Wichita State University www.becklaboratory.com/James "Beck, James" <James.Beck@wichita.edu>

Researcher Database

The communications team at the Society for the Study of Evolution has a new initiative to improve science communication. We are creating a database of researchers who would be willing to be contacted by the media to comment on others' research in their area of expertise. With increasing specialization of research, it can be difficult for science communicators to find appropriate sources to comment on new research. By joining this database, you can be a resource for science communicators and contribute to accurate science reporting.

*To sign up, fill out this 5-minute survey: https://goo.gl/forms/WebYdDmf2wngujk92 Thank you! Please contact Kati Moore at communications@evolutionsociety.org with any questions.

Kati Moore *Communications Specialist* *Society for the Study of Evolution* communications@evolutionsociety.org www.evolutionsociety.org communications@evolutionsociety.org

SouthAfrica Volunteers EvolutionSmallMammals

Volunteers needed for the period Oct /Nov 2017 to April 2017

Evolution and Socio-Ecology of small Mammals in the Succulent Karoo of South Africa

Opportunity: This is a great opportunity for anybody who wants to get more experience in field work related to animal behavior, evolution, eco-physiology, and ecology before starting an MSc or PhD project.

Project: We study the evolutionary and ecological reasons as well as physiological mechanisms of group living, paternal care, communal nesting and social flexibility in the striped mouse. One focus is on the adaptation to droughts, combining physiological, behavioral, ecological and evolutionary research. As this species is diurnal and the habitat is open, direct behavioral observations in the field are possible.

What kind of people are needed? Applicants must have an interest in working in the field and with animals. Hard working conditions will await applicants, as the study species gets up with sunrise (between 5 and 6 AM), and stops its activity with dusk (7 PM). Work during nights might also be necessary. Work in the field will be done for 5 days a week. Applicants must be able to manage extreme temperatures (below 0 at night in winter, sometimes over 40Â^{o}C during summer days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small social group.

Work of volunteer field assistants: Trapping, marking and radio-tracking of striped mice; direct behavioral observations in the field. Volunteers will also see how blood samples are collected for physiological measurements. Volunteers are expected to help with maintenance of the research station (water pump, solar power, etc.).

Confirmation letter: Students get a letter of confirmation about their work and can prepare a report of their own small project to get credit points from their university for their bachelor or masters studies.

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 1600 (around 110 Euro) must be paid for accommodation at the research station. Students must buy their own food etc in Springbok. Including extras (going out for dinner; shopping), you should expect costs of about 450 Euros or 600 US$ per month. Students get an invitation letter which they can use to apply for funding in their home country.

Place: The field site is in the Goegap Nature Reserve near Springbok in the North-West of South Africa. The vegetation consists of Succulent Karoo, which has been recognized as one of 25 hotspots of biodiversity. It is a desert to semi-desert with rain mainly in winter (June to September).

When and how long: We are looking for volunteers to start in Oct / Nov 2017 as well as beginning of 2018. Volunteers are expected to stay for a minimum of 2-3 months, though longer periods are preferred.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to succulent.karooo.research.station@kabelbw.de.

Dr. Carsten Schradin, DR2, http://www.iphc.cnrs.fr/-Carsten-Schradin-.html

Video presentation: https://www.youtube.com/-watch?v=vZmAXySr-EM

Institut Pluridisciplinaire Hubert Curien, Département d'Ecologie Physiologie et Ethologie, 23, rue Becquerel, UMR 7178 CNRS UdS, 67087 Strasbourg cedex 2, France

Tel: +33 (0)3 88 10 69 19

Titularprofessor, University of Zurich, Switzerland, http://www.ieu.uzh.ch/research/behaviour/-endocrinology.html

Honorary Professor at the University of the Witwatersrand, Johannesburg, South Africa

Director of the Succulent Karoo Research Station http://-/www.stripedmouse.com

Carsten Schradin <carsten.schradin@iphc.cnrs.fr>

STEM women program ClimateChange

Programme to encourage STEM women to become leaders in climate change

Applications are currently open for the Homeward Bound programme < http://-homewardboundprojects.com.au/application/ >, a global enterprise that uses creative approaches to train professional STEM women who investigate the causes and consequences of climate change.

Homeward Bound aims to give researchers with leadership potential innovative tools with which they can influence the design of policies and actions, for the sustainable management of our natural resources. The year-long programme provides individual coaching, leadership training and the developing of various projects related to the effects of climate change. At the end of this training phase, participants meet in person and take part in a 3-week Antarctic expedition, which includes further workshops on leadership, strategic planning and climate change education. Applications for the Homeward Bound programme are open until *25 September*.

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Adriana Humanes

www.adrianahumanes.com Participant of *Homeward Bound: * To support my participation in this program please visit my fundraising page < https://-www.chuffed.org/project/adrianahumanes >.

Postdoctoral Associate Researcher

Ridley Building 2 Newcastle University Claremont Road Newcastle upon Tyne NE1 7RU Telephone: +44 (0)191 208 6441 <+44%20191%20208%206441>

Adriana Humanes <adrihumanes@gmail.com>

PostDocs

AuburnU EvolutionaryGenomics

Postdoctoral Position in Evolutionary Genomics at Auburn University

The Stevison Lab (http://sites.google.com/site/lstevison/) at Auburn University is seeking a creative and highly motivated postdoc with research interests in evolutionary genetics and genomics. The Stevison Lab is in the Biological Sciences Department, located in Auburn Research Park, featuring both a computational dry lab and a shared wet lab space for tackling a variety of scientific questions. Several research projects are available including primate genomics, variation in recombination rate, population genomics, and topics in speciation, such as islands of speciation and biogeography of speciation. Ongoing projects include work with both primates and fruit flies.

A strong background in evolutionary biology and excellent communication, organizational, and leadership skills are required. The applicant should have a strong work ethic, and is expected to develop new ideas that promote current research and her/his own future independence. The post-doc will be expected to assist with training graduate and undergraduate students in the lab, develop synergistic projects, write grants, produce first authored papers, and contribute to co-authored papers.

Ideal applicants will have:

* Strong written and oral communication skills * Be a productive member of a research team * Proficiency in computational biology * Ability to code in at least one programming language * Produce high quality research (as evidenced by first authored publications) * Work effectively and collegially with colleagues

?Other traits not required, but ideal:

* Experience with best practices for analyzing NGS data * Familiarity with GBS methods * Molecular Skills (e.g. generating NGS library preps)

Full support is available for one year with additional years possible pending satisfactory performance and available funds. Selected applicants will also benefit from funds to travel to national meetings annually, opportunities for mentoring and career development. Additional lab funds for independent projects are available upon written proposal submission. Anticipated start date is January 2018.

The selected applicant would be joining a strong research community in the Southeastern US. Nearby universities/research facilities (within 2 hours) include UGA, Georgia Tech, Emory, Yerkes Primate Center, Hudson Alpha, and UAB. The wider SE Community also includes UF, Clemson, UNC, and Duke with local area meetings annually to network within this community.

Applicants must have a Ph.D. in an appropriate field. The candidate selected for this position must be able to meet eligibility requirements to work in the United States at the time the appointment is scheduled to begin and continue working legally for the proposed term of employment. Women and minorities are strongly encouraged to apply.

This announcement is informal in nature and candidates of interest will be asked to submit a formal application for complete consideration after initial screening.

If interested, please send a cover letter/statement of interest with a list of relevant skills, a CV, including a list of peer-reviewed publications, and contact information for two references by email to Laurie Stevison at lss0021 (at) auburn (dot) edu (please note our mail system is limited to 25Mb messages) with “Postdoc Position” in the subject line. Receipt of application will be confirmed within 3 days. Review of applications will begin October 15, 2017, and continue until a suitable applicant is found.

Weblink to position: https://sites.google.com/site/-lstevison/prospective-members/postdoc-positions Laurie Stevison <lss0021@auburn.edu>

BangorU AdaptationGenomics

3 year, full-time postdoctoral researcher in School of Biological Sciences, Bangor, UK

The genomics of rapid, parallel adaptation to heavy metal toxicity

We are seeking a highly motivated post-doctoral researcher to join the Molecular Ecology and Fisheries Genetics Laboratory (http://mefgl.bangor.ac.uk/) at Bangor University as part of a new research team led by Alex Papadopulos (http://labadopulos.co.uk). The successful candidate will be integral to an exciting, NERC-funded project investigating the genomics of rapid, parallel adaptation to heavy metal toxicity in sea campion (Silene uniflora). Silene uniflora has rapidly adapted to heavy metal contaminated soils at abandoned mines within the last 200 years. Using state-of-the-art genetic/genomic analyses, quantitative genetics and experimental evolution studies, the project will explore the roles of standing genetic variation in the adaptive process, reveal the key signatures of rapid parallel evolution and investigate the potential for strong natural selection to drive reproductive isolation of populations at very small scales.

Candidates should hold a PhD in evolution, ecology or genetics and have research experience in evolutionary biology, molecular ecology or a related discipline, preferably in relation to adaptation and speciation genetics. The post-doc will be responsible for the generation and analysis of genomic (ddRADseq, RNAseq, whole genome re-/sequencing) and ecological/phenotypic data for population genomics and QTL analyses, supported by a dedicated research technician. Basic molecular genetic wet lab and data handling/analysis skills are essential, as is the ability to work collaboratively on writing and analysis for publication. Experience of high-throughput sequencing library preparation and bioinformatics analysis of genomic data is desirable, but training in all aspects will be provided if necessary. Occasional weekend working to conduct tolerance experiments and to maintain plants will be required.

This is a fixed term appointment for 36 months. Starting Salary: pounds 32,548 pa (Grade 7). Preferred start date is 01/12/17 or as soon as possible thereafter. Applications will only be accepted via the on-line recruitment website (jobs.bangor.ac.uk).

See https://tinyurl.com/yats25fm and/or http://tinyurl.com/y8zrwbfw for further details. Closing date for applications: 20/10/17.

For informal enquiries contact Alex Papadopulos (a.papadopulos@bangor.ac.uk)

About MEFGL Bangor The Molecular Ecology and Fisheries Genetics Laboratory (MEFGL) is a leading research division of the School of Biological Sciences (SBS), within the College of Natural Sciences at Bangor University. The MEFGL represents one of Europe's largest centres focusing on population, species and community diversity of aquatic animals, with additional activities on prokaryotic and eukaryotic groups, including plants, fungi and microbes throughout terrestrial and aerobiological biomes.

Alexander Papadopulos <a.papadopulos@bangor.ac.uk>

Barcelona EvolutionaryGenomics

Postdoctoral position at the Evolutionary and Functional Genomics LAB.

Institute of Evolutionary Biology (CSIC-UPF).

Parc de Recerca Biomedica de Barcelona.

http://www.biologiaevolutiva.org/gonzalez_lab/ The Evolutionary and Functional Genomics Lab led by Josefa Gonzalez is seeking a highly motivated postdoctoral researcher to join our research team at the Institute of Evolutionary Biology (IBE, CSIC-UPF), which is part of the Barcelona Biomedical Research Park (PRRB). The postdoctoral researcher will work on a project funded by a European Research Council Consolidator Grant that aims at identifying the genetic basis, the molecular mechanisms, and the functional traits relevant for environmental adaptation.

The postdoctoral researcher will be responsible for the functional characterization of the candidate adaptive mutations identified in Drosophila melanogaster. The tasks involved in the postdoctoral research project are: - to investigate the molecular mechanisms underlying candidate adaptive TE insertions, such as adding epigenetic marks and/or transcription factor binding sites.

- to investigate the structural changes induced by candidate adaptive TE insertions.

-to design and perform functional experiments such as stress resistance experiments (oxidative stress, heat stress, heavy metal stress, among others) and behavioral experiments (olfactory behavior, aggressive behavior, among others).

A PhD in Populations Genetics or a related field, experience handling Drosophila melanogaster stocks, experience with processing genome-wide datasets such as ChIP-seq, ATAC-seq or HiC datasets, and good writing skills are required. Previous postdoctoral experience will be considered.

We offer a full-time position for 2 years with the possibility of extension. Salary will depend on the experience of the candidate.

Starting date January 2018, but alternative dates can be discussed.

Application Please send your CV and a brief letter of motivation before the 31st October 2017 to: josefa.gonzalez@ibe.upf-csic.es

Josefa Gonzalez, PhD CSIC Tenured Scientist Institut de Biologia Evolutiva (CSIC-UPF) Passeig MarÃtim de la Barceloneta 37-49 08003 Barcelona. Spain.

+34 932309637 Co-organizer of DrosEU: European Drosophila Population Genomics Consortium Our most recent publication in Methods in Ecology and Evolution Lab website: www.biologiaevolutiva.org/gonzalez_lab Science Outreach: La Ciencia Al Teu Mon Follow us on twitter: @GonzalezLab_BCN

"GONZALEZ PEREZ, JOSEFA" <josefa.gonzalez@ibe.upf-csic.es>

Beijing AntVenomEvolution

Postdoc position open at Institute of Zoology, Chinese Academy of Sciences

This position is open to PhD. students or postdocs who have been working on ant venom related research work and would like to continue postdoctoral research in our institution in Beijing. Applicants need to apply for a special fund from the Chinese Academy of Sciences (CAS) to support postdoctoral position for internationals. The salary covered will be 250k RMB (equals to US $ 38k) per year for 2 years plus round-trip air-tickets. The program has to be initiated no later than April 30, 2018. The deadline for application is Sep. 24.

The application is highly competitive. Applicants should have nice publications. And those with physiological entomology, molecular biology, chemical biology, or chemical ecology background would have priority to be considered. My major research project is on the biosynthesis of fire ant venom alkaloids and evolution of fire ant venom. Please be aware that the postdoc position absolutely depends on the approval of application.

If anyone has interest, please contact Dr. Li Chen at chenli@ioz.ac.cn via email for more information.

chenli@ioz.ac.cn

Budapest 2 EvolutionaryGenomics

Budapest.2.EvolutionaryGenomics

Final call. Postdocs in evolutionary genomics and phylogenomics are available to join the ERC 'GENECLOCKS' project (http://cordis.europa.eu/project/rcn/207593_en.html) headed by Gergely Szollosi (http://ssolo.web.elte.hu) . Two positions are offered for 2 years with the possibility of extension up until the 2022 end date of the GENECLOCKS project. The position comes with a salary of up to EUR 43,200 per year (approx. up to EUR 2,400-2,900 net per month after taxes), as well as a travel and research funds.

We are looking for an individual who received his or her PhD preferably within the last six years, who is highly self-motivated and can work independently on a project that he or she will help develop in the context of GENECLOCKS.

A central theme of GENECLOCKS is disclosing new sources of information for dating the first three-quarters of Earth's evolutionary history that are independent from both fossils and molecular clocks. Life's early history has remained terra incognita until now, because the fossils needed to calibrate standard evolutionary timescales are simply not available for microbial life. Microbial fossils are scarce and difficult to interpret in a phylogenetic context with confidence. In previous work we have shown that patterns of lateral gene transfer inferred from modern genomes encode a record of co-existing lineages throughout the history of life, and that we can use this record to reconstruct the relative ages of microbial groups from the three domains of life in deep time.

This discovery is a game changer for anyone interested in the history of life, from either a geological or genomic perspective. It demonstrates the existence of a new and abundant source of dating information that is inscribed in the genome of any organism, provided a gene transfer occurred in its ancestry. This constitutes the overwhelming majority of the diversity of life.

Postdocs will undertake projects together with international collaborators with the goal of either i) developing new methods that systematically extract information on the pattern and timing of genomic evolution by explaining differences between gene trees, or ii) apply existing methods to resolve the timing of microbial evolution and its relationship to Earth history and answer long standing questions. Possible collaborations and associated projects include:

Reconstructing a dated phylogeny of Bacteria in collaboration with Vincent Daubin at the LBBE in Lyon.

Developing and implementing bayesian methods for the species tree aware reconstruction of gene trees with Nicolas Lartillot at the LBBE in Lyon.

Reconstructing a dated phylogeny of Eukaryotes including their position within Archaea in collaboration with Tom Williams at the University of Bristol.

Developing and implementing new methods for species tree reconstruction in the context of hierarchical gene tree-species tree methods with Jens Lagergren at the Science for Life Laboratory in Stockholm.

Implementing and applying methods to include transfer derived relative age constraints in molecular clock estimates with Bastien Boussau at the LBBE in Lyon.

Developing novel gene tree-species tree reconciliation methods that model correlated gene histories with Eric Tannier at LBBE in Lyon.

Research visits of up to several months are foreseen as part of potential collaborations.

To be considered, please send a single merged PDF to ssolo@elte.hu that contains your CV including publication list, preferably with a link to your google scholar profile, academic transcripts, a statement of research interests (3 pages or less) as well as three academic references. Please include 'GENECLOCKS17' in the subject of your email. Applications will be considered until October 1st, 2017, or until the position is filled. The position is available from the fall or winter of 2017.

The research group is lead by Dr. Gergely Szollosi (https://scholar.google.hu/citations?user=3DsPrYT-oAAAAJ) and is hosted at Eotvos Universities Institute of Physics in Budapest. The Institute of Physics has been included in the Excellence Group of European Universities, and has achieved top placement in the number of citations, the number of ERC grants, the time available for PhD research and the gender balance of master's students in the CHE Excellence Ranking. Budapest is a vibrant capital city with exciting cultural life, a unique atmosphere and affordable living costs (cf. https://goo.gl/86II3s).

Please direct any enquiries to Dr. Gergely Szollosi (ssolo@elte.hu, http://ssolo.web.elte.hu).

sszolo@gmail.com

Canada Conservation

Liber Ero Fellowship Program - call for post-doctoral applications

We are delighted to announce a call for post-doctoral applications for the Liber Ero Fellowship Program. The Liber Ero Fellowship Program supports exceptional post-doctoral fellows who address pressing conservation challenges of relevance to Canada. The Program aims to develop the next generation of conservation scientists, trained in the latest methods and in the skills necessary to affect policy and improve conservation of CanadaÂ¹s wild places and natural resources.

The Liber Ero Fellowship is open to candidates from any country whose research furthers conservation goals within Canada. Fellows must be hosted at a Canadian institution, with mentorship teams drawing from expertise in non-governmental organizations, government, and universities. Applications are now being accepted, with a deadline of November 1, 2017. See http://liberero.ca/ for more details.

Please see http://liberero.ca/meet-the-fellows/ to read about the current cohort of fellows and their projects.

Contact information: info@liberero.ca

Anita Miettunen Liber Ero Program Coordinator T: 604-822-5041 E: info@liberero.ca W: liberero.ca

"info@liberero.ca" <info@liberero.ca>

CNRS Montpellier AvianTimingOfReproduction

Two-year postdoctoral position in Evolutionary Ecology and Physiology of reproduction

Do birds time their reproduction based on the spring development of vegetation?

Context

The consequences of global warming can only be reliably estimated if we know how organisms respond to environmental changes. One way changes in climate and environment influence population resilience is through the modification of the seasonal timing of life-cycle events (i.e. phenology). However, species at different trophic levels usually do not respond at the same rate, and many organisms become increasingly mismatched with their food supply. In this context, central questions relate to how organisms adjust the timing of their life cycles to a changing world: Which environmental factors do they rely on to time their seasonal events like reproduction? Which components of the reproductive axis do these environmental factors influence?

Job description

The postdoc will take part in an on-going project in which we study the trophic relations between birds, insects, and vegetation. In particular, we investigate whether blue tits (Cyanistes caeruleus) use bud development of oak trees in spring to predict the peak of caterpillar abundance (i.e. the main food source for raising tits' chicks, and the main selection factor for tits' timing of breeding). This question will be addressed using a combination of experimental approaches in captivity, as well as field studies in several wild populations of blue tits that have been monitored for 20 to 40 years.

First, the successful candidate will link small-scale geographic variation in bud development of trees with variation in reproductive decisions of individual blue tits using remote-sensing imagery and field observations, and test the fitness consequences of matching the phenology of trees. Second, the postdoc will identify the main volatile components emitted by tree buds in spring. (S)he will then study whether birds are able to detect those compounds in a Y-maze apparatus, and test whether their reproductive behaviours and physiology are modulated accordingly (reproductive hormones, etc.). Third, time permitting, the postdoc might also investigate whether the influence of vegetation development on timing of breeding occurs through the ingestion, rather than the smell, of compounds present in growing tree buds, using a similar experimental approach as above.

Requirements

We are seeking a highly motivated candidate with a strong track record, who is willing to start a truly interdisciplinary study. The candidate should have interest and/or experience in behavioural ecology (behavioural tests), plant and animal physiology (tree development and avian endocrinology), spatial analyses (satellite image processing), and chemical ecology (characterization of plant volatile emissions). It is not necessary to have experience in all these fields, but the candidate should be interested in, and not afraid of, mixing these different approaches and techniques. Multi-tasking and organisational skills will be necessary and appreciated.

Location

The position will be held at the CEFE (Centre d'Ecologie Fonctionnelle et Evolutive, UMR 5175), a leading research institute in Ecology of the CNRS (Centre National de la Recherche Scientifique), situated at Montpellier, France. Montpellier has recently been ranked world second best for research in Ecology (http://www.shanghairanking.com/-Shanghairanking-Subject-Rankings/ecology.html), it is thus an ideal place for studies in the field, with many opportunities to interact with forefront scientists.

Conditions of employment

This is a temporary position for two years, full-time employment. Gross salary will be of minimum 31k€per year, which is comfortable in France.

The project and position are funded by an ANR grant (Agence Nationale de la Recherche, the main research funding agency in France). The grant will cover the salary of the postdoc, his/her research, as well as participation to conferences. Training will mainly be provided by Samuel Caro (Behavioural Ecologist and Physiologist), but also by other scientists present at the CEFE who are involved in the project: Francesco Bonadonna (Behavioural Ecologist), Michaël Staudt (Plant Ecologist and Physiologist) and Anne Charmantier (Evolutionary Ecologist).

Application:

Application to Samuel Caro (samuel.caro@cefe.cnrs.fr) should include a CV, a list of publications, a letter of motivation as well as contact details of at least 2 possible references.

Deadline for applying: October 25, 2017. Start of employment: January 2, 2018.

CARO Samuel <samuel.caro@cefe.cnrs.fr>

CornellU 2 EvolutionSocialBehavior

The Sheehan lab (sheehanlab.weebly.com) at Cornell University is looking to recruit 2 postdocs to work on projects to understand the genomic and neural basis of individual facial recognition in paper wasps. Among its close relatives, the paper wasp Polistes fuscatus is unique in that it uses highly variable facial patterns to recognize individuals. The recent evolution of this complex behavior, coupled with small genomes and very high recombination rates make paper wasps an unusually tractable systems for investigating the genetic basis of behavioral and cognitive evolution.

We are currently seeking postdocs to begin work on two inter-related aspects of a recently funded project:

1. The evolution of neural architecture underlying social cognition

Using a combination of staining, imaging and recording techniques the postdoc will determine regions of the wasp brain that are involved in processing individually distinctive facial signals.

For this aspect of the work, prior experience working with insect neurobiology is strongly desired.

2. Population, comparative and functional genomic approaches to identifying the genomic basis of social cognition

Preliminary work in the lab has identified a number of narrowly defined candidate regions under selection that have likely been evolving in response to selection for novel cognitive abilities related to individual recognition in P. fuscatus. We are now interested to further characterize their effects on brain development or processing.

For this aspect of the work, prior experience working in genomics is highly desirable.

Start dates for positions are flexible. Funding is available now, though I would anticipate start dates after January or even into the summer. In both cases, postdocs in the lab will be encouraged to develop independent projects related to the broader goals of the lab on the evolution of social behavior.

If the neural and/or genomic basis of social cognition is interesting to you, please be in touch!

The Sheehan lab is housed in the Department of Neurobiology and Behavior at Cornell University (nbb.cornell.edu), which brings together neurobiology and the study of the evolution of behavior. Cornell is a leading center for the development and implementation of neural imaging technology (https://neurotech.cornell.edu/) and also has a very strong presence of comparative and evolutionary genomics on campus (3cpg.cornell.edu).

Those interested in a postdoctoral position in the lab should contact Michael Sheehan directly (msheehan@cornell.edu) and send along your statement of your interests and a CV. There is no deadline per se, review will be rolling until positions are filled.

Michael J Sheehan Assistant Professor Nancy and Peter Meinig Investigator in the Life Sciences Neurobiology and Behavior Cornell University W303 Mudd Hall 215 Tower Rd Ithaca NY, 14853

"msheehan@cornell.edu" <msheehan@cornell.edu>

CzechRepublic GenomicsBiochemistryAdaptation

Postdoctoral positions in population genomics and biochemistry of oxidation stress response at the Czech Academy of Sciences.

Two postdoctoral positions are available with Petr Kotlik (http://www.researcherid.com/rid/B-4633-2009) at the Institute of Animal Physiology and Genetics of the Czech Academy of Sciences in Libechov (http://www.iapg.cas.cz/org_lab&id=23) to join a group of investigators studying microevolutionary response to climate change using a widespread European small mammal - the bank vole (Clethrionomys glareolus) - as the model system.

Research areas include (1) identifying postglacial population history and genetic adaptations in response to climate change, using large SNP datasets and genomic data, and (2) identifying how the difference in the resistance to oxidative stress conferred by haemoglobin contributes to the adaptation of bank vole populations to varied environmental conditions. Research projects will be aligned with the interests of the successful candidates.

