EvolDir

August 1, 2016

Month in Review

Foreword

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

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

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

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Conferences

BatonRouge SocietyofSystematicBiologists Jan8-10

The Society of Systematic Biologists is pleased to announce its second standalone meeting to take place at Louisiana State University in Baton Rouge from January 8th-10th, 2017. The meeting will feature panel discussions, debates, lightning talks, workshops, and more! Details will be available through the SSB website (www.systbio.org), with speakers and schedule to be posted this fall. We hope you can join us!

dewitt832@gmail.com

Cambridge InsectImmunityEvolution Dec16

"Insect Infection and Immunity in Insects: from Mechanisms to Evolution"

Emmanuel College, Cambridge, UK

Friday, 16th December, 2016.

This is a one-day meeting that aims to bring together people working on different facets of insect infection and immunity. As guest speaker we will have Dr. Sylvia Cremer who has pioneered the study of cooperative defences in eusocial insects.

Registration and more information at: http://infectionandimmunity.strikingly.com/ The Royal Entomological Society sponsors this meeting.

Best regards,

The organizing committee:

Frank Jiggins

Sinead English

Alexandre Leitāo

Mara Lawniczak

Alexandre Leitāo <ac2016@cam.ac.uk>

Cambridge MathematicalMolBiol Oct3-4

Call for contributions

Workshop on Mathematical and Statistical Aspects of Molecular Biology

http://www.cl.cam.ac.uk/events/masamb2016 26th annual workshop, Computer Science Laboratory, Cambridge, UK

Important dates: August 5 2016: Submission deadline for oral presentations September 5 2016: Author notification date September 5 2016: Late submission deadline for poster presentations October 3/4, 2016: Workshop date

WORKSHOP DESCRIPTION

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

The workshop will host presentations of emerging problems and statistical techniques in molecular biology. —We encourage contributions describing either progress on new molecular problems or work on established problems using new approaches that are substantially different from established approaches. Kernel methods, graphical models, semi-supervised approaches, feature selection and other techniques applied to relevant problems would all be appropriate for the workshop.—

SUBMISSION INSTRUCTIONS

The MASAMB program will be compiled from submitted abstracts. Researchers interested in contributing should upload a one-page abstract in PDF format to the MASAMB submission site—

https://easychair.org/conferences/?conf=masamb2016 by August 5, 11:59pm (BST).

All submissions will be peer reviewed and will be evaluated on the basis of their technical content. —A typical submission to the workshop represents a new mathematical or statistical approach applied to a problem in molecular biology. We encourage submissions both for established as well as new and emerging fields.

The workshop allows submissions of abstracts that are based on papers that are currently under review or have been recently published in a conference or a journal. The authors should clearly state any overlapping published work at time of submission.—

LOCAL ORGANIZERS

Max Convey (University of Cambridge) Pietro Lio? (University of Cambridge) Oliver Stegle (EMBL-EBI) Lara Urban (EMBL-EBI)

"goldman@ebi.ac.uk" <goldman@ebi.ac.uk>

Cambridge PlantEvolution Sep15-16

Registration is now open for the second UK Plant Evolution meeting, to be held at Cambridge University Botanic Garden on 15 and 16 September 2016.

Registration will close in just over one month, on August 19th.

We have a great line-up of invited speakers including Doug Soltis, Sandy Knapp, Chiara Airoldi, Robert Scotland, Vincent Savolainen, Minsung Kim, Kirsten Bomblies, and Dmitry Filatov.

The Accommodation section of the website now includes a live link to book college accommodation, in addition to a list of suggested hotels.

Registration is only 40 (student) or 60 (standard), including lunches and all tea/coffee breaks, and the opportunity to tour the CU Botanic Garden and/or herbarium.

To register or submit an abstract see

http://www.plantsci.cam.ac.uk/research/-sambrockington/uk-plant-evolution-2016 or email bjg26@cam.ac.uk with any questions.

"bjg26@hermes.cam.ac.uk" <bjg26@hermes.cam.ac.uk>

Marseilles 21thEvolutionaryBiology Sep26-29

Dear all the the program of the

20th evolutionary biology meeting at Marseilles is available see : sites.univ-provence.fr/evol-cgr/ or aeeb.fr

The date for the 21st evolutionary meeting are september 26-29

Best regards

Pierre

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

MaxPlanckInst Ploen ExptEvolution Sep19-21

Dear colleagues,

we would like to bring to your attention a symposium on 'Experimental Evolution & Community Dynamics" which will take place this fall (September 19th-21nd) at the Max Planck Institute for Evolutionary Biology (Plön, Germany). The aim of the meeting is to bring together a mix of people working in fields of ecology, evolution and microbiology using experimental evolution and/or theory.

Registration and additional information: https://eecd2016.wordpress.com/ Best wishes, Teppo Hiltunen & Lutz Becks

Lutz Becks Emmy Noether research group leader Max Planck Institute for Evolutionary Biology August Thienemann Str. 2 24306 Plön Germany

Telephone: +49 4522 763 230

Lutz Becks <lbecks@evolbio.mpg.de>

MNHN Paris Holobionts Apr19-21

International Conference on Holobionts,

Paris (Natural History National Museum), April 19-21, 2017

It is becoming increasingly clear that the development, nutrition, physiology and health of most organisms are influenced by the complex microbial communities they host, hereby shaping their ecology and evolution. Biology is indeed undergoing a paradigm shift, where individual phenotypes are seen as a result of the combined expression of the host and associated microbe genomes, leading to the popularization of the holobiont concept (the host and its microbiota) and the hologenome (the collective genomes of a holobiont). Ecological and technical advances, especially in next generation sequencing technologies, have greatly contributed to this conceptual shift, thereby revealing the diversity and roles of the microbes hosted by diverse organisms, from people and plants, to sponges and insects. The scientific community has now recognized that the host organisms cannot be studied without taking resident microbiomes into account, making holobiont research imperative across numerous fields of the life and medical sciences.

The objective of the International Conference on Holobionts, Paris 2017 is to, for the first time, bring scientists together who are interested in holobiont systems and their study. This conference will highlight major advances in defining the key roles of host-borne microbiota in the ecology and evolution of higher organisms and the potential implications for human health, food production and ecosystem functioning. In addition, the conference will offer a platform for debate related to the definition, assembly and evolution of holobionts. By bringing a range of holobiont researchers together, the International Conference on Holobionts seeks to help consolidate the field, facilitate exchange of knowledge across systems and approaches and stimulate further developments in this emerging discipline.

Scientific program. This conference will address the following topics:

1. Holobionts and evolution
2. Emerging approaches to holobiont research
3. Microbiota and host health
4. Mechanisms for holobiont assembly

5. Metabolic interactions between host and microbiota

For each topic, we encourage oral and poster communications on holobiont systems from different perspectives including theoretical, empirical, fundamental and applied researches.

Provisional list of invited speakers (to be updated soon):

Thierry Heulin (CEA Cadarache, France), confirmed

Nancy Moran (University of Texas, Austin, Texas, USA), confirmed

Jeroen Raes (Vrije Universiteit, Brussel, Belgium), confirmed

Eugene Rosenberg (Tel Aviv University, Israel), confirmed

Paul Schulze-Lefert (Max Planck Institute Koln, Germany), confirmed

Practical aspects. This conference will last 2.5 days, from April 19^th 2 p.m. to from April 21^st 4 p.m. It will take place right in the center of Paris, in the heart of "Quartier Latin" in the prestigious Grand Amphitheatre of the Natural History National Museum (https://www.mnhn.fr/fr). Note that for space constraints, we won't be able to take more than 300 registrations. Registrations will open by November 15, 2016 and be closed by January 30, 2017. A dedicated website for registration and practical information is under construction at https://symposium.inra.fr/holobiont-paris2017 . Organizing institutions: CNRS (Centre National de la Recherche Scientifique), INRA (Institut National de la Recherche Agronomique), MNHN (Museum National d'Histoire Naturelle). This conference is a joint initiative of the Groupe de Recherche en Genomique Environnementale (GDR GE) and the INRA Metaprogramme Meta-omiques et ecosystemes microbiens (MEM).

Members of the Scientific Committee: Bourguet-Kondracki Marie-Lise (CNRS, MNHN Paris), Bourtzis Kostas (FAO/IAEA, Vienna, Austria), Buee Marc (INRA Nancy, France), Faure Denis (CNRS Orsay, France), Heulin Thierry (CNRS Marseille, France), Joly Dominique (CNRS Paris, France), Kowalchuk George (Utrecht University, The Netherlands), Marchesi Julian (Imperial College, UK), Medigue Claudine (CNRS Genoscope Evry, France), Mougel Christophe (INRA Rennes, France), Selosse Marc-Andre (MNHN Paris), Simon Jean-Christophe (INRA Rennes, France), Vandenkoornhuyse Philippe, (University Rennes 1, France)

Marc-André SELOSSE <ma.selosse@wanadoo.fr>

NHM London YoungSystematists Nov25

18th YOUNG SYSTEMATISTS' FORUM

Friday, 25 November 2016, 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 no later than Friday 28 October 2016. 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).

Dr Ellinor MICHEL Department of Life Sciences The Natural History Museum Cromwell Road SW7 5BD London UK tel: +44-207-942-5516

http://nhm.academia.edu/EllinorMichel www.researchgate.net/profile/Ellinor_Michel Ellinor Michel <e.michel@nhm.ac.uk>

Oxford MolecularArchaelogy Sep14-16

Come to the 7th International Symposium on Biomolecular Archaeology (ISBA7) from 14th -16th September 2016 hosted in Oxford, UK.

The registration deadline closes on August 12th and more than 150 people have registered already.

The 2016 Conference is expected to attract 200+ delegates and will encourage and promote interdisciplinary research - ideally in combination with archaeology - by means of DNA, RNA, proteins, lipids or stable isotopes and will feature plenary and parallel sessions with an outstanding line up of speakers from around the word.

Please bookmark our website http://palaeobarn.com/-isba7 where details about the conference will follow, including information on registration, abstract submission and the scientific programme. Online registration and abstract submission will open in early April and we will let you know as soon as this goes live so you can take advantage of the early bird discount!

We are proud to build on the success of previous ISBA conferences held in Amsterdam, Stockholm, York, Copenhagen, Beijing, and most recently Basel in 2014, however we are very much looking forward to being able to welcome you to our city and to our University. Nine centuries of development have gone into building the University of Oxford and its colleges and we are fortunate to be able to hosting ISBA7 in two of the finest University and college settings; the day sessions will take place at the Oxford Museum of Natural History (http://www.oum.ox.ac.uk/) and the conference will conclude on the Friday evening with a drinks reception and banquet in the spectacular dining hall at Balliol college http://www.balliol.ox.ac.uk/) one of the oldest Oxford colleges.

Getting to Oxford could not be easier. We are at the heart of the UK and fast and efficient train and coach services link Oxford with London and the north and south of the country, and the M40 and A34 ensure easy access by road.

Please forward information about ISBA7 onto anyone who might be interested and let us know if you have any queries by emailing the organizers at isba7@arch.ox.ac.uk

We look forward to welcoming you in September!

“greger.larson@arch.ox.ac.uk”

Paris HumanPopGenetics Dec7-10

HUMAN POPULATION GENETICS CONFERENCE; PARIS 7-10 DECEMBER 2016 - EXTENDED CALL FOR ABSTRACTS

The 6th international conference of the series DNA POLYMORPHISMS IN HUMAN POPULATIONS will be held in Paris (France), 7-10 December 2016 at the Musee de l'Homme. The conference has a general topic: (Cross-Disciplinary) Human Population Genetics. The conference will be hybrid, allying plenary sessions and three specialized workshops. While a preliminary program is available, we have some room for more presentations, this why an extended *call for abstracts* is now open until the *3^rd of September, 2016*.

Registrations will start in late September.

We invite you can submit abstracts concerning posters, or talks in plenary sessions or talks in the frame of the workshops.

Multiple abstracts are accepted. To submit, just send an abstract through the conference website.

Conference website: http://ecoanthropologie.mnhn.fr/-DPHP2016/DPHP2016.htm Contact: dna-paris2016@gmail.com

Franz MANNI <fmanni@mnhn.fr>

Portland ASN Jun23-27 CallSymposium

Symposium at Evolution 2017

Due September 1, 2016

The American Society of Naturalists invites symposium proposals for a special symposium to be held at the 2017 annual joint meeting of the Society for the Study of Evolution, the American Society of Naturalists, and the Society of Systematic Biologists, to be held June 23-27, 2017 in Portland, Oregon.

Symposium topics should support the Society's goal to advance the conceptual unification of the biological sciences and further knowledge in evolution, ecology, behavior and organismal biology. The committee will consider all submitted proposals. However, because 2017 marks the 150th anniversary of the founding of The American Naturalist, we are especially keen to sponsor a symposium that broadly celebrates the journal and the society. For instance, a symposium might bring together talks that use diverse natural history approaches to investigate a conceptual issue, or target speakers that have a track record of publishing in the journal, or highlight topics that promise to be especially pressing for the society in the coming decades. A travel, registration, and accommodation budget of $8,000 is provided to help with expenses.

*****

Symposium at ESA 2017

Due September 1, 2016

The American Society of Naturalists invites symposium proposals for a special symposium to be held at the 2017 Ecological Society of America annual meeting August 6-11, 2017 in Portland, Oregon. By holding this second annual symposium at ESA, ASN hopes to strengthen ties between the society and ecologists.

Symposium topics should support the Society's goal to advance the conceptual unification of the biological sciences and further knowledge in evolution, ecology, behavior and organismal biology. Proposals are encouraged on topics that are synthetic, interdisciplinary or that address important emerging issues in evolution, ecology and behavior. Because this symposium is in conjunction with the ecology meeting, special weight will be given to integrative topics of interest to ecologists. A travel, registration, and accommodation budget of $8,000 is provided to help with expenses.

*****

Proposal Procedures

Proposals should include (1) a title; (2) a description of the symposium topic (one page); (3) a tentative list of six speakers, including institutional affiliations; (4) a justification for the symposium explaining why the topic and speakers are appropriate for a Society- sponsored symposium (up to one page).

Please submit proposals by midnight Eastern Standard Time on September 1, 2016 by email (emilies@umn.edu) as a single pdf attachment, under subject heading: ASN Symposium Proposal: ESA (or Evolution) 2017. Proposals that include women, young investigators and individuals from underrepresented groups are especially encouraged.

The Society's selection committee will evaluate proposals based on the significance and timeliness of the topic, and on it being substantively different from recent symposia sponsored by the Society. All applicants will be notified of the decision within a month of the deadline.

Emilie Snell-Rood ASN Symposium Committee Chair Department of Ecology, Evolution and Behavior University of Minnesota emilies@umn.edu

Portland EvolutionEcology 2017 ASNSympCall

American Society of Naturalists Call for Symposium Proposals for 2017

Symposium at Evolution 2017

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Emilie Snell-Rood ASN Symposium Committee Chair Department of Ecology, Evolution and Behavior University of Minnesota emilies@umn.edu

Emilie Snell-Rood <emilies@umn.edu>

SanDiego AvianGenomics Jan14-18

Dear all,

The registration for the PAG meeting is open: International Plant & Animal Genome XXV - http://www.intlpag.org/ - January 14-18, 2017 - San Diego, CA, USA

This meeting is among the largest for non-human genomics globally (thousands of attendants; including a genomics technology fair). Much of it is about plant and animal breeding but over the last few years there is a growing community of Ecology and Evolution sessions with hundreds of attendants across sessions. Last year we successfully hosted a session about non-model avian genomics ("Avian Genomics - Going Wild!") which was well perceived. Please have a look at the speakers and topics of #PAGXXIV: https://pag.confex.com/pag/xxiv/meetingapp.cgi/Session/3531. And here for reference the overall workshop list of #PAGXXIV: https://pag.confex.com/pag/xxiv/meetingapp.cgi/Program/1051 . The conference starts on Saturday, 14th January. On the Friday 13th we will do a pre-conference birding tour around San Diego for everyone who is interested (not only the speakers!!). If you are at PAG and can't give a talk, please be in touch about the birding tour nonetheless.

In our Avian Genomics workshop we seek to present current states of *omics in ecology and evolution of birds, as broadly as possible. I herewith invite contributions from the community for giving a talk. Please send your abstract of 200-300 words to me until 27th August.

Feel free to forward to approach me with questions.

Very best regards, Robert Kraus

robert.kraus@uni-konstanz.de

Seville EcolEvolNGS Jan31-Feb4

Symposium: Investigating ecological and evolutionary processes with NGS

Global change drivers create new environmental scenarios and selective pressures, affecting animal and plant species in various interacting ways. Understanding how the genome of an organism evolves and copes with environmental challenges is the main goal of Ecological and Evolutionary Genomics (EEG). EEG involves the integration of genomic data to the phenotype and ecosystem function of the organism. The development of next-generation sequencing (NGS) technologies offers an unprecedented opportunity to understand the genetic architecture of fundamental ecological and evolutionary processes such as migration, foraging behavior, energetics, and communication in natural populations as well as to identify the environmental factors that drive local adaptation. The aim of this symposium is to discuss the promise of NGS technologies in order to study ecological adaptation and bring together field biologists along the molecular to theoretical continuum to exchange ideas and perspectives.

Invited speaker, Aaron Schafer (Trent University), Canada: "Using genomic data to infer demographic and adaptive processes in natural populations".

The online abstracts submission for the symposium is open until the 5th of September. This symposium is part of the XIV MEDECOS & XIII AEET meeting, which will take place in Seville, Spain, from January 31 to February 4, 2017.

For more information about the meeting, please visit: http://www.medecos-aeet-meeting2017.es/ For abstract submission, please visit: http://www.medecos-aeet-meeting2017.es/Call_for_Abstracts_330_p.htm Miguel Gallach Center for Integrative Bioinformatics Vienna (CIBIV) Max F. Perutz Laboratories(MFPL) Telf: +43 1 4277 74330 Campus Vienna Biocenter 5, Ebene 1 CIBIV, MFPL 1030 Vienna, Austria e-mail: miguel.gallach@univie.ac.at migaca2001@gmail.com

Miguel Gallach <miguel.gallach@univie.ac.at>

Stockholm ScandinavianOrigins Nov7-8

Symposium: Origins and Natural History of the Scandinavian Biota

7-8 November 2016

Swedish Museum of Natural History, Stockholm, Sweden

Scandinavia was covered by a large ice sheet during the last glacial maximum, which means most modern-day animals, plants and humans have a recent origin in the region. But their origins and subsequent history have until recently remained unresolved.

The Swedish Museum of Natural History invites you to a symposium where some of the world's leading researchers in genetics, paleobiology and archaeology present the latest research results on the origins and natural history of the Scandinavian biota.

Invited speakers: Inger Alsos - University of Tromsø Ingela Bergman - Institute for Subarctic Landscape Research Love Dalén - Swedish Museum of Natural History Ãystein Flagstad - Norwegian Institute for Nature Research Anders Götherström - Stockholm University Rolf Ims - University of Tromsø Sven Isaksson - Stockholm University Mattias Jakobsson - Uppsala University Jan StorÃ¥ - Stockholm University Eske Willerslev - Natural History Museum of Denmark

Read more and register here: www.nrm.se/scandorigins "Love.Dalen@nrm.se" <Love.Dalen@nrm.se>

Tempe Arizona EvolGenomicsSex Nov17-19

Evolutionary Genomics of Sex Conference 2016

Abstract Deadline Extended to July 7,ˆ 2016

When: November 17-19, 2016.

Location: Tempe, Arizona #EvSex16

Sponsored by the American Genetic Association and the Center for Evolution and Medicine at Arizona State University

ABSTRACT SUBMISSION NOW OPEN

https://easychair.org/conferences/?conf=3Devsex16 Deadline extended to July 7, 2016

TRAINEE TRAVEL AWARDS AVAILABLE

REGISTRATION WILL OPEN AFTER ABSTRACTS ARE ACCEPTED Expected Registration ˜$75-$125 Expected Registration Opening: August 1, 2016

Trainee travel awards will be notified before registration opens.

To stay up-to-date with announcements about the conference, join the google group: https://groups.google.com/d/forum/evsex16 Public Speakers

Tia-Lynn Ashman, University of Pittsburg: http://www.pitt.edu/~tia1/ Doris Bachtrog, University of California, Berkeley: http://ib.berkeley.edu/labs/bachtrog/ Justin Blumenstiel, University of Kansas: http://www.blumenstiellab.org Amanda Larracuente, University of Rochester: http://blogs.rochester.edu/larracuente/? John Logsdon, University of Iowa: http://biology.uiowa.edu/people/john-logsdon Judith Mank, University College, London: http://www.ucl.ac.uk/mank-group/ Nicole Valenzuela, Iowa State University: http://www.public.iastate.edu/~nvalenzu/ Melissa A. Wilson Sayres, Arizona State University: http://www.wilsonsayreslab.org Lenora L. Ott

Communications and Events Coordinator

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Lenora Ott <Lenora.Ott@asu.edu>

Tuscany Speciation Feb19-24 Registration

We are pleased to announce SPECIATION 2017, a Gordon Research Conference (GRC) dedicated exclusively to speciation research. The conference — the world's largest of its kind — will be held at the Renaissance Tuscany Il Ciocco Resort & Spa in Italy during the week of February 19-24, 2017. Invited presentations and discussion sessions will cover a broad array of timely topics in speciation research. A preliminary program for the GRC is now posted.

The conference will be directly preceded by a two-day Gordon Research Seminar (GRS), co-chaired by Amanda Hund and Laurel Symes, that offers opportunities for early-career scientists to get involved at the forefronts of modern speciation research. Participants will engage in scientific discussions on salient topics of interest, thereby gaining knowledge and confidence for their participation in SPECIATION 2017.

The GRC conferences on speciation raise to a trans-Atlantic level a tradition of international conferences on speciation research that was initiated by the European Research Networking Programme 'Frontiers of Speciation Research'. The three conferences held thus far, in 2010, 2013, and 2015, have helped facilitate bridge-building between disparate approaches to speciation research and have attracted hundreds of participants from all facets of speciation research.

Registration for SPECIATION 2017 is open at https://www.grc.org/programs.aspx?id=16903 and will continue until the venue's capacity is filled.

With many thanks and best wishes, Ãke Brännström & Rebecca Safran Amanda Hund & Laurel Symes

Dr. Rebecca Jo Safran Associate Professor N317 Ramaley Hall Ecology and Evolutionary Biology University of Colorado Boulder, Colorado 80309 USA http://safranlab.weebly.com/ rebecca.safran@colorado.edu

Rebecca J Safran <rebecca.safran@colorado.edu>

Vienna MindTheGap Oct31-Nov1 2

MIND THE GAP 5 Conference Vienna, Austria October 31 and November 1, 2016

Bridging the gap between theoretical and empirical population genetics

The students of the Vienna Graduate School of Population Genetics are proud to announce the fifth MIND THE GAP conference to be held on October 31 and November 1, 2016 at the campus of Vetmeduni Vienna, Austria.