Representative publications of related projects from the lab can be found below.

The relevant projects are in collaboration with the lab of Jeremy Searle (Cornell University).

The starting date is flexible and can be as early as November 2017. Applications will be accepted until the positions are filled. The positions are available for up to four years.

The ideal candidates will have a strong publication track record in peer-reviewed journals and a background in, respectively, population genetics/genomics and biochemistry/oxidative stress biology.

We seek individuals who are enthusiastic, highly motivated, and willing to work independently as well as in a team.

We expect good written and oral communication skills in English for candidates of any nationality.

The gross salary of the postdocs is 35.000 CZK/month (ca 1300 EUR), and may increase based on their achievements during the project (note that living expenses in the Czech Republic are generally lower than in Western European countries or the United States).

Interested applicants should send a PDF with CV, a brief description of research interests and experience, and contact information for three senior scientists who may provide a reference, to kotlik@iapg.cas.cz.

Representative publications:

Kotlik et al. (2014) Adaptive phylogeography: functional divergence between haemoglobins derived from different glacial refugia in the bank vole. Proc. R. Soc. B 281, 20140021.

Searle et al. (2009) The Celtic fringe of Britain: insights from small mammal phylogeography. Proc. R. Soc. B 276, 4287-4294.

Filipi et al. (2015) Mitogenomic phylogenetics of the bank vole Clethrionomys glareolus, a model system for studying end-glacial colonization of Europe. Mol. Phylogenet. Evol. 82, 245-257.

Kotlik et al. (2006) A northern glacial refugium for bank voles (Clethrionomys glareolus). Proc. Natl. Acad. Sci. USA 103, 14860.

Kotlik@iapg.cas.cz

EmoryU BehavioralEvolutionaryGenet

POSTDOCTORAL POSITION in BEHAVIORAL/EVOLUTIONARY GENETICS

We are recruiting a postdoctoral fellow for a project linking genetic differentiation with social behavior in a unique animal model. The position will span Emory University (PI Donna Maney) and Georgia Institute of Technology (PI Soojin Yi) and will integrate the fields of comparative genomics and behavioral neuroendocrinology. We are investigating how a prevalent chromosomal polymorphism in the white-throated sparrow leads to two distinctive and complex behavioral phenotypes. We use genomic and epigenomic tools as well as behavioral and physiological approaches. These techniques include ATAC-seq, bisulfite sequencing, reporter assays, and gene knockdown. Applicants with strong quantitative (e.g. bioinformatics) skills are especially encouraged to apply. Interested candidates should send a CV, including contact information for three references, to dmaney@emory.edu.

“Maney, Donna” <dmaney@emory.edu>

Evry France CoralMetagenomicAndTranscriptomic

PostDoc: Bioinformatic analysis of genomic and functional diversity of coral holobiont from Tara Pacific expedition.

SCIENTIFIC CONTEXT: Although covering only 0.02% of the ocean’s surface, coral reefs harbour 25% of ocean biodiversity. They provide direct livelihood in terms of food and ecological services from coral reefs (fisheries, tourism and coastal protection) are estimated at about 30 billion USD per year. Recent estimates indicate that about 20% of reefs have disappeared forever, 25% are in grave danger and an additional 25% will be threatened by 2050 [1].— In this context, Tara Pacific expedition (2016-2018) aims to understand the evolution of coral reefs [2]. This expedition is unique by the large geographical area covered: 35 islands in the Pacific Ocean, and by the breadth of the sampling: about 40 000 samples of water, fishes and corals. Following the success of protocols and results obtained during Tara Oceans expedition [3,4], a similar DNA and RNA sequencing program in the Genoscope has been established in order to analyse at a molecular level the diversity and the activity of the coral holobiont at each sampling location. Genomic analyses of coral reef ecosystems at the oceanic scale provide new approaches to study their capacities of resistance, adaptation and resilience to environmental change.

PROJET: The post-doc will have in charge to analyse metagenomic and metatranscriptomic data of three representative coral species(Millepora platyphylla, Pocillopora meandrina and Porites lobata) as well as planktonic eukaryotes surrounding coral colonies. Two different aspects of coral reef biology should be addressed in this project: 1) Transcriptional activity of coral holobiont in each sample will be analysed to understand the regulation of key genes in relation to the geographic location and the activity of planktonic communities around the colony. 2) In collaboration with other teams of Tara pacific, a global analysis of genomic variations between coral samples— will be realized in order to find genes under selective pressure without a priori and to study population structure within and between sampling sites. The candidate will address these questions taking environmental (e.g. ocean temperature, acidity) and coral trait data into account to identify drivers of adaptation and selection.

TEAM: The candidate will work in the Laboratory of Genomic Analysis of Eukaryotes (LAGE), part of the Genoscope at Evry in France, in a team of 15 researchers and students led by Patrick Wincker working on several Tara projects. The project will lead to close collaborations with several scientific teams of Tara Pacific consortium.

CONTRACT: The position will start in January 2018 for 24 month. The salary is based on the CEA salary grid and depends of qualifications and experience.

PROFIL: -——— PhD in bioinformatics, genomic or biology. -——— A strong background in NGS manipulation (Metagenomics and/or large datasets). -——— A sound knowledge of cellular biology, genomic and evolution as well as biostatistics. -——— Experience in programming languages: Python or Perl, R and familiar with UNIX OS. -——— Experience in marine biology is a plus.

APPLICATIONS: Send CV, references and letter of motivation (in French or English) by email to Quentin Carradec: qcarrade@genoscope.cns.fr until the end of September.

REFERENCES: 1.——— Hughes, T.P., et al., Global warming and recurrent mass bleaching of corals. Nature, 2017. 543(7645): p. 373-377. 2.——— Tara website: http://oceans.taraexpeditions.org/m/qui-est-tara/les-expeditions/tara-pacific/ 3.——— Alberti, A., et al., Viral to metazoan marine plankton nucleotide sequences from the Tara Oceans expedition. Sci Data, 2017. 4: p. 170093. 4.——— Bork, P., et al., Tara Oceans. Tara Oceans studies plankton at planetary scale. Introduction. Science, 2015. 348(6237): p. 873.

Quentin Carradec <qcarrade@genoscope.cns.fr>

Harvard EvolutionaryGenomics

Title:— Postdoctoral Fellowship in Evolutionary Genomics School: Faculty of Arts and Sciences Department/Area: OEB Position Description: Gene flow between butterfly species in the Amazon URL: https://academicpositions.harvard.edu/postings/7826 The James Mallet Group seeks two Postdoctoral Fellows to investigate the causes and genomic effects of gene flow among species of the butterfly genus Heliconius.

We have recently identified a number cases of hybridization and introgression among a group of closely related species of Heliconius butterflies. In one publication (Simon Martin et al. 2013, Genome Research), we documented that up to 42% of the genome had been exchanged between a pair of occasionally hybridizing species. We now have unpublished evidence from a different pair of Heliconius from the Amazon for an even more extraordinary case. Up to 98% of the genetic material has been exchanged between these two species, leading to very low divergence across most of the genome, punctuated by scattered “genomic islands” of high divergence. In these Heliconius, and in the Anopheles gambiae group of malaria mosquitoes, introgression has swamped the original signal of speciation history, giving a highly misleading impression of phylogenetic relationships across most of the genome.

We aim to understand how this situation could be maintained, and the “speciation genes” involved in keeping such species apart. Genes for differences in flight behavior, ecology and host plant use, pheromones, mating behavior, and genes involved in female hybrid sterility are all of interest. We need to understand the population genetics of the interactions between the species, both empirically via analysis of genome data and functional analysis, and in theory. In doing so, we will advance the understanding of speciation with gene flow, and of introgression among species. It is hoped to apply this understanding to very similar situations among the African malaria mosquitoes and other disease vectors.

Basic Qualifications Requirements: - Candidates must have completed their PhD in biology (biology, molecular biology, integrative biology or similar); - Relevant experience in population genetics, genomics, functional genetics, and/or data analysis; - A record of scientific publications

Additional Qualifications The successful applicants will have: - An interest in evolution and population genetics - Laboratory skills, especially in functional genetics or next-generation sequencing - Bioinformatics, statistics, and data analysis skills. Knowledge of population genetic theory - Good communication skills, both written and oral - Field experience is not required, but could be helpful

Special Instructions Materials should include: - A cover letter (2 pages maximum) describing your research experience and motivation, with special attention to your training in ecological statistical modeling; - Curriculum vitae; - Up to three relevant scientific publications on which you were an author; - Names, addresses and email addresses for three referees

Application review will begin on October 15, 2017 and will continue until the positions are filled. See: https://academicpositions.harvard.edu/postings/7826— The target start date can be adjusted to accommodate the selected candidates.

Contact Information Contact James Mallet (jmallet@oeb.harvard.edu) for questions regarding the position or application process. For further information about OEB visit http://www.oeb.harvard.edu . Contact Email: jmallet@oeb.harvard.edu Equal Opportunity Employer 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, national origin, disability status, protected veteran status, or any other characteristic protected by law.

Minimum Number of References Required——— 3 Maximum Number of References Allowed——— 5

James Mallet Organismic & Evolutionary Biology Harvard University 16 Divinity Avenue - BioLabs Cambridge, MA 02138 USA tel: +(1)617-496-5350 Web: mallet.oeb.harvard.edu/

James Mallet <jmallet@oeb.harvard.edu>

HebrewUJerusalem MethodsHumanPopulationGenetics

A position is available for a post-doctoral fellow at Shai Carmi's research group at the Hebrew University of Jerusalem in Israel. The lab is computational, focusing on statistical and population genetics. It is located at the Hebrew University medical campus, in a scenic area at the outskirts of Jerusalem.

The research project will involve the development and application of statistical methods for reconstructing demographic events based on human modern and ancient genetic variation. One aim is to improve the modeling of the effect of founder events on the number and length of "identical-by-descent" haplotypes (long genomic segments that are nearly identical between individuals due to recent co-ancestry). Other aims are to develop new methods for inferring the parameters of complex admixture events and for modeling the ancestry of ancient genomes. In all projects, methods will be tested and applied on large-scale datasets from the Jewish and other Israeli populations.

Other projects in the lab are in medical genetics: association studies, imputation, technologies for carrier testing, and genetic risk prediction. The lab has access to high performance computing and enjoys collaborations with a wide network of computational biologists, physicians, and computer scientists.

For more details on the lab, please visit http://-scarmilab.org . Requirements for the position are formal education or research experience in a quantitative field, experience in programming for computational biology (Linux, R/Matlab, and preferably one of Python, C/C++/Java, etc.), an excellent publication track record, and a solid understanding of probability and statistics. Background in population genetics is an advantage.

For more details on the position and to apply, please email Dr. Shai Carmi: shai.carmi@huji.ac.il.

"shai.carmi@mail.huji.ac.il"
<shai.carmi@mail.huji.ac.il>

IBValencia TuberculosisMolEvol

Postdoctoral position in tuberculosis epidemiology and evolution

Job position

Applicants for a postdoc position in microbial bioinformatics and microbial genomic epidemiology are invited. The primary focus of the work will be to the evolution and epidemiology of the pathogen Mycobacterium tuberculosis using different genomic datasets.

Start

The position will be opened as soon as possible and will run until June 2020 at least.

Qualifications Candidates should have a PhD degree or equivalent

* Must have a strong research background in bioinformatics and/or statistical approaches * Preferably have experience with bioinformatic methods for snp calling, inferring phylogenies and determining evolutionary rates * Preferably have experience with analysis of complex sequence data * Have a strong interest for health surveillance and combining microbiology and genomics with bioinformatics and epidemiology

To apply for the position please email me: icomas@ibv.csic.es

– Iñaki Comas Espadas, PhD Head of Tuberculosis Genomics Unit

https://tbgenomics.wordpress.com/ Biomedicine Institute of Valencia (IBV) Spanish Research Council (CSIC) C/ Jaume Roig, 11 46010 - València (Spain) Telf: (+34) 96 339 3773 Correo-e: icomas@ibv.csic.es (note: inaki.comas@uv.es and comas_ina@gva.es are being redirected here)

Para envío de muestras/for sample delivery: LUIS VILLAMAYOR BSL3 Lab Manager FISABIO Avda. Cataluña, 21. 46020 Valencia Tel: (+34) 96 192 63 64 email:villamayor.lm@gmail.com villamayor_lui@gva.es

Iñaki Comas <icomas@ibv.csic.es>

IGFL Lyon EvoDevo

The team of Michalis Averof, at the Institut de Génomique Fonctionnelle de Lyon (IGFL) in France, is recruiting a post-doctoral researcher with expertise in transcriptional profiling and data analysis. The project will explore fundamental questions on regeneration, including the identity and evolutionary relationships of progenitor cells, the cellular diversity that these generate, and whether the process of regeneration mirrors the mechanism of leg development in the embryo. The project is funded by an ERC Advanced Grant.

The project will involve analyzing large datasets of bulk and single-cell transcriptomes during the course of limb regeneration. The research will be carried out in the crustacean Parhyale hawaiensis, a new model that combines good regenerative ability with genetic tractability and live imaging (seeScience 343: 788-791, eLife 5: e19766). The Parhyale genome sequence and regenerating limb transcriptomes are already available(eLife 5: e20062).

Candidates should have a strong background in genome-wide computational analysis, including coding skills for data analysis and statistics. Previous experience with single-cell RNAseq and/or transcriptomics in non-model organisms would be an advantage. Laboratory skills (or a wish to acquire them) would allow the recruited candidate to generate his/her own data.

The researcher will be integrated in the Averof lab (www.averof-lab.org),in the new laboratories of the IGFL at the Ãcole Normale Supérieure de Lyon,an exciting environment for research at the interface of development, physiology, evolution and genomics. The working language of the team is English.

The researcher will receive a salary and health/social security coverage from the CNRS. The contract will be initially for one or two years, with possible extensions until the end of the project (December 2021).The starting date is negotiable.

This call has an open deadline; applications will be examined until the relevant position is filled. Potential applicants are encouraged to contact Michalis Averof as early as possible, sending a brief description of interests and a CV to michalis.averof@ens-lyon.fr.

The position is described here: https://averof-lab.org/web/news_files/ERC_postdocs_Transcriptomics_Sept2017_2.pdf

“mathilde.paris@univ-amu.fr” <mathilde.paris@univ-amu.fr>

InstitutoButantan Brazil SnakeAndVenomEvolution

Theme: Comparative transcriptomic analysis of snake venom glands

Supervisor: Inacio Junqueira de Azevedo

Place: Special Laboratory of Applied Toxinology, Instituto Butantan, Sao Paulo, BRAZIL

We are selecting candidates for a Post-Doctorate position granted with a FAPESP fellowship to work in a thematic project called “Scales of Biodiversity - Integrated studies of snake venom evolution and function across multiple levels of diversity”. This is a project conducted in partnership with researchers from USA, aiming at a broad-scale study on the evolution of snake venom and its role in the diversification of snakes in the Americas.

The postdoctoral fellow should act in the generation but mostly in the analysis of transcriptomic data from oral glands of snakes. It is expected that he/she will aid in the wet-lab part of the project (RNA extraction, library preparation, sequencing in Illumina system), but will focus majorly on dry-lab activities, aiming the transcriptomic assembly, gene identification and comparison of expression levels of toxin genes and their correlation with the diversification of the phylogenetic groups studied. There will also be the possibility of accessing the links between genomics, transcriptomics and proteomics of the species with the functional variability of the venoms. The postdoctoral fellow may also participate in the activities carried out by the other groups involved, both in Brazil and in the USA.

Qualifications for position: (1) Candidates must present, at the time of the implementation of the fellowship, a doctoral degree in area related to the project. (2) have proven experience in projects involving transcriptomic analysis by Next Generation methods (RNAseq) (prerequisite); (3) mastering the use of bioinformatic tools for the analysis of transcriptomic data, including de novo assemblers and tools for the quantification of gene expression (prerequisite); (4) have the ability to develop bioinformatic tools and scripts in a Linux system (highly desirable); (5) have knowledge about venoms and animal toxins and/or on evolution of gene families (desirable);

(6) Fluency in English is desirable.

Those interested in the position should send an e-mail to biodiversity.scales@butantan.gov.br until 09/27/2017, containing:

- CV; - cover letter explaining the interest in the position; - contacts (name, Institution, telephone and email) of two to three researchers who can give information about the candidate.

The documents submitted will be analyzed by the principal investigators of the project, Drs. Inacio Junqueira-Azevedo (coordinator), Hussam Zaher, Erika Zaher and Ana M. Moura da Silva, who will select the suitable candidates for the fellowship through the curricula and possible interviews (face-to-face or by Skype).

The selected candidate will be indicated to a pre-granted FAPESP Post-Doctorate fellowship, subject to the approval of candidate CV by the agency according to its criteria (http://www.fapesp.br/en/5427). The copy of the doctoral degree or certificate of completion will be mandatory for the implementation of the fellowship. The fellowship has the value of R$ 7,174.80/month (proximately $2,200.00), plus a Technical Reserve, and it lasts for two years with annual evaluations. The Technical Reserve is equivalent to 15% of the annual value of the fellowship and is intended to cover unforeseen expenses directly related to the research activity.

Inacio de L. M. Junqueira-de-Azevedo, PhD

Scientific Researcher Lab. Especial de Toxinologia Aplicada Instituto Butantan Av. Vital Brasil, 1500 05503-900 - Sao Paulo SP, Brazil Phone: +55 11 2627-9731 e-mail for this subject: scales.biodiversity@butantan.gov.br

"inacio.azevedo@butantan.gov.br" <inacio.azevedo@butantan.gov.br>

InstitutoButantan Brazil SnakeVenomEvolution

Theme: Comparative transcriptomic analysis of snake venom glands

Supervisor: Inacio Junqueira de Azevedo

Place: Special Laboratory of Applied Toxinology, Instituto Butantan, Sao Paulo, BRAZIL

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Qualifications for position: (1) Candidates must present, at the time of the implementation of the fellowship, a doctoral degree in area related to the project. (2) have proven experience in projects involving transcriptomic analysis by Next Generation methods (RNAseq) (prerequisite); (3) mastering the use of bioinformatic tools for the analysis of transcriptomic data, including de novo assemblers and tools for the quantification of gene expression (prerequisite); (4) have the ability to develop bioinformatic tools and scripts in a Linux system (highly desirable); (5) have knowledge about venoms and animal toxins and/or on evolution of gene families (desirable); (6) Fluency in English is desirable.

Those interested in the position should send an e-mail to scales.biodiversity@butantan.gov.br until 09/27/2017, containing:

- CV; - cover letter explaining the interest in the position; - contacts (name, Institution, telephone and email) of two to three researchers who can give information about the candidate.

The documents submitted will be analyzed by the principal investigators of the project, Drs. Inacio Junqueira-Azevedo (coordinator), Hussam Zaher, Erika Zaher and Ana M. Moura da Silva, who will select the suitable candidates for the fellowship through the curricula and possible interviews (face-to-face or by Skype).

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KunmingInstZoology Metabarcoding

The Chinese Academy of Sciences offers 1-to-2-year postdoctoral fellowships and 2-to-9-month visiting fellowships for faculty, under its PIFI program (Presidential International Fellowship Initiative).

All fellowships come with an internationally competitive salary and round-trip airfare.

http://international-talent.cas.cn/front/index.html#/-bicsite/pifiIntroduce/pifi My lab at the Kunming Institute of Zoology welcomes environmental scientists from anywhere in the world who are working with environmental-DNA, metabarcoding, and/or mito/metagenomic data for biodiversity conservation. This includes scientists working in statistical ecology, who would like to start using these new data sources. My lab is fully funded for coffee and sequencing.

We are particularly interested in collaborations in these areas: The biodiversity impact of the One Belt One Road Initiative and of climate change. The integration of remote-sensing data, joint species distribution modelling, and high-throughput data for monitoring biodiversity and ecosystem functions and services. See this article for more detail: https://www.nature.com/-articles/s41559-017-0176 The Kunming Institute of Zoology is very active in evolutionary biology, especially in evolutionary and functional genomics and phylogeography. KIZ also has an active DNA barcoding center. PIFI applicants interested in these areas can also contact me for quick introductions to other KIZ faculty.

Kunming, in Yunnan province, China, is a very pleasant place to live and visit, with several new microbreweries and great weather (see gokunming.com)

Douglas Yu

– Prof. Douglas W. Yu School of Biological Sciences, University of East Anglia, Norwich, Norfolk NR4 7TJ UK, mob +44-7510-308-272

Kunming Institute of Zoology, 21 Qingsong Lu, Kunming, Yunnan 650201 China ofc +86-871-519 9178, mob 1860-871-7369

www.uea.ac.uk/bio/People/Academic/Douglas+Yu, eastanglia.academia.edu/DouglasYu/Papers for pdfs

Douglas Yu <dougwyu@gmail.com> Douglas Yu <dougwyu@gmail.com>

LundU PlantDrivenSpeciation

I have an opening for a postdoc to work with me on host plant driven speciation in the fly Tephritis conura at Lund University, Sweden. The research will have both genomic and ecological components, and the research agenda will be decided together with the successfull candidate. Lund University is ranked among the top 100 universities (73rd) and has a strong evolutionary ecology and molecular ecology research environment.

The postdoc will be part of a group working on host plant interactions together with me, Magne Friberg and our PhD- and MSc-students and another post doc. Samples for the first study/ies are available and will allow for a fast first publication. The position is for one year with possibilities for a one year extention.

The candidate must have defended their thesis within the last 5 years and can't have a PhD from Sweden. Please contact me if you have any questions!

All the best, Anna Runemark

anna.runemark@ibv.uio.no / anna.runemark@biol.lu.se https://www.mn.uio.no/cees/english/people/-researcher-postdoc/annaru/ (researcher home page for Lund University under construction)

For more on the Tephritis thistle fly system: http://onlinelibrary.wiley.com/doi/10.1111/j.1365-294X.2006.02792.x/abstract More on Lund University: http://www.lunduniversity.lu.se/-

about/about-lund-university Anna Runemark <anna.runemark@biol.lu.se>

MichganStateU KelloggBioStation ConservationGenomics

The Fitzpatrick Lab (www.swfitz.com) at the W.K. Kellogg Biological Station, Michigan State University is searching for an enthusiastic and motivated postdoctoral researcher to work on projects focusing on landscape/conservation genomics of threatened species and genomic architecture of genetic rescue. The Fitzpatrick Lab is interested in the evolutionary and ecological processes that determine adaptation, fitness, and ultimately persistence in small populations. We primarily work on freshwater fish, including the model Trinidadian guppy system, as well as with a diverse set of non-model organisms, including amphibians, reptiles, and birds.

The primary responsibility of this position will be to carry out a range-wide population genomic study of Arkansas darters, a stream fish that occurs in small, fragmented populations and is a species of conservation concern. In addition to the funded work (U.S. Fish & Wildlife; Kansas Dept. of Parks, Wildlife, & Tourism), there will be opportunities to develop related experimental or theoretical projects related to genetic rescue, including the potential to take advantage of previously collected datasets from multi-generational genetic rescue experiments using Trinidadian guppies.

The position is based at MSU's Kellogg Biological Station, located in Hickory Corners, MI ~65 miles from the main campus. KBS is home to 14 resident faculty and their graduate students and post-doctoral researchers, with interests focusing on ecology, evolution, and conservation, as well as full-time research staff, visiting research scientists, and many summer undergraduates. KBS is home to the KBS Long Term Ecological Research (LTER) program (www.lter.kbs.msu.edu), the Great Lakes Bioenergy Research Center (GLBRC), and a newly developed Molecular Ecology and Genomics Laboratory. The successful candidate will have opportunities to interact with faculty on main campus in the Departments of Integrative Biology; Fisheries & Wildlife; members of the Ecology, Evolutionary Biology, & Behavior (EEBB) program; and the NSF BEACON Center for the Study of Evolution in Action. KBS and the Fitzpatrick Lab are committed to postdoctoral research career development, providing postdocs with opportunities to gain experience in mentoring, teaching, and other professional skills.

Requirements: We seek an individual with a PhD in a related field (ecology, evolution, genetics, conservation biology, organismal biology), demonstrated expertise in population and/or landscape genomics, and excellent writing ability. The candidate should have experience in the collection of NGS data (especially RADseq and/or WGS), bioinformatics pipelines to filter and assemble Illumina reads and call SNPs, GIS, and landscape genetic analysis.

Additional valuable qualifications include: coding skills, reference genome annotation, database management, experience working with live vertebrates in lab or field settings, and experience mentoring undergraduate students.

Start date and duration: The position start date is somewhat flexible, but we hope to employ someone by November 15, 2017. Funding is for one year with likely multi-year extension pending satisfactory performance.

Salary: $47,500 - $49,000 USD plus benefits

How to apply: Interested candidates should apply by sending an email to sfitz@msu.edu that includes: (1) cover letter describing research interests and motivation, including a discussion of how your skills are aligned with the needs of projects described above, (2) CV, (3) names and emails of 3 references, and (4) 2-3 published papers or manuscripts in preparation. Review of applications will start October 1st and will continue until a strong candidate is hired.