MIND THE GAP aims at bringing together theoretical and empirical population geneticists. This conference is the fifth meeting in a series of conferences held in Freiburg (2009), Plön (2010), Cologne (2011), and Vienna (2013).

As in these past meetings, there are different main topics for this conference. This year's themes are:

- Evolutionary inference using time series data - Adaptive QTLs and their genomic signatures - Phenotypic plasticity - Introgression: signatures of selected and neutral alleles

Several invited speakers have already confirmed their attendance: Nick Barton (IST Austria, A) Alan Bergland (Univ. of Virginia, USA) Luis-Miguel Chevin (CEFE/CNRS, FR) Oscar Gaggiotti (Univ. of St. Andrews, UK) Anna-Sapfo Malaspinas (University of Bern, CH) Fernando Racimo (Univ. of California, Berkeley, USA) Wolfgang Stephan (LMU Munich, GER) Lev Yampolsky (East Tennessee State Univ., USA)

A few remaining speaker slots are still available for which we invite you to apply by July 17th. Attendance to the conference will be free of charge but space is limited. Details about registration can be found on our website: http://www.popgen-vienna.at/news/mind-the-gap-5.htm Julia Hosp <Julia.Hosp@vetmeduni.ac.at>

WashingtonDC EvolTheory Sep22

INVITATION to the Hierarchy Group Workshop and launch of the book “Evolutionary Theory: A Hierarchical Perspective”

A symposium centered around the upcoming publication of the multi-authored book,

EVOLUTIONARY THEORY: A HIERARCHICAL PERSPECTIVE (N. Eldredge, T. Pievani, E. Serrelli and I. Tëmkin, eds.), Chicago University Press (September 2016; http://press.uchicago.edu/ucp/books/book/-chicago/E/bo25468890.html),

will be held at the National Academy of Science (NAS, Washington, DC) on September 22 (Thursday) 2016, 2:30-5:00 PM.

The day after, September 23, the Northern Virginia Community College (NOVA; Annandale, VA) will host a series of workshops with the contributing authors of the book and several discussants to discuss issues related to the hierarchy theory in biology in an informal atmosphere, and to foster further collaborative work. Beside the workshops at NOVA, an hour-long public event promoting the book is scheduled for the middle of the day at NOVA, a more abbreviated and less formal version of the NAS symposium.

More detailed information and tentative schedules of the events are available on the Hierarchy Group website (www.hierarchygroup.com), where you also find further information on the hierarchy theory of evolution.

We extend our invitation to students, scholars, researchers, and educators interested in evolution to attend both events and contribute to the discussions. As the number of attendees is limited, we kindly ask you to contact us at grouphierarchy@gmail.com to reserve your seat in advance.

We look forward to seeing you in September.

Respectfully,

Andrea Parravicini, Ph.D. & Ilya Tëmkin, Ph.D. on behalf of the Editorial team, Evolutionary Theory: A Hierarchical Perspective

“TemkinI@si.edu” <TemkinI@si.edu>

GradStudentPositions

ArizonaStateU PopulationGeneticsGrad

PhDStudent Positions in Population Genetics

Threestudent positions are available in the Jensen Lab in the School of Life Sciences and the Center for Evolution & Medicine at Arizona State University (ASU).

Researchin the lab focuses on the study of adaptation, utilizing approaches from theory and statistical inference as well as experimental evolution and empirical population genetics. Particular projects of interest include theoretical work extending multiple merger coalescent models, and data analysis investigating the evolutionary dynamics of viral infection and the evolution of drug resistance. Additional information on current lab members, alumni, research, funding, and publications may be found at: http://jjensenlab.org Potentialapplicants are encouraged to contact Prof. Jensen to express their interest in the position: jeffrey.d.jensen@asu.edu andto investigate the application procedures related to the Evolutionary Biology PhD program for the upcoming Fall deadline: https://sols.asu.edu/degree-programs/-evolutionary-biology-phd ASUprovides an intellectually engaging research and training community at the interface of evolution, genetics, computer science, statistics, and medicine; with strong interactions among multiple groups of related interest including the Stone, Wilson Sayres, Taylor, Pfeifer, Cartwright, and Hedrick Labs.

jeffrey.jensen@epfl.ch

Auckland InsectOdorantEvolution

Postal Address: Plant & Food Research Private Bag 92169, Auckland Mail Centre, Auckland, 1142, New Zealand Physical Address: Plant & Food Research 120 Mt Albert Road, Sandringham, Auckland, 1025, New Zealand

PhD student position

Plant & Food Research, Auckland, NEW ZEALAND

Professor Richard Newcomb (Richard.Newcomb@plantandfood.co.nz)

Assoc. Professor Thomas Buckley (BuckleyT@landcareresearch.co.nz)

The origin of odorant receptors in insects

A PhD position is available to study the origins of a unique family of receptors for odorants and pheromones that arose early in the evolution of insects. Supported from a grant from the prestigious Marsden Fund, the PhD project will address the timing and role of the first insect odorant receptors. Our hypothesis is that they appeared just before the origin of insect flight and expanded to fill roles in detecting food, predators and/or mates in this new three dimensional environment. The research will involve the isolation of candidate odorant receptors from the transcriptomes and genomes of early insects and their deorphaning in surrogate cell systems.

http://www.royalsociety.org.nz/2015/11/05/was-the-first-smell-of-a-meal-or-a-mate/ The successful candidate will conduct their research within the Auckland laboratories of Plant and Food Research, while being enrolled through the School of Biological Sciences at the University of Auckland. Support includes a $27k p.a. three year stipend with university fees paid. You will work alongside postdoctoral fellows also working on the problem and other members of the Molecular Sensing team within Plant & Food Research, together with collaborators from Landcare Research in New Zealand and the Max Planck Institute for Chemical Ecology in Germany. Candidates should have some background or at least interest in evolutionary genomics, bioinformatics and cell biology.

Richard Newcomb <Richard.Newcomb@plantandfood.co.nz>

EawagETH Zurich EvolutionaryPhysiology

Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is an internationally networked aquatic research institute within the ETH Domain (Swiss Federal Institutes of Technology). Eawag conducts research, education and expert consulting to achieve the dual goals of meeting direct human needs for water and maintaining the function and integrity of aquatic ecosystems.

The Department of Aquatic Ecology seeks a Ph.D. student to study

Evolutionary physiology and adaptation to multifarious selection

Organismal physiology and its genetic basis are key determinants of how natural populations respond to environmental stress on short and long time scales. The goal of this project is to understand how the corticosterone hormonal pathway mediates adaptation to multiple stressors along an environmental stress gradient (acidification). Specifically, the study focuses on adaptive divergence of the moor frog (Rana arvalis) to simultaneous selection via pH, predation and parasites. The work involves field surveys, laboratory and mesocosm experiments as well as genomics and transcriptomics. The student will be based at Eawag, with annual visits to Sweden for field & lab work.

A diploma or M.Sc. (or equivalent) degree in biology or related area is mandatory. The ideal candidate has a strong interest in evolutionary ecology, previous experience with molecular genetic tools, laboratory rearing experiments and field work, is independent and works well in a team. This Swiss National Science foundation position is funded for three years and will be filled as soon as a good candidate is found (earliest starting date 1. October 2016).

The Department of Aquatic Ecology is situated in Dübendorf (near Zürich) and offers an enjoyable and dynamic working environment with broad expertise in ecology and evolution. The working language is English. The project is conducted in collaboration with Doc. Anssi Laurila, Dept. of Ecology and Evolution, EBC, Uppsala University, Sweden and Dr. Otto Seppälä, Dept. of Aquatic Ecology, Eawag/ETH-Zurich, Switzerland and the Genetic Diversity Center (GDC) of ETH-Zurich.

For further information consult www.eawag.ch or

Dr. Katja Räsänen, (katja.rasanen@eawag.ch) or

Personal webpage: http://www.eawag.ch/˜rasaka Additional information

Eawag offers a unique research and working environment and is committed to promoting equal opportunities for women and men and to support the compatibility of family and work. Applications from women are especially welcome.

The closing date for applications is 20 August 2016. We look forward to receiving your application including an application letter (with a statement of research interests and relevant experience), a CV and a list of publications (if any), copies of academic qualifications and the names and e-mail addresses of three referees. Please submit your application via the Eawag Jobs & Career webpage, any other way of applying will not be considered. The LINK below will take you directly to the application form.

https://apply.refline.ch/673277/0455/pub/1/-index.html Dr. Katja Räsänen

Homepage: www.eawag.ch/ ˜ rasaka E-Mail: katja.rasanen@eawag.ch Phone: +41 58 765 5186 Fax: +41 58 765 5802 Address: Eawag Ãberlandstrasse 133 Postfach 611 8600 Dübendorf

Office:

BU G15

"Räsänen, Katja" <Katja.Rasanen@eawag.ch>

GreenwichUK AedesOviposition

Information on Postgraduate Research Scholarship - Ref: DTA-ES-01-16

Faculty: Engineering and Science, Medway Campus

The Natural Resources Institute is aiming to recruit a fully funded PhD bursary to support the following key area of research in the Institute:

Project Title: Identification of chemical signals which modulate oviposition behaviour of the disease vector Aedes aegypti in urban environments

Project Description: The mosquito Aedes aegytpi transmits the etiologic agents of serious viral diseases, including Dengue and Zika, across South America. These viruses are passed from human to human through the blood-feeding behaviour of female A. aegypti. Protein from the blood is required for A. aegypti to produce eggs, which in urban environments are laid in small pools of water close to human habitation. Finding and eliminating oviposition sites is the major focus of Dengue and Zika control strategies in Brazil, with water tanks, discarded containers and plant pots all frequently encountered as containing larvae and pupae. Egg-laying A. aegypti are attracted to odours derived from infusions of plant material, which in natural habitats may indicate a suitable egg laying site containing bacteria on which larvae can feed. However, the extent to which analogous chemical cues are used to locate and choose oviposition sites in urban environments is not yet known. This information is essential to predicting where breeding sites are most likely to occur, and to develop new methods of attracting A. aegypti to oviposition traps, and away from people.

The work will comprise both chemical analysis and behavioural elements, using water odour samples and A. aegypti which have been collected from Brazil. It will build on the framework set out by the collaborative MRC-Newton grant awarded to Dr R. Hopkins at NRI and our collaborators at Instituto Oswaldo Cruz in Brazil. There is the possibility to conduct some of the work in Brazil, to demonstrate the potential impact of the results in a field setting.

For further information contact: Dr Daniel Bray (D.Bray@greenwich.ac.uk) Duration: 3 years, Full-Time Study Bursary available (subject to satisfactory performance):

Year 1: 14,296 Year 2: In line with RCUK rate Year 3: In line with RCUK rate

In addition, the successful candidate will receive a contribution to tuition fees equivalent to the university's Home/EU (4,052) rate for the duration of their scholarship. International applicants will need to pay the remainder tuition fee of 8,029 for the 2016/17 session (the tuition fee is subject to an annual increase.

Making an application: Please read this information before making an application. Information on the application process is available at: http://www2.gre.ac.uk/-research/study/apply/application_process .Applications need to be made online via this link. No other form of application will be considered.

All applications must include the following information. Applications not containing these documents will not be considered.

+Scholarship Reference Number (DTA-ES-01-16)- include in the personal statement section together with your personal statement as to why you are applying + a research proposal related to the subject topic* + a CV including 2 referees * + academic qualification certificates/transcripts and IELTs/English Language certificate if you are an international applicant or if English is not your first language or you are from a country where English is not the majority spoken language as defined by the UK Border Agency * *Attachments must be a PDF format and uploaded to the qualification section. Before submitting your application you are encouraged to liaise with the Lead Supervisor on the details above.

Natural Resources Institute

The Natural Resources Institute (NRI) of the University of Greenwich is a leader in natural resources research, promoting efficient management and use of renewable natural resources in support of sustainable livelihoods. Research is primarily focused on developing and emerging economies. NRI's presence and research partnerships in developing countries, and its training and capacity building programmes, provides the platform for the Institute to develop and disseminate key technologies and knowledge. This has resulted in substantial impact at farmer and community level, and has made significant contributions to the international research community. Much of the work also involves interaction with the developed world where it is equally applicable

Closing date for applications: midnight UTC on 12 July 2016 University of Greenwich, a charity and company limited by guarantee, registered in England (reg. no. 986729). Registered office: Old Royal Naval College, Park Row, Greenwich, London SE10 9LS.

Daniel Bray <D.Bray@greenwich.ac.uk>

iDivLeipzig BiodiversitySynthesis

iDiv invites application to PhD position in Biodiversity Synthesis

https://www.idiv.de/fileadmin/content/-Vacancies_PDF/PhDannouncementChase2.pdf
The German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig is one of the four National Research Centres funded by the German Research Foundation (DFG). It is located in the city of Leipzig and jointly hosted by the MLU, the Friedrich Schiller University Jena (FSU), the University of Leipzig (UL), and the Helmholtz Centre for Environmental Research (UFZ). It is supported by the Max Planck Society, the Leibniz Association, the Klaus Tschira Foundation and the Free State of Saxony. Its central mission is to promote theory-driven synthesis and data-driven theory in this emerging field. The concept of iDiv encompasses the detection of biodiversity, understanding its emergence, exploring its consequences for ecosystem functions and services, and developing strategies to safeguard biodiversity under global change. The Martin Luther University Halle-Wittenberg, in cooperation with iDiv, offers the following positions, salary scale 13 TV-L:

1 PhD researcher on “Biodiversity Synthesis”

(65 percent of a full-time employment, earliest possible start date)

The position is affiliated to the professorship Biodiversity Synthesis of Prof. Jonathan Chase in Leipzig.

The Biodiversity Synthesis group (led by Jonathan Chase) seeks an enthusiastic and creative new member to start a PhD in the summer or fall 2016. The overarching mission of our group is to develop a cohesive framework for understanding the patterns of biodiversity and the processes that explain its heterogeneous distribution across multiple scales.

Topics:

- You will employ novel analytical tools being developed in the group to disentangle the importance of species' total and relative abundances, as well as spatial aggregations, in driving the species-energy relationship.

- There will be three facets to this PhD project: (i) a meta-analysis of the species-energy relationship derived from the published literature, (ii) analyses of global terrestrial and aquatic databases where species-energy data can be derived, (iii) field collected data on the species-energy relationship in grassland plots distributed in multiple locations across the world.

- You will be integrated in our research group composed of international experts who can transmit their expertise, and in close proximity to experts of adjacent fields, providing opportunities for interdisciplinary collaboration. In addition, you will integrate the yDiv doctoral program which offers courses and activities for a successful dissertation and be prepared for the rest of your career while having the recognition of an excellent track.

Requirements /expected profile:

- Masters degree (MSc) (or one that will be delivered by July) in a relevant field and excellent records.

- Fluent in English with excellent communication skills.

- We are looking for a motivated researcher interested in how biodiversity varies with increasing energy inputs (i.e., the species-energy relationship), which is one of the most important environmental gradients structuring biodiversity on the planet.

Postdoctoral associates will develop collaborations with Professor Chase and other members of the iDiv community that complement and extend the overall aim of the working group, including (but not limited to) extending these approaches to include temporal aspects of biodiversity change through time, responses of phylogenetic and functional diversity (and beta-diversity), microbial communities, and theoretical approaches that examine biodiversity patterns and processes in space and time. In addition, postdocs will have the opportunity to collaborate with working groups of visiting international researchers through the associated Synthesis of Centre for Biodiversity Sciences (sDiv), to participate in the training of master's and PhD students through the Young Biodiversity Research Training group (yDiv) and MLU, and to help develop and implement workshops for biodiversity analysis and interpretation to be held in locations across the world. Application should consist of a single pdf file including a letter of motivation (describing your main interests in biodiversity synthesis and main results of your master thesis), a CV, a scan of your most relevant degrees and the names and email addresses of two individuals who could provide an evaluation of the candidate upon request.

For any queries please contact Bettina Zschille, E-mail: bettina.zschille@idiv.de

Please submit your application only in English and in electronic form addressed to Jonathan Chase and sent by mail to the above mentioned email address with registration number 4-5458/16-D in the subject line until August 1^st 2016.

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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

IRI Berlin EvoDevo

The Integrative Research Institute for Life Sciences (IRI) and Humboldt Universität zu Berlin invite applications for

PhD Students (2)

in the research group "Evolutionary Biology" of Dr. David Garfield

Our group focuses on understanding the evolution of developmental gene expression from a population genetics perspective. We are currently recruiting for two projects involving the characterisation of new mutations affecting development (in Drosophila) and the evolution of gene regulatory networks between related species (sea urchins). The positions offer training primarily in experimental biology, though students interested in computational and analytical methods are also encouraged to apply.

PhD candidates will have a Masters degree in Molecular Biology, Evolution, Genetics, or a related field and an interest in understanding evolutionary processes as well as the molecular mechanisms underlying development. Previous experience with modern genomics methods (e.g. high-throughput sequencing) is encouraged. Recruitment is through the IRI Graduate School, which offers numerous training opportunities as well as close interactions with our partner institutions (Charité and the Max Delbrück Center for Molecular Medicine) and collaborators at the nearby Museum of Natural History.

Successful candidates will preferably join the group 1. November 2016 or shortly thereafter. Both positions are highly collaborative, and involve interactions with partners in Berlin and internationally. As such, successful candidates will demonstrate strong communication and organisational skills.

We offer a competitive salary according to German E13 TVöD/Bund (65%). Contracts are 3 years in duration with the possibility of extension. While the working language of the laboratory is English, some knowledge of German (or a willingness to learn) is encouraged. The positions requires a flexible commitment of ~3 hours of teaching per week during the academic semester.

Applications, including a motivation letter, CV, and contact details for two academic references, should be sent as a single PDF to info@garfieldlab.org. Applications will be considered initially until July 31st.

http://www.garfieldlab.org/ http://www.garfieldlab.org/open-positions/
"david.garfield@embl.de" <david.garfield@embl.de>

LiverpoolJMU InheritanceEnvironmentalInfo

Afully funded 3-year PhD position is available in the School of Natural Sciences and Psychology at Liverpool John Moores University:

Title:"Epigenetic inheritance of ecological information"

Description:Organisms are thought to adapt to changing environments through either short term (e.g. phenotypic plasticity) or long term processes (e.g. genetic mutation & evolution, gene flow). Accumulating evidence, primarily from rodents, suggests that there is an additional mechanism, epigenetic inheritance, which facilitates adaption to challenges over the medium term. However disentangling epigenetic inheritance from maternal effects is problematic in mammals due to viviparity: internal fertilisation and development permit the mother to exert considerable influence on offspring phenotype during embryonic development, potentially masking direct epigenetic inheritance. This project will investigate the role of epigenetic inheritance in vertebrates using the classical genetic model organism the zebrafish (Danio rerio). As an externally-fertilising species with no parental care, zebrafish are an ideal, genetically tractable model organism in which to study the mechanisms of epigenetic inheritance while controlling other transgenerational influences such as maternal effects.

Thisproject will involve manipulation of the parental environment to identify experiences and ecological challenges which produce transgenerational behavioural or physiological effects. Following characterisation of parental and offspring phenotypes, RNAseq will be used to identify differentially expressed genes associated with different phenotypes in offspring. Associated changes in epigenetic status of DNA and chromatin will be characterised to investigate the epigenetic mechanisms involved in the observed transgenerational effects.

Theproject will involve both molecular biology and bioinformatics as well as behavioural and physiological analysis and would suit a student with either a genetics/molecular biology background and a keen interest in whole animal biology, or a zoology/organismal biology background and strong molecular biology knowledge and skills. The project will be supervised by Dr Will Swaney, Dr Craig Wilding and Dr Prim Singh, all at LJMU.

Duration:3 years, full time, starting by 1st November 2016 Funding:the successful student will receive a stipend in line with RCUK rates (e.g. pounds 14296 in year 1), and tuition fees will be waived Eligibility:UK/EU citizens only, with the equivalent of a UK 1st class or 2:1 Bachelors degree in biology/genetics/zoology or related subject as a minimum, good spoken & written English. Desirable/relevantknowledge: bioinformatics, PCR, biostatistics/R, behavioural analysis, fish biology, relevant MSc

Applicationprocess: email an application letter explaining your interest in the project, your relevant experience and suitability, as well as a CV and the contact details for two academic referees (former tutors/supervisors). Applicationdeadline: Friday 19th August, shortlisted candidates will be interviewed in early September. Applicationsand informal enquiries should be sent to Dr Will Swaney (w.t.swaney@ljmu.ac.uk)

W.T.Swaney@ljmu.ac.uk

MasseyU Auckland BacterialBehaviour

PhD Scholarship in Evolutionary Microbiology

Massey University, Auckland, Institute of Natural and Mathematical Sciences

We are looking for an enthusiastic and motivated student with interests in microbiology, evolution, and genomics to work on the evolution of behaviour and memory in natural populations of E. coli. The project will involve characterising the behaviour of bacteria using a range of cutting-edge techniques, including microfluidics, (https://www.youtube.com/watch?v=-3DUVT-zxDj8wQ), automated image analysis, and high-throughput flow cytometry. Modern techniques in experimental evolution, genomic analysis, and computational / statistical analyses will also be used. The precise research direction of the project will depend on where the student's passions lie.

Applicants with a background in molecular biology and microbial genetics are especially encouraged to apply. Previous experience in R / Python / (Perl) is also highly desirable.

The Silander Lab is a newly established lab in the Institute of Natural and Mathematical Sciences at Massey University, Auckland. We are interested in microbial evolution, with a focus on the evolution of transcriptional regulation and other quantitative phenotypes, especially on the single-cell level.

The Institute of Natural and Mathematical Sciences has a young and dynamic faculty with a broad range of research interests, from statistics to ecology to evolution. Massey University is located on the North Shore of Auckland, a city which is regularly ranked among the most liveable cities in the world.

The three year scholarship covers all university fees and includes an annual tax-exempt stipend of $25,000 NZD.

To apply, please send a cover letter and CV, including the names of two references, as a single pdf to Dr. Olin Silander (olinsilander@gmail.com). See osilander.wordpress.com for more information on the lab. Application deadline is Sept. 1 2016. Start date upon mutual agreement, preferably before the end of 2016.

olinsilander@gmail.com

MaxPlanckInst Jena InteractionEvolution

4 PhD positions in Molecular and Chemical Ecology

International Max Planck Research School: “The Exploration of Ecological Interactions with Molecular and Chemical Techniques”

The International Max Planck Research School (IMPRS) “The Exploration of Ecological Interactions with Molecular and Chemical Techniques” in Jena, Germany, invites applications for 4 PhD positions beginning in January 2017. The overarching research topic is the use of molecular, chemical and neuroethological techniques to experimentally explore ecological interactions under natural conditions. The main focus is on the relationship between plants, microbes and herbivores, and their environment, as well as the evolutionary and behavioral consequences of these interactions. We offer 6 exciting projects focusing on different organisms and approaches. The complete list of projects offered including project descriptions is available on our website.

We are looking for enthusiastic PhD students with strong interests in the above-described central topic. Applicants should have a firm background in one of the following fields: ecology, bioinformatics, analytical chemistry, entomology, neurobiology, molecular biology, biochemistry, plant physiology and genetics. All our projects are highly integrative and require willingness to closely collaborate with researchers of different backgrounds.

The Research School is a joint initiative of the Max Planck Institute for Chemical Ecology, Friedrich Schiller University, and the Leibniz Institute for Natural Product Research and Infection Biology Jena. We offer state-of-the art equipment, an excellent research environment, supervision by a thesis committee and a structured training program including scientific courses, training in transferable skills and internal conferences. Successful candidates will receive a Max Planck support contract. There are no tuition fees and the working language is English.

Application deadline is August 19, 2016. For detailed information on the IMPRS, projects offered and application requirements, please visit our website http://-imprs.ice.mpg.de/ . Please apply online at https://-imprs-reg.ice.mpg.de

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MPIO Seewiesen
EvolutionCognition

MASTER PROJECT/INTERNSHIP OPPORTUNITIES - PARROT COGNITION (TENERIFE)

Comparative Cognition Research Group, Max-Planck Institute for Ornithology, Tenerife, Spain

The Max-Planck Comparative Cognition Research Group, a part of collaboration between the Max-Planck Institute for Ornithology, Seewiesen, Germany, and the Loro Parque Fundación (LPF), Tenerife, Spain is currently accepting applications for Autumn/Winter term 2016/2017as part of research projects on social cognition in parrots (social learning capacity and cooperation) and a comparative study on physical cognition and problem solving abilities of parrots. CCRG invites applications for master theses and internship projects in a dynamic, international research environment. Successful applicants can expect to gain a solid insight in the field of Animal Cognition/Experimental Psychology and gain experience with working on parrots. The research is carried out on captive parrots of the LPF, which holds the largest parrot collection and gene reserve in the world (ca. 350 subspecies) for conservation and research purposes.

Possible research topics:

- The social learning project is to study the social learning capacity of young individuals of slowly maturing, long-lived and large-brained psittacid species, as well as revealing potential underlying social learning mechanisms, with particular focus on imitation ability. Parrots, as plastic vocal learners, good vocal imitators and flexible, innovative species that probably exhibit life-long learning, represent interesting study candidates for testing their ability to copy novel behaviour from others.
- The aim of the cooperation project is to study prosocial tendencies and perspective taking in a cooperative context in parrots of different social and mating systems.
- The physical cognition project focuses on flexibility and innovative problems solving skills and underlying cognitive mechanisms across different parrots species.

Logistics:

Internship/Master Project start and end dates are flexible but preference will be given to students that can start in September/October 2016. The position requires a minimum of 4 months, but ideally 6 months, continuous commitment at the research station in Tenerife, Spain. The position is not paid but free accommodation in a shared student apartment can be provided. It requires a contribution to the running costs (electricity, water and internet) of ca. 50 Euro per month. Successful applicants will be responsible for their own transportation expenses to and from the research centre (Puerto de la Cruz, Tenerife, Spain).

Important skills/qualifications:

Successful candidates will have:

- for internship projects students with a completed degree in Biology or any related field will be preferred - a strong interest in comparative cognition - high motivation and commitment to the project - reliability and an ability to work independently - confidence to interact with animals - previous research experience is advantageous - good verbal and written English skills - an ability to work in an organised and reliable manner and to manage avariable and demanding workload - initiative to develop the project - good team work attitude and social skills (shared accommodation between 3 students)

To apply:

Please send your CV and a cover letter reporting any relevant experiencehave and motivation to participate in the project to Dr. Auguste von Bayern (avbayern@orn.mpg.de) or Dr. Anastasia Krasheninnikova (akrashe@orn.mpg.de). Contact details of 2 referees may be requested. may be requested.

Roscoff France MarineParasiteEvolution

Open PhD position at Roscoff (France)

http://www.sb-roscoff.fr/en The paradox of being a specialist for a parasite of marine blooming dinoflagellates

The parasitism is a frequent lifestyle in nature and a major source of evolutionary pressure for both the host and the parasite. Given the ubiquity of host-parasite interactions, understanding the factors that generate, maintain, and constrain these associations is of primary interest with implications for a wide range of ecological issues, including dynamics of emerging infectious diseases and invasions (Daszak et al. 2000, Keane and Crawley 2002). Although little studied, many extremely virulent microeukaryotic parasites infecting microalgae have been detected in the marine plankton. Among them are Syndiniales, which constitute a diverse and highly widespread group (Guillou et al. 2008). Because of their virulence and abundant offspring, such parasites have the potential to control dinoflagellate populations, and therefore toxic microalgal blooms (Alves de Souza et al. 2015). These parasites usually exhibit a narrow host spectrum (Chambouvet et al. 2008). Such specialization strongly relies on the life-history traits and ecology of the host. However, coastal planktonic ecosystems are by nature characterized by strong environmental fluctuations and rapid turnovers, even at the population level (Dia et al. 2014). Considering the short generation time and the high dispersal capacity of microalgae, their parasites must adapt at a significantly faster rate than for larger hosts (e.g. plants or animals). All of these considerations should theoretically lead to the natural selection of generalist parasites at the expense of specialists. The persistence and ecological success of specialists among marine planktonic parasites is thus an intriguing paradox.

We hypothesise that host specialization is constrained by evolutionary processes underlying key steps during the infection (such as penetration inside the host and the takeover of the host). We will explore this hypothesis at the cellular level, using molecular approaches

Strategy

We will screened intra and inter variability of > 70 parasitic strains corresponding to 7 genetic clusters (based on their ITS). All of these parasites belong to the same genus (Amoebophrya, Syndiniales) and infect dinoflagellates, but have different host range. NGS reads (RAD and/or MIG-seq) will be mapped on two complete genomes recently acquired from two strains having contrasting host range (one specialist and one able to infect several species and at least two genera), and for which a model of gene prediction is available (using transcripts acquired every 6 hours during a complete life cycle). Genes under positive selection will be screened with the hypothesis that such genes could be involved in speciation, host-parasite interactions, or sex determination. Special attention will be given to homologues with a known function find in other dinoflagellates and closely related parasites such as Apicomplexa (e.g. Plasmodium falciparum) and Perkinsozoa. Novel hypotheses will be then tested in the laboratory using living strains. The PhD student will also actively participate in the expert annotation of genomes, being fully integrated to the international consortium.

Skills

- Strong background in Microbiology
- Knowledge of NGS analysis tools and methods
- Knowledge in population genetics and/or molecular biology
- Ability to work and integrate a team
- Autonomy, rigor and openness

Applications should be sent to Laure Guillou (lguillou@sb-roscoff.fr).

Context of the project:

This project is part of the ANR HAPAR (Head L. Guillou), in collaboration with the ABiMS platform (Analysis and Bioinformatics for Marine Science) at the Station Biologique of Roscoff (France), the University of Ghent (Belgium, S. Rombauts, Y. Van de Peer), and the Genoscope (France, P. Wincker, B. Porcel, France).

The student will work at the Station Biologique of Roscoff (UMR7144, France) under the supervision of L. Guillou (Team Diversity and Interactions in oceanic plankton, http://www.sb-roscoff.fr/en/diversity-and-interactions-oceanic-plankton),and will work in a very dynamic group working on marine plankton (> 50 persons). The Station Biologique of Roscoff has a long tradition in the study of plankton. Its major achievements include the development of flow cytometry methods applied to Oceanography, the creation and development of the Roscoff Culture Collection hosting now more 2500 strains of microalgae, viruses and parasites, and a pioneering role in meta-"omics" approaches of marine picoeukaryotes from marine environments (TARA cruise, OSD).

Other partners of the project:

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SenckenbergResInst 2 EvolutionaryBiol

Senckenberg Gesellschaft für Naturforschung has an international reputation in all fields of Natural History research. It runs six research institutes and two museums in Germany and is also custodian of the UNESCO World Heritage Site at Messel.

The Department "Palaeoanthropology and Messel Research" of the Senckenberg Research Institute and Natural History Museum in Frankfurt invites applications for a

PhD position (Geosciences) in "Pattern of element loss in the autopodial and axial skeleton of extant and fossil mammals" (55%)

This position is part of the joint research project "Forward Genomics", which aims at identifying the genomic causes of phenotypic differences between placental mammals. This project is funded by the Leibniz Association (Leibniz Competition).

Your tasks: The successful applicant will be working in the Module 1 "Phenotyping skeletal traits" that focusses on systematically exploring phenotypic traits of mammals and provide the other modules with solid, calibrated, and evolutionary as well as developmentally understood characters in a practical way (e.g., establishing morpho-matrices). He/she will investigate the evolutionary patterns of vertebral formula and autopodial skeleton: analysis of the thoracolumbar vertebral formula in key-fossil mammals (e.g. from Messel), study on the evolution and variation of sacral and caudal vertebrae count in fossil and extant taxa, analysis of the loss/fusion of basipodials and fingers using ontogenetic observations. The project brings together palaeontology and biology with advanced imaging techniques. It provides a unique opportunity to combine anatomical and genetic field studies to bridge the gap between phenotype and genotype. Finally, the results could even find application in the medical field. The project will be conducted in close collaboration with other PhD students (Senckenberg Dresden, Max Plank Institute Dresden) and other members of the research project.

Your profile:

• You hold a Master degree (or equivalent) in Palaeontology, Biology or a related field • Strong interest in mammal evolution and ontogeny with a background in vertebrate comparative anatomy • Experience in collection based research on fossil and extant vertebrates, as well as in investigating histological serial sections • Good knowledge of image processing in particular ÂμCT data and virtual 3D reconstructions (e.g., VG StudioMAX, Amira, Avizo) • Very good written and oral communication skills in English (knowledge of German is desirable) • Strong ability to work independently, and interest for interdisciplinary teamwork is highly recommended

Salary and benefits are accordance with a public service position in Germany (TV-H E13, 55%). The contract shall start between October and December 2016 and will be initially limited to a 3-year term. The Senckenberg Research Institute supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment station will be Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung.

Please submit your application before August 1st, 2016 by e-mail (attachment in a single pdf document), mentioning the reference of this position (Ref. #01-16027) and including a letter outlining your suitability for the post, a detailed CV including relevant certificates, a 1-page summary of your Master thesis and contact details of 2 potential referees to the address below.

Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt am Main recruiting@senckenberg.de

For scientific enquiries please contact Dr. Thomas Lehmann (thomas.lehmann@senckenberg.de) or PD Dr. Irina Ruf (irina.ruf@senckenberg.de).

The Senckenberg Gesellschaft für Naturforschung (SGN) is a member of the Leibniz Association and is headquartered in Frankfurt am Main, Germany. SGN conducts natural history research with almost 800 employees and research institutions in six federal states. SGN also supervises the Messel Pit Fossil Site, a UNESCO World Heritage Site.

The Department Senckenberg Naturhistorische Sammlungen Dresden, Section Mammalogy invites applications for a

PhD position (Ref.# 07-16008) in Zoology/Mammalogy

within the project funded by the Leibniz Association: Identifying genomic loci underlying mammalian phenotypic variability using Forward Genomics with Semantic Phenotypes.

The successful applicant will be working in the Module 1 Phenotyping skeletal traits that focuses on systematically exploring and mapping craniodentale characters of a series of mammal species. The project aims at identifying the genomic causes of phenotypic differences between mammal species. A matrix of characters (presence and absence) has to be established and the characters documented.

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TrentU 2 EvolBiolGrad

PhD position or Post-Doctoral Fellowship investigating carnivore responses to landscape heterogeneity - Trent University

We are currently seeking a highly motivated PhD student or Post-Doctoral Fellow to examine relationships between landscape heterogeneity and physiological, genetic, and genome-level variation in carnivores. Building on our 35,000+ repository of wolf, coyote, fox, lynx and bobcat fur and tissue samples, we aim to determine how carnivore stress levels, diet breadth, and genetics vary according to environmental factors like climate, habitat, or anthropogenic activity. There is further opportunity to investigate processes underlying spatio-temporal variation in patterns of dispersal and population connectivity, and the contribution of environmental variability and intrinsic features of the individual animal to such processes. Of particular interest is the role of climate change on stress levels and diet breadth, as well as potential variation in functional genes especially in environments undergoing rapid change. Our recent work (mostly on lynx and coyotes) sets the foundation for this work, and our next challenge is to develop a more comprehensive understanding of physiological-dietary-genetic linkages across carnivore species and through space and time. Our team has access to abundant samples and state-of-the-art analytical facilities and equipment to address these research questions, and the successful candidate will have the opportunity to develop his/her own research interests within the scope of the broader program.

Applicants must have a strong academic record and graduate degree(s) in Biology, Physiology, Ecology, Genetics or a related field. Candidates with an interest in and/or knowledge of hormone assays, stable isotope analysis, DNA extraction, bioinformatics, or other relevant procedures, will be highly sought. Candidates should demonstrate evidence of research potential (including scientific publications), a strong work ethic, and willingness to work in a large, dynamic, and collaborative research environment. The funding package is competitive and will include a foreign tuition waiver, if the successful applicant is an international PhD student.

The position will be offered through an NSERC CREATE program in Environmental Monitoring and Assessment (www.create-enviro.ca). The position will be closed as soon as a suitable candidate is found, so apply early! To apply, please submit: cover letter, unofficial transcripts, curriculum vitae, and names of three references to: Dennis Murray (dennismurray@trentu,ca; www.dennismurray.ca).

PhD position or Post-Doctoral Fellowship investigating mechanisms underlying the plasticity of amphibian responses to environmental stressors - Trent University

We are currently seeking a highly motivated PhD student or Post-Doctoral Fellow who will examine mechanisms governing the effects of environmental stressors on phenotypic and behavioural plasticity in amphibian models. Building on our longstanding research on amphibian responses to environmental stressors (including disease, predation risk, and contaminants), we aim to further establish a mechanistic link among ecological, physiological, and genome-level responses in amphibian tadpoles to natural or human-caused stressors. We are especially interested in building a bioinformatics approach to help identify the mechanisms involved in stressor-induced phenotypic and behavioural plasticity. Our preliminary work indicates differences in gene expression that are related to tadpole exposure to different stressors, and our next challenge is to establish the functional link between expressed genes and type of stressor. Our team has access to state-of-the-art facilities and equipment allowing us to address these cutting-edge research questions, and the successful candidate will have the opportunity to develop his/her own research interests within the scope of the broader program.

Applicants must have a strong academic record and graduate degree(s) in Biology, Physiology, Ecology, Genetics or a related field. Candidates with an interest in and/or knowledge of bioinformatics platforms/resources, experience in extracting genetic material or other relevant lab procedures, and conducting lab experiments with larval amphibians, will be highly sought. Candidates should demonstrate evidence of research potential (including scientific publications), a strong work ethic, and willingness to work in a large, dynamic, and collaborative research environment. The funding package is competitive and will include a foreign tuition waiver, if the successful applicant is an international PhD student.

The position will be closed as soon as a suitable candidate is found, so apply early! To apply, please submit: cover letter, unofficial transcripts, curriculum vitae, and names of three references to:

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UCanterbury ChytridPopulationGenetics

A fully-funded three-year PhD position is available at the School of Human and Life Sciences at Canterbury Christ Church University (CCCU).

Project title: Evolution and epidemiology of chytridiomycosis in an amphibian biodiversity hotspot

The research project revolves around the distribution and evolution of the fungal infection chytridiomycosis in Cusuco National Park, Honduras. This park is a major biodiversity hotspot, characterised by exceptional species diversity and is one of the top 25 areas of global significance to amphibian biodiversity. We have a large collection of samples collected from a number of tree frog species (including three that are endangered) over the last five years. Alongside the disease genetics the project will also seek to characterise and study the population genetics of Major Histocompatibility Complex loci in the host species. The project will include both wet-lab work and bioinformatics and students with a keen interest in either are encouraged to apply. The project will be supervised by Dr Samit Kundu at CCCU.

The ideal candidate for this PhD position will have a Bachelors degree in Molecular biology, Molecular Ecology, Evolution, Genetics or a related discipline. A Masters degree in a relevant area is also desirable, but not essential.

The studentship includes a salary of 12500 GBP and an additional bursary of 6500 GBP (in total about 19000 GBP) per year

Enquiries and applications, which should include a cover letter stating why you are interested in the position and a Curriculum vitae that includes the names of two referees, should be sent to Dr. Samit Kundu (samit.kundu@canterbury.ac.uk). Applications will be accepted until the position has been filled.

"Kundu, Samit (samit.kundu@canterbury.ac.uk)"

UGroningen 12 EvolutionaryBiol

12 PhD positions in Evolutionary Life Sciences

The University of Groningen has an international reputation as a dynamic and innovative institution of higher education, offering high-quality teaching and research. The Groningen Institute for Evolutionary Life Sciences (GELIFES), the largest institute of the Faculty of Mathematics and Natural Sciences fills a special niche in the life sciences by covering and integrating mechanistic, evolutionary and ecological approaches, aiming to understand adaptation on all levels of biological organisation. Researchers pursue fundamental questions while collaborating with partners from industry, medicine and other realms of society. For its new research programme, Adaptive Life, GELIFES is looking to fill 12 Scholarship PhD positions. For more information on available positions, qualification requirements and the application procedure, please consult our website: http://www.rug.nl/research/fmns/themes/adaptive-life/research/phd-projects .

More information about the PhD-training programme and scholarship can be found via: https://www.rug.nl/education/phd-programmes/-

phd-scholarship-programme/ Maartje Giesbers <m.c.w.g.giesbers@rug.nl>

UHaifa Evolution

Biology, mathematics, computer science and bioinformatics students/researchers are needed

Dr. Livnat's new lab for the study of evolution at the University of Haifa in Israel is seeking applications for Ph.D, postdoc and other positions from individuals with a background in biology, mathematics, computer science or bioinformatics and a record of past excellence.

We study the deep principles of how evolution works both theoretically and experimentally. 1) Students with a background in theoretical computer science or other branches of mathematics may participate in work at the interface of evolutionary biology and theoretical computer science whose goal is to form a new mathematical framework for evolution. Our lab works in collaboration with leading computer scientists abroad and in Israel. 2) Students with a background in bioinformatics and students with molecular biology lab skills may participate in evolutionary research involving cutting-edge sequencing methods. 3) Students interested in the evolution of behavior are also encouraged to apply.

Applicants should send a cover letter and a CV to alivnat@univ.haifa.ac.il, including the names of 2-3 references. More info at http://sci3.haifa.ac.il/~alivnat/ adi.livnat@gmail.com

UKansas CnidarianGenomics

The Cartwright Lab at the University of Kansas is seeking graduate students (masters or PhD) to work on cnidarian genomics. Our lab focuses on many aspects of cnidarian evolution, including phylogenomics and development. In particular, we are seeking someone to characterize genomes and transcriptomes of parasitic myxozoans and their relatives. Additional projects include applying CRISPR technologies to cnidarian model systems, hydrozoan phylogenomics and comparative gene expression.

Student must be highly motivated, have a demonstrated ability to work independently and show a keen interest in cnidarians, phylogenetics, developmental processes and evolution.

The EEB department at the University of Kansas guarantees five years of support (two years for masters students). If interested, please contact Paulyn Cartwright at pcart@ku.edu.

Paulyn Cartwright Associate Professor Department of Ecology and Evolutionary Biology 1200 Sunnyside Ave. Haworth Hall University of Kansas Lawrence, KS 66045 https://eeb.ku.edu/paulyn-cartwright http://www.people.ku.edu/~pcart/labwebsite/Home.html Paulyn Cartwright <pcart@ku.edu>

UKansas EvolGenetics

Graduate Opportunities in Evolutionary Genetics at the University of Kansas

The Department of Ecology and Evolutionary Biology at the University of Kansas has several graduate positions open in Evolutionary Genetics. The Evolutionary Genetics group in the KU EEB department comprises multiple labs with funded research programs that apply cutting edge techniques to address questions in evolutionary mechanisms, phylogenetics, genomics and population genetics. The group is highly interactive and holds a weekly graduate seminar.

The EEB department at the University of Kansas guarantees five years of support (two years for masters students).

Please see https://eeb.ku.edu/prospective-students to learn more about our graduate program.

The application deadline for Fall 2017 is December 1, 2016.

Below are brief descriptions of some of the graduate opportunities in our department:

The Cartwright Lab is seeking graduate students (masters or PhD) to work on cnidarian genomics. Our lab focuses on many aspects of cnidarian evolution, including phylogenomics and development. In particular, we are seeking someone to characterize genomes and transcriptomes of parasitic myxozoans and their relatives. Additional projects include applying CRISPR technologies to cnidarian model systems, hydrozoan phylogenomics and comparative gene expression. For more information please contact Paulyn Cartwright at pcart@ku.edu

The Glor Lab investigates the evolution of species diversity through studies of reptiles. Current lab projects include sequencing, assembly and annotation of new Anolis lizard genome; experimental laboratory crosses designed to characterize patterns of reproductive isolation between closely related species as well as the genetic basis for species differences; and field studies of species, speciation and hybridization in the Dominican Republic and Cuba. For more information please contact Rich Glor at glor@ku.edu

The Hileman Lab is seeking graduate students (masters or PhD) to work on the evolution of flower diversity. Our research focuses on understanding the genetic and developmental basis of floral form, with special interest in the genetics of convergent trait evolution. We integrate diverse methods ranging from phylogenomics to gene silencing. We are particular interested in identifying creative and enthusiastic students to join our group. For more information, please contact Lena Hileman at lhileman@ku.edu

The Blumenstiel Lab is seeking graduate students (masters or PhD) to work on genome evolution and the evolution of genome stability mechanisms. We are especially interested in the population dynamics of selfish DNA, the evolution RNA silencing and the evolution of meiosis. For more information please contact Justin Blumenstiel at jblumens@ku.edu

The Kelly Lab is seeking graduate students (masters or PhD) for work in evolution genetics. Students can pursue theoretical and/or experimental studies. Currently, we are particularly interested in mating system evolution in plants and quantitative trait evolution in general. For more information please contact John at jkk@ku.edu.

The Orive Lab is seeking graduate students interested in theoretical evolutionary biology and population genetics. Areas of current research in the lab include evolutionary genetic models of complex life histories, modeling the effects of clonal reproduction on rates of evolution and evolutionary lag, and models of within- and between-host pathogen and symbiont population dynamics. For more information please contact Maria Orive (morive@ku.edu).

“jblumens@ku.edu” <jblumens@ku.edu>

ULincoln MacaqueConservationGenetics

MSc by Research project on genetic diversity of the Barbary macaque of Algeria

This is an MSc by Research studentship with a full fee waiver for UK/EU students and a partial fee waiver for international students.