Michigan State University, Kellogg Biological Station, and the Fitzpatrick Lab are interested in candidates who are committed to the highest standards of scholarship and professional activities, and to the development of a climate that supports equality and diversity. Michigan State University is an affirmative action/equal opportunity employer.

pelagicfitz@gmail.com

MNHN Paris HumanPopulationGenetics

Post-doc in Human Population Genetics, Eco-Anthropology, Paris A one-year post-doctoral position starting in November 2017 is available in the Human Population Genetics group at MNHN (Museum National d'Histoire Naturelle), Paris. The project is aimed at exploring the biological and cultural factors influencing mate choice in Humans using genomic data. Mate choice in humans is mainly under the influence of socio-cultural factors, but previous works (Chaix 2008; Laurent 2012a; Laurent 2012b) suggest that some biological factors such as the MHC (Major Histocompatibility Complex), as well as other regions of the genome (Laurent 2012c), may also influence mate choice.

Previous studies have been performed on samples of small sizes from a restricted number of populations. Here we aim at extending this research to new samples. We have developed a powerful methodological framework enabling to detect similarities or differences between husbands and wives from genomic data. This framework allows distinguishing biological factors that leave local genomic signatures, from socio-cultural factors (such as cousin marriages or a tendency for geographical endogamy) that leave genome-wide signatures. We wish to explore new population samples, more precisely several hundreds of couples sampled in Central Asia and South-East Asia in populations having different social organizations.

The ideal candidate will have expertise in population genomics and/or bioinformatics, a solid background in statistics and computing (R, python, ;) and a strong interest in social sciences.

To apply, please send a cover letter detailing experience and research interests, a current CV, and contact information for three professional references to raphaelle.chaix@mnhn.fr, romain.laurent@mnhn.fr and bruno.toupance@mnhn.fr before the 20th of September 2017.

Contact: Raphaelle Chaix, Bruno Toupance, Romain Laurent Human Population Genetics group Unit of Eco-Anthropology and Ethnobiology MNHN, Paris, France Email: raphaelle.chaix@mnhn.fr, romain.laurent@mnhn.fr, bruno.toupance@mnhn.fr

References Chaix R, Cao C and Donnelly P (2008) Is mate choice in humans MHC-dependent? PLoS Genet 4(9): e1000184.

Laurent R and Chaix R (2012) HapMap European American genotypes are compatible with the hypothesis of MHC-dependent mate choice (response to DOI 10.1002/bies.201200023, Derti and Roth). Bioessays 34(10): 871-872.

Laurent R and Chaix R (2012) MHC-dependent mate choice in humans: why genomic patterns from the HapMap European American dataset support the hypothesis. Bioessays 34(4): 267-271.

Laurent R, Toupance B and Chaix R (2012) Non-random mate choice in humans: insights from a genome scan. Mol Ecol 21(3): 587-596.

Raphaelle Chaix Chargee de Recherche CNRS / CNRS researcher CNRS/MNHN/University Paris Diderot/Sorbonne Paris Cite UMR7206 Ecoanthropology and Ethnobiology Musee de l'Homme 17, place du Trocadero 75016 Paris France chaix@mnhn.fr tel: +33 1 44 05 72 69

Raphaelle CHAIX <raphaelle.chaix@mnhn.fr>

MPIDS Goettingen Germany ImmunePathogenCoevolution

Postdoctoral position to study immune-pathogen coevolution

The Max Planck Research Group (MPRG) "Statistical Physics of Evolving Systems", led by Dr. Armita Nourmohammad is offering a postdoctoral position at the Max Planck Institute for Dynamics and Self-organization (MPIDS) in Göttingen, Germany. The institute has strong ties with the George August University of Göttingen, which is the largest university in Germany. There are a number of groups at MPIDS with interests in biological systems, fostering an ideal environment for interdisciplinary research. Moreover, the newly established International Max Planck Research School for Genome Science at the Göttingen campus provides many opportunities for collaborations at the interface of biophysics and genomics. The focus of our group is on out-of-equilibrium processes in evolutionary systems by combining mathematical modeling and inference from molecular data.

Job Description Similar to the evolution of organisms adapting to their environment, rapid evolution of cellular populations occurs within our bodies, as the adaptive immune system works to eliminate infections. Chronic pathogens, such as HIV, are able to persist in a host for extended periods of time, during which they also evolve to evade the immune response. Our goal is to characterize the mode and tempo of somatic co-evolution of the adaptive immune repertoire together with chronically infecting pathogens, within individuals. This project requires development of inference technique for out-of-equilibrium coevolutionary processes, and application of such methods to molecular sequence data of antibodies and pathogens collected over time from individuals.

This data is often a highly under-sampled representation of the underlying distributions. Statistical inference is necessary to characterize the evolutionary dynamics based on such incomplete information. The goal is to identify the molecular signatures of coevolution, and ultimately, to predict the fate of an antibody or a viral sequence, dependent on the accumulated information of their interacting evolutionary histories.

Requirements For this interdisciplinary project we seek an enthusiastic postdoctoral candidate with background in topics related to statistical / theoretical physics, mathematical biology or population genetics, and preferably (but not required) familiarity with genomic data analysis. The ideal candidate should be motivated, curious, and analytically and numerically competent.

The position will be open from November 1st onwards. The contract will be limited to one year with potential for extension.

Interested candidates should contact armitan.applications@gmail.com with a CV, publication list, a brief description of their research experience and why they are interested in this project, and a list of people whom I can contact for references.

Armita Nourmohammad Max Planck Research Group Leader Max Planck Institute for Dynamics and Self-organization Göttingen, Germany https://scholar.princeton.edu/armitan armitan.applications@gmail.com

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Netherlands OriginsOfLife

SIX POSTDOC POSITIONS FOR INTERDISCIPLINARY ORIGINS OF LIFE RESEARCH (full time, three year, the Netherlands)

The http://www.origins-center.nl is a recent, multidisciplinary and multi-institute initiative of a large number of top tier scientists in the Netherlands, who responded to questions submitted by the public on fundamentals of life in the universe in the context of the http://www.wetenschapsagenda.nl/?lang=en. Recently we defined the outlines of five three-year pathfinder projects that together should lay the groundworks for a future, far larger research programme, which aims at game-changing understanding of the origin of life and of life-bearing planets, predicting evolution, building and steering life from molecule to biosphere, finding extraterrestrial life and developing the mathematical understanding needed for bridging large spatial, temporal and organisatorial scale differences.

For these five pathfinder projects we are now recruiting six postdoctoral research fellows with a strong background in astronomy, biophysics, chemistry, microbiology, ecology, evolutionary biology, mathematics, computational science, molecular biosciences, or planetary and geosciences, and with the ability to perform innovative and multidisciplinary research. The recruited fellows will, jointly with research groups in the Netherlands, further define and execute the projects. They will thereby be centrally involved in advanced and multidisciplinary research of great scientific and public interest.

JOB DESCRIPTION Fellowships are available within each of the following five projects (detailed info available at http://www.origins-center.nl/vacancies/):

217354 Developing, testing and operating the Origins Simulator 217355 Identifying key factors involved in predictability of evolution 217356 Building and directing life 217357 Modelling planet earth as an exoplanet 217358 Mathematically understanding downward causation

Each fellow will be hosted by a research group involved in the Origins Center initiative and be employed by the host's university or research institute, and will cooperate with at least one other research group in another field of expertise and preferably in another university or research institute. The fellow's tasks will include: - further conceptualising, planning, and executing one of the pathfinder projects - reaching out to and collaborating with research groups in the Netherlands and abroad - forging linkages between the five pathfinder projects and with the relevant research community at large - contributing to a programme of public outreach.

QUALIFICATIONS The successful candidate will have: - a recently obtained PhD in a relevant field as indicated above - an excellent track record as shown by publications, invitations, awards and honorary positions - a sound grasp of issues, concepts and methods linked to the pathfinder project targeted in the application, and the ambition, resourcefulness, perseverance and- cooperative skills needed to bring the project to a successful closure. - strong communication skills both towards direct collaborators and towards the wider research community - an interest in science communication targeted at a variety of audiences - excellent written and oral knowledge of English. Some specific requirements linked to the separate projects are indicated in the separate pathfinder project descriptions.

To apply go to http://www.rug.nl/about-us/work-with-us/job-opportunities/overview?details=00347-02S0005TNP Closing date for applications: 25

September 2017 12:00 h pm CEST The aimed-for starting date is 1 January 2018 or soon afterwards; interviews will be on 5 and 11 October 2017.

Applicants can contact the Origins Center coordinator Jan-Willem Mantel (j.w.e.mantel@rug.nl) ahead of application for further information

"Ellers, J." <j.ellers@vu.nl>

Netherlands PredictabilityOfEvolution

IDENTIFYING KEY FACTORS INVOLVED IN PREDICTABILITY OF EVOLUTION One full-time research fellow position, 3 years Project reference: 217355

Ever since Darwin, understanding how life has evolved in interaction with the environment has been at the forefront of science. More recently, however, the emphasis has shifted to a forward-looking perspective of evolution, aiming at understanding how species can adapt, in an evolutionary sense, to current and future changes of their world.

Predicting evolution requires a deep understanding of the evolutionary processes across different levels of biological organisation and scale. The field of evolutionary genetics/ecology/biology has made considerable progress towards this understanding. Crucially, propelled by technological advances in modelling, bioinformatics and molecular genetics, the role of non-genetic forms of inheritance, genomic networks and the feedback between organisms and their environments, can be addressed. Although these aspects are increasingly recognized to be important for adaptation and transmission of information to the next generation, but predicted effects on evolutionary trajectories remain to be established.

The Dutch research community has developed a Roadmap towards Predicting Evolution to align the on-going research and to look ahead to the next 15-20 years. We are therefore recruiting a Fellow to carry out a Pathfinder project to proceed on this road. The Pathfinder project's aims are (i) to generate new insights by addressing the possibilities and challenges of predicting evolution, (ii) to strengthen the research community in the Netherlands around this theme, and (iii) to further shape and develop the Roadmap. In a joint effort the research community has defined the contours of this Pathfinder project, described here.

The Fellow will investigate what factors are of key importance for the predictability of evolution, including (i) components of the genomic architecture (Genotype-Phenotype map) such as epistatic interactions and the complexity of the gene regulatory network underlying the phenotype, as well as the standing genetic variation, (ii) the characteristics of the abiotic and biotic drivers of selection and (iii) the traits to be predicted.

The first step is to make predictions about the relative importance of the different factors using theoretical modelling. This theoretical work will be carried out in complement with a set of experimental studies, which will address the same factors empirically and can validate the predictions.

To facilitate building a research community in the Netherlands around predicting evolution, the empirical work will be carried out by a large number of Dutch research groups, using a single model system*. All participating groups will be invited to run a standardized experimental evolution experiment and to run one or more variants of this experiment, for instance varying the same factors as used in the theoretical work described above (incl. experiments under natural conditions). The fellow will be involved both in the theoretical and the empirical work and will be instrumental in integrating these two components. Furthermore, the Fellow will coordinate the experiments of the different research groups. The Fellow will perform a meta-analysis on the results and will link the empirical results with the outcome of the theoretical work.

*A suitable experimental system would be Caenorhabditis remanei as it is likely that many groups could use this system to address questions which link to their own research. This species is relatively easy to culture with fast generation times, has sexual reproduction, computational models exist, and it is possible to include evolutionary processes in wild populations. By focussing on a single system, the results can be analysed in a single analysis by the Fellow.

QUALIFICATIONS The successful candidate will have: - a PhD in a relevant field as indicated above - an excellent track record as shown by publications, invitations, awards and honorary positions - a clear vision on evolutionary processes, and thorough expertise in modelling and/or experimental evolution research - the ambition, resourcefulness, perseverance and- cooperative skills needed to bring the project to a successful closure. - strong communication skills both towards direct collaborators and towards the wider research community - an interest in science communication targeted at a variety of audiences - excellent written and oral knowledge of English.

HOSTING RESEARCH GROUPS AND INSTITUTES Several highly qualified research groups in the Netherlands are willing to contribute to the overall Origins Center research programme by hosting one of the research fellows we are presently recruiting. Contact details of these groups and links to further information can be found

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NHM London BeeGenomics

Postdoctoral Researcher, Natural History Museum, London.

Genomic Analysis of Museum Bumblebees

Apply here:

https://careers.nhm.ac.uk/templates/CIPHR/jobdetail_344.aspx A NERC-funded PDRA position is available for 34 months working at the Natural History Museum, London, with Professor Ian Barnes and Dr Selina Brace, on the recovery and analysis of DNA from bumblebee museum specimens. This work is part of a larger project investigating insect pollinator responses over a century of UK land-use change. The advertised position will focus on whole genome sequencing of museum specimens, and analysis of these data to infer past patterns of population size change, admixture and selection. The post-holder will work closely with Dr Richard Gill and his team in the Department of Life Sciences at the Silwood Park campus of Imperial College London, who are conducting population trait evolution and manipulative experiments as complementary components of the project. The project also involves working with the imaging and digitisation teams at the Natural History Museum, and museum curators and other leading researchers from around the UK. The overall aim for the project is to better understand the dynamics of how insect pollinator populations have (and will) change in response to changes in land-use and associated factors, and how they adapt to newly emerging environments and the impact on fitness.

The post will be based at the Natural History Museum, and will make use of the Museum's excellent molecular laboratory facilities and extensive collections. The successful applicant will be interested in the recovery of DNA sequences from museum specimens, and the application of these data in evolutionary biology and applying this to eco-evolutionary questions.

Salary will be 33,416 per annum plus benefits.

Informal enquiries can be addressed to Dr Selina Brace (s.brace@nhm.ac.uk) or Prof Ian Barnes (i.barnes@nhm.ac.uk).

Closing date: 9am on Monday 16 October 2017.

"I.Barnes@nhm.ac.uk" <I.Barnes@nhm.ac.uk>

NOAA-FisheriesSeattle SeascapeGenomics

The Conservation Biology Division at the Northwest Fisheries Science Center in Seattle seeks a National Research Council (NRC) postdoctoral research associate in genetic mixture analysis and genomics. The Genetics and Evolution Program is the oldest fishery genetics laboratory in the county and played a pivotal role in the development of genetic mixture analysis applied to fishery science and management (modeled stock composition and individual assignment). Currently, researchers have implemented next generation sequencing methods in a wide range of evolutionary and ecological studies. The goals for the NRC postdoctoral fellow are both technical in further developing genotyping-by-sequencing methods and building the reference baseline datasets, as well as theoretical and descriptive in the analysis and interpretation of contemporary and historical Chinook salmon samples from ocean fisheries (including a 40-year time series ideally suited to climate and ocean ecology studies). The research will involve building genomic DNA libraries, bioinformatics processing of sequence data, and analyze stock composition in ocean fisheries, stock-specific migration, and association with ocean conditions. A theoretical population genetics background with extensive computational/bioinformatic experience is essential along with experience in computing languages and programs that facilitate population genomic and seascape genomic studies.

The NRC Research Associateship Program is administered by the National Academies of Sciences, Engineering and Medicine. The initial funding period for the award is one year, renewable for up to three years pending funding. NRC research associates receive a competitive stipend, health insurance and travel allowance. Details on eligibility, terms, and application for the award may be found at http://bit.ly/2hpWj5g, research opportunity number 26.03.39.C0079. The online application is now open, with applications due 1 November 2017. Applications include a research proposal, which will be developed by the applicant in discussing the project with the research advisers. Applications and supporting documents are to be submitted by the deadline to the NRC WebRAP system (https://nrc58.nas.edu/nrcwebrap/rap/login/login.asp). For more information, please contact prospective co-advisers Dr. Paul Moran (paul.moran@noaa.gov) or Dr. Krista Nichols (krista.nichols@noaa.gov).

Paul Moran <paul.moran@noaa.gov>

OberlinC Ohio EvolutionMetabolicPathways

The Goldman lab in the Department of Biology at Oberlin College invites applications for a full-time postdoctoral research position in computational biology. This is a one-year, non-continuing position with the potential of renewal for one additional year. The postdoctoral fellow will work with Dr. Aaron Goldman on a NASA-funded research project investigating the early evolution of metabolic pathways. The research, which will be entirely computational in nature, seeks to identify the earliest metabolic pathways and is part of a larger research collaborative involving origin of life laboratories at NASA Jet Propulsion Laboratory and the University of Southern California. The postdoctoral fellow will have the opportunity to mentor Oberlin undergraduates assisting with the research. The position has a preferred start date between October 15 and November 30, 2017. Questions about the position can be addressed to Dr. Aaron Goldman at agoldman@oberlin.edu. To apply, please follow the link... http://jobs.oberlin.edu/postings/5244 Aaron Goldman <agoldman@oberlin.edu>

OregonStateU ForestMetagenomics

Postdoctoral scholar: Developing and applying multi-species metagenomic assessments in Pacific Northwest forests.

Oregon State University

We are seeking a skilled and enthusiastic post-doctoral research scholar to provide bioinformatics and genomics leadership on a project developing multi-species metabarcoding approaches for assessing diversity and health in forest riparian ecosystems in the Pacific Northwest of North America. The goal of the project is to develop and apply multigene multiplexing approaches that characterize and quantify species-level diversity, and developing analytical pipelines that convert next-generation sequencing data into count data that describe presence/absence, abundance, and spatial genetic diversity of target organisms. This full-time position (Postdoctoral Scholar, 1.0 FTE, salary $52,000/year with health care benefits) requires a one-year commitment, with the potential of a one-year extension, starting as early as November 1, 2017. Qualified applicants are invited to electronically submit an application, including (1) a cover letter; (2) a full-length curriculum vitae (CV); and (3) the names and contact information of three referees. We invite you to visit the application web site https://jobs.oregonstate.edu/postings/47422 for further details about position # P01495UF and information on how to apply. OSU is an AA/EOE/Vets/Disabled employer

Brooke Penaluna, PhD | Research Fish Biologist USFS PNW Research Station | Corvallis, OR bepenaluna@fs.fed.us|brooke.penaluna@oregonstate.edu (541) 758-8783

"Penaluna, Brooke" <Brooke.Penaluna@oregonstate.edu>

Paris EvolutionaryEcology Phylogenetics

Postdoctoral positions. Evolutionary ecology - phylogenetics. Ecole Normale Supérieure, Paris

Several postdoctoral positions are available to work in Hélène Morlon's group at the Ecole Normale Supérieure (http://www.phyloeco.biologie.ens.fr/) on a project supported by a five-year grant from the European Research Council (ERC), in the general area of evolutionary ecology and phylogenetics. The project integrates across diverse fields (macroevolution, macroecology, community ecology, ecological networks, paleobiology, microbial ecology) with a focus on phylogenetic approaches. Applicants with diverse backgrounds are encouraged to apply (e.g. mathematics, physics, ecology, evolutionary biology, genomics, bioinformatics). Interest/experience in advancing phylogenetic comparative methods, studying diversification and/or phenotypic evolution at large spatial and temporal scales, studying the (macro)evolution of species interaction networks, or developing a research project at the interface between genomics and macroevolution will be particularly appreciated.

Applicants should have solid quantitative, programming, and/or bioinformatics skills, as well as good writing skills. Speaking French is not mandatory.

The postdoctoral researchers will work in Hélène Morlon's group at the Institue of Biology of the Ecole Normale Supérieure (http://www.biologie.ens.fr/depbio/). The IBENS is a multidisciplinary research centre in Biology conveniently located in the Latin Quarter in downtown Paris. The centre develops research in a wide range of disciplines, including evolutionary biology, ecology, computational biology, genetics, and comparative genomics.

Review of applications begins immediately and will continue until the positions are filled. Starting dates are flexible and salaries depend on experience. To apply, please submit: i) a cover letter summarizing research interests and expertise ii) a Curriculum Vitae (including publications), and iii) the names and contact information for at least two references. Questions and application should be sent to Hélène Morlon (morlon@biologie.ens.fr).

Helene Morlon <morlon@biologie.ens.fr>

RiceU RiceAcademy EvolBiol

Rice University is pleased to invite applications for the Rice Academy Postdoctoral Fellows Program.

The 2018 competition is open to all research areas, but applications/proposals broadly related to evolutionary biology are encouraged. (In fact, two of the first five postdocs awarded in 2016 had an EEB topic.)

Please contact potential faculty mentors/collaborators from our Ecology & Evolutionary Biology program if interested: http://biosciences.rice.edu/Content.aspx?id=2147484507 < http://biosciences.rice.edu/Content.aspx?id=2147484507 >

The two-year Rice Academy Postdoctoral Fellowships are open to exceptional scholars who have recently earned the doctoral degree in any area, including medicine, and who want to pursue research with faculty at Rice University. Applications are particularly welcome from those who are interested in interdisciplinary approaches to scholarship. The Fellowship term will begin on September 1, 2018. The Rice University Academy of Fellows is a vibrant interdisciplinary community composed of Rice Academy Postdoctoral Fellows and Rice Academy Faculty Fellows. Academy Postdoctoral Fellows can be housed in any department at Rice University. Postdoctoral Fellows are appointed to a two-year term, and they take a concurrent complementary non-tenure track faculty appointment in an appropriate department at Rice. Fellows are generally expected to remain in residence in or near Houston to actively participate in the Academy. Rice Academy Postdoctoral and Faculty Fellows hold regular gatherings that support social interactions, as well as intellectual and academic pursuits. Fellows should attend regularly and present their work at least once a year. Professional development is a central focus, and Academy Postdoctoral Fellows will receive close mentorship in pursuit of the NIH K99 or other career development awards. The research of each Academy Postdoctoral Fellow is mentored by two professors at Rice University.

The Rice Academy Senior Fellows will begin application reviews as early as December 1, 2017. All applications for the 2018 competition are due January 10, 2018.

For detailed information about the fellowship: https://riceacademy.rice.edu/about Scott P. Egan Assistant Professor Department of Biosciences Rice University

https:///sites.google.com/site/scottpegan/ Scott Egan <scott.p.egan@rice.edu>

Szeged Hungary FungalEvolution

Three ERC-funded postdoctoral positions in fungal genomics, bioinformatics and evolution

Applications are invited for 3 postdoctoral positions by candidates with an interest in pursuing groundbreaking research on the evolution of multicellularity and organismal complexity and its relationship to the cis-regulatory genome in fungi. The projects use fungi as a model system and employ various molecular biology, NGS-based, genetic engineering, single-cell RNA and phylogenetic approaches.

The Project

The aim of the project is to understand the general principles of the evolution of complex multicellularity in fungi as a model system. What genomic prerequisites does the evolution of complex multicellularity (and increased organismal complexity in general) have? How does cis-regulatory evolution contribute to the evolution of novel phenotype? What is the genetic toolkit of fruiting body development in fungi? Are there major patterns of genome-evolution associated with the multicellularity? The project aims to test broad hypotheses related to the above questions using a combination of state of the art experimental and computational approaches.

The Candidates

The successful candidates are highly motivated, experienced in and capable of developing protocols and workflows for one or combinations of the above-mentioned approaches (with help from the PI), have good problem solving and team player skills. The position involves working independently and with other members of the research team, and provides the opportunity to interact with the wide knowledge base in molecular and systems biology at the Synthetic and Systems Biology Unit (http://group.szbk.u-szeged.hu/sysbiol/). Experience in RNA-Seq, the CRISPR/Cas9 system, genetic manipulation of filamentous fungi, in vitro protein expression or phylogenetics/genomics is a plus.

The Lab

The successful candidate will join the Fungal Genomics and Evolution lab (http://group.szbk.u-szeged.hu/sysbiol/nagy-laszlo-lab-overview.html) recently funded by the European Research Council (project duration: 2018-2023). The Lab is part of the Synthetic and Systems Biology Unit of the Institute of Biochemistry, BRC-HAS, a vibrant systems and evolutionary biology research unit, comprising young PI-s and an inspiring atmosphere. It is located in Szeged, a mediterranean-feeling city in southeast Hungary, centered around a strong pedigree in higher education (the University of Szeged has ca. 30000 students), providing an inspiring and welcoming environment for open-minded postdocs.

Contact and application If interested, please send a motivation letter along with your CV to Laszlo G. Nagy (lnagy@fungenomelab.com).

László Nagy <cortinarius2000@gmail.com>

UArkansas EvolutionaryGenomics

The Alverson Lab at the University of Arkansas is recruiting a Post-Doctoral Fellow to work on the evolutionary genomics of marine-freshwater transitions in diatoms. The project combines comparative genomics and experimental transcriptomics to address basic questions about the rate and mode of environmental adaptation in microbial eukaryotes. The researcher will be encouraged to develop and pursue his or her own questions in this area. More information, with instructions on how to apply, is available here: https://jobs.uark.edu/postings/22582 The start date is flexible.

The University of Arkansas is located in Fayetteville, Arkansas, in the middle of the beautiful Ozark Mountains. Fayetteville is consistently ranked among the top 5 places to live in the United States < https://realestate.usnews.com/places/rankings/best-places-to-live >.

Please contact me with questions.