We are looking for a qualified and motivated student to work on a project on the genetic diversity of the Barbary macaque (Macaca sylvanus). The project will run at the University of Lincoln (UK) under supervision of Dr Bonaventura Majolo (School of Psychology; http://staff.lincoln.ac.uk/bmajolo) and Dr Malgorzata Pilot (School of Life Sciences; http://staff.lincoln.ac.uk/-mpilot). This is a unique opportunity to assess genetic diversity on an endangered population of the Barbary macaque. Faecal samples of Barbary macaques have been collected over the last three years and the project will involve DNA extraction and genotyping. The successful candidate will receive training in genetic analysis and will conduct the study at Joseph Banks Laboratory in Lincoln. The successful candidate will enrol on our MSc by Research programme in the School of Life Sciences, starting in October 2016 (or as soon as possible after October, but no later than early December 2016) and lasting approximately one year. The student will be responsible for carrying out laboratory analyses, data analysis, and writing up their MSc thesis. They will be involved in the preparation of a report for our funding bodies (see below) and will co-author at least one paper. The student will have the opportunity to join a multi-cultural and inter-disciplinary research-oriented environment at Lincoln, including Evolution & Ecology and Animal Behaviour, Cognition and Welfare research groups at the School of Life Sciences and the Evolution and Development research group at the School of Psychology. This position is an excellent opportunity to gain research experience before enrolling on a PhD programme.

Qualifications/Experience: Priority will be given to applicants who have experience in population genetics and behavioural ecology. Applicants with the following skills/experiences are particularly welcome:

§A background in Genetics, Conservation Biology, Animal Behaviour, Primatology

§Some experience of laboratory based molecular genetics

§Good spoken and written English is an essential requirement for this post.

Funding: This project is funded by la Montagne des Singes, Affenberg Salem, Trentham Monkey Forest, and la Foret des Singes. The successful candidate will receive a full fee-waiver to enrol in our MSc programme. Please note that the full fee waiver only applies to UK or EU candidates. Non-EU candidates will receive a partial fee waiver equivalent to home student fees (4500). Moreover, the student will receive approximately 2,000 as a contribution to their living expenses. The costs of project consumables are fully covered by the funding bodies.

Term of Appointment: Starting date should be early October 2016 or as soon as possible after. The student is expected to be based in Lincoln for the duration of this project.

Application Deadline: 13 August 2016

How to apply: In order to apply please email a short cover letter (1 A4 page maximum) explaining previous experience, interest and suitability to the position along with a CV and the contact details of two referees. Referees should be former supervisors/ tutors and should be able to provide a reference when contacted. For informal enquiries please contact Malgorzata Pilot (mpilot@lincoln.ac.uk) or Bonaventura Majolo (bmajolo@lincoln.ac.uk).

Applicants who are invited to interview will subsequently need to complete online application form to enrol for MSc by Research.

The University of Lincoln, located in the heart of the city of Lincoln, has established an international reputation based on high student satisfaction, excellent graduate employment and world-class research.

Malgorzata Pilot <MPilot@lincoln.ac.uk>

UMonash Melbourne Microbial Evolution

Experimental evolution of microbes

Two PhD positions are available to undertake research at the interface of evolutionary genetics and microbial ecology. You will be using experimental evolution, whole genome sequencing and molecular genetic techniques. The research will involve the handling and passaging of yeasts and bacteria, whole genome sequencing, cutting edge molecular techniques and DNA sequence data analysis. Specific research projects will be discussed upon application.

The ideal candidate for this scholarship has experience in molecular biology techniques and either computer programming or statistical analysis. Prior experience in working with microbes and a strong background in evolutionary biology are of an advantage, but not strictly necessary.

The studentship covers all university fees and includes an annual stipend of AUD$25,000 for three years. The Monash University PhD program has been adapted to the multiple potential career outcomes of the 21^st century PhD graduate, including extensive training and support.

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

Monash University is located in Melbourne- a city consistently ranked as the most liveable city in the world. Monash is one of Australia's prestigious group of eight research institutions.

To apply for the position, please send a cover letter stating your interest in the position and why you think you would be a good candidate, a Curriculum Vitae, a copy of your academic transcript, and the names of two referees. Applications will be accepted until the positions are filled.

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

mike.mcdonald@monash.edu

for more information see:

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

UNewBrunswick EvolutionGreenAlgae

Graduate student position - Evolution in green algae; UNB, CANADA

A graduate student position is available in the laboratory of Aurora Nedelcu (http://www2.unb.ca/vip/amnedelcu/), in the Department of Biology (http://www2.unb.ca/biology/) at the University of New Brunswick (http://www.unb.ca/), Fredericton, CANADA. Research in our laboratory is directed towards understanding general, fundamental issues in evolution - such as the evolution of multicellularity, development, cell differentiation, sex, programmed cell death, altruism. Our research is rooted in the framework of transitions in individuality and evolution of complexity (at a conceptual level), and of cellular responses to stress (at a more mechanistic level). The experimental model-system we are currently using is the green algal group, Volvocales (see our Volvocales Information Project; http://www.unbf.ca/vip). Highly motivated students with interests in either theoretical/genomics or experimental/molecular approaches, and previous research experience are encouraged to apply. Interested applicants should e-mail a CV, summary of research experience and interests, unofficial transcripts, and contact information for three referees to anedelcu@unb.ca. Applicants should meet the minimum requirements for acceptance in the Biology Department Graduate Program (see http://www2.unb.ca/biology/Degree_Info/Graduate.html).

Aurora M. Nedelcu University of New Brunswick Department of Biology PO Box 4400 Fredericton, NB Canada E3B 5A3 phone: (506) 458-7463

Aurora Nedelcu <anedelcu@unb.ca>

UNewEnglandAustralia PlantSpeciation

We are seeking outstanding applicants to join an ARC-funded research program on speciation, hybridisation and adaptation in Eucalyptus. This project is run out of the University of New England, in Armidale, New South Wales, Australia (not Maine!), and is a collaboration between the groups of Dr Rose Andrew (UNE) and Prof. Justin Borevitz (Australian National University). — Why are there so many (700+) species of Eucalyptus? How do they come to share polymorphisms? Is hybridisation a regular—constructive force in their evolution? These are just some of the questions we're trying to answer with whole genome and reduced representation population genomic—sequencing. There is scope for student projects to incorporate quantitative genetics and ecological studies, to search for adaptive loci or speciation genes.

The ideal student will be highly motivated, enjoy writing, and show both independence and the ability to work well in a team. Skills in bioinformatics, empirical or theoretical population genetics, and/or field botany will be an asset. Armidale is a vibrant and diverse college town in regional Australia. It is surrounded by spectacular landscapes and rich plant communities, with exceptional hiking and climbing opportunities on its doorstep. The University of New England is world-class in Genetics and Ecology, and the Australian National University is a global—leader in research (top 20 universities in the world). — The next rounds for the UNE International Postgraduate Research Award (IPRA) and Australian Postgraduate Award (APA) scholarships will open on 29 July 2016 and close on 30 September 2016. Up to 20 UNE IPRA's and up to 35 APA's are available to outstanding applicants. On top of the AU$26,000 pa stipend, the School of Environmental and Rural Science contributes AU$3,500 pa for research and travel.

For more information, please contact Rose Andrew (rose.andrew@une.edu.au) by 30 August 2016.

Dr Rose Andrew Lecturer in Molecular Ecology School of Environmental and Rural Science

University of New England Armidale NSW 2351 Australia

Phone —61 2 6773 3160 Email —rose.andrew@une.edu.au http://www.une.edu.au/staff-profiles/randre20

www.une.edu.au CRICOS Provider Number: 00003G

"randre20@une.edu.au" <randre20@une.edu.au>

UOtago EvolutionaryModels

Ph.D. Scholarship at University of Otago, New Zealand

We're looking for an applied mathematician for a Ph.D. examining evolutionary models for ecological niches. The candidate would work with Prof David Bryant (Mathematics and Statistics) and Prof. Steven Higgins (Ecology) studying the ways that species niches change over time, their relationship with speciation, and how we can work with these mathematically.

The candidate needs to have some programming experience, and an enthusiasm (if not background) in the life sciences.

The postdoctoral scholarship is funded by a Marsden grant, paying NZ$25,000 plus fees and a travel budget.

For more information, contact David at david.bryant@otago.ac.nz

http://www.maths.otago.ac.nz/~dbryant Prof. David Bryant Department of Mathematics and Statistics University of Otago Dunedin 9054 New Zealand http://www.maths.otago.ac.nz/~dbryant ph: +64 3 4797889

David Bryant <davidjamesbryant@fastmail.com>

UQuebecTR HumanLifeHistoryAndDiseaseEvol

PHD OPPORTUNITY IN ECO-EVOLUTIONARY DYNAMICS AND DISEASE EVOLUTION IN MODERN HUMANS

Population Genetics Lab Â' prof. Emmanuel Milot, Universite of Quebec at Trois-Rivières

Send your application by August 12th 2016

A PhD candidate is sought to work on evolution in contemporary human populations. The aims of the project are 1) to measure selection on genetic variation shaping life history and diseases (e.g. asthma, neuropathy); 2) to assess how eco-evolutionary dynamics modulate this variation within the context of modernization (main collaborators: Simon Gravel, McGill University; Catherine Laprise, Universite of Quebec at Chicoutimi). While it is sometimes claimed that humans have stopped evolving, recent studies suggest that selection on heritable traits, thus the potential for evolution, is ubiquitous in our species. Moreover, abrupt changes that have occurred over the last centuries, such as the demographic transition, have profoundly modified the playground of natural selection. These processes may have important consequences on reproduction, health and ageing and could also be modulated by eco-evolutionary feedbacks between demography and genetic changes in traits.

The successful applicant will study the process of selection and genetic change generation-by-generation, using exceptional human data (pedigree and genome scans) from the Québec population since its foundation, which has become a model recognized worldwide in population genetics. He/she will join an interuniversity team in evolutionary biology that will provide opportunities to interact and collaborate with researchers from various disciplines (ecology, evolutionary ecology, epidemiology, anthropology, demography, medicine, etc.).

FUNDING AND CONDITION FOR ADMISSION The project is funded by the Natural Sciences and Engineering Council of Canada (NSERC) and the Québec Nature and Technologies Research Fund (FRQNT). We seek candidates with profiles good enough to apply for scholarships. Candidates must have undergraduate (bachelor$\hat{\text{A}}^1$s) and Master degrees in biology or bioinformatics or in a related domain, or expect to have completed their degree very soon. Profiles with a strong background in bioinformatics or statistics will be preferred.

DOCUMENTS REQUESTED TO APPLY

- Cover letter with a statement of the research interests of the candidate - CV - Name and Email of two referees

Do not hesitate to contact me for further information:

Emmanuel Milot E-mail : emmanuel.milot@uqtr.ca Phone : +1 819 376-5011, ext. 4397 Web page : www.uqtr.ca/emmanuel.milot/EN ABOUT THE UNIVERSITY AND THE CITY The University of Québec at Trois-Rivières is small-medium size (~15,000 students) institution that is currently expanding and very dynamic in research. The working language is French although many people also speak English. Founded in 1634, Trois-Rivières is the third oldest city in North America (after Québec City and Boston) with a small and nice old downtown. It is strategically located within an hour and half drive of Montreal and Québec City, along the St. Lawrence River and nearby vast forested landscapes. Access is thus easy to both the great cultural life of these cities and profuse outdoor activities, including winter sports.

"Emmanuel.Milot@uqtr.ca"

<Emmanuel.Milot@uqtr.ca>

UToulouse PopGenomics PlantMedicago

PhD: "Detecting networks of coadapted genes by genome-scale analysis of DNA polymorphisms: application to the model legume Medicago truncatula" A PhD position is available at Université Toulouse 3 (Paul Sabatier), France, starting on fall 2016, for three years.

The scholarship is founded by the ANR (Agene Nationale de la Recherche) project "DeCoD". The PhD activities will be conducted in the Plant Sciences Research Laboratory (Laboratoire de Recherche en Sciences Végétales - LRSV), in the city of Castanet-Tolosan, very close to Toulouse.

The PhD student will be co-supervised by Dr Maxime Bonhomme and Prof Christophe Jacquet. We are seeking for a recently graduated Master student in Bioinformatics, Biostatistics, or Evolutionary Biology with strong skills in population genetics, bioinformatics (analyses of SNP data) and programming.

For further details please contact: Dr Maxime Bonhomme (bonhomme@lrsv.ups-tlse.fr)

Dr. Maxime Bonhomme Pôle de Biotechnologie Végétale UMR CNRS UPS 5546 Chemin de Borde Rouge BP 42617 31326 Castanet tolosan cedex, France Tel : 33 (0) 5-34-32-38-14 Fax : 33 (0) 5-34-32-38-02 email: bonhomme@lrsv.ups-tlse.fr researchgate: https://www.researchgate.net/profile/Maxime_Bonhomme

Maxime Bonhomme <bonhomme@lrsv.ups-tlse.fr>

UTulsa EvolutionaryBiol

Department of Biological Sciences - University of Tulsa

The Booth lab at The University of Tulsa is currently seeking M.Sc and Ph.D students. Four projects are available:

1) Identifying the genomic signatures of host-associated differentiation. Through genome resequencing of 22 lines of haematophagous insect and the availability of two annotated reference genomes, we seek to understand genes driving differentiation to alternative mammalian hosts. This project will be primarily bioinformatic as the genome resequencing has taken place. This may also include transcriptomic and microbiomic components.

2) Spatiotemporal metapopulation dynamics and host-species expansion of a disease-vectoring avian ectoparasite. Using both nuclear and mitochondrial markers, we aim to understand variation in the temporal and spatial structure of an avian ectoparasite undergoing both a population range expansion and a host-species expansion. This project has the potential to include both genomic and microbiomic aspects also.

3) Understanding the dynamics of rapid and pervasive mitochondrial heteroplasmy and recombination. Using a mitogenomic approach this project seeks to 1) assess the influence of mitogenomic divergence on the frequency of paternal leakage driven heteroplasmy; 2) to empirically and theoretically evaluate heteroplasmy decay; and 3) determine whether recombination hotspots can be detected within the mitochondrial genome.

4) A genomic assessment of facultative parthenogenesis in snakes. We have generated RAD-Seq data for parthenogens, their mothers, and in one case, their offspring. Using this data, and two published genomes, we seek to address two main questions. 1) Can we identify the automictic mechanism underlying the production of parthenogens? This may be either terminal fusion or gametic duplication; and 2) what are the genomic characteristics of parthenogenesis and also sexual reproduction by facultative parthenogens, and can these be detected in wild populations?

Applicants for this position should have a strong background in population genetics/genomics, molecular ecology, bioinformatics, or evolutionary biology, and meet the admission requirements for the Department of Biological Sciences graduate program. (https://graduate.utulsa.edu/admission/eligibility-requirements/). If a non-U.S citizen, the applicant must already have a valid VISA permitting them to enter and study in the United States. Funds are not currently available to cover this as part of this project.

The students stipend, tuition, and medical insurance, is covered as part of the teaching assistantship (requires 20 hours per week teaching assistance).

Applications should include the following:

1) A letter of interest (not exceeding two pages).

2) A curriculum vitae.

3) Names and email addresses for at least two academics/researchers willing to provide a letter of recommendation

4) Copies of undergraduate/post-graduate transcripts

5) Electronic copies of published manuscripts, if any.

For more information about this opportunity, contact Dr. Booth (warren-booth@utulsa.edu). Anticipated start date can be as early as mid-August 2016.

Additional information regarding our research can be found at our website: www.booth-lab.org —

Dr. Warren Booth

Assistant Professor of Molecular Ecology

Department of Biological Sciences University of Tulsa
315 Oliphant Hall

Tulsa, OK 74104

Tel.

(918) 631-3421 - Office

(918) 631-3136 - Lab

Web site - TU academic

Lab website

"Booth, Warren" <warren-booth@utulsa.edu>

UVienna EvolGenomics

Hi, all

There will be one 3-year fully-funded PhD position available in the research group of Dr. Qi Zhou in the Department of Molecular Evolution and Development. My research is at the interface of evolution, epigenetics and development. We harness the latest sequencing technologies and genomic tools to address basic questions about how sex chromosomes evolve in Drosophila and birds. Candidates are expected to have a Master degree in Molecular Biology, Developmental Biology or Evolution. Research experience in Drosophila genetics, specifically with skills of CRISPR/Cas9, transgenics or fluorescence in situ hybridization is highly preferred. The project is going to use a recently evolved Drosophila young sex chromosome system to study how euchromatin and heterochromatin transit to each other on the sex chromosomes, and what are the role of small RNAs during this process. I invite the interested candidates to directly submit her/his CV, at least two recommendation letters, and a one-page research statement to muntjaczhou at gmail.com. I will interview the candidates until the position is filled.

More about my research can be refereed to www.qizhoulab.org Cheers, Qi

Qi Zhou <muntjaczhou@gmail.com>

UZurich DolphinGenomes

Project title:

Unraveling the genetic architecture of dolphin genomes using new sequence technologies and bioinformatics, and application of genomic data to populations

Project description:

Innovations in sequence technology and computational methods have prompted a shift towards individual bioinformatics-savvy laboratories being able to accurately assemble large and complex genomes. These developments make it feasible to generate detailed evolutionary analyses for non-model organisms. In this project, we will sequence and assemble a reference genome of the Indo-Pacific bottlenose dolphin (Tursiops aduncus) with a new protocol that gives long-range genetic information. We will then re-sequence relevant subpopulations to infer the demographic history and assess speciation patterns in the genus Tursiops. Among marine mammals, bottlenose dolphins are a fitting candidate to explore, given the detailed knowledge on their biology, high levels of adaption, global distribution, and their many convergent features with humans and great apes.

Comment:

This 4 year PhD position is based in the Robinson (http://goo.gl/d9V7ci) and Krutzen (http://goo.gl/tojCR1) labs at the University of Zurich and will be embedded in the Zurich Life Science Graduate School's program in Evolutionary Biology (http://www.lifescience-graduateschool.ch/). Remuneration is according to Swiss PhD salary scales (CHF 48'540 p.a. plus employer social security contributions). Expected start date will be 1 January 2017.

We are seeking a highly collaborative, motivated and dynamic student with a Bachelors or Masters degree in Evolutionary Biology. The student possesses a good mathematical grounding, in particular, sufficient training in mathematics, statistics, computer science, bioinformatics. The student will have a passion for collaborative and open science with a flare for developing high-quality tools for the community. In addition, the ideal student will have experience in evolutionary biology and population genomic data analyses and is knowledgeable in modern data science tools. A strong background in programming, scripting and managing large datasets will be considered an asset.

Application:

Interested students should send their application package to Mark Robinson (mark.robinson@imls.uzh.ch) and Michael Krutzen (michael.kruetzen@aim.uzh.ch) before 29 September 2016. The package must include, in a single PDF file:

1) A one-page cover letter expressing research interests relevant to the position

2) A complete CV

3) Names and email address of at least two academic referees

Please also attach low-resolution copies of your official academic transcripts and degrees, as well as copies of any publications and Diploma/MSc theses.

PD Dr. Michael Krutzen Anthropological Institute & Museum University of Zurich Winterthurerstr. 190 CH-8057 Zurich / Switzerland (p) +41 44 63-55412 (f) +41 44 63-56112

http://www.sharkbaydolphins.org http://www.aim.uzh.ch/research/orangutannetwork.html
Michael Krützen <michael.kruetzen@aim.uzh.ch>

UZurich EvolutionaryMicrobiology

The laboratories of Rolf Kümmerli and Andreas Wagner at the University of Zurich, Switzerland, offer a joint PhD position in evolutionary microbiology. Starting date of the position is January 2017.

Both labs run inter-disciplinary research programs, combining empirical research with computational approaches. Examples of current research projects can be found at http://www.botinst.uzh.ch/en/research/evolutionary/kuemmerli/research.html and http://www.ieu.uzh.ch/wagner/research.html For the current project, the successful candidate will work on the evolutionary diversification of bacterial cooperative traits using a combination of microbiological and genomic experiments with Pseudomonas bacteria, as well as computational modeling.

We are looking for a highly-motivated student, who is interested in working at the interface between microbiology, evolutionary and computational biology. The ideal candidate should have previous research experience in evolutionary microbiology and computational biology. We will also consider candidates with strong background in one of the disciplines (evolutionary biology, microbiology or computational biology), and who are keen to rapidly acquire skills in the other disciplines. Experimental and computational work will be carried out in the Kümmerli and the Wagner lab, respectively. There will be close collaboration between the PIs and the members of the two groups, including joint group meetings. Both groups are based at the Irchel Campus of the University of Zurich, in vicinity of one another.

Candidates must have a Masters or an equivalent degree. The working language in both laboratories is English. German skills, although helpful, are not essential.

Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

Applications should be sent to rolf.kuemmerli@uzh.ch, as a single (!) PDF file merged from the following parts: CV including publication list (if available), a scanned academic transcript (list of grades in university courses), a one-page statement of research interests, and three references. The application deadline is August 10, 2016.

Rolf Kuemmerli <rolf.kuemmerli@uzh.ch>

UZurich EvolutionOfInvasions

PhD Studentship in Evolution/Evolutionary ecology @ University of Zurich & Eawag, Switzerland

The Altermatt lab and the Wagner lab at the Department of Evolutionary Biology and Environmental Studies (IEE) of UZH and the Department of Aquatic Ecology of Eawag have a vacancy for a PhD position.

Project title: Understanding invasions - from the genetic basis to the ecological dynamics of spreading populations

Biological invasions are among the biggest threats to natural ecosystems. Unfortunately, the causes of invasions remain elusive, due to the large spatiotemporal scales involved and the poor integration of macroecology and evolutionary biology. Additionally, we lack an integration of ecological and evolutionary theory with experimental data. In this project the doctoral researcher will conduct laboratory invasion experiments, using the model organism /Tetrahymena thermophila/ in miniaturized landscapes suitable to study macroecological and evolutionary dynamics (Giometto et al. 2014 PNAS, Altermatt et al. 2015 Methods Ecol. Evol., Fronhofer & Altermatt 2015 Nature Comm.), in order to track and understand the resulting eco-evolutionary dynamics from genes to populations. During these invasions, /Tetrahymena/ undergoes evolutionary adaptations that alter its ability to invade which affects the ecological invasion dynamics. Whole genome sequencing and computational analyses of sequence data will reveal the genomic basis of observable phenotypic changes of invading organisms. The experimental findings will be integrated into a consistent theoretical eco-evolutionary framework using mathematical models and agent-based simulations. This interdisciplinary and synthetic project will promote our causal understanding of invasions and range dynamics.

Competitive applicants will have previous experience or a strong interest in evolutionary ecology, molecular ecology or evolutionary biology. They ideally have substantial programming skills and optimally experience in analyzing high-throughput sequence data. Excellent experimental skills are a wanted. A background in modeling is a plus. Candidates will be highly motivated, enthusiastic and independent persons with a passion for science. Excellent communication and writing skills in English, good work ethics, and creative thinking are desired. A Masters level degree (or equivalent) is necessary for admission. The working language is English.

The project will be co-supervised by Prof. Dr. Florian Altermatt, Prof. Dr. Andreas Wagner and Dr. Emanuel Fronhofer. The project will be based at University of Zurich and at Eawag. Zurich offers a stimulating and international research environment, excellent research facilities and a lively and social working place. The position will be for a period of four years, and should start in January 2017 or soon thereafter. The PhD student will be enrolled at University of Zurich and be part of the PhD Program in Evolution.

The project is financed by the University of Zurich Research Priority Program "Evolution in Action" (http://www.evolution.uzh.ch/en.html).

For further information, consult

Altermatt lab: http://homepages.eawag.ch/~altermfl/Home.html Wagner lab: http://www.ieu.uzh.ch/wagner/ or directly contact

Prof. Dr. Florian Altermatt, E-mail: florian.altermatt@eawag.ch or

Prof. Dr. Andreas Wagner, E-mail: andreas.wagner@ieu.uzh.ch

University of Zurich and Eawag offer a unique research and working environment and are committed to promoting equal opportunities for women and men. Applications from women are especially welcome. *Applications must be submitted by 15 August 2016.*

We look forward to receiving your application. Please submit your application including a motivation letter with a description of pertinent experience, a complete CV (incl. publication list), the names (with e-mail addresses) of three academic references, and copies of certificates of academic qualifications via the Eawag Jobs & Career webpage (https://apply.refline.ch/673277/0445/pub/1/index.html), any other way of applying will not be considered.

The following link will take you directly to the application form: https://apply.refline.ch/673277/0445/pub/1/index.html – Prof. Dr. Florian Altermatt Department of Evolutionary Biology and Environmental Studies, University of Zurich, Winterthurerstr. 190, CH-8057 Zürich, Switzerland.

Group address: Eawag, Swiss Federal Institute of Aquatic Science and Technology, Department of Aquatic Ecology, Ãberlandstrasse 133, CH-8600 Dübendorf, Switzerland

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UZurich OrchidEvolution

PhD Position Genomics of early-evolving reproductive barriers in orchids

A PhD position is open for a highly motivated student with a keen interest in plant evolutionary genomics, population genetics and bioinformatics/statistics. The project seeks to understand the genomic and molecular basis of pollinator-mediated reproductive isolation and ecological speciation between sexually deceptive orchids of the genus Ophrys. In particular, the successful candidate will analyse the extent of linkage, clustering and phyical interaction among candidate loci under pollinator-mediated selection. To do so, s/he will produce high-quality genome assembly and annotation data for the study organism using state-of-the-art tools and technology to enable the population genomic study of the architecture of traits controlling pollination. This will involve the integration of genomic with various phenotypic and Omics data sources. Potential field/research stays in the Mediterranean can be accommodated in the project. For background information on the study system, please see e.g. Schlüter & Schiestl (2008, Trends Plant Sci.) and Sedeek & al. (2013, PLoS One; and 2014, Mol. Ecol.).

The ideal candidate should be highly motivated and able to articulate her/his motivation for this project clearly. S/he should be well organised, with a thorough understanding of evolutionary biology, population genomics and molecular biology, and would ideally have an interest in orchid pollination. The candidate is expected to be proficient in statistical data analysis, with a good working knowledge of R and proven experience in bioinformatics, ideally with an ecological genomics background. Programming/scripting skills in other languages are an advantage. Since the student will have to prepare libraries for Illumina sequencing, laboratory skills are necessary; previous field experience is a plus. Proficiency in English and good communication skills are essential, as is a completed MSc degree (or equivalent) in biology or a related discipline, and the proven ability to carry out research independently. The candidate will be enrolled in the Life Science Zurich Graduate School (LSZGS) programme in Evolutionary Biology (www.evobio.uzh.ch/en.html) and therefore must be eligible to undertake a PhD at the University of Zurich (UZH). In particular, a recognised Masters certificate (or equivalent) must be produced prior to the start of the project.

We offer a 4-year PhD position at the University of Zurich, Switzerland, at a competetive salary (>45 kCHF/year before tax) funded by the Universitys Research Priority Programme Evolution in Action. The student will be a member of two collaborating labs at the Botanical Institutes (www.systbot.uzh.ch and www.botinst.uzh.ch), located in the beautiful Botanic Gardens and within walking distance of Lake Zurich. The successful candidate will work in a young, active, interdisciplinary and stimulating environment and will have access to state-of-the-art tools and techniques.

Your application should consist of a letter of motivation (1-2 pages), your CV and (if applicable) publication list, and the names and e-mail adresses of three academic referees. The letter of motivation should detail why you are personally interested in the project, why you find it relevant and why you think you are well-suited to undertake it. Please send your application (or any requests for further information) electronically to Dr Philipp Schlüter (philipp.schlueter at systbot.uzh.ch) as a single PDF file. Screening of applications will begin immediately and continue until the position is filled. The start date is 1st of January 2017.

Philipp Schlueter <philipp.schlueter@systbot.uzh.ch>

WesternSydneyU MetabolismEvolMammals

Opportunity for postgraduate students in animal physiological and evolutionary ecology at the Hawkesbury Institute for the Environment, Western Sydney University

Header: WesternSydneyU. MetabolismEvoEcologyMammals

Project: How does resting metabolic rate interact with environmental conditions to affect the energetic performance, survival and reproductive success of small mammals?

Research Leader: Dr Christopher Turbill, Hawkesbury Institute for the Environment, Western Sydney University

Project Description: We seek outstanding research students to join our group and lead projects that make use our unique modal study system, well-equipped laboratory and outdoor experimental facilities to determine the ecological function and evolutionary drivers of variation in the resting metabolic rate of small mammals. We have developed an innovative approach that combines artificial selection on resting metabolic rate with ecological experiments in field enclosures. Our selective breeding experiment has established replicated populations of mice with contrasting metabolic phenotypes. An exciting opportunity is now available to lead projects that use these selected mice populations to test predictions about i) the genetic and physiological causes underpinning these different metabolic strategies, and ii) the ecological consequences of these different phenotypes under manipulated conditions using semi-outdoor and large wild foraging enclosures. These projects would allow students to conduct unique field experiments to address questions at forefront of research in physiological and evolutionary ecology.

To Apply: Interested applicants should send a CV, academic transcript and a brief summary of their research interests to c.turbill@westernsydney.edu.au

Applications will be assessed as they are received. Students (domestic or international) with a high level of relevant qualifications, research experience and enthusiasm will be invited to apply for a Higher Degree Scholarship from Western Sydney University. To rank highly, students will need to have completed a Masters by Research (or international equivalent), first class Honours (domestic students) and at least one publication or extensive research experience.

Expressions of Interest for Higher Degree Scholarships at Western Sydney University < http://www.uws.edu.au/graduate_research_school/grs/scholarships/main_round_scholarships > close - 9th October 2016.

Benefits: Students that secure a scholarship (with the potential of fee waiver for high-quality international students) can apply for top-up funding to support living expenses, research costs, and conference attendance. Students will also enjoy the logistical, academic and social benefits of working in a very active, research-focused and internationally diverse institute within Western Sydney University. The Hawkesbury Campus (Richmond, NSW) is located at the foot of the Blue Mountains on the western outskirts of Sydney, Australia.

Dr Christopher Turbill Hawkesbury Institute for the Environment Western Sydney University Contact: +61 (0)2 4570 1456

C.Turbill@westernsydney.edu.au

Jobs

Berlin LabTech EvoDevo

The Integrative Research Institute for Life Sciences (IRI) and Humboldt Universität zu Berlin invite applications for

Laboratory Assistant (Biologielaborant)

in the research group "Evolutionary Biology" of Dr. David Garfield

Our group focuses on understanding the evolution of developmental gene expression from a population genetics perspective. We are currently recruiting a laboratory technician to help in the day-to-day running of the lab and to perform laboratory experiments (including the generation of libraries for high-throughput DNA sequencing). The position will also require some handling and maintenance of laboratory animals (Drosophila and sea urchins) as well as assisting in the teaching of students.

Candidates will have a degree equivalent to completed formal training as a biological laboratory assistant (Biologielaborant), a German Diplom (Masters degree), or comparable training. Previous experience with modern genomics techniques (e.g. high-throughput sequencing) is strongly encouraged, though the primary requirement is formal training in laboratory sciences or previous experience with basic techniques in molecular biology and a willingness to learn.

Our laboratory is located in the Mitte district of Berlin near the Charité main campus and the future site of the Berlin Institute for Medical Systems Biology. Our close interactions with these institutes allows access to a wide-range of numerous technical platforms as well as numerous training opportunities and an exciting, interdisciplinary environment.

Successful candidates will preferably join the group 1. October 2016 or shortly thereafter. Strong communication skills in both English and German are essential for this position, as is a willingness to interact with student researchers. We offer a competitive salary according to German E9 TVöD/Bund (100%). Contracts are offered for an initial term of 1 year with the possibility of extension.

Applications, including a motivation letter, CV, and contact details for two references, should be sent as a single PDF to info@garfieldlab.org. Applications will be considered initially until July 31st.

http://www.garfieldlab.org/ http://www.garfieldlab.org/open-positions/
"david.garfield@embl.de" <david.garfield@embl.de>

CornellU FishEvolutionaryDynamics

Assistant or Associate Professor of Fisheries and Aquatic Sciences

STARTING DATE: August 1, 2017

LOCATION: Department of Natural Resources College of Agriculture and Life Sciences Cornell University Ithaca, NY 14853

RESPONSIBILITIES: The successful candidate will develop an internationally-recognized research program focused on the ecological and/or evolutionary dynamics that influence the conservation and management of freshwater fish populations, including but not limited to Adirondack systems. The appointment is 50% research of which a principal component should build upon the 60-year legacy of research associated with the Adirondack Fishery Research Program by working within the program to address the consequences that changing environmental conditions have on the ecology and management of fishes and fisheries. The ideal candidate should be able to work across spatial and temporal scales and/or across levels of biological organization from physiology to ecosystems. In keeping with departmental research philosophy, the candidate is expected to actively engage stakeholders, resource managers and other decision-makers. The individual is further expected to secure external funding and contribute to the scholarly literature through journal articles and other peer-reviewed publications. Teaching responsibilities (50% of appointment) will include two courses offered each academic year and a graduate seminar offered at least once annually. Possible undergraduate courses include core environmental science courses in the Environmental and Sustainability Sciences major. The successful candidate will advise undergraduate and graduate students and supervise undergraduate and graduate research.

Service to society through consultation and other outreach activities is expected of all faculty members in addition to collegiality and service at the departmental, college and university levels. The position is a full-time, tenure-track, academic-year (9-month) appointment. It is anticipated that the successful candidate will be appointed director of the Adirondack Fishery Research Program at a future date.

QUALIFICATIONS: Ph.D. in fisheries science, aquatic ecology or an affiliated discipline Experience in teaching, student advising, and research related to this position, either postdoctoral or pre-doctoral. Evidence of ability to work with other researchers and stakeholders in collaborative inquiry. Demonstrated interest in working on topics related to contemporary challenges in aquatic conservation and management, and in working cooperatively with conservation/management agencies in applying results of scholarly research. Evidence of ability to attract extramural research support and coordinate and lead an innovative research program.

SALARY: Competitive, commensurate with background and experience within the Assistant or Associate Professor rank at Cornell. Cornell faculty receive an attractive fringe benefits package.

APPLICATIONS: Electronic application must be submitted through Academic Jobs Online: https://academicjobsonline.org/ajo/jobs/7455. Applications should include a letter of application, current curriculum vitae, statement of teaching and advising philosophy, statement of research interests and accomplishments, names (including mailing and email addresses, and phone numbers) of three references and three relevant publications.

Review of applications will begin on September 1, 2016.

Additional inquiries should be directed to Dr. Matt Hare, Fisheries and Aquatic Sciences Search Committee Chair, 205 Fernow Hall, Cornell University, Ithaca, NY 14853, Tel (607) 255-5685, FAX (607) 255-0349, email: mph75@cornell.edu.

Diversity and Inclusion have been and continue to be a part of our heritage. Cornell University is a recognized employer and educator valuing AA/EEO, Protected Veterans and Individuals with Disabilities. The University seeks to meet the needs of dual career couples and has a Dual Career program to assist with dual career searches.

Matthew Hare Associate Professor 205 Fernow Hall Department of Natural Resources Cornell University Ithaca, NY 14853 607-255-5685 http://www2.dnr.cornell.edu/HareLab/harelab.html
“mph75@cornell.edu” <mph75@cornell.edu>

CornellU QuantitativeGenetics

Quantitative Genetics - Assistant/Associate Professor

Faculty Position in Quantitative Genetics, School of Integrative Plant Science, Section of Plant Breeding and Genetics, College of Agriculture and Life Sciences, Cornell University

The School of Integrative Plant Science at Cornell University is seeking applicants for a 9-month tenure-track position at the level of Assistant/Associate Professor in Quantitative Genetics in the Section of Plant Breeding and Genetics, with research and teaching responsibilities. The successful candidate will conduct innovative, externally funded, and collaborative research on quantitative methods, statistical modeling, and optimization applied to plant breeding. Research outcomes should include new computational, systems biology, machine learning, and/or combinatorics tools to enable the improvement of genetic stocks, germplasm, or varieties. Collaboration with other faculty on analysis and selection in crops and model organisms is expected. The successful candidate will teach courses in quantitative methods to meet the needs of plant breeders and others in a data-driven era and guide graduate student research and learning in plant breeding, genetics, biological statistics , and computational biology. This position is 70% research and 30% teaching.

QUALIFICATIONS: Ph.D. in Plant Breeding, Plant Biology, Genetics, Statistical Genomics, Computational Biology, or related discipline, demonstrated ability to excel in a multi-disciplinary and multi- cultural setting, and an excellent publication record are required. Ph.D. in Animal Breeding or Animal Genetics also possible, contingent on candidate motivation to reach across kingdoms. Preferred qualifications include postdoctoral experience, successful collaborative experience, and ability to communicate effectively with diverse groups, including students, colleagues, and external stakeholders.

ANTICIPATED START DATE: August 2017. ACADEMIC RANK AND SALARY: Assistant/Associate Professor (tenure track) with salary competitive with peer institutions and commensurate with background and experience.

APPLICATIONS: Electronically submit a curriculum vitae, a research plan (2-3 pages) and teaching interests (1 page). In addition, applicants must arrange for three letters of recommendation to be submitted concurrently with the other application materials at Academic Jobs Online, https://academicjobsonline.org/ajo/jobs/7477. Application review begins on October 1, 2016. Questions about the position can be addressed to Search Committee Chair, Professor Walter De Jong (wsd2@cornell.edu).

ABOUT CORNELL: The new faculty member will join a collaborative, interdisciplinary community on the main campus of Cornell University, in Ithaca, New York. The Section of Plant Breeding and Genetics is part of Cornell's School of Integrative Plant Science (SIPS), a large internationally renowned group of academics with many interactions and joint projects. Members of the section also collaborate with colleagues in computational biology, and genetics. For more information about the position, SIPS, and the Section of Plant Breeding and Genetics, visit http://plantscience.cals.cornell.edu/ . Cornell comprises a varied array of academic units from music and literature to astrophysics and veterinary medicine and is a member of the Ivy League. The main campus of Cornell University, which overlooks 40-mile-long Cayuga Lake, is located in the Finger Lakes region of Upstate New York, a scenic environment of spectacular lakes, waterfalls, gorges, rolling hills, farmland, vineyards, and state parks. It is an area with outstanding recreational and summer and winter sports opportunities for individuals and families. The Cornell campus itself is one of the most beautiful in the country. The Ithaca community is culturally diverse with excellent theater, music, sports, and other activities befitting a major university town, yet also has the warmth and friendliness of a small community. The area is known for its many bookstores and restaurants, an extensive walking trail system, arboretum, Laboratory of Ornithology, marina, Farmers Market, a hands-on Science Center, and art and science museums. For more information and links to individual attractions, visit http://www.visitithaca.com/ . Application Materials Required: Submit the following items online at this website: * Cover Letter * Curriculum Vitae * Research Statement * Teaching Statement * Three Reference Letters (to be submitted by the reference writers at this site help popup)

And anything else requested in the position description.

Further Info: https://plbrgen.cals.cornell.edu/ Kim Cotton kec36@cornell.edu 607-255-2180 Plant Breeding and Genetics Section,

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LPF Tenerife DirectorConvservation

JOB ANNOUNCEMENT

Director of the Loro Parque Fundación

The organisation

The Loro Parque Fundación (LPF) is a private foundation, created in 1994 and legally registered in Spain as a charitable-status entity. It is a conservation NGO, and member of the International Union for the Conservation of Nature - IUCN. Its HQ is located at Loro Parque in Tenerife, Canary Islands, Spain. Although it has no national or regional branches, it operates at international level and is represented in many countries through its project partnerships with organisations in those countries.

Its recent average annual spend directly on projects, of which there are 36 active in 2016, is US$1 million. It is the owner of, and manages the world's largest, most diverse collection of Psittaciformes. The collection is a genetic reserve and resource for research and exhibition for education, as well as generating part of the income of the LPF. The private company Loro Parque is its principal sponsor, covering all operating costs so that 100% of all other donations go directly to the projects.

The larger proportion of projects is for the conservation of threatened species of parrots, each project including to a lesser or greater extent the direct protection of the target species, the protection and restoration of habitat, and the cooperation with and integration of the local community into the conservation effort. The LPF has increasing involvement in projects related to the conservation of the marine environment, in particular with whales and dolphins. More recently, the LPF is involved in the conservation of large terrestrial mammals in central southern Africa.

The LPF has a Board of Trustees (President, Secretary and Vocals) which has ultimate responsibility for its governance. An international advisory board meets annually with the trustees and principal staff to review progress and make recommendations about project support. There are also honorary vice-presidents.

More information at:

www.loroparque-fundacion.org Major duties and responsibilities of the Director

The Director is responsible for the institutional development of the organisation, and the promotion of a clear identity and profile of the LPF, with the objectives to highlight its scientific and conservation strengths, and to obtain external support for its activities. Duties include managing the LPF project portfolio, with particular emphasis on the terrestrial projects, and to provide suitable content for external communication of projects and activities. The Director will represent the LPF in the wider conservation arena, and is expected to maintain productive relations with other entities involved in conservation. The Director reports directly to the LPF President.

Requirements

Applicants will have a higher degree in a relevant subject, and will already have several years of experience in conservation management, including experience in the field as well as in an administrative capacity. Experience of project management from proposal to outcome will be essential, in particular the ability to discern valid goals and appropriate costs, and evaluate budgets correspondingly. Existing knowledge of bird conservation, especially of parrots, is important. Applicants will need a clear understanding of the positive interface between ex situ and in situ conservation. Good communication and interpersonal skills are indispensable especially to acquire resources for the LPF, and therefore applicants will demonstrate a trackrecord in fund-raising. Leadership skills, the ability to plan and prioritize, as well as to work independently and meet deadlines, will be necessary. Fluency in English is required. Existing fluency in Spanish is preferred, or rapid achievement of proficiency will be essential. German will also be advantageous.

Salary and starting date

The remuneration package will be commensurate with qualifications and experience. The expected commencement date will be 1st September 2016

A CV and covering letter

(addressed to: The President, Loro Parque Fundación, Av. Loro Parque s/n, 38400 Puerto de la Cruz,Tenerife, Spain) should be emailed at the earliest convenience to: lpf@loroparque-fundacion.org

"Bayern, Auguste von" <avbayern@orn.mpg.de>

LundU ResTech

We are looking for a highly skilled and motivated research technician who is interested in working in different projects addressing research questions at the interface of ecology, evolution and molecular biology.

Our research involves collecting data from wild, captive and laboratory organisms using a range of approaches including experimental evolution, molecular genetics and bioinformatics, field experiments, and literature searching. Our primary study organisms are algae, damselflies, moths, lizards and birds. Tasks involve data collection in the field and the laboratory, support for sample curation/organisation, data organisation and processing including statistical analyses, and coordination and management of the research group's daily routines, including organism husbandry and administrative support. It is expected that the person assigned to this post will pursue opportunities to acquire further skills through national and international courses. The position is aimed at a junior level and it is therefore expected that any postdoctoral experience is limited to two years.

Required qualifications It is essential that the applicant has:

* An MSc or PhD in Ecology, Evolution or Molecular Biology or a closely related field with strong emphasis on either or both of these subjects. * Experience of working with microorganisms, particularly experimentation and maintaining laboratory populations * Experience of molecular genetics including DNA extractions, PCR, next-generation sequencing

It is desirable that the applicant has:

* Experience of experimental evolution * Experience of working with algae particularly identification and culturing of clones * Experience of organizing databases and analyzing sequence data * Experience with statistical analysis of data from field studies or experimental settings as well as experimental design * A good command of the software R for programming, statistical analyses or graphical visualization of data * Motivation to work in a team and desire to take responsibility * Fluent in English. A good understanding of Swedish is advantageous but not required * A full drivers license.

Applicants should send a cover letter explaining their background and a CV that includes publications and the contact information for two referees. Applicants are evaluated based on how well they fulfill the requirements detailed above. Such evidence may include documentation of completed coursework, scientific publications, technical and analytical know-how, evidence of organizational skills and enthusiasm for ecology and evolution. Where possible, statements to these effects should be accompanied by objective or independent assessment of the candidate's track record and potential. These may include links to access published or unpublished (e.g., thesis) research material or letters of support from supervisors or previous employers.

Additional Information For more information and informal discussion about the position candidates can contact Charlie Cornwallis (charlie.cornwallis@biol.lu.se), Erik Svensson (erik.svensson@biol.lu.se), or Tobias Uller (tobias.uller@biol.lu.se). For more general information see: http://www.biology.lu.se/research/research-groups/ To apply: https://lu.mynetworkglobal.com/en/what:job/-jobID:108188/ charlie.cornwallis@biol.lu.se

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Melbourne StatisticalGenomics

We are looking for a quantitative geneticist / statistical genomicist to join our growing group in Melbourne. The successful candidate will primarily contribute towards an exciting project on Genomic Selection for Heat Tolerance in Wheat, which is an Australian Grain Research Development Corporation funded project in collaboration with Prof. Richard Trethowan, University of Sydney. The position will report to Dr. Hans Daetwyler. There will also be opportunities to collaborate with other team leaders including Assoc. Prof. Matt Hayden, Prof Mike Goddard, and Dr. Jennie Pryce. The closing date for this position is August 10th, 2016. Research Scientist §$77,418 - $87,838 AUD per annum (plus superannuation) §Fixed Term / Full Time - 3 Years §Bundoora location, AgriBio, La Trobe University Campus

The position of Research Scientist forms a part of the Biosciences Research branch of the Agriculture and Rural division, within the Agriculture and Resources group.

The Research Scientist Computational Biology will develop tools enabling faster genetic gain for important crop and forage species through research on genomic selection, with a focus on heat tolerance during grain fill in wheat. The role is required to deliver on specific research milestones for large, collaborative, industry co-funded projects.

The incumbent will be required to provide a substantial individual contribution to the science of the Computational Biology group, through cutting-edge research in the areas of quantitative genetics and statistical genomics applied to plants. In this position you will analyse empirical genomic and phenotype data to produce genomic breeding values for key crop traits and develop genomic plant pre-breeding programs that enrich germplasm for these traits using advanced algorithms that are demonstrated in real and simulated data.