Thanks,

Andy

Andrew Alverson University of Arkansas Department of Biological Sciences 1 University of Arkansas, SCEN 601 Fayetteville, AR 72701-1201

office: 479-575-7975 lab: 479-575-4886

http://alversonlab.com/ “alversoa@umail.iu.edu” <alversoa@umail.iu.edu>

UBern 4PDF PhD EvolutionCooperation

4 PhD- and postdoc positions are available at the University of Bern, to study the

Evolution of cooperation based on relatedness, negotiation and trading

All major transitions in the evolution of life are characterized by the necessity of cooperation and sacrifice of constituent parts transforming into higher complexity. Conceptually, the evolution of cooperation seems to be well understood. However, critical tests of the predictions from alternative mechanisms responsible for the establishment of evolutionarily stable levels of cooperation hardly exist. For instance, the seemingly overwhelming evidence for the importance of kin selection to the evolution of altruism is almost entirely correlational. Few studies have manipulated relatedness and measured behavioural responses and corresponding fitness effects, and several have found that relatedness in fact hampers cooperative behaviour instead of promoting it, opposite to predictions from kin selection theory. The relative significance of alternative mechanisms in addition to kin selection, such as negotiation and reciprocal trading, to explain cooperation in nature is as yet unclear. In this project we aim to develop and experimentally test predictions regarding the relative and interactive influence of relatedness and negotiation/trading on cooperation between social partners.

Our previous work has suggested that mutual help and trading of service and commodities are important and widespread variants of cooperative interactions among animals, which can elicit high levels of evolutionary stable cooperation. A crucial parameter in reciprocal trading is the potential time delay between subsequent interactions among social partners, because this affects the perceived or true probability to receive returns for provided help. One aim of this project will be to vary the time axis of social decisions between concurrency and delays of different magnitude to span the entire range from coaction to long-term reciprocity. Another important issue is that in nature most social interactions involve some sort of asymmetry between concerned individuals, regardless whether this is sex, age, dominance status, body condition, individual quality, need, resource holding potential, reproductive status, residual reproductive value, etc. Consequently, in virtually any social interaction the involved individuals have different abilities and expectations about potential pay-offs from the interaction. The current project aims to experimentally scrutinize the significance of asymmetries for the negotiation process between social partners about their respective cooperative effort.

Hitherto, effects of experimental manipulation of cooperation on direct and indirect components of fitness have hardly been scrutinized. We aim at estimating fitness effects of experimentally controlled cooperative behaviour in natural and semi-natural settings by manipulating at the same time relatedness and the negotiation rules applied by all involved parties. Our model organisms will be wild-type Norway rats and cooperatively breeding Lake Tanganyika cichlids.

Within the framework of this SNF-funded project, we offer one post-doc and three PhD-positions. We seek highly-motivated and well organised candidates who can work independently as well as drive collaborative projects. Scientific curiosity is a must and good English language skills are important. Previous experience with studying animal behaviour is mandatory. The PhD-applicants will need an MSc-degree (or equivalent) in biology. Applications must include a letter of motivation, CV, list of publications, copy of degree certificates, and two names of referees who should have sent their recommendation letter separately before the mentioned deadline. Applications should be submitted before

Wednesday 25 October 2017

by e-mail (all documents merged into one PDF file) to Claudia.Leiser@iee.unibe.ch.

Late applications will be considered until all positions are filled. Starting date of all positions is as soon as possible. Duration of contracts is up to 3 years.

Principal investigator: Prof. Dr. Michael Taborsky

Behavioural Ecology Division, Institute of Ecology and Evolution

michael.taborsky@iee.unibe.ch

http://behav.zoology.unibe.ch/index.php?p=-109 "michael.taborsky@iee.unibe.ch" <michael.taborsky@iee.unibe.ch>

UCalifornia Davis PopulationBiol

DEADLINE: October 30, 2017

POSTDOCTORAL FELLOW IN POPULATION BIOLOGY–The Center for Population Biology at UC Davis invites applications for a Postdoctoral Fellowship in Population Biology, broadly defined to include ecology, phylogenetics, comparative biology, population genetics, and evolution. We particularly encourage applications from candidates that have recently completed, or will soon complete, their PhD.

The position is for TWO YEARS, subject to review after one year, and can begin as early as July 1, 2018. This position is covered by a collective bargaining unit. It has a starting annual starting salary of $48,216 plus benefits, and $6,000 per annum in research support. The Fellow will be a fully participating member in the

Center for Population Biology and will be expected to have an independent research program that bridges the interests of two or more CPB faculty research groups. We strongly encourage candidates to contact appropriate faculty sponsors before applying. We also ask that each Fellow propose a workshop, discussion or lecture series that they could offer to the community of population biologists at UC Davis; faculty sponsors or the Director of CPB, Artyom Kopp, can provide additional input on this aspect of the fellowship. For samples of past workshop abstracts and more information about UC Davis programs in population biology, see https://-cpb.ucdavis.edu/cpb-postdoc-fellowship . ONLINE APPLICATION: Interested candidates should submit a cover letter, CV, a short (1-2 page) description of research accomplishments, a short (1-2 page) description of proposed research including potential faculty mentors, a brief (1 page or less) description of their proposed workshop, and copies of two publications, all in PDF format at: https://recruit.ucdavis.edu/apply/JPF01868. Applicants should also provide the information requested for three referees. Once entered, applicants will electronically request letters from referees who will then be prompted by email with upload instructions. Refer to the on-line instructions for further information. For full consideration, applications (including letters of reference) must be received by October 30, 2017. The University of California is an Equal Opportunity/Affirmative Action Employer with a strong institutional commitment to the development of a climate that supports equality of opportunity and respect for diversity. E-mail questions to smmann@ucdavis.edu.

John J. Stachowicz, Professor and Chair Department of Evolution and Ecology University of California Davis CA 95616

jjstachowicz@ucdavis.edu http://-stachlab.wordpress.com Jay Stachowicz <jjstachowicz@ucdavis.edu>

UCIrvine EvolutionaryResponseEnvironmentalChange

Postdoctoral Position in Evolutionary Responses to Environmental Change

The Campbell lab in Ecology & Evolutionary Biology at the University of California at Irvine (http:/-/faculty.sites.uci.edu/campbelllab/) invites applications for a post-doctoral position examining how climate influences natural selection. The project is part of a NSF-funded research program designed to test models for evolutionary rescue and determine if plant populations can adapt quickly enough to environmental change to avoid extinction. The postdoc will investigate impacts of snowmelt timing and summer precipitation on the strength of selection on vegetative and floral traits. The project will involve extensive field research based at the Rocky Mountain Biological Laboratory (http://www.rmbl.org/), ideally beginning in spring 2018. The successful candidate will have the opportunity to combine field data with quantitative genetic and demographic modeling and to develop expertise in gas chromatography - mass spectrometry of flower volatiles. The postdoc will also be able to collaborate with a dynamic group of ecologists and evolutionary biologists at both UC Irvine and RMBL.

Required qualifications include a Ph.D. in ecology, evolutionary biology, or a related field, demonstrated experience in conducting field experiments, strong statistical skills, and a successful publication record. The ideal candidate will also have expertise in one of the following areas: chemical analysis of plant volatiles, plant ecophysiology, population modeling.

The initial appointment is for one year with potential for renewal. The salary is competitive and commensurate with experience.

Review of applications will begin October 21, 2017, and will continue until the position is filled. Candidates should submit curriculum vitae, statement of research interests and experience, and names and contact information for three references to the following on-line recruitment site:

https://recruit.ap.uci.edu/apply/JPF04298 For more information about this position, contact Dr. Diane Campbell at drcampbe@uci.edu. See also: Campbell, D.R. and J.M. Powers. 2015. Natural selection on floral morphology can be influenced by climate. Proceedings of the Royal Society B 282: 21050178. DOI: 10.1098/rspb.2015.0178

The University of California, Irvine is an Equal Opportunity/Affirmative Action Employer advancing inclusive excellence. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age, protected veteran status, or other protected categories covered by the UC nondiscrimination policy.

– Diane Campbell Professor, Ecology & Evolutionary Biology University of California, Irvine Irvine, CA 92697 USA

Research Scientist, Rocky Mountain Biological Lab

drcampbe@uci.edu http://www.faculty.uci.edu/profile.cfm?faculty_id=2124&name=Diane%20R.%20Campbell http://faculty.sites.uci.edu/campbelllab/ Diane Campbell <drcampbe@uci.edu>

UCLondon Multivariate yeast adaptation

Postdoctoral Research Associate at University College London

The effects of genetics, mutation and selection on Evolutionary Rescue in complex environments

We are looking for a postdoctoral research associate to work with Max Reuter and Jürg Bähler at University College London. The position is available for three years and funded by a grant from the BBSRC, which also includes Daniel Jeffares (University of York) and Doug Speed (UCL Genetics Institute) as collaborators.

The project will study how the interplay between genetics and evolutionary forces shapes the capacity of populations to show rapid adaptive responses. The project will use high-throughput phenotyping, genomics and quantitative genetics in fission yeast to investigate the genetic basis of growth responses to different environmental gradients (salinity, temperature), and establish how genetic correlations between responses arise from overlap in genetic pathways. We will then asses how mutation and selection acting within these genetic constraints shape standing genetic variation and how this, in turn, affects population survival in the face of sudden shifts in their multivariate environment. The project thus combines fundamental evolutionary concepts with functional genetic aspects that are accessible in a tractable microbial model. The results will be relevant in the context of sudden, strong selection, be it in relation to climate change, antibiotic treatments or agricultural pest control.

The postdoctoral research associate will interact with both the groups of Max Reuter, working on evolutionary constraints on phenotypic adaptation (http://www.homepages.ucl.ac.uk/~ucbtmre/Labsite), and Jürg Bähler, working on genome regulation (http://www.bahlerlab.info/home/). Both are based in UCL's Research Department of Genetics, Evolution and Environment, which offers a stimulating and interactive environment across the fields of evolutionary and human genetics to biodiversity research. Further afield, UCL offers a great diversity of world-class research right in the centre of London.

The position is an opportunity for a highly motivated, ambitious and independent individual. The candidate will have (or be about to obtain) a PhD in a relevant discipline, a strong interest in evolutionary genetics and/or microbiology, proven research skills (as evident in publication record and prior research findings), experience in relevant approaches (such as quantitative genetics/genomics, molecular microbiology, high-throughput phenotyping, statistics) and excellent verbal and written communication skills.

The post is available from 1st November 2017 (negotiable) for up to 36 months, with a starting salary between 34,045 (31,076 plus 2,980 London Allowance) and 41,163 per annum (38,183 plus 2,980 London Allowance), depending on experience. In line with UCL regulation, candidates who have not yet obtained their PhD will be paid at a lower grade until the date of their final thesis submission.

For more information on the application process and to submit applications, search reference 1669963 on the UCL Jobs database or follow this link: https://atsv7.wcn.co.uk/search_engine/jobs.cgi?SID=amNvZGU9MTY2OTk2MyZ2dF90ZW1wbGF0ZT05NjUmb3duZXI9N In case you have difficulties with the online system, please email biosciences.staffing@ucl.ac.uk. For informal enquiries or more information on the project, email Max Reuter (m.reuter@ucl.ac.uk).

The closing date for applications is 16 October 2017.

Max Reuter

Research Department of Genetics, Evolution and Environment Faculty of Life Sciences University College London Darwin Building Gower Street, London WC1E 6BT, UK

Phone: +44-20-76792201 (internal 32201)

Lab: http://www.homepages.ucl.ac.uk/~ucbtmre/Labsite/ Department: http://www.ucl.ac.uk/gee m.reuter@ucl.ac.uk

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UCollegeLondon StatisticalGeneticsRiceChickpea

Research Associate in Statistical Genetics and Bioinformatics, - Ref:1671499

We are recruiting a talented statistical geneticist/bioinformatician to determine the genetic basis of complex phenotypes in rice and chickpea, with the aim of improving these important crops. The methodologies developed by the project will apply to many crops and animals. The post is funded by the UK Global Challenges Research Fund and the BBSRC.The post-holder will join the group of Richard Mott in the Genetics Institute (UGI) University College London (UCL), and will work in close collaboration with the International Rice Research Institute (IRRI), Philippines, and the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT), India, and the National Institute for Agricultural Botany (NIAB), Cambridge. The postholder will join a dynamic team of statistical geneticists working on a variety of problems. The project focuses on (i) the imputation of genome sequence from crop populations sequenced at low coverage, adapting methods developed previously in the group (e.g. Davies et al Nature Genetics 2015) (ii) the use of low-coverage population sequence to identify structural variants implicated in phenotypes (Imprialou et al Genetics 2017) (iii) The development and implementation of quantitative genetics and genomic prediction methods in crop development, particularly in relation to multiparental advanced intercrosses. (iv) Close collaboration, support and knowledge exchange with partner laboratories. The project will involve visits to both IRRI and ICRISAT.

The post is available from now until 30 June 2021 with possibility of extension.

Key Requirements PhD in Statistical Genetics, Bioinformatics or a related field is essential as is a good understanding of the statistics of genetic association and experience of manipulating and analysing Next-Gen sequence data. It is essential candidates demonstrate programming fluency in R, Perl/Python, or C/C++. The successful candidate must have experience of conducting research in statistical genetics or bioinformatics.

Grade7 34,635 - 41,864 per annum (inclusive of London allowance) Full details on the role available from http://tinyurl.com/ycfqjv9v Please ensure you read these carefully before applying for the post as candidates must meet all essential criteria to be considered. If you would like to discuss the post please contact Professor Richard Mott, r.mott@ucl.ac.uk Closing Date15 Oct 2017

r.mott@ucl.ac.uk

UCopenhagen 2yr NarwhalPopulationGenomics

Postdoctoral Position in Narwhal Population genomics

Applications are invited for a two-year postdoctoral researcher position in the field of population genomics in the group led by Assoc. Prof. Eline Lorenzen at the Natural History Museum of Denmark, University of Copenhagen from 01.01.2018 - 31.12.2019.

The postdoctoral researcher will generate and analyze population genomic data from modern narwhal, to investigate the population dynamics and evolutionary history of the species. Applicants should have completed a PhD in the fields of Population Genomics, Evolutionary Genomics or Computational Science and have an established record of research productivity and publications in high-profile scientific journals.

We are seeking a highly motivated and productive scientist who is interested and capable of contributing to a research team consisting of molecular biologists, bioinformaticians, and evolutionary biologists. S/he should have strong research interests in evolutionary biology and large-scale genome analyses as well as a solid training in statistical and population genomics.

The ideal candidate will show great abilities to work in a team environment and strong expertise in the molecular tools and/or computational procedures used in next-generation sequencing and population genomics. S/he will have documented experience with NGS methods and data, and strong bioinformatics skills. While not mandatory, high proficiency in R, Perl, Python and/or C++ programming, as supported by a track record of software implementation will be highly considered.

The successful candidate will also be responsible for the daily management of his/her research project in coordination with other members of the group. S/he will be actively involved in the training and co-supervision of other staff members and students. Strong teaching experience is, thus, recommended.

The post may also include performance of other duties including teaching and outreach.

Due to the developmental nature of the position, for consideration, applicants must be able to document the following skills:

* Expertise in the laboratory skills required for Illu-

mina based sequencing * Expertise in the informatics skills required for population genomic analysis * Research dissemination through at least 3 peer-reviewed publications

Further information on the Natural History Museum of Denmark is linkedat: http//snm.ku.dk/english/. Information about Section for Evolutionary Genomics canbe found at: http//snm.ku.dk/english/research/sections/evolutionary_genomics

Inquiries about the position can be made to Associate Professor Eline Lorenzenat elinelorenzen@snm.ku.dk

The deadline for applications is Monday October 9th 2017, 23:59 GMT +1.

To apply, please go to this link: http://jobportal.ku.dk/-videnskabelige-stillinger/?show=145502 Eline Lorenzen <elinelorenzen@snm.ku.dk>

UCopenhagen PopulationGenomics

Postdoctoral Position in Population genomics Applications are invited for a two-year postdoctoral researcher position in the field of population genomics in the group led by Assoc. Prof. Eline Lorenzen at the Natural History Museum of Denmark, University of Copenhagen from 01.01.2018 - 31.12.2019.

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The successful candidate will also be responsible for the daily management of his/her research project in coordination with other members of the group. S/he will be actively involved in the training and co-supervision of other staff members and students. Strong teaching experience is, thus, recommended.

The post may also include performance of other duties including teaching and outreach.

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* Expertise in the laboratory skills required for Illumina based sequencing * Expertise in the informatics skills required for population genomic analysis * Research dissemination through at least 3 peer-reviewed publications

Further information on the Natural History Museum of Denmark is linkedat: http://snm.ku.dk/english/. Information about Section for Evolutionary Genomics canbe found at: http://snm.ku.dk/english/research/-sections/evolutionary_genomics Inquiries about the position can be made to Associate Professor Eline Lorenzenat elinelorenzen@snm.ku.dk

The deadline for applications is Monday October 9th 2017, 23:59 GMT +1.

To apply, please go to this link: http://jobportal.ku.dk/-videnskabelige-stillinger/?show=145502 Eline Lorenzen <elinelorenzen@snm.ku.dk>

UEdinburgh ClimateAdaptationTits

A three-year postdoctoral research position is available in a NERC funded project studying the relationship between temperature and optimal breeding phenology of blue tits over space and time. The research will involve field data collection and manipulative experiments replicated across 44 sites along a 200km transect in the Scottish Highlands, combined with analysis of metabarcoding derived diet data, and application of novel statistical models. The relationship between temperature and optimum phenology is key to predicting population responses to climate change and the postdoc will establish (i) whether this relationship varies among populations; (ii) its mechanistic underpinnings and (iii) whether space can substitute for time in estimating the relationship. Essential experience includes the statistical analysis of complex data sets and the use of hierarchical (mixed) models. Some experience with large-scale fieldwork would be useful and the applicant must have good communication skills and be able to manage a team of field assistants.

The project is funded by a Natural Environment Research Council (UK) grant to Dr Ally Phillimore and Dr Jarrod Hadfield (University of Edinburgh), and Dr James Pearce-Higgins and Dr Dave Leech (British Trust for Ornithology). The postdoc would join a large and active research group in Edinburgh working on the evolutionary ecology of wild populations.

This post is full time and fixed term for 3 years. The post is available from 1st Jan 2018.

Informal enquiries to: Ally Phillimore, Institute of Evolutionary Biology University of Edinburgh, Edinburgh EH9 3JT, UK Tel. (44) 131 650 5413 albert.phillimore@ed.ac.uk http://phillimore.bio.ed.ac.uk/ For further details and to apply please use this link https://www.vacancies.ed.ac.uk/pls/corehrrecruit/erq_jobspec_version_4.jobspec?p_id=041392
PHILLIMORE Ally <aphillim@exseed.ed.ac.uk>

UEdinburgh PopulationGenomics

Two postdoctoral research positions to work on a newly funded ERC project with Konrad Lohse (Institute of Evolutionary Biology, University of Edinburgh, UK) 'ModelGenomLand - Modelling the genomic landscapes of selection and speciation':

1) Postdoc in population genomics

Enthusiastic and motivated postdoc wanted to:

i) develop analytic and simulation based methods for modelling selection and demography from whole genome data ii) apply these new tools to whole genome datasets to quantify genome- wide selection and make inferences about the speciation process

Applicants should have a strong interest in statistical inference and population genetics, a PhD in a relevant subject area (population genetics, statistics, computer science or a related quantitative field) and a strong track record of independent and creative thinking.

2) Postdoc in butterfly speciation genomics

I am looking for an enthusiastic and motivated postdoc interested in comparative genomics and speciation. The postdoc will collaborate closely with Lepbase (http://lepbase.org/) to generate and analyse whole genome data for several European butterfly species and investigate the genomics of speciation in a comparative framework

Applicants should have a strong background in comparative and evolutionary genomics and a PhD in a relevant subject area (genetics, bioinformatics). Experience working with whole genome data is essential, as is a strong track record of independent and creative thinking. Experience with long read data, genome assembly and genome analysis/interrogation would be very advantageous.

Both postdocs will collaborate with several Project Partners in the UK and abroad and there is ample scope within the project to develop independent lines of research with a view to establishing themselves as independent investigators. The grant includes substantial funds for computing, sequencing and to attend international conferences.

Both positions are for 3 years from 1st February 2018 and can be extended for a further 2 years based on performance.

To apply, go to http://www.ed.ac.uk/human-resources/jobs and search for vacancies 041050 and 041051.

Closing date for applications: 6th of October 2017

Applicants are strongly encouraged to contact konrad.lohse@ed.ac.uk ahead of application.

LOHSE Konrad <klohse@exseed.ed.ac.uk>

UExeter SocialBees

POSTDOCTORAL POSITION: SOCIAL EVOLUTION IN SWEAT BEES

A 3 year full time ERC-funded postdoctoral position is available starting 1 January 2018 in the research group of Professor Jeremy Field, based in the Centre for Ecology & Conservation, University of Exeter, Cornwall Campus, UK (http://biosciences.exeter.ac.uk/cec/staff/index.php?web_id=Jeremy_Field&tab=profile). The successful applicant will work on a project investigating the evolution of queen-worker caste differences and social behaviour in sweat bees (Halictidae: Lasioglossum, Halictus). A 4th year of funding may be available, depending on the needs of the project.

The post will include work carrying out field transplants, behavioural observations and experiments, together with transcriptomic work relating behaviour to gene expression (see Field et al. 2010 Current Biology 20:2028-31 for an example of our behavioural work). The successful applicant will have relevant experience in evolutionary or behavioural ecology and/or transcriptomics with non-model organisms.

The closing date for completed applications is midnight on 8th October. Interviews are expected to take place during 26-31 October 2017.

For full details, including how to apply, see the link at:

https://jobs.exeter.ac.uk/hrpr_webrecruitment/wrd/run/ETREC107GF.open?VACANCY_ID=037271JanP&WVID=3817591jNg&LANG=USA Or enter the job reference number (P58889) as a keyword in the University of Exeter job search engine at:

https://jobs.exeter.ac.uk/hrpr_webrecruitment/wrd/run/etrec105gf.open?wvid=3817591jNg Jeremy Field Professor of Evolutionary Biology Centre for Ecology and Conservation University of Exeter Penryn Campus Cornwall TR10 9EZ

“Field, Jeremy” <J.P.Field@exeter.ac.uk>

UHelsinki 5 ClimateAdaptation

The Department of Biosciences at the University of Helsinki invites applications for 5 post doc positions to utilize long-term ecological data to understand impacts of global change

The post doc positions are part of the Research Centre for Ecological Change and are funded by the Jane and Aatos Erkko Foundation for 1.1.2018-31.12.2020. PIs of the Centre are prof. Anna-Liisa Laine, prof. Otso Ovaskainen, prof. Tomas Roslin, assist. prof. Jarno Vanhatalo and dr Marjo Saastamoinen. The starting date is 1.1.2018, but a later starting date can be negotiated. The overreaching aim of the Centre is to generate a coordinated analysis of long-term ecological data to understand impacts of global change. To unravel how populations and interactions between species in nature are responding to ongoing environmental change, the project takes advantage of the unique long-term datasets collected in Finland. The centre also develops state-of-the-art methodology for analysing long-term spatially structured data sets within a joint species distribution modeling framework. For more information on the Centre, please visit https://www.helsinki.fi/en/researchgroups/research-centre-for-ecologica l-change

The salary of the successful candidate will be based on level 5 - 6 of the demands level chart for teaching and research personnel in the salary system of Finnish universities. In addition, the appointee will be paid a salary component based on personal performance. The starting salary will be ca. 3300 - 3800 euros/month, depending on the appointee’s qualifications and experience.

The deadline for submitting the application is 7 October 2017.

A link to the University of Helsinki Recruitment System where applications can be submitted will be available after mid September at: https://www.helsinki.fi/en/researchgroups/research-centre-for-ecologica l-change

3 POST DOC POSTITIONS IN POPULATION/COMMUNITY ECOLOGY

We are seeking three post docs to analyse extensive ecological datasets. The successful candidates will take part in developing the specific research questions, and in linking spatial and temporal data on the abundance and distribution of species and on community composition to data on habitat structure, population harvesting, fragmentation, land use and/or weather. Examples of questions of interest include the role of environmental change on biodiversity in different habitats, on the spread of pests, disease, and invasive species, on the threat status of endangered species, and on potential mismatches in phenology among interacting species. The data and research questions concern both aquatic and terrestrial ecosystems. The focus of the specific research questions can be modified in accordance with the background and interests of the candidate. The successful applicant should have completed a PhD in ecology or a related field, and have a strong background in statistics, spatial statistics, and/or GIS. We seek candidates with excellent written and verbal communication skills, and the ability to conceive, execute and complete research projects, and to think independently and creatively. The post docs will work as a part of a team at the Centre but also with researchers from other environmental institutes. Overall, excellent social skills are required for extensive collaborations. For more information, contact prof. Anna-Liisa Laine, prof. Tomas Roslin and/or Dr. Marjo Saastamoinen by email: anna-liisa.laine@helsinki.fi, tomas.roslin@helsinki.fi, marjo.saastamoinen@helsinki.fi

References

Jousimo, J, Tack, AJM, Ovaskainen, O., Mononen, T.,

Susi, H., Tollenaere, C. & Laine, A.-L. 2014. Ecological and evolutionary effects of fragmentation on infectious disease dynamics. Science, 344: 1289-1293.

Saastamoinen, M., Ikonen, S., Wong, S.W., Lehtonen, R. & Hanski, I. 2013. Plastic larval development in a butterfly has complex environmental and genetic causes and consequences for population dynamics. Journal of Animal Ecology 82: 529-539.

Schmidt, N., Mosbacher, J., Nielsen, P., Rasmussen, C., Hoye, T., & Roslin, T. 2016. An ecological function in crisis? - the temporal overlap between plant flowering and pollinator function shrinks as the Arctic warms. Ecography 39: 1250-1252. DOI: 10.1111/ecog.02261.

2 POST DOC POSTITIONS IN STATISTICAL ECOLOGY

The post docs take part in the development of statistical methods for analyzing long-term ecological data and in statistical analyzes within the Research Centre for Ecological Change.

The methodological work focus on development of Hierarchical Modelling of Species Communities (HMSC) and hierarchical multivariate Gaussian processes. HMSC is a joint species distribution modelling framework that can be used for the statistical analysis of data on species

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UIdaho ConservationGenomics

The Waits and Hohenlohe labs at the University of Idaho are recruiting a postdoc in conservation genetics/genomics. See details below.

A one-year postdoctoral position, with the possibility of extension, is available to join our interdisciplinary conservation genetics research group (http:// http://www.uidaho.edu/cnr/faculty/waits). Our group focuses on using molecular methods to study the ecology, evolution and conservation status of wildlife populations. We conduct research on genetic diversity and gene flow, landscape genetics, mating system and behavior, predator-prey interactions, hybridization, environmental DNA monitoring, metabarcoding and noninvasive genetic monitoring of population demographics of wildlife. This active research group includes five graduate students, 1 research scientist, 2 laboratory technicians and multiple undergraduate students. The postdoc will be collaboratively mentored by Paul Hohenlohe in the Department of Biological Sciences (http://hohenlohelab.github.io/) and work on collaborative projects between the Hohenlohe and Waits labs. The successful candidate will (1) conduct research and contract work in conservation genetics and genomics; (2) assist in training and mentoring undergraduate and graduate students; and (3) assist in teaching a graduate level conservation genetics course and/or landscape genetics course. The successful candidate will be based in the Department of Fish and Wildlife Sciences and will be a member of the Laboratory of Ecological, Evolutionary and Conservation Genetics at the University of Idaho. We have state-of-the art facilities for genetic and spatial analyses and collaborate extensively with faculty and students in the Institute for Bioinformatics and Evolutionary Studies - IBEST(http://www.ibest.uidaho.edu).

For full details see, https://uidaho.peopleadmin.com/postings/19308 Review of applications will begin Sept 28th but applications will be accepted until a suitable candidate has been identified. Position is available starting Nov 2017.

Thanks,

Lisette Lisette Waits, PhD Distinguished Professor Department Head Fish and Wildlife Sciences University of Idaho Moscow, ID 83844-1136 (208) 885-7823

lwaits@uidaho.edu

UIdaho ModellingEvol

Multiple Openings for Postdoctoral Fellows at the University of Idaho

We seek to hire three postdoctoral fellows-two modeling and one empirical-to join our research team at the University of Idaho. The two modeling postdocs will be housed within the Center for Modeling Complex Interactions (CMCI). CMCI is funded by the National Institutes of Health and serves as an epicenter for research at the university. The central concept behind CMCI is that by housing modelers in proximity to each other and having them interact regularly with empiricists, synergies will emerge that drive research. For all three postdocs, we seek individuals who are creative in applying their skills to new problems, who are good at communicating across disciplines, and who sees themselves thriving in our highly collaborative environment. Researchers from CMCI, in collaboration with faculty from Brown University and the University of Vermont were recently awarded a major NSF EPSCoR grant with the goal of using biophysical protein models to map genetic variation to phenotypes. The empirical postdoc position will work on this NSF grant, in close collaboration with modelers from CMCI and researchers at Brown and Vermont.

For the two CMCI modeling postdocs, we are interested in applicants with many potential skill sets, including but not limited to: applied mathematics and mathematical biology (e.g., dynamical systems, PDEs, stochastic processes), systems biology, ecological modeling, statistical modeling, epidemiology, computer programming and novel package development, bioinformatics, and molecular modeling. Postdocs are expected to integrate into one or more CMCI workings groups. These groups are diverse and evolving. Some current examples include: studying the pathogenic effects of viral co-infection in drosophila and mice; modeling spectral shifts in opsin proteins; modeling how human social dynamics, e.g. peer influences on vaccination rates, generates feedback with disease dynamics; using microbiome data to model population dynamics of microbial communities; and modeling reproducibility in science.

The empirical postdoc will initially carry out lab work to assess how mutations in the fusion glycoprotein of respiratory syncytial virus (RSV) affect protein stability and antibody affinity and neutralization. The goal of the project is to combine molecular and mathematical modeling with empirical research to develop a framework for predicting how mutations - alone, in combination, and in different environments - influence protein stability, affinity for substrates and partners, and mapping to higher-level phenotypes. The empirical work will include the generation and characterization of mutation libraries in an RSV infectious clone and biochemical analyses of mutant fusion glycoproteins and antibodies. Collaboration with molecular and mathematical modelers will determine how well models can predict antibody escape. In time, this project will be extended to additional systems being studied at Idaho. We seek applicants with molecular biology and protein biochemistry skills, including targeted mutagenesis, high throughput molecular techniques, and protein expression.

All three positions will be located at the University of Idaho in Moscow. The empirical postdoc will work in the labs of Tanya Miura (http://www.webpages.uidaho.edu/miuralab/) and Paul Rowley (https://www.rowleylab.com/) in Biological Sciences and the modeling postdocs will be located within CMCI. CMCI is in a gorgeous, 3000 ft2 space on the top floor of the University of Idaho's new flagship research building, the Integrated Research Innovation Center. The University of Idaho is only eight miles from Washington State University in Pullman, Washington, providing an academically and culturally rich community. Moscow is a friendly mid-sized town on the rolling hills of the Palouse, with great parks, bike paths, restaurants, farmer's market and fantastic opportunities for recreation in the adjacent mountains and rivers. For more information about CMCI, the NSF EPSCoR project, the University of Idaho, and Moscow, go to http://www.cmciuidaho.org/ , https://ddg2phenome.org/, http://www.uidaho.edu/ and https://www.ci.moscow.id.us/.

To apply, submit to cmci@uidaho.edu : 1) a letter of application specifying which position (empirical or modeling) you are interested in and how you fit the job requirements; 2) a CV; 3) contact information for three individuals who can provide recommendations; and 4) PDFs of up to three publications. Please use POSTDOC APPLICATION as the subject line.

“mmattoon@uidaho.edu” <mmattoon@uidaho.edu>

UIllinois BeeGenomics

UNIVERSITY OF ILLINOIS URBANA-CHAMPAIGNâ€ DEPARTMENT OF ENTOMOLOGYâ€ FUNCTIONAL GENOMICS OF DISEASE AND PESTICIDE SUSCEPTIBILITY IN BUMBLE BEES

POSTDOCTORAL POSITION SALARY $43,000-$47,500 per yr.

Applications are invited to join the Cameron Lab in the Department of Entomology at the University of Illinois. Research will focus on experimental studies of the functional genomics and ecological effects of the fungal pathogen Nosema bombi, and its interactive effects with neonicotinoid pesticides, on bumble bee health. We are looking for expertise in the laboratory production and bioinformatic analysis of gene expression data (RNAseq, qPCR, etc.).

The collaborative research team includes Dr. Ben Sadd, Illinois State University, (https://faculty.sharepoint.illinoisstate.edu/bmsadd) and James Strange, Utah State USDA Bee Biology Lab (https://www.ars.usda.gov/pacific-west-area/logan-ut/pollinating-insect-biology- management-systematics-research/people/dr-james-strange/).

The research includes experiments on both declining and stable populations of bumble bees, with the broad goal of understanding causal factors of decline in U.S. bumble bee populations. We will examine how different species vary in susceptibility to pathogens and pesticides, investigating how these stresses can interact to the detriment of bee viability. An integration of colony-level, whole-organism, cellular, and transcriptomic approaches will address how susceptibility is linked to decline status. The postdoc will play a key role in setting up and analyzing RNAseq data. The ultimate goal is to identify expression and genetic diversity associated with infection and pesticide susceptibility. Major responsibilities will be to participate in experiments and develop the transcriptome datasets.

A strong bioinformatics or statistical genetics/population genetics background with a PhD degree in a relevant area is required. Communication skills are essential; programming skills are desirable.

To apply for this position, please submit your CV and a Statement of your interest in the position, including discussion of how your skills interface with the project's research needs, along with names and complete contact information for three professional references.

APPLICATION DEADLINE 20 September 2017.

For informal inquiries please contact Sydney Cameron (scameron@life.illinois.edu).

The University of Illinois is an Equal Opportunity, Affirmative Action employer. Minorities, women, veterans and individuals with disabilities are encouraged to apply. For more information, visit http://go.illinois.edu/EEO. To learn more about the University's commitment to diversity, please visit http://www.inclusiveillinois.illinois.edu. The University of Illinois conducts criminal background checks on all job candidates upon acceptance of a contingent offer.

Dr Ben Sadd Assistant Professor of Infectious Disease Ecology School of Biological Sciences Illinois State University Normal, IL 61790-4120

email: bmsadd@ilstu.edu twitter: @Saddlab < https://twitter.com/saddlab > web: https://faculty.sharepoint.illinoisstate.edu/bmsadd tel: +1 (309) 438 2651 fax: +1 (309) 438 3722

"Sadd, Benjamin" <bmsadd@ilstu.edu> "Sadd, Benjamin" <bmsadd@ilstu.edu>

UKentucky InsectEvolution ResistanceManagement

Post-doctoral position in insect evolutionary biology

Project: Funding is available for a post-doc to build theoretical models that integrate Integrated Pest Management (IPM) tactics with Insect Resistance Management (IRM), considering eco-evolutionary and metapopulation dynamics of adaptation. We aim to integrate past knowledge of pest systems with new modeling paradigms to identify novel solutions for insect resistance management. In particular, we seek an individual to extend a recently developed model of insect resistance evolution to investigate the influence of spatial structure, dispersal, type of refuge, crop rotations, insecticide application, and biocontrol strategies on the success of resistance management strategies. Outcomes of this research will include tests of hypotheses about resistance evolution and pest life history evolution in response to management strategies with the goal of identifying novel resistance management methodologies that improve pest suppression and the extend the life of pest control products. Additional details about the project are available upon request.

Qualifications: Interested individuals must have a PhD in entomology, ecology, evolutionary biology or a related field with expertise in modeling of ecological and/or evolutionary dynamics, particularly in a metapopulation context. Experience with C and R is desirable.

Hiring: Preferred start date is January 2018 or as soon thereafter as possible, though starting earlier might be an option. Initial funding is through December 2018; funding for additional years depends upon satisfactory completion of the Year 1 goals and extension of funding by our funder. Salary is dependent on experience.

Research PIs: Research funding for this project was awarded to Charles Fox (http://www.uky.edu/~cfox/) at the University of Kentucky.

To apply: Please email Charles Fox at cfox@uky.edu with your CV, a statement discussing your interest in this position and your experience as it relates to the project, and the names plus contact details of at least three references.

Deadline: The position will remain open until a suitable applicant is found.

– Dr. Charles W. Fox Professor and Director of Graduate Studies Department of Entomology University of Kentucky Lexington, KY 40546-0091 phone: 859-257-7474 e-mail: cfox@uky.edu web: www.uky.edu/~cfox Charles Fox <cfox@uky.edu>

ULausanne 4PDF 2PhD EvolutionaryGenomics

4 postdoctoral and 2 PhD positions: Evolutionary genomics/behaviour

University of Lausanne, Department of Ecology and Evolution

We are looking for PhD students and postdoctorals to work on three lines of research:

1. Ant behaviour. The idea is to study the evolution of division of labour with a new system based on fiducial identification labels and video tracking. This system which automatically follow all the individuals in a colony allows quantitative studies of behaviour.

2. Ant genetics. We previously identified a supergene influencing social organization in the fire ant Solenopsis invicta. We have sequenced five closely-related species and found that the same genomic element is also responsible for variation in social organization. The aim of the project is to analyse how this large non-recombining region is evolving.

3 Evolutionary genomics. We are sequencing + generating RNAseq data for queens and workers of ca. 80 ant species. These data will be available for all sorts of analyses related to social evolution and the study of the genetic basis underlying differences between castes.

These positions will be funded by an ERC grant and the Swiss NSF. Other topics of research on social behaviour are also possible if they fit the research interests of our group :

http://www.unil.ch/dee/page7717.html The Department of Ecology and Evolution is a well-funded and vibrant research institution, with superb facilities.

http://www.unil.ch/dee/keller-group Applications should comprise a CV, a list of publications, 1 page describing why you are interested in joining our group and contact information for three referees. Only applications with all these information will be considered. Applications should be sent laurent.keller@unil.ch Laurent Keller Department of Ecology and Evolution Biophore University of Lausanne 1015 Lausanne Switzerland http://www.unil.ch/dee/keller-group Laurent Keller <laurent.keller@unil.ch>

UMontana BacterialEvolutionaryGenomics

Postdoctoral Research Associate - Bacterial Evolutionary Genomics, University of Montana

The Miller Lab at the University of Montana, Missoula (http://hs.umt.edu/dbs/labs/miller) is searching for a postdoctoral research associate to investigate the evolutionary mechanisms responsible for the maintenance and expression divergence of gene duplicates in bacteria with exceptionally high gene duplication rates. Projects will involve analyses of large genomic and transcriptomic data sets. A Ph.D. in biology or a related field is required, and the successful candidate will demonstrate a strong background in molecular evolution and genomics as well as proficiency with programming in Python, Perl and/or R.

The Division of Biological Sciences at the University of Montana (hs.umt.edu/dbs) is home to a diverse and highly interactive faculty, and the Miller lab is housed in newly constructed space dedicated to evolutionary genomics research. Missoula is a great college town located in the heart of the Rocky Mountains with an exceptional quality of life. For further information on this position and our research, please contact Dr. Miller directly at scott.miller@umontana.edu.

To apply, please visit http://umjobs.silkroad.com and click the job title for this position (Tracking Code 1811-254) under All Openings. Candidates must apply online and will be asked to upload the following application materials: a cover letter describing your research interests and qualifications, a CV, and the names and contact information for three references. Review of applications will begin on October 1 and the position will remain open until filled. The appointment is a 12-month Letter of Appointment with flexible start date, renewable for up to two years with possible extension to a third year.

University of Montana is an ADA/EOE/AA/Veteran's Preference Employer

"Scott.Miller@mso.umt.edu"
<Scott.Miller@mso.umt.edu>

UMontana UNebraska EvolGenomics

Postdoctoral positions: Genome-to-phenome connections in wild populations

THE UNIVERSITY OF MONTANA and THE UNIVERSITY OF NEBRASKA are seeking applications for two 2-year postdoctoral research associate positions. The positions are funded by a recent NSF award aimed at establishing a collaborative research and training network to advance the science of genome-to-phenome connections in wild populations.

https://www.nsf.gov/awardsearch/-showAward?AWD_ID=3D1736249&HistoricalAwards=-false Research activities will center around three core projects, which are united by their conceptual focus on adaptation to spatiotemporal environmental variation: 1.) high altitude adaptation and hypoxia resistance in deer mice, 2.) adaptation to climate change in snowshoe hares and other species that undergo seasonal phenotypic change and 3.) thermal adaptation in yellow monkeyflowers. Successful applicants may extend these core projects in novel directions or propose to work on complementary questions in independent experimental systems with active mentorship from one or members of the UNVEIL network (see below).

The expected salary is approximately $48,000 and the postdoctoral research associates will be provided generous research funds to support their work (up to $30,000/year for two years).

To apply, please visit http://bit.ly/um1826. Candidates must apply online and will be asked to upload the following application materials: a CV, a 1-page description of previous or current research, and a 2-3 page description of proposed research. In addition, the applicant must provide contact information for 3 references.

Review of applications will begin on November 1, 2018 and the position will remain open until filled. The appointment is a 12-month Letter of Appointment, and while the start date is flexible, a start date of January 15, 2018 is preferred. The position renewable for up to two years.

In evaluating applicants, a panel of network members will weigh research creativity, the potential for synergy, and the overall quality of the proposed research. Emphasis will be placed on researchers with integrative programs that would benefit from interaction and technical training by members of the UNVEIL network, and whose programs will stimulate new interactions among network members.

Applicants are strongly encouraged to contact one or more the following project PIs to further refine their application materials:

Zac Cheviron (Ecophysiology and Evolutionary Genomics, www. chevironlab.org)

Lila Fishman (Evolutionary Genetics and Genomics; http://hs.umt.edu/dbs/labs/fishman/)

Jeff Good (Ecological and Evolutionary Genomics, www.thegoodlab.org)

Scott Mills (Population Ecology and Global Change Biology, www.umt.edu/research/millslab/)

Kristi Montooth (Evolutionary and Physiological Genetics, http://montoothlab.unl.edu)

Colin Meiklejohn (Evolutionary and speciation genomics, http://biosci.unl.edu/colin-meiklejohn)

Jay Storz (Evolutionary genetics and physiology, http:/-/storzlab.unl.edu/)

General inquires can be addressed to Zac Cheviron (zac.cheviron@mso.umt.edu)

ADA/EOE/AA/Veteran's Preference Employer

Zac Cheviron Assistant Professor Division of Biological Sciences Graduate Program in Organismal Biology and Ecology University of Montana Missoula MT 59812

ph. 406-243-4496 email. zac.cheviron@mso.umt.edu web. chevironlab.org

"zac.cheviron@mso.umt.edu" <zac.cheviron@mso.umt.edu>

UMontana UNebraska EvolutionaryGenomics

Program announcement: Genome-to-phenome connections in wild populations

We are pleased to announce the establishment of a new collaborative research and training network created to advance evolutionary and ecological genomics in natural populations. The UNVEIL network (Using Natural Variation to Educate, Innovate, and Lead) is funded by a recent NSF EPSCoR award, and brings together researchers from the University of Montana and the University of Nebraska. The network seeks to advance our understanding of the genetic basis of fitness-related traits in wild populations and to train the next generation of integrative biologists to solve pressing societal challenges in ecological and conservation genomics.

https://www.nsf.gov/awardsearch/-showAward?AWD_ID=1736249 The research and training activities of the UNVEIL network will center around three core projects, which are united by their conceptual focus on adaptation to spatiotemporal environmental variation - high altitude adaptation and hypoxia resistance in deer mice, adaptation to climate change in snowshoe hares and other species that undergo seasonal phenotypic changes, and thermal adaptation in yellow monkeyflowers. Network members and trainees will work collaboratively on these projects to meet the following goals:

1. Advance the science of genome-to-phenome connections through the development of novel approaches for the integration of functional and genomic data.

2. Develop ethical guidelines for the application of genomic interventions for wildlife conservation.

3. Create a unique interdisciplinary training environment to broaden participation in the STEM workforce, and to train integrative biologists that are both technically and ethically equipped to leverage genomic approaches to solve ecological and conservation challenges.

In the coming years, the network will provide a variety of opportunities that may be of interest to the community:

Postdoctoral Fellowships: Over the next four years, we will fund four postdoctoral fellowships within the network. We anticipate filling two of these positions this year. In addition to a competitive salary and benefits package, fellows will be provided generous research funds ($50,000; $25,000/year over two years) to allow them the freedom to creatively extend the core projects in novel directions or to work on complementary questions in independent experimental systems with active mentorship from one or more members of the UNVEIL network.

Graduate Student Research Assistantships: We will also fund graduate student research assistantships on both campuses. Two UNVEIL Diversity Fellowships will be available in the Fall of 2018 and will support one graduate fellow on each campus for a three-year tenure. Additional research assistantships will be available for students to work on aspects of the core projects outlined above.

Annual symposia: Finally, to aid in the exchange of ideas and to advance research and training activities both within and beyond the network, we will hold yearly UNVEIL conferences. These conferences will feature 1.) a scientific program focused on evolutionary and ecological genomics in wild populations, 2.) technical and analytical workshops, and 3.) working group sessions to develop ethical frameworks for the application of genomic interventions for wildlife conservation. We anticipate broad participation from biologists, philosophers, and land managers in the ethics working groups and these sessions will serve as catalysis meetings to formulate policy position white papers, synthesis papers for academic audiences, and ethics training materials.

Specific announcements of all of these activities will be disseminated periodically as deadlines approach, but interested postdoctoral and graduate fellowship candidates are strongly encouraged to contact one or more of the following UNVEIL PIs to discuss these opportunities further:

Zac Cheviron (Ecophysiology and Evolutionary Genomics, www.chevironlab.org)

Lila Fishman (Evolutionary Genetics and Genomics; http://hs.umt.edu/dbs/labs/fishman/)

Jeff Good (Ecological and Evolutionary Genomics, www.thegoodlab.org)

L. Scott Mills (Population Ecology and Global Change Biology, www.umt.edu/research/millslab/)

Kristi Montooth (Evolutionary and Physiological Genetics, http://montoothlab.unl.edu)

Colin Meiklejohn (Evolutionary and Speciation Genomics, http://biosci.unl.edu/colin-meiklejohn)

Dane Scott (Environmental Ethics, www.cfc.umt.edu/-personnel/details.php?ID45)

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UNorthCarolina SpeciationHybridZones

Postdoctoral position: Dynamics of hybrid zones

The Matute lab (dm-incompatibilities.org) at the University of North Carolina at Chapel Hill is looking for a postdoc for research in Evolutionary genetics. The Postdoctoral Research Associate will work in the field of speciation genetics in Drosophila. In particular, the project will focus on the study of hybrid zones in the oceanic islands of Africa. The aim of the project is to quantify the frequency of introgression in natural populations. The postdoc will be encouraged to develop independent lines of research within the broader goals of the project and the lab. The ideal candidate will be creative, enthusiastic, motivated by experimental and analytical challenges, and be proficient in a range of bioinformatics and molecular techniques. The candidate must have experience in at least two of the three following topics: fly genetics, bioinformatics, or population genetics. The appointment could begin as early as October 2017 and can persist for up to three years.

Required Qualifications: PhD in relevant field (evolution, organismal biology, computational biology, etc.) Strong coding skills are absolutely essential.

The University of North Carolina at Chapel Hill is an equal opportunity, affirmative action employer and welcomes all to apply regardless of race, color, gender, national origin, age, religion, genetic information, sexual orientation, gender identity or gender expression. We also encourage protected veterans and individuals with disabilities to apply.

Interested applicants should send a CV, brief statement of research interests (one page), and contact information for three references to dmatute@email.unc.edu. Relevant information can also be found at: https://unc.peopleadmin.com/postings/127000. The application deadline is September 30, after which the position will remain open until filled.

Daniel R. Matute

University of North Carolina, Chapel Hill

“dmatute@email.unc.edu” <dmatute@email.unc.edu>

UOregon Bioinformatics EvolutionaryGenomics

Phillips Lab, University of Oregon

Postdoc in Bioinformatics/Evolutionary Genomics

The Phillips Lab in the Institute of Ecology and Evolution (IE2) at the University of Oregon seeks applications for a postdoctoral research The successful candidate will provide research leadership for several NIH-funded projects utilizing the analysis large-scale DNA sequence and functional genomic information from natural populations, experimental evolution, and genetic crosses to understand the genetics and evolution of complex traits and/or the systems genetics of aging. The ideal candidate would have strong computer and quantitative skills, as well as some background in genomic analysis and/or evolutionary genetics. Further information on Phillips Lab is available at http://www.uoregon.edu/~pphil. Application materials available at http://careers.uoregon.edu/cw/en-us/job/521009/postdoctoral-research-scholar . Patrick C. Phillips, Ph.D. Acting Executive Director | Professor of Biology Phil and Penny Knight Campus for Accelerating Scientific Impact https://www.uoregon.edu/accelerate https://www.uoregon.edu/~pphil pphil@uoregon.edu | 541-346-0916

“pphil@uoregon.edu” <pphil@uoregon.edu>

UOregon BiologyAging Biodemography

Phillips Lab, University of Oregon

Postdoc in Biology of Aging/Biodemography

The Phillips Lab in the Institute of Ecology and Evolution (IE2) at the University of Oregon seeks applications for a postdoctoral research fellowship in the biology of aging and/or biodemography. The successful candidate will provide research leadership for a set of projects aimed at investigating demographic variation within and between species from the standpoint of understanding the effects of compounds that extend individual lifespan and/or the causes and consequences of genetic, environmental and stochastic variation in reproductive patterns among individuals. This work is supported by multiple NIH grants, including the Caenorhabditis Intervention Testing Program (CITP) and a special program in biodemography. These projects involve the use microfluidic devices and automated lifespan scanners to generate the largest and highest precision demographic database ever assembled for an animal system. The ideal candidate would have strong quantitative skills and a desire to inv estigate fundamental questions in aging biology and demography using advanced approaches for survival and demographic analysis. Further information on Phillips Lab is available at http://www.uoregon.edu/~pphil. Application materials available at http://careers.uoregon.edu/cw/en-us/-

job/521005/postdoctoral-research-scholar . Patrick C. Phillips, Ph.D. Acting Executive Director | Professor of Biology Phil and Penny Knight Campus for Accelerating Scientific Impact https://www.uoregon.edu/accelerate https://www.uoregon.edu/~pphil pphil@uoregon.edu | 541-346-0916

"pphil@uoregon.edu" <pphil@uoregon.edu>

UOtagoNZ 2 Bioinformatics

Post-doctoral position in developing bioinformatic methods for genomic identification of bacterial virulence

http://www.ucbioinformatics.org/opportunities.html As large-scale pathogen genome sequencing efforts become more common, the need to comprehensively analyse genome variation is real and immediate. Typically phenotype-genotype association studies (e.g. GWAS) are underpowered due to the size and complexity of variable genomes. We are interested in developing context-dependent models of genome variation to boost the performance of association analyses. Our methodology will be applied to a range bacteria including those with commensal lifestyles, those involved in chronic infection, or hypervirulent strains. We aim to use our results to predict the pathogenic potential of bacteria using genome sequence alone.