Communicating key results and new methodologies to industry, and engaging with industry partners will also be a key part of the role. Publications in key international journals are expected and encouraged. The position offers a unique opportunity to fast track the latest research in genetics and genomics into industry application. You will be expected to support other scientists as well as PhD students working in the same area and build a positive culture.

For a confidential discussion, please call or email Hans Daetwyler on +61 (0)3 9032 7037. hans.daetwyler@ecodev.vic.gov.au

For more info, please check https:/-/jobs.careers.vic.gov.au/jobtools/-jncustomsearch.viewFullSingle?in_organid=-14173&in_jnCounter=222654002&in_jobDate=all The Department of Economic Development, Jobs, Transport and Resources is an equal opportunity employer and welcomes applicants from a diverse range of backgrounds. The Department strongly encourages applications from Aboriginal and Torres Strait Islander people. We assist successful candidates with attaining work visas.

Dr. Hans Daetwyler | Research Leader Computational Biology Biosciences Research | 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

MilwaukeeMuseum InvertebrateCurator

Research Curator in Invertebrate Zoology Milwaukee Public Museum

The Milwaukee Public Museum is seeking a mid-career research curator with a Ph.D. to oversee the Zoology Department. The person in this leadership role will plan, direct, implement and coordinate activities of the Zoology Department (Invertebrates and Vertebrates) to ensure the effectiveness and balance of scholarly research, collections, public service/education, and exhibit development. The candidate will maintain an active invertebrate zoology research program, with preference for research in the areas of museum strength –Lepidoptera or Coleoptera. At least one of their research interests should incorporate aspects of citizen science. The curator will be responsible for providing content expertise for the development of museum exhibits and reviewing educational program aspects, serving as a representative of their research to the print, broadcast, and online media, and speaking on a range of topics to diverse audiences. We are seeking an individual with a proven publication record and a history of successful funding.

Key Responsibilities - Oversee Invertebrate and Vertebrate Zoology collections - supervise Collection Manager, Puelicher Butterfly Wing Supervisor, and other personnel. - Conduct research and oversee growth of the collections in invertebrate zoology and direction of growth for the vertebrate collections as related to the Museum's mission. - Work closely with other research curators to design, implement and deliver at least one citizen science research project. - Oversee and provide the best standards of care for the zoology collections. - Seek funding from a variety of sources to support research. - Collaborate with local universities and other institutions with regard to research and other activities. - Present research findings through publication and presentation, including peer-reviewed journals, books, and proceedings of professional meetings. - Serve as content expert for the development of museum exhibits and review of educational materials.

Qualifications - Doctoral Degree in relevant field. - Highly motivated, with demonstrated success working as a team member in a fast-paced interdisciplinary environment. - Familiarity with databases. - Ability to thrive in both independent and in team-oriented settings. - Excellent verbal and written communication skills. - Ability to communicate findings with a diverse array of technical and non-technical audiences. - Experience in a museum or collection desirable. - Passion for field of inquiry.

To apply please go to: https://mpm.hyrell.com/-VirtualStepPositionDetails.aspx?TemplateId=141183 *Ellen J. Censky, PhD*

Senior Vice President/Academic Dean

Milwaukee Public Museum

414-278-2786 | censky@mpm.edu <Youremail@mpm.edu> | www.mpm.edu "Censky, Ellen" <censky@mpm.edu>

NatlTaiwanU PopulationDynamics txt

Assistant Professor (or higher rank) in Behavioral Ecology, Population Dynamics, Ecosystem Simulation, or ecological related disciplines

Organization: National Taiwan University (NTU)

Application Deadline: September 2, 2016

Job Starting Date: February 1, 2017

Place: Taipei, Taiwan

Type of Position: Academic

Education Requirement: Ph.D. (or equivalent)

Description The Department of Life Science, National Taiwan University seeks an outstanding scientist to fill one position at the rank of Assistant Professor (or higher). The successful candidate is expected to teach General Biology, Vertebrate Biology and Behavioral Ecology, and develop an internationally recognized research program. Applicants having strong commitment to undergraduate education and academic research are cordially welcomed.

Qualifications The applicant is required to have a Ph.D. (or equivalent) degree, post-doctoral training, and international academic exchange experience.

Evidence of exemplary scholar achievement (funding, publications, presentations, etc.) commensurate with position and years of experience is expected. The candidate should have effective communication skills (oral and written) and the ability to collaborate with other scientists.

How to Apply / Contact Applicants should submit a cover letter indicating their suitability for the advertised position. Additional materials should include curriculum vitae, research and teaching plans, a copy of official transcript of doctoral program, list of publications since February 1, 2010, and PDF files of related publications. All documents must be sent via e-mail to: fumee@ntu.edu.tw. Three recommendation letters are required, and should be sent by the referees directly to the above e-mail address.

Mee <fumee@ntu.edu.tw>

RockefellerU ResAssist SocialEvolutionBehavior

The Laboratory of Social Evolution and Behavior We use an integrative approach to understand how natural selection shapes the evolution of insect societies and how social life is regulated at different hierarchical levels: the gene, the individual and the colony. More information can be found on our lab website at: http://lab.rockefeller.edu/kronauer/about . The Rockefeller University The Rockefeller University is the world's leading biomedical research University. Our groundbreaking discoveries in basic and clinical research are transforming medicine. We share a singular commitment to advancing science for the benefit of humanity. Our collaborative culture drives each of us to achieve a higher level, fueling the breakthroughs for which we are known.

Research Assistant Responsibilities We are seeking a highly motivated individual to participate in different ongoing projects on ants that involve DNA sequencing and genotyping, gene expression and CRISPR Genome Engineering using candidate genes. The position will involve mainly ant colony maintenance, egg incubation, and larval rearing and also ant dissections and injections, as well as behavioral observations.

Qualifications - Bachelor's degree in science - Excellent organizational and interpersonal skills - Driven by scientific curiosity - Experience in maintaining laboratory organisms - Strong interest in insects, ants in particular

How to Apply To apply for this position, please visit the URL below and apply to job code IRC19328. Please make sure to upload your resume/CV, a letter of interest, and a reference list.

http://www.rockefeller.edu/hr/jobs Leonora Olivos-Cisneros <lolivos@mail.rockefeller.edu>

SanDiegoZoo ResearchAssociate

San Diego Zoo Global - Research Associate

The Research Associate will work in the Genetics Division at the San Diego Zoo Institute for Conservation Research. Applicants must have knowledge of standard laboratory procedures and safety practices and be skilled in the use and basic maintenance of general laboratory equipment. Experience in nucleic acid preparation and quantitation from various source materials is highly desired. Proficiency with PCR, automated sequencing, and microsatellite fragment analysis is preferred. Training in establishing, culturing, and freezing somatic cells is helpful. Competence in Microsoft Office computer programs is essential, and understanding of molecular data analysis programs is a plus. The applicant must have the ability to take direction, multitask, work as part of a team, and follow through on assignments in a timely fashion. This position requires high attention to detail and good record-keeping with the ability to neatly organize high volumes of biological samples and electronic data.

Complete information about the position and procedures for applying can be found at http://zoo.sandiegozoo.org/jobs HDavis@sandiegozoo.org

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TempleU LabManager BiodiversityScience

A full-time position of LAB MANAGER is available at Temple University's Center for Biodiversity within the joint lab of Drs. Matthew Helmus and Jocelyn Behm. The lab mission is to integrate biodiversity science with human ecology to understand contemporary patterns of biodiversity and its functioning within ecosystems. The lab manager be will be responsible for research activities and overseeing day-to-day operations of the lab including:

- data mining - genetic sequencing - functional trait measurement - biodiversity sampling - ecosystem-service assessments (in the lab and the field) - managing undergraduate research assistants - database maintenance - lab administration

Proficiency in all of these areas is not expected, instead applicants must have the ability, background, and enthusiasm to learn relevant techniques.

Applicants must have a bachelor's degree (Master's degree preferred) in biology, environmental science, or other relevant field. Ideal applicants are those with relevant prior research experience, but most importantly, the successful applicant will be well-organized, able to work both independently and in a team setting, and motivated to learn. This position is ideal for those craving experience in the exciting, fast-paced world of biodiversity science before pursuing a higher degree.

Please email applications to biodiversity@temple.edu. Include your CV, unofficial transcript, contact information for three references, and a brief letter of interest that describes your relevant background experiences, managerial skills, and why you are interested in the position. Review of applications will begin August 12, 2016 and will continue until the position is filled. The start date is negotiable, salary is commensurate with experience, and the position includes a competitive benefits package. The position is initially for one year, and can be extended two more years given positive work reviews. Possible extensions of the position are also likely as funding is acquired.

The Center for Biodiversity is located in a new LEED-Gold certified building on Temple's main campus in historic Philadelphia. The Center provides state-of-the-art biodiversity research facilities along with support staff with expertise in media development, GIS technology, and genetics. Temple University, founded in 1884, is a public R1 university with a diverse student body of ca. 40,000 students. It is the sixth largest provider of graduate school education in the U.S., is within the top 4% of research institutions in the U.S., and is in the top ten of the fastest gainers in ranking by the US News & World Report's Best Colleges. Philadelphia is the birthplace of America, filled with numerous attractions (e.g., Philadelphia Museum of Art, Philadelphia Zoo, Academy of Natural Sciences), amazing food, and a quick train ride to New York City and Washington DC. Philadelphia is nestled within an extensive national/state trail and park system, and is very close to Valley Forge National Park, the Pocono Mountains, the unique Pine Barren ecosystem, and the beaches of the Atlantic shore.

Temple University is an equal opportunity, equal access, affirmative action employer committed to achieving a diverse community.

For more information see: http://www.matthelmus.com/ http://www.jocelynbehm.com/ http://www.biodiversitycenter.org/ Matthew R. Helmus, Ph.D. Center for Biodiversity Department of Biology Temple University Philadelphia, PA 19122 www.matthelmus.com Phone: 215 204-4244 Email: mrhelmus@temple.edu Office: 502 SERC, Main Campus

Matthew Helmus <mrhelmus@temple.edu>

TexasAMU NontenureTrack ConservationBiol

Title: Non-tenure track lecturer at Texas A&M Univ, Dept. Wildlife and Fisheries Sciences

http://wfscjobs.tamu.edu/jobs/non-tenure-track-lecturer-texas-am-university/ Agency: Texas A&M University Department of Wildlife and Fisheries Sciences Location: College Station, Texas Job Category: Faculty Appointments Salary: 9 Month Non-Tenure Track $45,000.00 Year Start Date: August 15, 2016 Last Date to Apply: July 15, 2016

General Duties and Responsibilities: The Department of Wildlife and Fisheries Sciences seeks to fill the position of Lecturer. Responsible for teaching some combination among the following undergraduate courses: Wildlife in a Changing Environment, Animal Behavior, Urban Wildlife and Fisheries, and Ecology and Society, plus a 1-credit writing course. Some courses may have both classroom and distance education sections.

Administrative Relationships: The person will report to the Head of the Department of Wildlife and Fisheries Sciences.

Qualifications: Ph.D. degree in Ecology, Conservation Biology, Wildlife Management Human Dimensions of Wildlife, or a related field. Excellent communication and organizational skills. Experience teaching undergraduate university students in topics related to organismal biology, ecology, conservation biology, wildlife management, or fisheries science. Experience in publishing scientific research papers.

Evidence of a strong commitment to teaching, including development of student problem solving skills and awareness of complex issues associated with biodiversity conservation and sustainable use of renewable natural resources.

Headquarters: Office space in Nagle Hall on the main campus of Texas A&M University.

Areas Served: Texas, the nation and the world.

Facilities: Teaching and laboratories are located primarily on the main campus of Texas A&M University in College Station, Texas, but also include numerous other facilities across the state.

Closing Date for Applications: July 15, 2016 Date Position is Available: August 15, 2016 Application process: Submit electronically as a single PDF a CV, statements of teaching and research, plus contact information for three references to: Dr. Kirk Winemiller, Search

Committee Chair, kwinemiller@tamu.edu. Submission deadline is July 15, 2016.

The Texas A&M University System is an Equal Opportunity Employer committed to building a diverse faculty, staff, and student body reflecting the population and educational needs of Texas and the Nation. All applicants are invited to address how their teaching, mentoring, or other activities could support Texas A&M's commitment to diversity and inclusion (see http://diversity.tamu.edu/).

Contact Person:

Dr. Kirk Winemiller: kwinemiller@tamu.edu

Sincerely,

Mariana Mateos, Ph.D. Associate Professor Department of Wildlife and Fisheries Sciences (wfsc.tamu.edu) Ecology and Evolutionary Biology PhD. Program (eeb.tamu.edu) Faculty of Genetics (genetics.tamu.edu) Texas A&M University 320B Heep Laboratory Building 2258 TAMUS College Station, TX 77843-2258 Phone(office/lab): 979-847-9463 Fax 979-845-4096 Email: mmateos@tamu.edu http://people.tamu.edu/ ˜ mmateos My ResearcherID: http://www.researcherid.com/rid/B-5235-2008 Mariana Mateos <mmateos@tamu.edu>

TunghaiU ResAssist Biodiversity

Research Assistant: Algal Biofuel Improvements and BiodiversityEffects

Department of Life Science, Tunghai University, Taiwan

Job details: A full-time research assistant position is readily available for 12-36 months at Shao-Lun Liu's lab in the Department of Life Sciences Tunghai University (Taiwan). More lab information can be found at the following website (http://algae.thu.edu.tw/lab/). The research project mainly focuses on the interplay between biodiversity effects and microalgal biomass production. Individuals with an interest in microalgal eco-physiology and biodiversity are highly welcomed. Prospect candidate will be mainly responsible for the cultivation and biomass estimation of microalgae, the operation of laminar flow bench and microscopy, and spectrophotometer analyses. Although experience in cultivation of microalgae and/or microbes and relevant lab skills would be appreciated, full training will be available in all aspects of the work.

Qualifications: (1) BSc/MSc in Biology, Ecology, Evolution.

(2) Microalgal/Microbial Isolation and Cultivation Lab Experience. (3) Ability to work in small teams and sociable personality.

Deadline: 31 August 2016 for application. Initial review of applications begins 1 August 2016 and continues as needed to ensure a large, high quality, and diver se applicant pool. For first consideration, please apply before 31 July 2016. Th e position is expected to start in late September 2016 or early October 2016.

Application Materials: CV, Cover letter with the description of relevant researc h experience and motivation (1 page), and the name of two referees.

Salary: Depending on the exchange rate, approximately USD$ 1200/month for MSc and USD$ 1000/month for BSc. Health insurance included.

Contact:

Shao-Lun Liu, Ph.D.

Associate Professor

Department of Life Science, Tunghai University, Taichung, Taiwan

Email: shaolunliu@gmail.com or shaolunliu@thu.edu.tw Sincerely yours, Shao-Lun (Allen) Liu Associate Professor Department of Life Science, Tunghai University Taichung 40704, Taiwan Web: http://algae.thu.edu.tw/lab Shao-Lun Liu <shaolunliu@gmail.com>

UBath ResTech EvolutionaryGenomicsMicrobes

We are excited to be recruiting a Research Technician to work on a project focused on the genetic basis and evolution of social and life-history traits in a microbe (a social amoeba). The project will combine high throughput measurements of traits with genome sequencing to understand the genetic basis to variation in natural populations. The technician will be required to work independently and will oversee several different technical components requiring different skill sets. The technician will support all aspects of the project, including culturing of strains, performing phenotyping assays, the preparation of genomic DNA samples and the processing of data sets.

The successful candidate will have a university degree in biology and relevant experience with laboratory based research in biology, including knowledge of basic molecular biology. Previous experience with microbiological techniques is desirable.

The position is fixed-term of 18 months and available to start as early as September 2016, but later start dates may be possible, subject to negotiation and approval. A contract extension for a longer term of employment may be possible (but is not guaranteed) subject to funding availability.

The technician will be based in Jason Wolf's lab in the Milner Centre for Evolution (and Department of Biology & Biochemistry) at the University of Bath, but will have opportunities to work in collaboration with Chris Thompson's lab at the University of Manchester and Reinaldo de Brito's lab at the Federal University in Sao Carlos (UFSCar).

For further information and to apply please see: https://www.bath.ac.uk/jobs/Vacancy.aspx?ref=FY4144 For an informal discussion about the role, please contact Prof Jason Wolf via email: j.b.wolf@bath.ac.uk (telephone or Skype consultations can be arranged)

Jason Wolf <jason@evolutionarygenetics.org>

UCalifornia Davis ChairPlantGenetics

Department Chair and Professor of Plant Sciences The University of California, Davis College of Agricultural and Environmental Sciences is pleased to announce an open recruitment for a tenured professor and chair of the Department of Plant Sciences (http://www.plantsciences.ucdavis.edu). The department portfolio covers a broad array of research and extension activities in the areas of ecology, genetics, and physiology of agricultural and natural systems in California, the U.S. and abroad. The department has a large effort in cooperative extension programming and mission-oriented research activities consistent with the CA Agricultural Experiment Station.

Criteria for appointment: a Ph.D. in plant sciences or a related discipline, a record of excellence in scholarly research in plant sciences that aligns with the interdisciplinary foci of the department, and demonstrated ability to establish a competitively-funded research program. The candidate is expected to have a record of strong teaching/mentoring of undergraduates and graduates, and evidence of strong outreach and stakeholder engagement experiences. Administrative experiences and skills are expected commensurate with the capacity to chair a large and diverse unit of faculty, students and staff.

Applicants should submit materials via the following website: http://apptrkr.com/829465 Additional inquiries should be directed to Search Committee co-chairs Ed Lewis eelewis@ucdavis.edu or Jeffrey Ross-Ibarra rossibarra@ucdavis.edu.

The position will remain open until filled but to ensure consideration, applications should be received by August 31, 2016.

The University of California, Davis, and the College of Agricultural and Environmental Sciences are interested in candidates who are committed to the highest standards of scholarship and professional activities, and to the development of a campus climate that supports equality and respect for differences based on gender, cultural ethnicity, level of disability, and sexual orientation. 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.

Tearsheets <tearsheets@jobelephant.com>

UCambridge EvolutionaryBiol

A named chair is available in the Dept of Genetics, University of Cambridge, UK:

The Board of Electors to the Al-Kindi Professorship invite applications for this Professorship from persons whose work is connected with the quantitative dynamics of living systems to take up appointment on 1 October 2017, or as soon as possible thereafter.

Candidates will have an outstanding research record of international stature in an interdisciplinary area concerning quantitative approaches to biological systems. They will have the vision, leadership, experience and enthusiasm to build on current strengths in genetics and physical biology while maintaining and developing a leading research presence and contributing to the strategic development of the discipline within Biological Sciences and more widely across the University. They will hold a PhD or equivalent postgraduate qualification.

Standard professorial duties include teaching and research, examining, supervision and administration. The Professor will be based in Cambridge.

A competitive salary will be offered.

To apply online for this vacancy and to view further information about the role, please visit: http://www.jobs.cam.ac.uk/job/10801. This will take you to the role on the University's Job Opportunities pages. There you will need to click on the 'Apply online' button and register an account with the University's Web Recruitment System (if you have not already) and log in before completing the online application form.

Further information is available at: www.admin.cam.ac.uk/offices/academic/secretary/professorships/ or contact the Academic Secretary, University Offices, The Old Schools, Cambridge, CB2 1TT, (email: ibise@admin.cam.ac.uk).

Applications, consisting of a letter of application, a statement of current and future research plans, a curriculum vitae and a publications list, along with details of three referees should be made online no later than Monday 5 September 2016.

Informal enquiries may be directed to Professor Anne C Ferguson-Smith, Head of the Department of Genetics, Cambridge, telephone +44 (0)1223 333834 or e-mail afsmith@gen.cam.ac.uk.

Please quote reference PC09542 on your application and in any correspondence about this vacancy.

The University values diversity and is committed to equality of opportunity.

The University has a responsibility to ensure that all employees are eligible to live and work in the UK.

"fmj1001@cam.ac.uk" <fmj1001@cam.ac.uk>

UFlorida Biodiversity

Biodiversity Faculty Search, University of Florida. Two positions at the Associate or Full Professor level (or Assistant Professors in process for tenure).

The Department of Biology in the College of Liberal Arts and Sciences at the University of Florida is seeking applicants for two positions at the Associate or Full Professor level (or Assistant Professors whose tenure package is already under review) in the area of Biodiversity, including the generation, maintenance, dynamics, conservation, structure, or functional consequences of biodiversity. One position targets researchers who creatively explore biodiversity science using mathematical, statistical, and/or computational tools, at scales from single species to entire communities and biogeographical realms. The other position is more broadly defined, and we welcome candidates with strong empirical (field, lab, or comparative) and applied research dimensions in biodiversity science, working in terrestrial, freshwater, marine, or coastal ecosystems. Successful candidates must have obtained a Ph.D. in biological sciences, mathematics, statistics, or a related field, and will be expected to have an internationally recognized research program and contribute to training and education in biodiversity science.

These hires are part of a new Biodiversity Initiative launched by the University of Florida, a campus-wide initiative bridging multiple units (and including the establishment of a Biodiversity Institute), and aiming at fostering collaborations among scientists, students, resource managers, and policy analysts, formulating strategies to meet the biodiversity challenges of the 21st century and beyond. Such strategic questions include gauging the effects on biodiversity, ecosystem processes, emerging diseases, and resource sustainability of factors such as climate change, sea level rise, invasive species, and environmental degradation. The University of Florida is uniquely positioned to take a leadership role in biodiversity science, capitalizing on its status as a land grant, sea grant, and space grant university, with the most comprehensive academic health center in the Southeastern US. The Biodiversity Initiative will leverage extraordinary data resources and computing power (including one of the most powerful university supercomputers), one of the nations largest natural history museums, and a strong collaborative culture across disciplines.

Applications must be submitted at http://explore.jobs.ufl.edu/cw/en-us/job/497559/preeminence-associate-full-professor-in-biodiversity and must include: (1) a letter summarizing the applicant's qualifications, ongoing research directions, and interests in the Department, (2) a complete curriculum vitae, and (3) names and contact information for three references. Applications will be reviewed beginning August 22, 2016 as received and the position will remain open until filled. Questions about these positions may be emailed to Jeremy Lichstein (jlichstein@ufl.edu) with subject BIODIVERSITY SEARCH.

The University of Florida counts among its greatest strengths and a major component of its excellence that it values broad diversity in its faculty, students and staff and creates a robust, inclusive and welcoming climate for learning, research and other work. UF is committed to equal educational and employment opportunity and access, and it seeks individuals of all races, ethnicities, genders and other attributes who, among their many exceptional qualifications, have a record of including a broad diversity of individuals in work and learning activities.

The final candidate will be required to provide an official transcript to the hiring department upon hire. A transcript will not be considered official if a designation of Issued to Student is visible. Degrees earned from an educational institution outside of the United States must be evaluated by a professional credentialing service provider approved by the National Association of Credential Evaluation Services (NACES), which can be found at http://www.naces.org/ . The University of Florida is an Equal Opportunity Institution.