The successful candidate will join a research group that has a broad range of interests including the application of bioinformatic methods to analyse comparative genomic, transcriptomic and proteomic datasets. In particular we are interested in RNA biology and the consequences of prokaryotic genome variation.

You will join the Gardner research group who has recently joined the University of Otago. We will work in close collaboration with A/Prof. Peter Fineran (Otago), Prof. Murray Cox (Massey) and Dr Nicole Wheeler (Sanger Institute). Our groups are diverse, and we collaborate widely, including with groups in the UK, Denmark, US, the Netherlands, Sweden, Germany and Australia. We work towards the free and rapid dissemination of research discoveries.

For further enquiries please contact: Paul Gardner (paul.gardner@otago.ac.nz)

Required background: A PhD in bioinformatics or computational biology. Ideally with experience analysing next-generation sequencing data. A demonstrated interest in microbial evolution would be an advantage.

Please email a CV and cover letter to Paul Gardner (paul.gardner@otago.ac.nz). If short-listed, we will request further details from you.

Closing date 1 December, 2017.

A salary starting at $66,000 NZD including fees will be provided by the Bio-Protection Research Centre.

Positions available for a Postdoctoral Fellow and a PhD Student to develop computational tools for tuning protein expression

http://www.ucbioinformatics.org/opportunities.html The Gardner Lab is seeking two fantastic researchers with strong programming skills to design new software tools for tuning protein expression. One of the determinants of protein expression level is the rate of translation. The rate is highly sequence-dependent and is highly variable across the vast number of synonymous messenger RNAs that encode a single protein.

The candidates will integrate the discoveries made in this recent eLife paper (https://elifesciences.org/articles/-13479), and will extend the work into more complex biological systems. The successful candidates will be collaborating with an international research team that includes Sinan Umu and Eivind Valen (Norway), Ivo Hofacker (Vienna) and Gregorsz Kudla (Edinburgh).

For further enquiries please contact: Paul Gardner (paul.gardner@otago.ac.nz).

Required background: A degree or equivalent with a strong computational modelling component (e.g. computer science, physics, ...). Experience in bioinformatics, computational biology, probabilistic modelling and/or machine learning would be considered an advantage.

Please email a CV and cover letter to Paul Gardner (paul.gardner@otago.ac.nz). If short-listed, we will request further details from you.

Closing date 1 November, 2017.

A salary/stipend of up to $75,000 NZD/$28,000 NZD will be provided by funding from MBIE Smart Ideas (Building bioinformatic software for controlling protein expression) for the Postdoc/PhD.

ppgardner@gmail.com

UppsalaU Bioinformatics

Postdoc opportunity in Bioinformatics in Uppsala

We are looking for highly motivated post-doctoral fellows in bioinformatics, for two-year positions at the Department of Medical Biochemistry and Microbiology, Uppsala University in Prof. Leif Andersson's research group (http://www.imbim.uu.se/Research/-+Genomics/Andersson_Leif/?languageId=1).

Major ongoing projects where strong bioinformatics expertise is needed include (PMID for recent publications illustrate ongoing research efforts): The genetic basis of ecological adaptation in Atlantic herring (see eLife: PMID: 27138043 and PMID: 28665273; PNAS: PMID: 28389569) The evolution of Darwin's finches (see Nature: PMID: 25686609; Science: PMID: 27102486) The genetics of male mating strategies in Ruff (see Nature Genetics: PMID: 26569123) The genetics of animal domestication and phenotype evolution (see Science: PMID: 25170157; Nature Genetics: PMID: 26691985) Duties: Take part in bioinformatic analysis of population whole genome sequence data, transcriptome data, DNA methylation and ChIP-seq data.

Take part in improving assemblies as well as in generating a better functional annotation of genomes using for instance transcriptome data, ribosome profiling and histone modifications. Depending on previous experience the development of better models for analysing whole genome population data is also a possibility.

Qualifications: A PhD in bioinformatics or a related area not later than 5 years ago (time spent on parental leave can be deducted). Experience in handling large scale next-generation sequence data is an absolute requirement. Competence in computational biology, population genetics and/or genome assembly is a merit. Since the project requires interacting with other team members and other research groups, an ability to interact with others is an asset.

Further information and applications: Prof. Leif Andersson, Department of Medical Biochemistry and Microbiology, Uppsala University, email: leif.andersson@imbim.uu.se Please include CV, a letter describing your research interest and skills, and the names and contact information (address, email address, and phone number) of at least two reference persons.

Deadline: You are welcome to submit your application no later than October 16, 2017 to email: leif.andersson@imbim.uu.se

Leif Andersson <leif.andersson@imbim.uu.se>

UppsalaU GenomicsUnculturedMicrobialEukParasites

Postdoc position in genomics of uncultured microbial eukaryote parasites In the Department of Organismal Biology at Uppsala University (Sweden)

See full description and how to apply here: http://www.uu.se/en/about-uu/join-us/details/?positionId=162255 NOTE: deadline is fast approaching, Sept 17, 2017

Project description: Study the evolution and specific adaptations to parasitism in Ascetosporea, an emerging threat in marine environments that has remained beyond reach of modern molecular tools. Ascetosporea is a collection of poorly characterized microbial eukaryote parasites of marine invertebrates. It is best-known for including deadly pathogens of oysters and mussels, costing millions of dollars to the growing aquaculture industry. To date, however, Ascetosporea is absent from models describing the evolution of parasites because comparative genomic data is lacking. This is due to multiple factors, including minute cell size, obligate intracellular lifestyle, lack of suitable host cell lines, and techniques for in vitro culture. Here, we propose to overcome these challenges by using micromanipulation and single-cell genomic/transcriptomic methods. We will sequence de novo the genome and transcriptome of several uncultured parasites encompassing the diversity of Ascetosporea, as well as their closest free-living outgroups. With these data, we will broadly look at the evolution of parasitism in Ascetosporea, i.e. identify pre-parasitic conditions, ancestral parasitic innovations, and lineage-specific adaptations using comparative genomics.

Requirements: Doctoral degree, or an equivalent foreign degree, in Biology. To be qualified for an appointment as a postdoctoral fellow you must hold a doctorate or a foreign degree equivalent to a doctorate, and have completed the degree within three years before the application deadline. In special circumstances, the PhD can have been completed earlier, including leave of absence due to sickness, parental leave, etc.

Additional qualifications: Highly motivated individual with strong academic proficiency within the field of (microbial) eukaryote evolution. We are looking for a combination of wet lab and bioinformatic skills: documented skills in single-cell genomics/transcriptomics and/or micromanipulation techniques; proven experience in bioinformatics to assemble and annotate genomes. Experience in phylogenetics/phylogenomics would be an asset. Candidates must be fluent in English.

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

The position is placed in the group of Dr. Fabien Burki in Systematic Biology (http://www.iob.uu.se/research/-systematic-biology/burki-lab/) and co-supervised by Dr. Jan Andersson at the Department of Cell and Molecular Biology (http://www.icm.uu.se/molecular-evolution/-andersson-lab/).

“fabien.burki@ebc.uu.se” <fabien.burki@ebc.uu.se>

USouthFlorida EvolutionaryGenomics

Postdoctoral Position in Evolutionary Genomics

University of South Florida

The Cassin Sackett Lab at the University of South Florida is looking for a highly motivated postdoctoral scholar to study population and conservation genomics in prairie dogs. The lab uses ancient DNA, field methods, next-generation sequencing and bioinformatic approaches to answer fundamental questions in evolutionary biology, especially those with practical conservation applications. Some major questions being asked in the lab are:

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

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

Please visit the lab website for more details on current projects: www.cassinsackett.com The postdoc will be involved in a project that uses genomic approaches to analyze genetic diversity in prairie dogs and investigate the potential for resistance to plague. Specific duties may include: 1) sampling historical museum specimens, 2) developing and optimizing genomic assays (e.g., SNP capture, highly multiplexed amplicon sequencing), 3) performing wet lab work to genotype individual prairie dogs (both modern and historical), 4) conducting bioinformatic analyses of population genomics and adaptation, 5) writing and submitting manuscripts related to the project.

The position is funded for one year, and candidates are encouraged to work with lab members and collaborators to pursue additional funding for extension. The position will be based at the University of South Florida in the Department of Integrative Biology, but requires travel to at least one museum (e.g., Smithsonian), including the possibility of a short-term stay in another city. Application review will begin September 15 and will continue until the position is filled. The desired start date is November 1, but is negotiable.

Qualifications:

Applicants should have a PhD in ecology, evolution, genetics, bioinformatics, or a related field. We are looking for a scientist with a record of scholarly publication, excellent organizational and communication skills, experience working in a Unix environment, and the desire/willingness to engage in occasional outreach. Preference will be given to candidates with experience working on ancient DNA and with strong bioinformatics skills. The Cassin Sackett lab is committed to increasing diversity in STEM, and we especially encourage applications from women, minorities, veterans and other underrepresented groups. We also welcome applications from international candidates. The University of South Florida conducts background checks on all job candidates upon acceptance of an offer.

How to apply:

Interested candidates should apply by sending an email to SackettL@usf.edu that includes: (1) cover letter describing research interests and motivation, including discussion of how your skills are aligned with the needs of the project, (2) CV, (3) names and emails of 3 references, and (4) 2-3 published papers or manuscripts in preparation.

Please email SackettL@usf.edu with any questions.

– Loren Cassin Sackett, Ph.D. Assistant Professor, Integrative Biology University of South Florida 4202 E Fowler Ave, SCA 312 Tampa, FL 33620-5200 www.cassinsackett.com Loren Cassin Sackett <sackettl@usf.edu>

Uvienna GenomicArchitectureOfAdaptation

Genomic architecture of adaptation

A postdoctoral position is available at the Institute of Population Genetics, Vetmeduni Vienna (Austria). The research focus of the Institute of Population Genetics is on understanding the genetics of adaptation in sexual organisms. This central question in evolutionary biology is being tackled using up-to-date methods and a variety of approaches, including experimental evolution, quantitative genetics, functional genetics, empirical population genetics, bioinformatics and statistics.

The successful candidate will be part of a team of scientists studying adaptation of experimental Drosophila populations to temperature stress. She/he can build on several highly replicated Drosophila populations that have evolved under various temperature regimes. With up to 15 replicate populations from different founder populations evolving for more than 100 generations, we host one of the best data sets currently available for a genuinely outcrossing species. The postdoc will integrate data from whole genome time-series sequencing, RNA-Seq and targeted phenotyping to understand the genetic architecture of adaptation to a new thermal environment.

We are looking for candidates with good quantitative training and experience in handling large data sets. A background in population genetic data analysis and/or quantitative genetics is a bonus, but not required. Active contribution to fly work during common garden experiments is expected, as well as a keen interest in linking the data to the biology of the fly.

The position is available starting from January 2018. The application should be emailed to christian.schloetterer@vetmeduni.ac.at as a single pdf containing CV, list of publications, a statement of research interests, and the names of references with contact details. While the search will continue until the position is filled, applications should be received by 30.9.2017 to ensure full consideration.

Background:

1. S. U. Franssen, N. H. Barton, C. Schlötterer, Reconstruction of haplotype-blocks selected during experimental evolution. *Molecular Biology and Evolution*, (2016).

2. S. U. Franssen, V. Nolte, R. Tobler, C. Schlötterer, Patterns of linkage disequilibrium and long range hitchhiking in evolving experimental *Drosophila melanogaster* populations. *Molecular Biology and Evolution* *32*, 495-509 (2015).

3. C. Schlötterer, R. Kofler, E. Versace, R. Tobler, S. U. Franssen, Combining experimental evolution with next-generation sequencing: a powerful tool to study adaptation from standing genetic variation. *Heredity* *114*, 431-440 (2015).

4. N. Barghi, R. Tobler, V. Nolte, C. Schlötterer, *Drosophila simulans*: a species with improved resolution in evolve and resequence studies. *G3* *7*, 2337-2343 (2017).

5. F. Mallard, V. Nolte, R. Tobler, M. Kapun, C. Schlötterer, A simple genetic basis of adaptation to a novel thermal environment results in complex metabolic rewiring in *Drosophila*. *BioRxiv*, DOI: 10.1101/174011 (2017).

Christian Schlötterer Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 1 1210 Wien Austria/Europe

phone: +43-1-25077-4300 fax: +43-1-25077-4390 http://www.vetmeduni.ac.at/en/population-genetics/ Vienna Graduate School of Population Genetics http://www.popgen-vienna.at schlotc@gmail.com

UWisconsin Milwaukee GeneticSelectionKelp

Post-Doctorial Research Associate

The Department of Biological Sciences at the University of Wisconsin-Milwaukee (UWM) is currently accepting application submissions for a postdoctoral appointment in Dr. Filipe Alberto's laboratory, studying genetic improvement for aquaculture of the giant kelp Macrocystis pyrifera.

A postdoctoral researcher to conduct the development of a germplasm collection of haploid strains of kelp (brown algae) is available in the Alberto lab at UW-Milwaukee, US. The collection will be the basis for a genetic improvement program aimed at faster growth and temperature and low nutrient tolerance in aquaculture. The project will require experience setting a large number of individual gametophyte cultures, medium preparation, environmental chamber work, excellent organizational skills and capacity to work under strict deadlines. Individual haploid cultures will have their biomass bulked up to provide sufficient biomass to extract DNA in quantity and quality required for genomic analysis. A research assistant will work closely with the postdoctoral researcher and the PI to achieve the project goals. Experience in population genomics lab techniques is a plus. Microsatellite marker analysis will also be used to monitor strain identify and purity at different stages of growth. The germplasm collection will at the basis of a Marker Assisted Selection program developed with partner institutions (UC Santa Barbara, U Southern California and JCVI) involving genome sequencing and annotation, phenotype typing of outplanted sporophytes in Southern California, capture sequencing of genetic variants (SNP) and the estimation of a predictive model linking genotype and phenotype for traits of interest.

Applicants are required to have a PhD in evolutionary ecology, plant breeding, population genetics/genomics or genetics. Experience in breeding experiments and seaweed biology and culturing are preferred. Familiarity with population genetics software is essential, as well as high-level of motivation to produce and write her or his results. Computer programming skills are important merits.

Other broad research interests in the Alberto lab are population genetics and evolutionary ecology of seaweeds and marine plants. Our focus is both on empirical research through the acquisition of population genetics data, using molecular marker techniques, and simulation based hypothesis testing.

Informal inquiries about the project are encouraged. Please apply by sending a pdf document including 1) CV, 2) a declaration of research interests, 3) previous experience and fit for the position and 4) the email address and telephone number of potential contacts for reference letters.

Applications should be emailed to Dr. Filipe Alberto, albertof(at)uwm.edu. Initial contract will be for one year with possible extension to three years. Benefits information can be found at: http://www.wisconsin.edu/hr/benefits/gradben.pdf . Review of applications starts on the 16th of September, 2017, and will continue until position is filled. The position is expected to start January 2018.

UWM is an AA/EEO employer.

For more information about the lab see: http://alberto-lab.blogspot.com/ . UWM has an active group of researchers studying evolutionary ecology and behavior:

https://uwm.edu/biology/research/ecology-evolution-and-behavior/ Filipe Alberto Associate Professor

Dept. of Biological Sciences University of Wisconsin - Milwaukee 3209 N. Maryland Ave. Milwaukee, WI 53211

URL: http://alberto-lab.blogspot.com/ Email: albertof@uwm.edu Tel: 414-229-6343

Filipe Aos Alberto <albertof@uwm.edu>

U Zurich ModellingEcoEvoDynamics

Postdoctoral position in modelling species' response to environmental change

University of Zurich, Switzerland 2-year SNSF-funded position starting January 2018

Deadline for application: 15 October 2017

We seek a strong candidate to model the demographic and evolutionary responses (eco-evo responses) of (plant) species to environmental changes at large geographical scales. The candidate will investigate the ecological and evolutionary conditions leading to species persistence when facing rapid climate/environmental changes. The project will be a mix of evolutionary modelling with the software Nemo (http://nemo2.sourceforge.net/), ecological niche modelling, and population dynamics modelling. Strong and documented expertise in one of those fields is required. Preference will go to candidates that have developed strong computational skills and/or a deep understanding of eco-evolutionary processes. With this project, we seek to improve on our current individual-based modelling approach (http://rdcu.be/rOCD) by developing new approaches, for e.g. population-based or multi-species approaches, depending on the candidate's background and motivations. Partners and potential collaborators on this project include Prof Arpat Ozgul (population ecology, UZH), Prof Nick Zimmermann (niche & climate modelling, ETH-WSL), and Drs. Felix Gugerli and Christian Rellstab (tree genetics/genomics, ETH-WSL).

The position is available in Prof Frederic Guillaume's lab at the Department of Evolutionary Biology and Environmental Studies, University of Zurich (http://www.ieu.uzh.ch/en/research/evolbiol/ecoevo.html). We offer a competitive working environment in the beautiful international city of Zurich, one hour from the closest mountains. The work-related activities are conducted in English.

Please send your application package as a *single* PDF to frederic.guillaume@ieu.uzh.ch with your CV, publication list, a one-page summary of research interests explaining why you want to join our group, and the contact information of min. two references. Application review will begin October 15th 2017, and continue until the position is filled. Direct inquiries are welcome.

Frederic Guillaume (frederic.guillaume@ieu.uzh.ch)

refs: Cotto O., Wessely J., Georges D., Klonner G., Schmid M., Dullinger S., Thuiller W., Guillaume F. (2017) A dynamic eco-evolutionary model predicts slow response of alpine plants to climate warming. Nature Communications, 8, 15399. DOI: 10.1038/ncomms15399

Schmid M., Guillaume F. (2017) The role of phenotypic plasticity on population differentiation. Heredity DOI: 10.1038/hdy.2017.36

Guillaume F., Rougemont J. (2006) Nemo: an evolutionary and population genetics programming framework. Bioinformatics 22 (20), 2556-2557

"frederic.guillaume@ieu.uzh.ch"
<frederic.guillaume@ieu.uzh.ch>

Versailles France PlantVirologyBioinformatics

Postdoctoral Position to Explore the Expanding Field of Plant Virology

Scientific context Sequencing and assembling the genomes of eukaryotes can help elucidating the evolution of viruses. Indeed, genomes of plants, animals and protists can contain viral sequences that have been inserted either by active or by passive integration mechanisms and in many cases retained there over extended periods of time, sometimes millions of years. The study of endogenous viral elements (EVEs), coined "paleovirology", does allow the evolution of viruses to be traced, much like a fossil record (Aiewsakun and Katzourakis, 2015). For example, the study of endogenous retroviruses has enabled to uncover their hidden diversity and host range, and has provided evidence that retroviruses have a marine origin, and that they developed in parallel with their vertebrate hosts more than 450 million years ago (Hayward et al., 2013) (Hayward et al., 2015) (Aiewsakun and Katzourakis, 2017). The Caulimoviridae is one of the five families of reverse-transcribing viruses or virus-like retrotransposons that occur in eukaryotes (Pringle, 1998), and is the only family of viruses with a double-stranded DNA genome that infects plants. Unlike retroviruses, Caulimoviridae do not integrate their DNA in the genome of their host to complete their replication cycle. Nevertheless, caulimovirid DNA can occasionally integrate their host genome passively. Using paleovirology approaches, we have determined that EVEs from several Caulimoviridae genera are found in virtually all vascular plant genomes, including ferns, gymnosperms and angiosperms, often at high copy number (Geering et al., 2014) (Diop et al., 2017). A major conclusion stemming out from previous work is that, instead of representing a single element, endogenous Caulimoviridae often appear to define complex networks of related sequences with structural and genetic variants. For instance, Caulimoviridae EVEs can be re-organized in plant genomes into sequences capable to generate episomal infection (Gayral et al., 2008). In addition, several Caulimoviridae genera have bipartite genomes (Geering et al., 2014) - each viral genome is defined by two "chromosomes" - but it is unclear whether this genomic organization has emerged once or repeatedly. Furthermore, in the oak genome, we found a very high number of short Caulimoviridae segments with movement protein domain relative to the number of full length viral genomes (Plomion et al., submitted), suggesting that they represent satellite sequences and so that their duplication relies on the production of proteins by autonomous entities, either from exogenous Caulimoviridae, or from endogenous elements.

Proposed work Combining information from several endogenous copies enables reconstructing consensus sequences that closely determine native elements. To disentangle the genetic relationships and functional interactions defining these networks, we will perform an accurate reconstruction of Caulimoviridae and related EVE sequences in several plant genomes, starting with species such as oak, vine, and citrus, for which we have collected exemplary data. The acquired methodology will be automatized and transposed to dozens of plant genomes to identify, characterize and compare Caulimoviridae sequence networks. Comparing Caulimoviridae networks across plant families with high

EVE content and for which a substantial set of genomes are publicly available (e.g. Solanaceae) or to which we have access in the context of collaborations (e.g. Rutaceae) will allow determining the time of emergence and performing detailed co-evolution analyses to gain further insights into the evolution of this complex plant pathosystem.

Profile §The successful applicant will have a Ph.D in bioinformatics and substantial experience in the fields of evolutionary biology, virology or genomics. §He/She will be familiar with different programming languages. §He/She will be autonomous, creative and dedicated, and will have good English writing proficiency.

Working environment §The host lab (URGI) is located in the INRA Center of Versailles, approx. 15km from Paris. URGI is a transdisciplinary unit dedicated to genome analysis and data integration. It is composed of over 20 permanent members, including several developers and researchers. The genome analysis team is internationally recognized for his expertise in the annotation and analysis of selfish genetic elements, including transposable elements and endogenous viruses. §URGI will provide a friendly and formative environment. The INRA Versailles Center can rent on-site institutional temporary accommodation under specific conditions. §The position is for 18 months to begin early 2018 in the frame of the ANR-funded project EVENTS (coordinated by Pierre-Yves Teycheney). §Monthly salary is approx. 2,000 euros (net). §Incoming researchers are welcome to apply for mobility allowance

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WageningenU ExperimentalEvolutionAntibioticResistance

Postdoc position - Experimental evolution of plasmid-mediated Î^2-lactam resistance in the chicken microbiome

Job description Plasmid-mediated antimicrobial resistance (pAMR) occurs in both humans and animals and requires One-health solutions, which include a holistic approach integrating veterinary, medical and environmental disciplines. The transfer dynamics of pAMR depend on ecological and evolutionary processes in the microbiota of the host. A consortium of Utrecht University (UU) and Wageningen University (WU) will study the ecological and evolutionary dynamics of pAMR in gut microbiota of chickens using mathematical modelling and experiments in the project, entitled “Microbiome Invasion and Transmission of plasmid-mediated Antimicrobial Resistance” (MITAR), supported by a grant of ZonMW.

We are seeking a motivated postdoctoral candidate, who wants to contribute to our fundamental understanding of the ecology and evolution of pAMR with an eye for application of the results to obtain better interventions and risk analyses. Tasks of the candidate include in vitro experiments to estimate key model parameters, including fitness cost of plasmid carriage, dynamics of compensatory evolution for these costs and transfer rate of the plasmid to other members of the chicken microbiome. The candidate will work at the Laboratory of Genetics at WU in close collaboration with a PhD student responsible for the modelling and in vivo experiments at UU. The project will be supervised by Prof Arjan de Visser (WU), Dr Mark Zwart (NIOO), Dr Egil Fischer (UU) and Prof Arjan Stegeman (UU).

Qualifications We seek a highly motivated scientist holding a PhD in (Medical) Microbiology or Biotechnology with solid knowledge of microbial ecology and evolution, or a PhD in Evolutionary Biology with a quantitative mind and experience with working with microbes, preferably bacteria. A further requirement is ample experience with the latest methods of molecular genetics. Assets include analytical skills, affinity with next generation sequencing and bioinformatics, excellent communicative abilities and the ability work both independently and in a multidisciplinary team. We expect the postdoc to write up and publish the results of the planned experiments as peer-reviewed articles in scientific journals, as well as to present them at international conferences and stake-holder meetings. Therefore, a suitable candidate has a high level of English in writing and speech according to CEFR proficiency level C.

Offer We offer a 1,0 fte position for one year with the possibility of extension for another year. Salary is according to postdoc scale depending on experience, and there are outstanding secondary benefits < http://www.uu.nl/en/organisation/working-at-utrecht-university/terms-of-employment > such as a minimum of 29 days holiday per year and membership of Research school Production Ecology and Resource Conservation (offering diverse courses and career guidance). For further information, see: working at WUR < http://www.wur.nl/en/Jobs.htm >.

About the organization Wageningen University and Research < https://www.wur.nl/ > (Wageningen UR) is a leading international organization in the life sciences, particularly in the field of healthy nutrition and living environment. With 6,500 employees and 10,000 students from more than 100 countries, Wageningen UR is a truly international organisation operating across the world. The scientific quality of research performed at Wageningen UR is evidenced by several international rankings and citation indices. The quality of Wageningen University as an institute of academic education is shown by its repeated top rank in the Netherlands for several studies, including biology. Research within the Laboratory of Genetics centers around the interrelationship between genetics, heredity and evolution, and takes place within the Department of Plant Sciences. Current research addresses the following three themes: (1) Generating variation; (2) Genetics and levels of selection, and (3) Genetics of adaptations. A range of experimental model systems are used, including bacteria, fungi, plants and insects. The group of Prof Arjan de Visser uses the approach of microbial experimental evolution to address fundamental evolutionary questions. A major recent line of research involves the evolution of antibiotic resistance, particularly beta-lactams.

Application Applications, including a motivation letter, CV and the names of 2 references, should be sent to Hedwig Casteels (hedwig.casteels@wur.nl) before 1 October 2017. For more information about this position, please contact Arjan de Visser, arjan.devisser@wur.nl, + 31 317483144.

Prof. dr. J.A.G.M. (Arjan) de Visser Laboratory of Genetics Wageningen University

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WorkshopsCourses

Barcelona PhenotypeGenotype Jan23-26

Dear colleague,

Transmitting Science (www.transmittingscience.org) is offering new courses for PhD students, postdocs and senior researchers. The courses are on-site, intensive (one week) and international. Below you will find the upcoming courses that can be of interest for members in this list:

-FROM PHENOTYPE TO GENOTYPE: THE GENETIC BASIS OF SHAPE - 4^th ed. January 23rd-26th, Barcelona (Spain). More info: http://www.transmittingscience.org/courses/genetics-and-genomics/phenot ype-genotype-genetic-basis-shape/

Instructors: Dr. Neus Martínez-Abadías (Centre for Genomic Regulation, Spain) and Dr. Nicolas Navarro (Ãcole Pratique des Hautes Ãtudes, France)

-AN INTRODUCTION TO METAGENOMICS AND METABARCODING. Marc h 19th-23rd, Crete (Greece). More info: http://www.transmittingscience.org/courses/genetics-and-genomics/introd uction-metagenomics-metabarcoding/

Instructor: Dr. M. Lisandra Zepeda-Mendoza (Chr. Hansen - Bacterial Physiology & Improvement, Denmark).

-INTRODUCTION TO EVOLUTIONARY QUANTITATIVE GENETICS. April 9th-13th, Barcelona (Spain). More info: http://www.transmittingscience.org/courses/genetics-and-genomics/ introduction-evolutionary-quantitative-genetics/

Instructors: Dr. Erik Postma (University of Zurich, Switzerland) and Dr. JesÃºs Martínez-Padilla (Universidad de Oviedo, Spain).

Please, do not hesitate to c ontact us if you have any question.

With best regards

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Soledad De Esteban-Trivigno,PhD. Scientific Director Transmitting Science www.transmittingscience.org soledad.esteban@transmittingscience.org

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Berlin AdvancedPythonForBiologists Nov13-17

Advanced Python for biologists

13-17 November 2017, Berlin (Germany)

https://www.physalia-courses.org/courses/course12/ Instructor: Dr. Martin Jones (founder, Python for Biologists)

http://www.physalia-courses.org/instructors/t1/ Registration deadline: 20th October 2017

Overview

Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. This workshop is aimed at people who already have a basic knowledge of Python and are interested in using the language to tackle larger problems. In it, we will look in detail at the parts of the language which are particularly useful in scientific programming, and at the tools Python offers for making development faster and easier. The workshop will use examples and exercises drawn from various aspects of bioinformatics work. After completing the workshop, students should be in a position to (1) take advantage of the advanced language features in their own programs and (2) use appropriate tools when developing software programs.

Who should attend

This workshop is aimed at researchers and technical workers with a background in biology and a basic knowledge of Python. The Advanced course is aimed at people who want to develop bigger or more complicated programs in Python, or to learn more about the language, or to explore different approaches (object-oriented, functional) to programming. The material covered is very general purpose and can be applied to any kind of problem.

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). They should also have basic Python experience (the Introduction to Python for Biologists course will fulfil 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.

Session content

Monday 13th - Classes from 09:30 to 17:30

Session 1: Data structures in Python

In this session we will briefly recap Python's 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. We'll 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 we'll 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, we'll 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 we'll 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.

Tuesday 14th - Classes from 09:30 to 17:30

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. We'll 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, we'll 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 we'll discuss the basic concept, the scenarios in which it's

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Berlin GeometricMorphometrics Mar5-9

Course: Geometric Morphometrics

5-9 March 2018, Berlin (Germany):https://www.physalia-courses.org/courses-workshops/course22/ Instructor:

Dr. Carmelo Fruciano (Queensland University of Technology (Brisbane, Australia))

https://www.physalia-courses.org/instructors/t11/ Topic

Introductory and intermediate Geometric Morphometrics.

Overview

Geometric Morphometrics has become a standard in biological research because it combines statistical rigour and ease of interpretation. Through geometric morphometrics, biological form is quantified, analysed and the results are expressed as easily interpretable and visually impactful shape changes. This course covers the main common practices of modern geometric morphometrics, including: acquiring data, analysing it, visualizing and interpreting the results.

Course Format

The course will be delivered over five days and will comprise both lectures and hands-on sessions. The lectures will cover both basic theoretical aspects and their practical implementation in research practice and software. During the hands-on sessions, the attendees will have the chance of both using example datasets and applying the knowledge acquired to their own data. The course will be focused mainly on 2D data and on easy-to-use software with graphical user interface to maximize the ability to understand concepts and apply them. However, some information on 3D data and on R implementations will be provided, as appropriate.

Who Should Attend

This course is aimed at beginners and intermediate users. In other words, it is aimed at researchers who intend to use geometric morphometrics or who have started performing geometric morphometric analyses but feel they need a more structured background.

Requirements

Attendees should have a background in biology and a basic understanding of statistical concepts.

Session content

Monday 5th - Classes from 09:30 to 17:30

Geometric morphometrics: overview and potential applications:

* Traditional and geometric morphometrics * An overview of common analyses * Examples of geometric morphometrics applied to biological problems

>From biological objects to numerical representation:

* Overview of typical devices used to digitalise biological objects * Landmarks, semilandmarks, outlines and surfaces - different types of geometric morphometric data * Most commonly used geometric morphometric software * Data quality, most common pitfalls in study design and data acquisition

Tuesday 6th - Classes from 09:30 to 17:30

Generalized Procrustes analysis (GPA) - the core of most geometric morphometrics:

Principal component analysis (PCA)

Comparing groups:

* Between-group PCA * Canonical variate analysis (CVA) * Tests of difference in means

Wednesday 7th - Classes from 09:30 to 17:30

Co-variation between size and shape:

* Allometry, regression and general linear models

Co-variation between shapes:

* Partial least squares analysis (PLS) * Modularity and integration

Thursday 8th - Classes from 09:30 to 17:30

Combining analyses in a basic workflow:

* Preliminary assessment of data quality * Typical basic workflow

Expanding the basic workflow: variation in geographic space

Expanding the basic workflow: association between shape and environmental variables

Friday 9th - Classes from 09:30 to 17:30

Expanding the basic workflow: elements of phylogenetic comparative analyses

Review and open discussion

Presentation of attendees' analyses on their own data

Packages available:

1) Course-only (430 euros VAT incl.) includes all course materials and coffee breaks;

2) All-inclusive (695 euros VAT incl.) includes all course materials, coffee breaks, accommodation and meals (breakfast, lunch and dinner).

The full list of our courses and Workshops: https://www.physalia-courses.org/courses-workshops/ –

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR

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https://groups.google.com/forum/#!forum/physalia-courses Carlo Pecoraro <info@physalia-courses.org>

Berlin GWASusingR Oct23-27

Practical GWAS Using Linux and R

23-27 October 2017, Berlin (Germany)

https://www.physalia-courses.org/courses/course15/ Registration deadline: September 22nd , 2017.

INSTRUCTOR

Dr Jing Hua Zhao (https://www.physalia-courses.org/instructors/t20/)

Trained in medicine, medical statistics and statistical genetics, he had worked on statistical and computational methods for epidemiological and public health studies at several institutions until 2005, when he joined the MRC Epidemiology Unit, University of Cambridge, to work on design and analysis of GWAS such as the EPIC-Norfolk, the Fenland and the InterAct. He has also participated in numerous genetic analysis workshops which involve both simulated and real data such as those from the Framingham heart study. Besides methodological development, data analysis, and other academic activities, he has also had tutorials on genetic dissection of complex traits with focus on GWAS at UseR! 2008, 2009, and 2010 Conferences and contributed a Henry-Stewart talk on genetic association with R.

Overview

The past decade has witnessed an astonishing development and the universal use of genome wide association studies (GWAS) in identification and characterisation of genetic variants underlying disorders and other variations in human and other species, which has an immense impact in biomedical research. This is owing to the ability to efficiently generate and process large quantity of genetic polymorphisms as well as to integrate with other sources such as gene expression and methylation. To tackle challenges in GWAS, a lot of methods and techniques have been established but many others are still evolving. The workshop therefore intends to give a grand picture as well as practical aspects of GWAS.

Targeted audience and assumed background

The purpose of this workshop is to render both a broad picture and computational details of GWAS to biomedical researchers and related fields. It sets to explore the biological, statistical, and computational concepts, methodologies and practices involving a variety of software based on Linux and R. Examples of consortium contributions will also be given. These will be particularly beneficial to those who come with their own problems and wish to implement the analysis.

Structure

The workshop contains both lecture and computer sessions, designed to help participants to understand the background, methodology and implementation. The computer session is designed to facilitate data analysis and interpretation.

Session content

Monday 23rd - Classes from 09:30 to 17:30

Module 1 -Overview

The purpose of this module is provide a grand view of genetic dissection of complex traits as well as the technological development which lead to GWAS. It will also set stage for later parts of the workshop.

* Introduction - background, purpose * The roadmap to GWAS * Background, study designs, implementations * GWAS catalog http://www.ebi.ac.uk/gwas/ * Workshop outlines

Tuesday 24th - Classes from 09:30 to 17:30

Module 2 - Elements of genetic association

The purpose of this module is to get into the basic considerations of the genetic association studies. At end of the module, you will be able to conduct the relevant analyses.

* Chromosomes, DNA, QC, alleles, genotypes, HWE, mode of inheritance, haplotypes and linkage disequilibrium, GxG and GxE interactions * Phenotype: QC, transformation * Study designs: case-control, case-cohort, family * Association models: linear, logistic, Cox regression models; R^2, AUC, Cstat * Meta-analysis: fixed and random effects models * Missing data models * Population stratification and genomic controls

Wednesday 25th - Classes from 09:30 to 17:30

Module 3 -GWAS

This module focuses on main analyses for GWAS.

* gene chips, HapMap, 1000 genomes project * QC-HWE, call rates, MAF * Genotype imputation, imputation quality * Multiple testing, FDR, q-value * Discovery, replication studies * Report of results and GSEA * Prediction

Thursday 26th - Classes from 09:30 to 17:30

Module 4-Advanced topics

This module covers several areas of GWAS in more details.

* Rare variants * Longitudinal data * Polygenic modelling * Bayesian methods * Marchine learning

Friday 27th - Classes from 09:30 to 17:30

Module 5 - Additional topics

The module will look further into several other areas of research in GWAS.

* Conditional/joint analysis * Mendelian randomization * Microarray, methylation, TWAS

Available packages:

1) Course-only: includes course material and refreshments (430 euros; VAT incl.)

2) All-inclusive: includes course material, refreshments, meals (breakfast, lunch and dinner), accommodation (695 euros; VAT incl.)

The full list of our courses and Workshops:

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Berlin LandscapeGenomics Nov6-10

Course: "Landscape Genomics" https://www.physalia-courses.org/courses-workshops/course17/ 6-10 November, Berlin (Germany)

Application deadline is: October 6th, 2017.

https://www.physalia-courses.org/courses-workshops/course17/ Instructors:

1) Dr. Stéphane Joost (Laboratory of Geographic Information System (LASIG), Swiss Federal Institute of Technology of Lausanne (EPFL)). Dr. Joost is specialized in the contribution of Geographic Information Science for the conservation of plant and animal genetic resources. He applies spatial statistics and geocomputation methods to conservation genetics and landscape genomics (https://www.physalia- courses.org/instructors/t13/)

2) Oliver Salmoni, MSc (Laboratory of Geographic Information System (LASIG), Swiss Federal Institute of Technology of Lausanne (EPFL)). https://www.physalia-courses.org/instructors/t24/ Course Overview:

Landscape genomics is an emerging research field that studies how genetic diversity distributes across space and how environmental features can modify this structure through local adaptation. In this workshop, students will learn the basics of this approach and train using state of the art methods. The course will provide an overview of the type of dataset that can be used for a landscape genomics analysis. Firstly, students will learn how to obtain environmental data from publicly available databases, how to process it with Geographic Information Systems (GIS) and how to use the latter to produce indicators able to describe the characteristics of the landscape. Next, the course will discuss the different approaches to obtain genetic data and subsequently show how to study genetic variation and population structure across space in the R environment. Students will be given an overview of the different statistical approaches to study local adaptation, and will be trained in using two of them, Sambada and LFMM. The course will also cover the critical task of the interpretation and validation of the results. Finally, the workshop will consider the crucial aspects and good habits to account for when planning a landscape genomics experiment (e.g. sampling design).

Targeted Audience & Assumed Background:

This workshop is aimed at all biologists, ecologists, geneticists, veterinarians that want to implement the landscape genomics approach in their own studies of evolutionary biology and conservation. Even though the course is not intended for a specialized audience, basic knowledge in evolutionary biology and population genetics would help. Students will learn how to use GIS, but basic computer skills are desirable (e.g. in the R environment). A basic understanding of statistics is also necessary.

Teaching Format:

The course is organized in ten learning sessions. During the first two sessions, the course will provide a contextualization of the research field. Then, students will be guided through a landscape genomics experiment with sessions that couple brief theoretical introductions with practical work.

Session content:

Monday 6th ÂC Classes from 09:30 to 17:30

Session 1-Introduction

- Overview of the course program
- Introduction on Landscape Genomics
- Examples

Session 2 - Dataset

- The environmental data
- The genetic data

Tuesday 7th ÂC Classes from 09:30 to 17:30

Session 3-Environmental Data 1

- GIS basics
- Main environmental databases
- Derived environmental variables

Session 4- Environmental Data 2

- Environmental characterization of the samples
- Point versus surface
- Analysis of environmental diversity of samples

Wednesday 8th ÂC Classes from 09:30 to 17:30

Session 5- Genetic Data 1

- Sequencing strategies

- Data filtering

Session 6- Genetic Data 2

- Spatial genetic variation

- Population structure

Thursday 9th ÂC Classes from 09:30 to 17:30

Session 7-Statistical Analysis

- Overview of statistical methods (univariate, multivariate, w/wo population structure)

- samÂ£ada: logistic regression

Session 8-Interpreting Results

- Spatial autocorrleation

- Process samÂ£ada output in R

- Validation of results

Friday 10th ÂC Classes from 09:30 to 17:30

Session 9- Planning a Landscape Genomics Experiment

- Scale and Resolution

- Sampling Design

Session 10-Conclusion

- Take home messages

- Question time

Available packages:

1) Course-only: includes course materials and refreshments (480 euros; VAT incl.)

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Berlin PopulationGenomics May14-18

2nd edition of the Workshop "Introductory Population Genomics: from Data to Inference"

May 14-18 2018, Berlin (Germany)

http://www.physalia-courses.org/courses/course9/ Instructors: 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.

Program:

Monday 14th-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 15th-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 16th-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 17th-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 18th-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

Available packages:

Course-only: course materials and coffee breaks (480 euros; VAT included)

All-inclusive: course materials, coffee breaks, accommodation and meals (795 euros; VAT included)

Full list of our courses and Workshops

https://www.physalia-courses.org/courses-workshops/

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cE3c Portugal EvolutionaryBiol Oct-Nov

Subject: Portugal-cE3c-Course: four advanced courses with deadlines October-November 2017

cE3c - Centre for Ecology, Evolution and Environmental Changes is organizing several Advanced Courses: see below the four courses with closer deadlines.

Additional informations at:

http://ce3c.ciencias.ulisboa.pt/training/?cat Course Bioinformatics analysis of biological sequences by Teresa Nogueira and Rita Ponce - October 23rd to October 27th 2017 @ Lisbon, Portugal

Objectives This five-days intensive course has as main objective to provide the participants with knowledge about the biological sequences from reliable databases, as well as with autonomy and critical attitude in the use of bioinformatics software freely available in the Internet.

Course INSTRUCTORS Teresa Nogueira (cE3c collaborator) http://ce3c.ciencias.ulisboa.pt/member/teresa-nogueira And Rita Ponce (cE3c collaborator) https://www.linkedin.com/in/rita-ponce-7189283b Intended audience: The course will be open to a maximum of 20 students, being directed to PhD or MSc students, postdocs, clinical analysts and other professionals working in Biology, Biochemistry and related topics. Minimum formation: bachelor degree in Biology, Biochemistry or related areas.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of fees for other participants see the programme details (access link below).

Deadline for applications: October 2, 2017

For additional details about the programme of the course, fees and to know how to register, click here, and access the specific course http://ce3c.ciencias.ulisboa.pt/training/?cat For more information about the course, please contact: teresainogueira@gmail.com

Course Natural History Collections and Biodiversity Organized by Maria Judite Alves, Raquel Barata, Cristiane Bastos-Silveira et al. | November 6th to November 10th 2017 @ Lisbon, Portugal

Objectives This course aims to: - evidence the importance of natural history collections for the study of biodiversity. - show new tools and approaches to extract and disseminate biodiversity data from natural history collections - increase awareness of young researchers for the scientific and culture value of Natural History Museums.

Course coordinator Maria Judite Alves (Researcher at the Centre for Ecology, Evolution and Environmental Changes (cE3c), and MUHNAC- Museu Nacional de História Natural e da Ciência)

http://ce3c.ciencias.ulisboa.pt/member/maria-judite-silva-cardoso-alves Intended audience This five days intensive course will be open to a maximum number of 16 participants, being directed to PhD or MSc students in Biology, Evolution, Ecology or related areas, and postdocs and other professionals working in related topics. Minimum formation: Bachelor in Biology or related area.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of fees for other participants see the programme details (access link below).

Deadline for applications: October 13, 2017

Candidates should send a short CV and motivation letter to Maria Judite Alves (mjalves@fc.ul.pt)

For additional details about the programme of the course, fees and to know how to register, click here, and access the specific course http://ce3c.ciencias.ulisboa.pt/training/?cat For more information about the course, please contact by email: Maria Judite Alves (mjalves@fc.ul.pt) Course Production of Science Communication Activities Organized by Cristina Luís, Filipa Vala & Patricia Garcia Pereira| November 13th to November 17th 2017 @ Lisbon, Portugal

Objectives To introduce participants to the details of communicating science to non-specialized audiences, including, but not exclusive to, public and private stakeholders, students and teachers, and media professionals. The course will particularly address the design, organisation, implementation and impact assessment of public engagement activities such as exhibitions, science festivals or games. At the end of the course, students should be able to develop and produce small-budget events or products to communicate scientific results and ideas.

Course INSTRUCTORS

Cristina Luís (Post-doc at MUHNAC- Museu Nacional de História Natural e da Ciência)

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CEREEP France LinearModelsForEvolutionaryEcol Nov20-24

Announcement course “Generalized Linear Models for Evolutionary Ecologists” 20-24/11/2017, CEREEP Ecotron IledeFrance.

The staple of data in evolutionary ecology consist of counts, proportions and durations. This course will enable participants to represent and analyse their own data using GLM and mixed models (GLMM) developed for the analysis of such data.

The course is organized by team VPA (Phenotypic Variability and Adaptation) from iEES Paris, the Institute of Ecology and Environmental Sciences and hosted by CEREEP in Nemours. Instructors will be Tom Van Dooren, Thomas Tully, Andrés López-Sepulcre, David Rozen-Rechels and Mathieu Bruneaux (JyU Finland).

Registration: Via https://glm2017vpa.sciencesconf.org/, before November, 1, 2017. The cost of the course will be around 400 euro, with the exact amount depending on the total number of participants. It includes on-site lodging, meals and lecture material. Please consult the website or contact tvdooren@gmail.com for further information.

tvdooren@gmail.com

DukeU Phenoscape Dec11-14

Call for Participation:

Computable evolutionary phenotype knowledge: a hands-on workshop

The Phenoscape (http://phenoscape.org) project is hosting a hands-on workshop on Dec 11-14, 2017, at Duke University in Durham, North Carolina.

Evolutionary phenotype data that is amenable to computational data science, including computation-driven discovery, remains relatively new to science. Therefore use-cases and applications that effectively exploit these new capabilities are only beginning to emerge. If you are interested in discovering, linking to, recombining, or computing with machine-interpretable evolutionary phenotypes, this is the workshop for you!

The event will bring together a diverse group of people to collaboratively design and work hands-on on targets of their interest that take advantage and promote reuse of [Phenoscape]'s online evolutionary data resources and services. The event is designed as a hands-on unconference-style workshop. Participants will break into subgroups to collaboratively tackle self-selected work targets.

The full Call for Participation, including motivation and scope, is posted here: https://hackmd.io/s/Sk6Xa7Eq-# To apply to participate in the event, please fill out the following form by Oct 9, 2017: < https://goo.gl/-tt18gR > Travel sponsorship is available but limited, as is space.

– Hilmar Lapp -:- genome.duke.edu -:- lappland.io

Leicester DNAseq Nov20-21

BBASH at University of Leicester is pleased to announce that applications for the upcoming training Next Generation Sequencing Introduction to DNA-seq workshop are now open.

Deadline for applications: 3rd November 2017

Notification of acceptance: 6th November 2017

Course dates: 20th-21st November 2017

Venue: University of Leicester - College Court Conference Centre, Leicester, UK (http://collegecourt.co.uk/)

Instructors:

Chiara Batini (University of Leicester, UK)

Matthew Blades (BBASH, University of Leicester, UK)

Benjamin Hunt (University of Leicester, UK)

Course description

This workshop serves as a standalone introduction to DNA-seq as well as the first of a two-part course in conjunction with our Exome Variants, Copy Number Calling, Variant Annotation and Reporting Workshop in December. The course will be delivered using a mixture of lectures and computer based hands on practical sessions using real data.

This course is aimed at clinicians and wet-lab biologists who are involved in research projects that will require the handling and analysis of DNA-seq data. A significant proportion of the course will be computer-based using command line tools in the Unix environment and applicants will find it useful to have a grasp of basic skills such as file navigation and management, though an introduction to the command line interface will be provided.

For additional information: https://www2.le.ac.uk/-colleges/medbiopsych/facilities-and-services/cbs/-bbash/training/workshop-webpages/dna-seq-ngs-nov2017 The Organisers

Chiara Batini (University of Leicester, UK)

Matthew Blades (BBASH, University of Leicester, UK)

Benjamin Hunt (University of Leicester, UK) "bh177@leicester.ac.uk" <bh177@leicester.ac.uk>

Leicester ExomeSeq Dec04-05

BBASH at University of Leicester is pleased to announce that applications for the upcoming training Exome Variants, Copy Number Calling, Variant Annotation and Reporting Workshop are now open.

Deadline for applications: 3rd November 2017

Notification of acceptance: 6th November 2017

Course dates: 4th-5th December 2017

Venue: University of Leicester - College Court Conference Centre, Leicester, UK (http://collegecourt.co.uk/)

Instructors:

Matthew Blades (BBASH, University of Leicester, UK)

Rob Hastings (University of Leicester, UK)

Peter Causey-Freeman (University of Leicester, UK)

Course description

This workshop is the second in a two-part course in conjunction with our Introduction to DNA-seq workshop in November. While attendance at the November workshop is not a pre-requisite, this workshop will requires experience with the topics covered therein (see link below). The course provides an introduction to calling variants and copy number alterations from exome sequencing data alignments, variant annotation, variant effect prediction and reporting recommendations. The course will be delivered using a mixture of lectures and computer based hands on practical sessions using real data.

This course is aimed at clinicians and wet-lab biologists who are involved in research projects that will require the handling and analysis of DNA-seq, exome data and sequence variation. A significant proportion of the course will be computer-based using command line tools in the Unix environment and applicants will require a grasp of basic skills such as file navigation and management.

For additional information: <https://www2.le.ac.uk/colleges/medbiopsych/facilities-and-services/cbs/bbash/training/workshop-webpages/dna-seq-ngs-nov2017>

For information on our Introduction to DNA-Seq November workshop see: https://www2.le.ac.uk/colleges/medbiopsych/facilities-and-services/cbs/bbash/training/workshop-webpages/dna-seq-ngs-nov2017

The Organisers

Chiara Batini (University of Leicester, UK)

Matthew Blades (BBASH, University of Leicester, UK)

Benjamin Hunt (University of Leicester, UK)

Rob Hastings (University of Leicester, UK)

Peter Causey-Freeman (University of Leicester, UK)

"Hunt, Benjamin" <bh177@leicester.ac.uk>

Leicester RNAseq Oct16-17

BBASH at University of Leicester is pleased to announce that applications for the upcoming training Next Generation Sequencing RNA-seq workshop are now open.