Stuart McDaniel Assistant Professor Department of Biology PO Box 118525 University of Florida Gainesville FL 32611

ph: 352 273 0123 fax: 352 392 3704 http://mcdaniellab.biology.ufl.edu/ Twitter: @mcdaniellab

"McDaniel, Stuart" <stuartmcdaniel@ufl.edu>

ULiverpool 10mnth TeachingEvolBiol

10 month teaching position in evolutionary biology at the University of Liverpool

https://www.liverpool.ac.uk/working/jobvacancies/currentvacancies/academic/000928/ "Saccheri, Ilik" <I.J.Saccheri@liverpool.ac.uk>

UManchester ConservationBiology

THEUNIVERSITY OF MANCHESTER

PARTICULARSOF APPOINTMENT

FACULTYOF ENGINEERING & PHYSICAL SCIENCES

SCHOOLOF EARTH, ATMOSPHERIC AND ENVIRONMENTAL SCIENCES

LECTURER(TEACHING AND SCHOLARSHIP) IN CONSERVATION BIOLOGY

Vacancyref: EPS-08491

Closingdate : 07/08/2016

Salary:Grade 6/7, Â£34,576 to Â£47,801 per annum

Hours:1 FTE

Duration:1 September 2016 until 31 August 2018

Location:Oxford Road, Manchester

Responsibleto: Professor Liz Sheffield

Enquiriesabout the vacancy, shortlisting and interviews:

ProfessorLiz Sheffield

Email:L.sheffield@manchester.ac.uk

Tel:0161 275 3905

OverallPurpose of the Job:

Youwill contribute to B.Sc. (Hons) and M. Sci. degree teaching in a rangeof biosciences programmes. You will offer teaching through a varietyof means including lectures, practicals, field courses, tutorialsand eLearning.

KeyResponsibilities, Accountabilities or Duties:

Thefollowing describes the type of work that is typically required of staffat this level. It is not expected that an individual will carry outall the activities mentioned below. Some staff may also carry out additionalduties.

Teachingand Learning Support

ïCo-ordinate, design and deliver teaching material to undergraduate students

ïUse appropriate teaching, learning support and assessment methods

ïSupervise student dissertations and projects

ïIdentify areas where current provision is in need of revision or improvement

ïContribute to the planning, design and development of objectives and materialparticularly in relation to conservation biology and/or ecologyand/or environmental biology lectures, practicals and field courses

ïSet, mark and assess work and examinations and provide feedback to students

PERSONSPECIFICATION

EssentialKnowledge, Skills, Experience and Qualifications:

ïYou will have a B.Sc. and Ph.D. in a relevant biosciences subject

ïYou will possess sufficient breadth or depth of specialist knowledge inthe discipline to deliver teaching programmes and provide learning support

ïYou will show evidence of scholarly activity: e.g. publications, conferencepaper presentations

ïYou will use a range of delivery techniques to enthuse and engage students

ïYou will contribute to administrative tasks within the School/Unit e.g.course development, assessment exercises, examinations, recruitment,and management of resources

ïYou will have HEA accreditation, or a PG Cert. or be willing to work towardssuch qualifications with our support when in post

Bestregards

Reinmar

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DrReinmar Hager

Lecturerin Evolutionary Biology

PostgraduateTutor

Computationaland Evolutionary Biology

Facultyof Life Sciences

TheUniversity of Manchester

ManchesterM13 9PT, UK

Tel.++ (0)161-275-1550

ReinmarHager <Reinmar.Hager@manchester.ac.uk>

UMaryland TeachingEvolution

Position Description: The First-Year Innovation & Research Experience (FIRE) is a major initiative at the University of Maryland, College Park. FIRE provides first-year students research experience, broad mentorship and social connectivity that impacts academic success and professional development.

The Office of the Provost and Senior Vice President in collaboration with Dr. Gerald Wilkinson of the Department of Biology is seeking a Clinical Assistant Professor to serve as the Research Educator for the FIRE Evolution of Exaggerated Traits innovation and research stream. The stream Research Educator works in collaboration with the stream-affiliated faculty members to design and implement the group research agenda and is responsible for all curriculum, instruction and broad student mentorship. The Research Educator will coordinate with a team of undergraduate peer mentors to oversee research operations including student research progress, infrastructure maintenance as well as management of the fiscal budget. The position empowers the individual to develop a strong portfolio of experience in curriculum development, instruction, mentorship, leadership and research group management.

Students in this FIRE stream will investigate how small genetic changes can profoundly influence the development and evolution of an extraordinary novel trait. They will use a group of flies from Southeast Asia that exhibit extreme sexual dimorphism in head shape with eyes on the ends of stalks. In males, these eyestalks can each exceed the length of the body. These flies provide a tractable laboratory model for understanding how organism shape can evolve rapidly and dramatically as a consequence of competition among males for mates. Using data available for these flies and other organisms, these studies will reveal how both highly conserved genes and newly evolved genes contribute to the development of a novel trait. Students in this stream will gain a comprehensive understanding of how traits evolve and will complete all aspects of the experiment, from dissecting tissue, selecting genes to study, quantifying gene expression, analyzing data using statistical methods, and int erpreting results.

Minimum qualifications: - Ph.D. degree in discipline related to cell, molecular or evolutionary biology or closely related field (ABD considered). - Record of success in presenting research at conferences and/or publishing research in peer-reviewed journals. - At least one year experience in teaching undergraduate students (either as the instructor of record or as a teaching assistant). - At least one year of research team experience.

Expectations of Position: Ability to lead a team of undergraduate peer mentors through clear communication and management. Ability to develop instructional curriculum and protocols for research-based inquiry and discipline understanding. Ability to effectively teach undergraduate students in lecture and research-based environments.

Ability to mentor students from research, academic and personal perspectives. Ability to assess student learning through development of formative and summative assessments appropriate for inquiry-based instruction. Ability to manage research operations including student progress, equipment, consumables and oversight of the fiscal budget. Ability to effectively communicate with stream faculty members, undergraduate peer mentors, students and institutional colleagues. Ability to problem-solve, prioritize and manage multiple projects and timelines. Strong organizational and interpersonal skills including the ability to communicate clearly and effectively. Ability to work autonomously and collaboratively.

Ability to coordinate multi-author publication development and submission. Ability to communicate stream and program accomplishment through presentation at relevant conferences. Ability to serve the FIRE program through oversight of some programmatic component (peer mentor oversight, outreach, marketing, assessment, etc). Flexibility to grow, adapt and change as FIRE develops at UMD.

Additional information: The Research Educator position will be supported from January 2017 through December 2019 (3 years) contingent on available funding and positive annual reviews (each December 2017 & 2018). The position co-reports to the Director of First-Year Research Programs in the Office of the Provost and Senior Vice President as well the stream affiliated faculty member Dr. Gerald Wilkinson.

More information about the FIRE program and the Research Educator position is available at the FIRE website: http://fire.umd.edu/ To apply for this position please submit the following documents: a cover letter; a curriculum vitae; a list of three professional references including names, addresses and telephone numbers; and, a statement of your teaching philosophy before Aug 31, 2016 to

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

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UMissouri ResTech LifeHistoryEvolution

A research specialist I position is available in the King lab (http://elizabethking.org) in the Division of Biological Sciences at the University of Missouri to join a project focused on the genetic and physiological basis of life history evolution using Drosophila melanogaster as a model system. Required responsibilities will include but are not limited to maintaining a set of selection lines, performing phenotyping assays, DNA and RNA extraction, and general coordination and organization of lab activities. The successful applicant will have a Bachelor's degree in a related field, some previous experience working in a laboratory setting, basic computer skills, and excellent written and oral communication skills. Ideally, we seek a highly motivated, enthusiastic individual, who works well with others and has a willingness to learn new skills and take on new challenges. Dr. King is committed to the career development of the successful applicant and welcomes applications from those with a desire to gain certain skills or develop independent research projects.

To apply, go to: http://bit.ly/2ah4SNI. Current employees of the University of Missouri should use this link instead: http://bit.ly/2a76kiu. In addition, applicants should email Elizabeth King (kingeg@missouri.edu) and provide a brief cover letter, a C.V., and names and contact information for 2 references. The cover letter should include a description of previous research experience, interest in the position, and future career goals. Application review will begin August 15th and will continue until the position is filled. The University of Missouri is an equal opportunity/access/affirmative action/pro-disabled and veteran employer.

The Division of Biological Sciences at MU (http://biology.missouri.edu/) has research strengths in evolutionary biology, genetics and genomics, and quantitative biology. MU also boasts a highly collaborative research environment between departments within the life sciences (e.g., animal sciences, plant sciences, biomedical sciences, statistics, etc.). Columbia is a vibrant college town located in mid-Missouri, 2 hours from both Kansas City and St. Louis (http://www.como.gov/).

kingeg@missouri.edu

UNevada Reno Bioinformatics

Assistant Professor Tenure-Track in Biochemistry and Molecular Biology

The University of Nevada, Reno (UNR) is the State of Nevada's land grant and historic flagship institution of higher education. Ranked in the Top Tier of "best national universities" by U.S. News & World Report, UNR plans to add up to 250 tenure-track faculty positions in 2015-2020. As integral components of the University, the Nevada Agricultural Experiment Station and the College of Agriculture, Biotechnology, and Natural Resources invite applications for the position of Assistant Professor of Bioinformatics in the Department of Biochemistry and Molecular Biology as part a research cluster of excellence in Dryland Agriculture. Preference will be given to applicants with demonstrated proficiency in emerging bioinformatics research areas including, but not limited to, integrated -omics methods, structural bioinformatics methods for generating protein-protein interaction or transcriptional regulatory networks, transcriptional and protein-protein network modeling, microbiomics, single-cell omics, proteomics, metabolomics, fluxomics, or other computational approaches to inform systems-level agricultural research.

Candidates must demonstrate a capacity to develop a high-impact, nationally recognized, and extramurally funded independent research program. Candidates will also have the opportunity to interact and collaborate with existing faculty to establish, utilize, and integrate cutting-edge experimental approaches. Candidates must demonstrate expertise to teach existing and/or newly developed undergraduate and graduate courses in such topic areas as Bioinformatics in the context of genomics, proteomics and metabolomics; Computational Systems Biology; Structural Bioinformatics; and Functional Genomics. Candidates must be able to mentor undergraduate and graduate students as well as postdoctoral scholars, and demonstrate the ability to work with a diverse group of research and teaching faculty, scientists, and students from diverse cultural and socioeconomic backgrounds.

The Department of Biochemistry and Molecular Biology holds a unique interdisciplinary position within the University as one of three departments in the College of Agriculture, Biotechnology, and Natural Resources and is located within the University of Nevada School of Medicine campus. The Department has approximately 380 undergraduate students, 15 graduate students, and 16 faculty members. The Department has access to modern laboratory facilities including Centers for Genomics, Proteomics, Bioinformatics and Imaging. With a growing and increasingly diverse student enrollment of approximately 21,000 undergraduate students and over 2,800 graduate students, and a total budget of over $500 million, the University offers a comprehensive selection of degree programs at the undergraduate, master, and doctoral levels along with post-graduate training opportunities.

Located in the picturesque Truckee Meadows on the eastern slope of the Sierra Nevada mountain range, the University is just a short distance from the state capitol, the stunning Lake Tahoe area, and 3.5 hours from the San Francisco Bay area. Relocate America named Reno as one of the top 100 places in America to relocate, and is listed as the 17th Safest City in America by Business Insider. Reno's high-desert climate allows for beautiful, four-season living, and a plethora of outdoor activities including skiing and snowboarding, hiking, biking, boating and fishing.

Inquiries about the position may be addressed to Dr. Karen Schlauch, chair of the search committee (schlauch@unr.edu; 775-784-6236). For full consideration, please apply by October 1, 2016.

Required Qualifications: The candidate must hold an earned Ph.D. degree in Bioinformatics, Biochemistry, Biology, Plant Sciences, Computer Science, Mathematics, or related field.

Preferred Qualifications: Preferred candidates will have completed at least two years of postdoctoral work or the equivalent.

How to Apply: Applicants should submit 1) a letter of application detailing required and preferred qualifications (no more than 1 page), 2) a current and complete curriculum vita, 3) a statement of research interests and vision of future research (no more than 3 pages),

4) a teaching statement (no more than 1 page), and 5) names and contact information of at least three references. Applications received by 10/1/16 will receive full consideration. Please apply for this job posting on E-Search- https://www.unrsearch.com/postings/21321 EEO/AA Women, under-represented groups, individuals with disabilities, and veterans are encouraged to apply.

Rebecca Mosher <rmosher@unr.edu>

UofStAndrews Bioinformatician

Bioinformatician post available in scenic southeast Scotland at University of St Andrews - School of Medicine ref. AR7802ML Salary: 31,656 to 37,768 per annum Hours: Full Time Contract Type: Contract / Temporary Closes: 19th August 2016

The University of St Andrews seeks to appoint a Bioinformatician to join a dynamic and multidisciplinary community and will play a key role in providing bioinformatic support and development to diverse projects across different research areas. St Andrews possesses a wide range of research programmes in functional genomics, bioinformatics and algorithm development applied to biomedical research, evolutionary biology and cell biology. St Andrews researchers lead large international projects in infectious diseases, neuro-developmental disorders and marine biology, all heavily involving bioinformatics approaches. Unique research opportunities are offered by the close links with research groups at the School of Computer Science working in algorithm development and machine learning.

The Bioinformatics Unit was established in 2012 to drive and assist world-class research in these areas. The Unit manages a recently installed a high memory computer cluster fully dedicated to bioinformatics research. We are recruiting an exceptional person to participate in the development and use of data-driven approaches within medical and biological research across the University.

The successful applicant will have a degree in bioinformatics or life sciences with experience in informatics or computing applied to biological questions. Applicants must be familiar with Linux and shell scripting, with experience in at least one major programming language.

Experience in the analysis of Next Generation Sequencing (NGS) data sets is required, for example: genome assembly, genome-wide association studies, gene expression, phylogenetic inference, RNA-Seq or genome informatics. Good communications and management skills, together with flexibility and clear vision and understanding of the advances in the field, are essential.

The role will include:

* Active participation in the design and implementation of bioinformatics analyses and pipelines. * Working with multiple research groups across St Andrews in order to provide bioinformatics support. * Testing, scripting, debugging and computation workflow development and refinement.

The post will be available immediately and is for 18 months in first instance to cover maternity leave, and will be based in the School of Medicine but will involve working with groups based in the Schools of Biology, Chemistry and Computer Science.

The University of St Andrews is committed to promoting equality of opportunity for all, which is further demonstrated through its working on the Gender and Race Equality Charters and being awarded the Athena SWAN award for women in science, HR Excellence in Research Award and the LGBT Charter; http://www.st-andrews.ac.uk/hr/edi/diversityawards/ . To apply, please visit http://www.jobs.ac.uk/job/AUH009/bioinformatician-ar7802ml Ramon Fallon <rf73@st-andrews.ac.uk>

UPennsylvania Lecturer EvolutionGeology

Lecturer in Earth and Life Through Time

The Department of Earth & Environmental Science at the University of Pennsylvania is seeking a leave-replacement lecturer for GEOL125: Earth & Life Through Time. The course is half earth processes and evolutionary concepts and half a survey of evolutionary history and past events, but may be reformulated. The course will be taught in the Spring 2017 semester. Enrollment in the course has been around 100-200 students, and is populated largely by non-science majors, with a small number of majors and potential majors in Earth Science. The course fulfills general education requirements. The course is structured as a large lecture section complimented by weekly, small group recitation sections. The course is supported by graduate teaching assistants to deliver the recitation and for grading. A complete syllabus and past course materials are available.

If interested, please contact Dr. Alain Plante (Undergraduate Chair, aplante@sas.upenn.edu). *Note that this course is held every year and is in high demand*

"Sallan, Lauren C" <lsallan@sas.upenn.edu>

USouthampton 2 EvolutionaryCompSci

Hello all -

Please see below the advert for two positions in the AIC group at Southampton. We are a multidisciplinary group in a top ranked computer science department with eclectic interests including Theoretical/Computational Evolutionary Biology, Evolutionary Systems Biology. e.g. see http://www.ecs.soton.ac.uk/people/raw Feel free to get in touch - best, Richard.

Please distribute widely (and responsibly) -

Lecturer*/Associate Professor (*USA translation = Assistant professor) https://jobs.soton.ac.uk/-Vacancy.aspx?ref=3D3D744016FP Agents, Interactions & Complexity research group Location: Southampton, UK Salary: £36,672 to £60,081 per annum Full Time Permanent Closing Date: Sunday 10 July 2016 Interview Date: Thursday 28 July 2016 Reference: 744016FP

The Agents, Interaction and Complexity (AIC) group within Electronics and Computer Science, at the University of Southampton, welcomes applications for a full time post at either Lecturer or Associate Professor level.

Electronics and Computer Science (ECS) is the largest and most distinguished School of its kind in the UK, with a worldwide reputation for its research,enterprise and research-lead teaching.

The AIC group undertakes world-leading, interdisciplinary research into the science and engineering of computing systems, in particular those that connect people and technology. We are interested in complex socio-technical, socio-economic and socio-ecological systems that underpin the most pressing challenges currently facing society. Problems as diverse as engineering resilient and sustainable smart infrastructure, or refactoring health-care systems to cope with demographic change, understanding voting patterns, or anticipating and mitigating the impacts of climate change, all involve building and analysing complex systems comprising many interacting agents, including people and other organisms, hardware robots and autonomous software agents.

AIC is a highly interdisciplinary group, not only collaborating across areas in Electronics and Computer Science, but across disciplines from physics and maths to psychology and the humanities. We are therefore actively seeking colleagues with excellent research track records and demonstrated ability to build collaborations, especially across disciplinary boundaries, and to engage in and to lead exciting, innovative work.

Applications are welcome in any of the group's key areas of interaction, complexity and agent-based systems as well as other areas that support the research themes and ongoing projects in the group. Information analytics and visualisation, serious games/play, machine learning are examples of areas of particular additional interest.

Further info, w. links to research areas, group members and application procedures etc:

https://jobs.soton.ac.uk/Vacancy.aspx?ref=-3D3D744016FP – Dr. Richard A. Watson Associate Professor Institute for Life Sciences/Electronics and Computer Science, University of Southampton http://www.ecs.soton.ac.uk/people/raw R.A.Watson@soton.ac.uk

R.A.Watson@soton.ac.uk

UWashington DrosophilaLabTech

The Promislow lab at the University of Washington in Seattle, WA, is seeking qualified applicants for a Research Tech I position to work in a Drosophila genetics lab. The Promislow lab uses a variety of approaches, including quantitative genetics, molecular genetics, systems biology, behavior, demography, and physiology, all with a view to better understanding the biology of aging. The ideal applicant will have at least a Bachelor's degree in a related field, and experience using genetic techniques, preferably in a Drosophila lab. Required tasks may vary, from routine stock maintenance and crosses, to DNA and RNA extraction and PCR, to behavioral observations and analysis. The successful candidate will have outstanding organizational skills, excellent verbal and written communication skills, basic computer skills (ideally with both PC and Mac), be comfortable with supervising others, and be willing to learn new techniques. To learn more about the lab, see http://www.promislowlab.org . Start date is flexible, but could be as early as Sept. 1st. To apply, go to http://www.washington.edu/admin/hr/jobs//, click on "START your job search", and enter the number 134690 in the Req# search space, or go to the following link: http://tinyurl.com/flylabjob2016. In addition to the online application, please send a cover letter, a copy of your CV and the names and contact info of two referees directly to Daniel Promislow at promislo@uw.edu. All applications received by July 22nd will be given full consideration.

The University of Washington is an affirmative action, equal opportunity employer. The University is building a culturally diverse faculty and staff and strongly encourages applications from women, minorities, individuals with disabilities and covered veterans.

Daniel Promislow Departments of Pathology and Biology University of Washington 1959 NE Pacific Street Box 357705, Room K-078 Seattle, WA 98195 ph: 206 616-6994 e: promislo@uw.edu

Daniel Promislow <promislo@u.washington.edu>

UWisconsinMadison InstituteDirector

Director, Wisconsin Institute for Discovery

WID is a transdisciplinary research institute at the University of Wisconsin-Madison exploring information across disciplines at the interfaces of research, education and business. The mission of WID is to enhance human health and welfare by facilitating interdisciplinary research spanning biotechnology, nanotechnology and information technologies. WID studies the information supporting life by advancing theoretical, applied, and laboratory research while seeking out connections among fields. http://wid.wisc.edu WID encompasses seven Research Themes: Bionates Core Computational Technology Epigenetics Games+Learning+Society Living Environments Laboratory Optimization Systems Biology

Applications (due 9/23) and inquiries: http://www.ohr.wisc.edu/Weblisting/External/PVLSummary.aspx?pvl_num=86822 I am sharing this vacancy but am not affiliated with the search. -JP

"jpool@wisc.edu" <jpool@wisc.edu>

UZurich FieldAssist BirdsLapland

Expenses paid field assistant positions to study the foraging ecology of Siberian Jays in Swedish Lapland

For the upcoming field season (15 August-31 October 2016) we are looking for a highly motivated expenses paid field volunteer to join our field project (main responsible Dr. Michael Griesser, University of Zurich, Switzerland) investigating life-history evolution in Siberian jays. The study site is located near Arvidsjaur, Swedish Lapland.

Our current project investigates the influence of habitat quality on the foraging and food storing behaviour of Siberian jays. The work of the field volunteers will be to help with field experiments, behavioural observations, catching birds, and data management. This work will give insight into exciting experimental fieldwork and will be carried out partly in managed forests and partly in scenic pristine boreal habitats. We will work 5-6 days per week in the field depending on the workload of the experiments. Observe that temperatures in the end of the season can be as low as -10C. The work is physically strenuous at times. The team will vary in size depending on the weeks, but at least two other people will be present during the whole field season.

Qualifications: (1) BSc/MSc in Biology, Ecology, Evolution or similar qualification (2) Previous field experience (3) Ability to work in small teams and sociable personality (4) Knowledge in observing (5) bird ringing and mist-netting experience (6) Driving licence (7) Fluent in English

We will cover for the accommodation, travel expenses from and to the study site (in total up to 300 Euros), as well as the living expenses.

Applications - including a CV, a letter of motivation (1 page) and the name of two referees - should be send to Michael Griesser michael.griesser@uzh.ch, preferably in a single PDF.

Applications received until 10 July 2016 will be given full consideration.

For further information on the project, see:

http://www.aim.uzh.ch/de/research/birdfamilies/JayResearch.html Michael Griesser Anthropological Institute & Museum University of Zurich - Campus Irchel Winterthurerstrasse 190 8057 Zürich Switzerland

http://www.aim.uzh.ch/research/birdfamilies/mgriesser.html michael.griesser@uzh.ch michael.griesser@uzh.ch

Other

ESEB outreach fund

ESEB Outreach Fund

The European Society for Evolutionary Biology (ESEB) welcomes applications to the ESEB Outreach Fund for projects that promote evolution-related activities. The goal of this initiative is to improve public knowledge about evolution globally.