Deadline for applications: 29th September 2017

Notification of acceptance: 2nd October 2017

Course dates: 16th-17th October 2017

Venue: University of Leicester - College Court Conference Centre, Leicester, UK (http://collegecourt.co.uk/)

Instructors:

Chiara Batini (University of Leicester, UK)

Matthew Blades (BBASH, University of Leicester, UK)

Benjamin Hunt (University of Leicester, UK)

Course description

This course will provide an introduction to next generation sequencing (NGS) platforms, data analysis and tools for data quality control, read alignment (mapping) and differential expression. The course will be delivered using a mixture of lectures and computer based hands on practical sessions using real data.

This course is aimed at wet-lab biologists who are involved in research projects that will require the handling and analysis of NGS data. A significant proportion of the course will be computer-based using command line tools in the Unix environment, therefore, in order to gain maximum benefit from the course all attendees should have basic Unix skills.

For additional information: https://www2.le.ac.uk/colleges/medbiopsych/facilities-and-services/cbs/

bbash/training/workshop-webpages/rna-seq-ngs-oct2017 The Organisers

Chiara Batini (University of Leicester, UK)

Matthew Blades (BBASH, University of Leicester, UK)

Benjamin Hunt (University of Leicester, UK)

"Hunt, Benjamin" <bh177@leicester.ac.uk>

Norway AdaptationsToSeasonality May22-Jun25

Dear colleagues,

Great if you could spread the word to potential participants.

MSc- and PhD-level course: Life History Adaptations to Seasonality (10 ECTS)

Five week course at The University Centre in Svalbard, Norway. 22 May to 25 June 2018 (a wonderful time of the year to study biology in the Arctic).

Application deadline is soon: 15 October 2017!

MSc version:

https://www.unis.no/course/ab-338-life-history-adaptations-to-seasonality/ PhD version:

https://www.unis.no/course/ab-838-life-history-adaptations-to-seasonality/ Kind regards,

Ãystein

Ãystein Varpe

Professor, Department of Arctic Biology, University Centre in Svalbard (UNIS)

Adjunct scientist, Akvaplan-niva, Fram Centre, Tromso

http://www.unis.no/staff/oystein-varpe/ Ãystein Varpe <Oystein.Varpe@unis.no>

SanDiego CamelidGenomics Jan13-17

Dear all,

It is time to start thinking about the next *Camelid workshop* at the Plant and Animal Genomic conference PAGXXVI 2018 < http://www.intlpag.org/2018/ >, Jan 13-17, San Diego.

Therefore, we would like to invite everyone interested in camelid genetics/genomics to *send your abstracts* to the workshop organizers Pamela Burger <pamela.burger@vetmeduni.ac.at> and Don Miller <dm96@cornell.edu>* by October 6th* 2017 or earlier. This gives us time to *select abstracts for oral presentatio*n at the workshop while the remaining will be posters.

If you have been invited to be a Workshop Speaker, you will receive an email with instructions regarding submission of your workshop abstract. This email will include a personalized link to submit and edit your abstract. All *poster abstracts* will need to be submitted to the PAGXXVI < https://pag.confex.com/pag/xxvi/-cfp.cgi > electronic system*.*

Looking forward for exciting contributions.

With best wishes,

Pamela Burger (chair) and Don Miller (co-chair)

Dr.med.vet. Pamela Burger Forschungsinstitut für Wildtierkunde und Ãkologie Vetmeduni Vienna Savoyenstraße 1 1160 Wien, Austria Tel: +43-(0)1-25077-7141 <+43%201%20250777141>; Fax: -7941

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Camels in Asia and North Africa < http://-hw.oeaw.ac.at/7244-4?frames=yes > —

Pamela Burger <pamela.burger@vetmeduni.ac.at>

SICB SanFrancisco PositiveSelectionPolarOrganisms Jan3

SICB_SanFrancisco Workshop PositiveSelectionPolarOrganisms Jan3rd

Workshop Announcement: Best practices for using NGS-based datasets to determine statistically robust evidence of positive selection and convergent evolution of polar organisms.

We will conduct a NSF-funded workshop using cross-disciplinary approaches for determining genetic adaptations in polar organisms using Next Generation Sequencing-based datasets. In particular, this workshop will focus on the following:

1) Establish collaborative research groups to test for genes under positive selection from diverse polar organisms using genomic and transcriptomic datasets.

2) Evaluate current analytical methods for determining positively selected genes and their statistical significance.

3) Explore current and novel methodologies for detecting genetic modifications acquired through convergent evolution in response to similar environmental conditions.

4) Review lab-based protocols for demonstrating the potential functions of candidate genes. Specifically, we will focus on techniques amenable to frozen or otherwise preserved samples that can be accomplished at the home institutional laboratory.

We will conduct a full-day meeting (9am-5pm) before the start of the next two conference meetings of the Society for Integrative and Comparative Biology (San Francisco, CA and Tampa, FL, January 3rd, 2018 and 2019, respectively) with collaborative work among the research groups during the interim period. The requested funds will be used to reimburse the costs of travel to each meeting (up to $300/meeting), SICB meeting registration, and one night of lodging (up to $200/meeting), for all workshop participants per meeting. Workshop participants will contribute to a final report summarizing our findings that will be available through the iDigBio website. We will also publish a multi-authored paper based on the relative contributions of participants towards data acquisition, NGS-based analyses, and the review of lab-based protocols.

Prospective participants should have documented research backgrounds in ONE or more of the following categories: 1) NGS-based studies of polar organisms, 2) Methodologies for determining genes under positive selection or showing evidence of convergent evolution (PAML, HyPHy, Phytools, etc.), 3) Phylogenomics of polar organisms, and 4) Physiological adaptations of polar organisms.

To apply please email scott.santagata@liu.edu (due date:09/06/17) with one attached PDF document containing: A) Current CV and B) One-page description detailing your experience in the research backgrounds listed above, and how this workshop fits into your overall career goals. Graduate students, post-doctoral researchers, and early career investigators from underrepresented groups are encouraged to apply. Applications may be accepted after the due date depending on the number of applicants and amount of available funds. The preliminary list of agreed participants currently includes investigators, post-doctoral researchers, and graduate students from Auburn University, California State University-Long Beach, Central Michigan University, Long Island University-Post, University of Alabama-Tuscaloosa, University of California-Santa Barbara, University of Florida, and the University of Hawaii.

Scott Santagata, Associate Professor Department of Biology Life Sciences Building, Room 261 Long Island University-Post Campus 720 Northern Blvd. Greenvale, NY 11548-1300 Phone:516-299-3029 Email:scott.santagata@liu.edu LIU Website: http://www.liu.edu/CWPost/Academics/Faculty/Faculty/S/Scott-Sa ntagata Labpage: http://sites.google.com/site/scottsantagata/ Researchgate: https://www.researchgate.net/profile/Scott_Santagata Scott Santagata <scott.santagata@liu.edu>

UGothenburg Sweden MetagenomicBioinformatics Nov6-10

Dear all,

Please find below the preliminary schedule and general aims of the course, “An introduction to bioinformatic tools for population genomic data analysis”, offered November 6-10 2017 at the Sven Lovén Centre for Marine Sciences on the island of Tjärnö outside of Strömstad on the Swedish West Coast (http://loven.gu.se/english/about_the_loven_centre/tjarno).

There is no course fee. Accommodation and meals for students are provided by the Royal Academy of Sciences of Sweden. Students will need to provide their own means of transportation to and from the course, however.

The course will be open to a maximum of 18 students, as large parts of the course will consist of hands-on exercises. The aim is a broad mix of students both from the University of Gothenburg and from the outside, mainly PhD students but postdocs are also welcome to apply.

Knowledge of general molecular biology and genetics is necessary, as is some previous experience with commandline interfaces. Previous experience working on a remote server will also be beneficial. No previous bioinformatics skills are needed, however.

For more information and registration, please visit the course web site at: https://sites.google.com/view/bioinformaticpipelines2017 Deadline for registration is

September 15th 2017.

Please note that ALL students must bring their own computers.

Best wishes,

Pierre De Wit

—

An introduction to bioinformatic tools for population genomic data analysis, 2.5 higher education credits Third Cycle

Faculty of Science; Department of Marine Sciences

The Swedish Royal Academy of Sciences

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1. Course content

This course aims at detailed understanding and hands-on experience of using state of the art bioinformatics pipelines for one"s own biological research questions. An important aspect of the course is to show how genomic data can be applied to address and answer research questions in the fields of genetics, ecology, population biology, biodiversity monitoring and conservation. The students will be trained in the latest bioinformatic methods to analyze high throughput sequencing data, which is present in many research projects. The course will cover basic computing tools required to run command line applications, processing high throughput sequencing data of whole genome / exome / restriction site digested (RAD) DNA for population genomic studies.

The first part of the course introduces general computing tools for beginners such as the UNIX command line environment, bash commands, data formatting using regular expressions and basic scripting in the unix shell with a series of examples and exercises using a remote server. The course introduces bioinformatics software for analysis of RAD-data, and downstream population genetic analysis of genotype data. The course also introduces basic and advanced concepts of population genomics data analysis such as genome/transcriptome assembly, alignment/mapping, differential Gene expression, functional enrichment tests, SNP genotyping, PCA, outlier tests. The course corresponds to 1 week of full time studies and and is composed of lectures, demonstrations and computer labs.

2. Outcomes

1. Knowledge and understanding 1a. Demonstrate advanced knowledge of experimental strategies, applications and bioinformatic tools for population genomics. 1b. Demonstrate advanced knowledge of the potential of genomics approaches to answer ecosystem-wide questions, in particular for biodiversity monitoring.

2. Skills and abilities 2a. Ability to use basic commands in the Unix command line environment (reformatting data with regular expressions, basic scripting, running python scripts from the unix shell)

2b. Ability to use different software tools to analyse sequence data from restriction-site digested DNA (data cleaning steps, clustering of reads, mapping to reference genomes, extracting and filtering genotype data.

2c. Ability to use population genomics software tools to assemble and a genome/transcriptome, and perform gene alignment/mapping, differential gene expression, functional enrichment tests, SNP genotyping, PCA, outlier tests.

3. Judgement and approach 3a. Formulate one's own research questions, identify data and tools needed to answer these questions and critically evaluate and analyse the results.

4. Required reading

Part 1: General computing tools. This will be the main textbook for the introduction to general computing tools: - Haddock and Dunn (2010). Practical computing for Biologists. Sinauer Associates.

Part 2: RAD data analysis. - Wang et al. (2012). 2b-RAD: a simple and flexible method for genome-wide genotyping. Nature Methods 9, 808-810. - Davey et al. (2011). Genome-wide genetic marker discovery and genotyping

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UK BioinformaticsUsingLinux Oct16-20

Introduction to Bioinformatics using LINUX

https://www.prinformatics.com/course/introduction-to-bioinformatics-using-linux-ibul02/ Instructor: Dr. Martin Jones

This course will run from 16th - 20th October at SCENE (the Scottish Centre for Ecology and the Natural Environment), Loch Lomond National Park, Glasgow.

Course overview: Most high-throughput bioinformatics work these days takes place on the Linux command line. The programs which do the majority of the computational heavy lifting â€genome assemblers, read mappers, and annotation tools â€are designed to work best when used with a command-line interface. Because the command line can be an intimidating environment, many biologists learn the bare minimum needed to get their analysis tools working. This means that they miss out on the power of Linux to customize their environment and automate many parts of the bioinformatics workflow. This course will introduce the Linux command line environment from scratch and teach students how to make the most of its tools to achieve a high level of productivity when working with biological data.

Availability: 15 places total.

Course programme Monday 16th - Classes from 09:00 to 17:00 (approximately) • Session 1 - The design of Linux In the first session we briefly cover the design of Linux: how is it different from Windows/OSX and how is it best used? We'll then jump straight onto the command line and learn about the layout of the Linux filesystem and how to navigate it. We'll describe Linux's file permission system (which often trips up beginners), how paths work, and how we actually run programs on the command line. We'll learn a few tricks for using the command line more efficiently, and how to deal with programs that are misbehaving. We'll finish this session by looking at the built in help system and how to read and interpret manual pages.

• Session 2 - System management We'll first look at a few command line tools for monitoring the status of the system and keeping track of what's happening to processor power, memory, and disk space. We'll go over the process of installing new software from the built in repositories (which is easy) and from source code downloads (which is trickier). We'll also introduce some tools for benchmarking software (measuring the time/memory requirements of processing large datasets).

Tuesday 17th - Classes from 09:00 to 17:00 (approximately)

• Session 3 - Manipulating tabular data Many data types we want to work with in bioinformatics are stored as tabular plain text files, and here we learn all about manipulating tabular data on the command line. We'll start with simple things like extracting columns, filtering and sorting, searching for text before moving on to more complex tasks like searching for duplicated values, summarizing large files, and combining simple tools into long commands.

• Session 4 - Constructing pipelines In this session we will look at the various tools Linux has for constructing pipelines out of individual commands. Aliases, shell redirection, pipes, and shell scripting will all be introduced here. We'll also look at a couple of specific tools to help with running tools on multiple processors, and for monitoring the progress of long running tasks.

Wednesday 18th - Classes from 09:00 to 17:00 (approximately)

• Session 5 - EMBOSS EMBOSS is a suite of bioinformatics command-line tools explicitly designed to work in the Linux paradigm. We'll get an overview of the different sequence data formats that we might expect to work with, and put what we learned about shell scripting to biological use by building a pipeline to compare codon usage across two collections of DNA sequences.

• Session 6 - Using a Linux server Often in bioinformatics we'll be working on a Linux server rather than our own computerâ€typically because we need access to more computing power, or to specialized tools and datasets. In this session we'll learn how to connect to a Linux server and how to manage sessions. We'll also consider the various ways of moving data to and from a server from your own computer, and finish with a discussion of the considerations we have to make when working on a shared computer.

Thursday 19th - Classes from 09:00 to 17:00 (approximately)

• Session 7 - Combining methods In the next two sessions â€i.e. one full day â€we'll put everything we have learned together and implement a workflow for next-gen sequence analysis. In this first session we'll carry out quality control on some paired-end Illumina data and map these reads to a reference genome. We'll then look at various approaches to automating this pipeline, allowing us to quickly do the same for a second dataset.

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UK BioinformaticsUsingLinux Oct16-20 reduced

Due to a late group cancellation PR informatics have 5 heavily reduced places available for the course "Introduction to Bioinformatics using LINUX"

The course fee price has been reduced to Â£250 (from Â£525.00) so as not to waste the spaces, we have 5 available, details below please feel free to email oliverhooker@prinformatics with any questions.

We have accommodation packages also available at Â£250 providing full board for the week.

https://www.prinformatics.com/course/introduction-to-bioinformatics-using-linux-ibul02/ Instructor: Dr. Martin Jones

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- Session 7 - Combining methods

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UK GeometricMorphometricsUsingR Feb19-23

Geometric Morphometrics Using R (GMMR01)

https://www.prstatistics.com/course/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 19th - 23rd February 2018 at Margam Discovery Centre, Wales, UK. — 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 Programme — Sunday 5th Meet at Millport field centre at approximately 18:30. — Monday 6th - Classes from 09:00 to 17:30 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 17:30 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 17:30 1: Phylogenetic shape variation 2: Group Differences & Trajectory Analysis 3: Allometry 4: Software demonstration and lab practicum — Thursday 9th - Classes from 09:00 to 17:30 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.com 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 — ECOLOGICAL NICHE MODELLING USING R #ENMR 16th - 20th October 2017, SCENE, Scotland, Dr. Neftali Sillero http://www.prstatistics.com/course/ecological-niche-modelling-using-r-enmr01/ — INTRODUCTION TO BIOINFORMATICS USING LINUX #IBUL 16th - 20th October, SCENE, Scotland, Dr. Martin Jones http://www.prstatistics.com/course/introduction-to-bioinformatics-using-linux-ibul02/ — REPRODUCIBLE DATA SCIENCE FOR POPULATION GENETICS #RDPG 23rd - 27th October 2017, Wales, Dr. Thibaut Jombart, Zhian Kavar https://www.prstatistics.com/course/reproducible-data-science-for-population-genetics-rdpg01/ — STRUCTURAL EQUATION MODELLING FOR ECOLOGISTS AND EVOLUTIONARY BIOLOGISTS USING R #SEMR 23rd - 27th October 2017, Wales, Prof Jarrett Byrnes, Dr. Jon Lefcheck http://www.prstatistics.com/course/structural-equation-modelling-for-ecologists-and-evolutionary-biologists-semr01/ —

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mcmaster.ca/~brian/evoldir.html

UK LandscapeGenomics Nov6-10 Scholarships

PARTFUNDED SCHOLARHPS for the course “Landscape genomics/genetics using R”

PR STATISTICS ARE PLEASED TO ANNOUNCE THAT THROUGH THEIR FUNDING SCHEME THEY CAN OFFER 5 PART-FUNDED SCHOLARSHIPS FOR OUR UP-COMING COURSE “Landscape genomics/genetics using R (LNDG02)”

SCHOLARSHIPS CONTRIBUTE TOWARDS COURSE FEES WITH 5 PLACES AVAILABLE AT 385.00 (Fees have been subsidised by 40% from 640.00).

Applications should be sent to oliverhooker@prstatistics.com and contain the following. 1. Full name 2. Institute name 3. PhD subject title or Post doc research questions 4. Do you hold a funded position 5. 150 words why this course would be relevant to your research or how it would help.

Application deadline is Tuesay 26th September 2017 and decisions will be made by Thursday 28th September 2017

We still have ’normal’ places available for anyone else interested.

Full course details are given below

“Landscape genomics/genetics using R”

Delivered by Prof. Rodney Dyer a leading expert in landscape genetics.

http://www.prstatistics.com/course/landscape-genetic-data-analysis-using-r- lndg02/

This course will run from 6th - 10th November 2016 at Margam Discovery Centre, Wales.

The term ’landscape genetics’ has been applied studies that integrate ecological context and intervening landscape into population genetic analyses of contemporary processes such as gene flow and migration. This course will cover the basics of both quantitative landscape ecology and population genetics, focusing on how we develop and evaluate spatial/genetic analyses using the R platform

Course content is as follows Day 1 - Spatial & Ecological Data - Installation & configuring R & RStudio - Acquiring spatial data, projections, and visualization - Vector and raster data

Day 2 - Genetic markers and basic analyses - Genetic markers and sampling - Genetic distance, diversity, and structure - Ordination techniques based upon genetic markers

Day 3 - Integrating spatial and genetic data - Barrier detection & population division - Resistance Modeling - Mantel and distance regressions - Remote sensing - LiDAR and Hyperspectral data

Day 4 - Integrating spatial and genetic data - Spatial autocorrelation - Network Approaches - PCMN & Redundancy

Day 5 - Adaptive Genetic Variance - Outliers & gradients - Quantitative genetics, why we should care. - Chromosome walking

Please email any inquiries to oliverhooker@prstatistics.com or visit our website www.prstatistics.com Please feel free to distribute this material anywhere you feel is suitable

Other up-coming courses are as follows

ECOLOGICAL NICHE MODELLING USING R #ENMR 16th - 20th October 2017, Scotland, Dr. Neftali Sillero http://www.prstatistics.com/course/ecological-niche-modelling-using-r-enmr01/ 2. REPRODUCIBLE DATA SCIENCE FOR POPULATION GENETICS #RDPG 23rd - 27th October 2017, Wales, Dr. Thibaut Jombart, Zhian Kavar https://www.prstatistics.com/course/reproducible-data-science-for-population-genetics-rdpg01/ 3. STRUCTURAL EQUATION MODELLING FOR ECOLOGISTS AND EVOLUTIONARY BIOLOGISTS USING R #SEMR 23rd - 27th October 2017, Wales, Prof Jarrett Byrnes, Dr. Jon Lefcheck http://www.prstatistics.com/course/structural-equation-modelling-for-ecologists-and-evolutionary-biologists-semr01/ 4. LANDSCAPE (POPULATION) GENETIC DATA ANALYSIS USING R #LNDG 6th - 10th November 2017, Wales, Prof. Rodney Dyer http://www.prstatistics.com/course/landscape-genetic-data-analysis-using-r-lndg02/ 5. APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS #ABME 20th - 25th November 2017, Scotland, Dr. Matt Denwood http://www.prstatistics.com/course/applied-bayesian-modelling-ecologists-epidemiologists-abme03/ 6. ADVANCING IN STATISTICAL MODELLING USING R #ADVR 11th - 15th December 2017, Wales, Dr. Luc Bussiere, Dr. Tom Houslay, Dr. Ane Timenes Laugen, http://www.prstatistics.com/course/advancing-statistical-modelling-using-r-advr07/ 7. INTRODUCTION TO BAYESIAN HIERARCHICAL

MODELLING #IBHM 29th Jan - 2nd Feb 2018, Scotland, Dr. Andrew Parnell

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UK ModellingEvolution Oct23-27 Scholarships

PARTFUNDED SCHOLARHPS for the course “Structural Equation Modelling for Ecologists and Evolutionary Biologists”

PR STATISTICS ARE PLEASED TO ANNOUNCE THAT THROUGH THEIR FUNDING SCHEME THEY CAN OFFER 5 PART-FUNDED SCHOLARSHIPS FOR OUR UP-COMING COURSE ”Structural Equation Modelling for Ecologists and Evolutionary Biologists (SEMR01)”

SCHOLARSHIPS CONTRIBUTE TOWARDS COURSE FEES WITH 5 PLACES AVAILABLE AT Â£405.00 (Fees have been subsidised by 40% from Â£670.00).

Applications should be sent to oliverhooker@prstatistics.com and contain the following. 1. Full name 2. Institute name 3. PhD subject title or Post doc research questions 4. Do you hold a funded position 5. 150 words why this course would be relevant to your research or how it would help.

Application deadline is Tuesday 12th September 2017 and decisions will be made by Thursday 14th September 2017

We still have â’ places available for anyone else interested.

Full course details are given below

“Structural Equation Modelling for Ecologists and Evolutionary Biologists”

Delivered by Dr. Jarret Byrnes and Dr. Jon Lefcheck

www.prstatistics.com/course/structural-equation-modelling-for-ecologists-and-evolutionary-biologists-semr01/ This course will run from 23rd - 27th October 2017 at Margam Park Discovery Centre, Wales, UK

Course only and all inclusive packages are available.

The course is a primer on structural equation modelling (SEM) and confirmatory path analysis, with an emphasis on practical skills and applications to real-world data.

Structural Equation Modelling (SEM) is a rapidly growing technique in ecology and evolution that unites multiple hypotheses in a single causal network. It provides an intuitive graphical representation of relationships among variables, underpinned by well-described mathematical estimation procedures. Several advances in SEM over the past few years have expanded its utility for typical ecological datasets, which include count data, missing observations, and nested or hierarchical designs. We will cover the basic philosophy behind SEM, provide approachable mathematical explanations of the techniques, and cover recent extensions to mixed effects models and non-normal distributions. Along the way, we will work through many examples from the primary literature using the open- source statistical software R (www.r-project.org). We will draw on two popular R packages for conducting SEM, including lavaan and piecewiseSEM. Participants are encouraged to bring their own data, as there will be opportunities throughout the course to plan, analyse, and receive feedback on structural equation models.

Course content is as follows

Day 1 Introduction to SEM Module 1: What is Structural Equation Modeling? Why would I use it? Module 2: Creating multivariate causal models Module 3: Fitting piecewise models Readings: Grace 2010 (overview), Whalen et al. 2013 (example)

Day 2 SEM Using Likelihood Module 4: Fitting Observed Variable models with covariance structures Module 5: What does it mean to evaluate a multivariate hypothesis? Module 6: Latent Variable models Module 7: ANCOVA revisited & Nonlinearities Readings: Grace & Bollen 2005, Shipley 2004 Optional Reading: Pearl 2012, Pearl 2009 (causality)

Day 3 Piecewise SEM Module 8: Introduction to piecewise approach Module 9: Incorporation of random effects models Model 10: Autocorrelation Reading: Shipley 2009; Lefcheck 2016

Day 4 Advanced Topics with Likelihood and Piecewise SEM Module 11: Multigroup models and nonlinearities Module 12: Composite Variables Module 13: Phylogenetically-correlated data Module 14: Prediction using SEM Module 15: How To Reject A Paper That Uses SEM Readings: Grace & Julia 1999, von Hardenberg & Gonzalezâ2013

Day 5 Open Lab and Final Presentations

Please email any inquiries to oliverhooker@prstatistics.com or visit our website www.prstatistics.com Please feel free to distribute this material anywhere you feel is suitable

Other up-coming courses are as follows

1. ECOLOGICAL NICHE MODELLING USING R #ENMR 16th - 20th October 2017, Scotland, Dr. Neftali Sillero http://www.prstatistics.com/course/ecological-niche-modelling-using-r-enmr01/ 2. REPRODUCIBLE DATA SCIENCE FOR POPULATION GENETICS 23rd - 27th October, Wales, Dr. Thibaut Jombart, Zhian Kavar http://www.prstatistics.com/course/genetic-data-analysis-exploration-using-r-gdar03/ 3. STRUCTURAL EQUATION MODELLING FOR ECOLOGISTS AND EVOLUTIONARY BIOLOGISTS USING R #SEMR

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Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.