Applications for funding will be accepted for educational initiatives that promote evolution, development of evolutionary material (books, films, web sites) intended for a general audience, public outreach seminars, public exhibitions, etc. While most projects will be financed for a sum between 1000-1500 Euro, exceptions can be made if a strong argument is provided for additional funds.

The application form can be found on www.eseb.org (click on the "Outreach Fund" link). Applications will be accepted twice yearly (deadlines March 15, September 15) and should be submitted by email to Ute Friedrich (office@eseb.org; Subject: Outreach).

Dr. Ute Friedrich ESEB Office Manager Email: office@eseb.org European Society for Evolutionary Biology - www.eseb.org office@eseb.org

Evolution2016 PresentationVideos

If you missed the Evolution conference in Austin or want to revisit talks from the meeting, visit the Evolution 2016 youtube channel: goo.gl/mwOpc8. There are more than 430 presentations recorded with playlists that group the talks by keywords. For an index of the talks with links to their specific video, visit the youtube station guide: https://goo.gl/7CPWRS There are also nearly 50 posters from the conference available for more detailed viewing on FigShare: https://goo.gl/OsXhqu Thank you to the conference organizers for such a great meeting, Howard Rundle for supporting and finding funding for the video recording initiative, the presenters that had their research documented to share with the broader community and the 58 student volunteers that video recorded and uploaded all of these talks.

Emily Behrman Ph.D. Candidate Schmidt Lab Department of Biology University of Pennsylvania 433 S University Ave Philadelphia, PA 19104 Bemily@sas.upenn.edu http://www.emily-behrman.com Emily L Behrman <bemily@sas.upenn.edu>

InputFiles SpamSoftware

Grettings dear Evoldir Members

I'm want to run a mixed stock analysis in SPAM using mitochondrial DNA sequences. I've read the manual for the input file format, but I still have some doubts about the input file for sequence data. Does anyone have an example input file (baseline data) for sequence/haplotype data that they would be willing to share?

best wishes.

MANUEL HOYOS

Biologo

Manuel Antonio Hoyos Rodriguez <mahoyosr@unal.edu.co>

LGBTQ survey

The Queer in STEM study of the career experiences of lesbian, gay, bisexual, trans, and other queer-identified individuals working in science is now soliciting responses for a new survey of science professionals ÃÂ euro " both LGBTQ and "straight." Volunteers can take the survey immediately at http://bit.ly/queerstem2 ÃÂ euro "see below or http://www.queerstem.org for more information. EvolDir was a big help with participant recruitment for our previous survey, and my collaborators and I would be very grateful for your participation in this new project, and assistance in passing the survey link along to folks who should participate.

Thanks! Jeremy Yoder

Postdoctoral Research Fellow Forest and Conservation Sciences University of British Columbia jbyoder@gmail.com http://jbyoder.org Introducing Queer in STEM 2.0

Three years ago, we launched Queer in STEM (http://www.queerstem.org) to take the first in-depth look at the experiences of lesbian, gay, bisexual, trans, or queer-identified (LGBTQ) professionals working in science, technology, engineering, or mathematics (STEM) fields. This summer, we're excited to announce a new chapter of the project: Queer in STEM 2.0.

The original Queer in STEM study

More than 1,400 people from across the U.S., Canada, and around the world answered the original Queer in STEM online survey, and 120 volunteered to answer in-depth follow-up questions. The results of that original online survey have now recieved substantial news coverage, and been reported in many seminar presentations, an upcoming book chapter, and a peer-reviewed research article (PDF available at https://drive.google.com/file/d/0B8WTovkBDKYWUUd1RnRXTmRkTU0/view?usp=sharing). We found that

- LGBTQ-identified people work in STEM fields from evolutionary biology to particle physics; - More than 40% have not disclosed their LGBTQ identity to colleagues, coworkers, or students, even if they are totally out of the closet at home; - LGBTQ-identified people are more likely to be open about their identities if they know their colleagues and employers support them, and if they work in STEM fields with more even representation of men and women.

Queer in STEM 2.0: New questions, new approach, new discoveries

As in all scientific projects, these discoveries lead to more questions. Do LGBTQ-identified people remain in the closet in STEM workplaces mainly because they feel a lack of support, or because STEM workplace cultures discourage discussion of personal lives outside the lab? How do LGBTQ-identified colleagues, mentors, and role models affect their careers? Does being out in the workplace affect their research productivity?

Queer in STEM 2.0 aims to answer these questions with a new online survey designed for more specific hypothesis testing. We hope to hear again from participants in the original Queer in STEM survey, and to achieve an even bigger sample from LGBTQ-identified STEM professionals across the U.S. and Canada. Finally, in our biggest innovation from the original study, we will also ask STEM professionals who don't identify as LGBTQ to answer many of the same questions we will ask LGBTQ-identified participants, to provide a powerful new tool for understanding the survey results: a control sample.

Queer in STEM 2.0 officially launched on June 20, 2016, and is now open for responses at http://bit.ly/queerstem2. We are asking LGBTQ-identified scientists, technicians, professors, lecturers, graduate students, engineers, and other professionals as well as their straight colleagues to answer the anonymous online survey, to help spread the word to everyone who should participate, and to volunteer for in-depth follow up questions if they are comfortable. Thanks in advance for your help! We're looking forward to some exciting new discoveries about the LGBTQ community and scientific careers.

Jeremy B. Yoder Postdoctoral Research Fellow Dept. of Forest and Conservation Sciences University of British Columbia

jbyoder@mail.ubc.ca jbyoder.org

Jeremy Yoder <jbyoder@gmail.com> Jeremy Yoder <jbyoder@gmail.com>

Phyloseminar JoeFelsenstein Aug4

Our next freely-viewable seminar:

A brief history of computational phylogenetics Joe Felsenstein (University of Washington) Thursday, August 4, 2016, 10:00 AM PDT

Abstract: I will discuss the history of the use of computers to infer phylogenies, starting in the late 1950s and giving particular emphasis to the introduction of the major methods in the 1960s. Much of this history I watched happen, from 1965 on. In particular I will explain the way that work in biological systematics, in population genetics, and in molecular evolution of multiple species gave rise to the early methods. I will touch on the controversies that developed in the 1970s and 1980s, a period of intense conflict over what should be the logical foundation of the reconstruction of phylogenies. Computational phylogenetics is becoming continually more statistical and continually less connected to the separable task of erecting a biological classification of organisms. Recent Twitter controversies show that arguments that were dominant and vehement in the 1980s are now taken seriously by few.

For instructions on how to attend this online seminar, see http://phyloseminar.org/attending.html – Frederick "Erick" Matsen, Associate Member Fred Hutchinson Cancer Research Center http://matsen.fredhutch.org/ Erick Matsen <matsen@fredhutch.org>

Resampling DistanceMatrices

Evoldir,

I have an SSR dataset collected from 360 individuals spanning the range of an autopolyploid prairie species comprising diploids, tetraploids, and hexaploids. Diploids are quite rare, so we are focusing in the 4x and 6x individuals. These 4x and 6x cytotypes demonstrate a highly non-random geographic distribution, and we would like to explore whether this came about through some sort of ecological sorting mechanism rather than historical contingency. In other words (and since hexaploids likely arose from tetraploids) that hexaploids are restricted to area X because they experience generally higher fitness than tetraploids in area X, not because area X is the only place where hexaploids arose from tetraploids. Said a third way, recurrent origins of the hexaploids from the tetraploids. Demonstrating that hexaploids tend to be more genetically similar to geographically proximate tetraploids would seem to offer some insight.

A) Does anyone know of a script(s) that would do this sort of thing (given genetic and geographic distance matrices, evaluate if group A individuals tend to be more genetically similar to _geographically proximate_ group B individuals)? It seems some sort of resampling approach would do it.

B) Are there any other approaches that come to mind for this sort of situation and dataset?

Thanks! James

James Beck Department of Biological Sciences Wichita State University james.beck@wichita.edu www.becklaboratory.com/-James "James.Beck@wichita.edu" <James.Beck@wichita.edu>

Software MPTP update

Dear community,

We just released a significantly faster and more accurate version of our species delimitation tool PTP:

Preprint: http://biorxiv.org/content/early/2016/07/-14/063875 Web-Service: http://mptp.h-its.org/ Documentation & Download: https://github.com/Pas-Kapli/mptp Cheers,

Alexis

– Alexandros (Alexis) Stamatakis

Research Group Leader, Heidelberg Institute for Theoretical Studies Full Professor, Dept. of Informatics, Karlsruhe Institute of Technology Adjunct Professor, Dept. of Ecology and Evolutionary Biology, University of Arizona at Tucson

www.exelixis-lab.org alexandros.stamatakis@gmail.com

SouthAfrica VolFieldAssist SmallMammalEvolution

Volunteers needed

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? Biology/zoology/veterinary students are preferred as candidates. 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 o‘ clock), and stops its activity with dusk (19 o‘ clock). 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°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 1450 (around 175 US$, 100 Euro) must be paid for accommodation at the research station. Students must buy their own food etc in Springbok (costs of about R 3000, approx. 350 US$ or 250 Euro/month). Including extras (going out for dinner; shopping), you should expect costs of about 600 US$ / 450 Euros 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 any time in 2016 as well as beginning of 2017. Volunteers are expected to stay for 2-3 months.

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.

More information under

http://stripedmouse.com/site1_3_5.htm

Dr. Carsten Schradin

Director of the Succulent Karoo Research Station (South African non-profit organization), Goegap Nature Reserve, PO Box 541, 8240 Springbok, South Africa

http://www.stripedmouse.com

Logo_June 2014

Director Succulent Karoo Research station <succulent.karoo.research.station@kabelbw.de>

YoungScientist prize

Science/AAAS and SciLifeLab, a coordinated effort of four universities, have joined forces in creating the Science & SciLifeLab Prize for Young Scientists. Each year, the grand prize winner will receive a prize of US$30,000; each of the three category winners will receive US$10,000.The grand prize winner will have his/her essay published in Science and the three category winners will be published online. The topic of the entrant’s thesis research (and the subject of the essay) must be in one of the following categories: Ecology and Environment, Cell and Molecular Biology, Genomics and Proteomics, Translational Medicine. The deadline for entry is August 1. For further information, see http://www.sciencemag.org/-site/feature/data/prizes/scilifelab/index.xhtml Barbara Jasny <bjasny@aaas.org>

PostDocs

ArizonaState EvolutionaryGenomics2

Postdoctoral Research Associate Genomics/Bioinformatcs

URL: http://cartwrig.ht/jobs/2016/05/19/Postdoc-Opening/ PDF: http://cartwrig.ht/postdoc-2016.pdf A Postdoctoral Research Associate position is available at the Biodesign Institute at Arizona State University (ASU). This new Postdoctoral Research Assocate will be part of the Cartwright lab (http://cartwrig.ht/) located in the Biodesign Center for Personalized Diagnostics. The lab is focused on evolutionary research related to mutation and population variation, as well as developing statistical software to process large, genomic datasets to identify and study somatic and germline mutation patterns. A successful candidate will participate in two NIH funded research programs: (1) analysis of mutation accumulation lines from the ciliate, Tetrahymena thermophila, and (2) development of DeNovoGear (https://github.com/denovogear/denovogear), a general toolkit for the study of mutation rates from next-gen sequencing of related individuals and cells. Corresponding projects in the lab involve the study of somatic and germline mutations in humans, chimps, trees, bacteria, bees, mice, and cancer.

In particular, under guidance from Dr. Cartwright, the candidate is expecte= d to:

1. Work both independently and closely with other members of the lab 2. Map and/or assemble next-generation sequencing data 3. Adapt existing genomic techniques to non-model organisms 4. Develop novel, high-throughput methodologies to identify de novo mutations by comparing related individuals and somatic samples. 5. Present the results of research at meetings, in publications, etc.

Requirements

- PhD in bioinformatics, computational biology, biostatistics, genomics, molecular biology or related fields - Proficiency in scientific computing and programming/scripting languages in UNIX platforms (e.g. Bash, Python, C/C++) - Experience in statistical computing (e.g. R/Bioconductor and Biopython)

Desired Qualifications

- Experience in development/maintenance of scientific software - Experience in next-generation sequencing data processing and analysis - Experience in statistical analysis and method development - Experience in high-performance parallel computing - Experience in collecting and processing large-scale scientific data

Instructions to Apply

The position will remain open until filled. To apply, please send cover letter, CV, summary of past work, and the names and email addresses of three references to Dr. Cartwright at cartwright@asu.edu by **June 30, 2016**. Please put "Postdoctoral Research Associate" in the subject line of your email.

The Cartwright Lab (http://cartwrig.ht/) offers a productive environment, in which researchers are given the freedom to explore new ways of solving scientific problems. There are opportunities to work with a large number of collaborators at both ASU and worldwide. We are located in the Valley of the Sun (Phoenix, AZ, USA), home to 4.5 million people, and short driving distances from numerous outdoor activities in the Sonoran Desert. Biking, hiking, mountain climbing, and bird watching are all popular activities in the area.

The Biodesign Institute Mission

The Biodesign Institute at ASU addresses today$B!G(Bs critical global challenges in healthcare, sustainability and security by developing solutions inspired from natural systems and translating those solutions into commercially viable products and clinical practices.

Arizona State University is a VEVRAA Federal Contractor and Equal Opportunity/Affirmative Action Employer. All qualified applicants will be considered without regard to race, color, sex, religion, national origin, disability protected veteran status, or any other basis protected by law.

ASU's full non-discrimination statement: https://www.asu.edu/aad/manuals/acd/acd401.html Title IX statement: https://www.asu.edu/titleIX/ Reed A. Cartwright, PhD Barrett Honors Faculty Assistant Professor of Genomics, Evolution, and Bioinformatics School of Life Sciences Human and Comparative Genomics Laboratory The Biodesign Institute Arizona State University

Availability: http://links.asu.edu/CartwrightCalendar Address: The Biodesign Institute, PO Box 875301, Tempe, AZ 85287-5301 USA Packages: The Biodesign Institute, 1001 S. McAllister Ave, Tempe, AZ 85287-5301 USA Office: Biodesign A-224A, 1-480-965-9949 Website: http://cartwrig.ht/ "rcartwri@asu.edu" <rcartwri@asu.edu>

ArizonaStateU PopulationGenetics

Postdoctoralpositions in Computational & Theoretical Population Genetics

Threepostdoctoral positions are available in the Jensen Lab at Arizona State University (ASU).

Researchin the lab focuses on the study of adaptation, utilizing approaches from theory and statistical inference as well as experimental evolution and empirical population genetics. Research topics are open to discussion and mutual interest, though specific interests include the development of inference related to time-sampled data and/or multiple merger coalescent models, as well as the analysis of natural and experimental data particularly pertaining to virus populations. Additional information on current lab members, alumni, research, funding, and publications may be found at: http://jjensenlab.org Startdates are flexible, though are anticipated to be in 2017. Applicants should email a CV, contact information for three references, and a brief statement of research interests by September 01 to: jeffrey.d.jensen@asu.edu

ASUprovides an intellectually engaging research community at the interface of evolution, genetics, computer science, statistics, and medicine; with strong interactions among multiple groups of related interest including the Cartwright, Hedrick, Jensen, Pfeifer, Stone, Taylor, and Wilson Sayres Labs. Additionally, the Center for Evolution & Medicine represents an innovative research community focused upon the crucial role of evolutionary biology in addressing issues of fundamental clinical and medical relevance.

JeffreyD. Jensen Professor ArizonaState University Schoolof Life Sciences Centerfor Evolution & Medicin

jeffrey.jensen@epfl.ch

AustralianNationalU EvolQuantGen

Postdoctoral Researcher in Evolutionary Quantitative Genetics at the Research School of Biology, Australian National University

Evolution of mating patterns in a cooperative songbird

A 36-month postdoctoral position is available to study the evolutionary quantitative genetics of mating systems in a wild bird population. The project would investigate the evolutionary processes that shape mating and breeding systems, and in particular the evolution of mate choice, the dynamics of sexual selection and the interaction of these factors with the social environment. It will use data from a long-term study of superb fairy-wrens, a cooperatively-breeding passerine bird with exceptionally high levels of extra-pair paternity. The data-set comprises detailed records on individual life histories, mating patterns, relatedness and population spatial structure. The aim of the project is to address fundamental evolutionary questions about patterns of variation in breeding success and the role of indirect genetic effects and inclusive fitness.

The post constitutes an exciting opportunity for a highly-motivated postdoctoral researcher with experience in evolutionary ecology and/or quantitative genetic analyses. It will involve statistical analyses of a long-term data-set as well as fieldwork, in collaboration with Loeske Kruuk and Andrew Cockburn in ANU's Division of Evolution, Ecology and Genetics.

Applicants should possess (or be nearing completion of) a PhD in a relevant area of evolutionary ecology or genetics. They should have strong skills in complex statistical analyses; in particular, whilst familiarity with quantitative genetic mixed models is by no means essential, it would be a strong advantage. They should also be able to demonstrate excellent writing skills and a strong track record of publication in academic journals.

The position is available for 36 months. Start date could be as soon as possible dependent on red tape, and the salary would be $81,122 p.a. plus 17% superannuation.

For informal enquiries or further information, please contact Loeske.Kruuk@anu.edu.au.

To apply: http://internaljobs.anu.edu.au/cw/en/job/-508972/postdoctoral-fellow Closing date 31 July 2016.

Professor Loeske Kruuk Division of Evolution, Ecology & Genetics Research School of Biology The Australian National University Canberra, ACT 2601 Australia Loeske.Kruuk@anu.edu.au www.biology.anu.edu.au/Loeske_Kruuk Loeske Kruuk <loeske.kruuk@anu.edu.au>

BarcelonaUPF HumanPopGenomics

Postdoctoral in Human ation Genomics

The goal of the postdoctoral position is to undertake large-scale analyses of human genome wide data and complete genomes at a population level to carry out independent research, contributing as a team member to the wider program of research led by Dr. David Comas (http://www.biologiaevolutiva.org/dcomas). This will involve contributions to the design and development of new studies, leading modest-scale research projects and playing a key role in collaborative human population genetics studies. Current research focuses on complete genome analyses in human populations to unravel the evolutionary processes (demographic and adaptive) that have shaped the extant genomic diversity.

Specifically the postdoctoral researcher will:

- Lead analyses of human genome wide and complete genomes data and bioinformatic analyses to explore evolutionary processes.
- Lead and undertake innovative research that will advance understanding of the genomic determinants of hu-

man diversity, using strategic vision, supervisory skills, innovative ideas and high-level research skills as an experienced researcher working at the interface of bioinformatics, genetics, human biology and biomedicine. This will include making significant contributions to journal papers and could include development of novel statistical genetic methods where relevant to on-going studies.

- Contribute to the international profile of the team by presenting research to research teams, local audiences and international conferences.
- Co-supervise junior members of staff and research students and provide advice and guidance to other members of the team and to collaborators.
- Contribute to broader team goals including the participation in University teaching of undergraduate and master students.

Qualifications, Knowledge and Experience:

Essential

- PhD in ation Genetics or a related field.

- Knowledge of human genomics.

- Experience of techniques used in bioinformatics, genomics and statistical genetics, with particular expertise in computational approaches to genomic analyses.

- Evidence of bioinformatic or statistical programming competency.

- Evidence of research productivity (including high-quality research publications, presentations) and involvement in innovative, high-level research.

Desirable

- Evidence of training students

- Experience of Linux, scripting and use of a High Performance Computing Linux cluster

Skills, Abilities and Competencies:

Essential

- High level of proficiency in English, sufficient to undertake research and teaching to communicate effectively with staff and students.

- Ability to work independently and also as part of a research team.

- Excellent written and oral communication skills.

- Effective interpersonal and organizational skills, excellent time management skills.

- To demonstrate research potential, high motivation and enthusiasm of the subject area and deliver high quality research.

- Strong computational skills, including statistical programming (ideally R) and ideally also a programming language such as Python, Perl or C++.

- Ability to supervise research students and junior staff

A full-time position for 2 years with the possibility of extension is offered. Salary will be similar to postdoc positions offered by the Spanish Ministry ("Juan de la Cierva" contracts). Starting date September 2016 but alternative dates can be discussed. Candidates are asked to supply contact details for referees, a CV and a covering letter to support the application. Candidates shortlisted for interview will be contacted by the team leader. Applications should be sent to david.comas@upf.edu. Review applications will begin on August 1st, 2016 and continue until the position is filled. Applications received by August 1st will be given priority consideration.

David Comas <david.comas@upf.edu>

Boston 5 DiseaseModeling

FIVE POSTDOCTORAL OPENINGS CENTER FOR COMMUNICABLE DISEASE DYNAMICS HARVARD T.H. CHAN SCHOOL OF PUBLIC HEALTH LIPSITCH, BUCKEE, HANAGE, and GRAD LABS

Postdoctoral Research Fellow Infectious Disease Modeling: Two openings are available immediately for postdoctoral fellows at the Center for Communicable Disease Dynamics at Harvard T.H. Chan School of Public Health. We are seeking a person with excellent skills in infectious disease transmission-dynamic modeling and parameter inference, including appropriate programming skills in one or more of R, Python, C++, or Matlab. The position is jointly in the research groups of Marc Lipsitch, CCDD Director and co-supervision from Caroline Buckee, Associate Director. Multiple projects are available, including evolutionary epidemiologic modeling of antigenic diversity in bacterial pathogens (extending recent work from the Lipsitch group (Science paper and J R Soc Interface paper) and the Buckee group (PLoS Pathog paper and Proc Biol Sci paper), inference of transmission dynamics from age-specific time series, spatial ecology of infectious disease dynamics and surveillance, and other projects in evolutionary and statistical epidemiology.

Postdoctoral Research Fellow in Statistics of Infectious Diseases: An opening is available immediately for a postdoctoral fellow at the Center for Communicable Disease Dynamics at Harvard T.H. Chan School of Public Health to develop methods to analyze data from randomized and observational studies of infectious diseases. Specific projects focus on 1) generalizing estimators for randomized vaccine effects to incorporate predictors of heterogeneity of baseline risk, as well as strain diversity in the pathogen 2) developing methods for simultaneous estimation of vaccine efficacy and identification of surrogates/correlates of protection; and 3) developing improved methods for vaccine effectiveness estimation from observational studies. The successful candidate will have experience with programming in one or more of R, Python, C++, as well as a publication record in statistics or biostatistics in a relevant area. Familiarity with causal inference preferred. The position is in the research group of Marc Lipsitch, CCDD Director, with possible collaborations with Ben Cowling at the University of Hong Kong or members of the Program in Causal Inference at Harvard Chan.

Postdoctoral Research Fellow in Bacterial Population Genomics: The Center for Communicable Disease Dynamics at the Harvard T.H. Chan School of Public Health is currently seeking an exceptional and creative scientist for a post-doctoral fellowship in the lab of Dr. William P. Hanage, to develop and apply innovative analytical approaches for studying the population genomics of antibiotic resistant Streptococcus pneumoniae. Efforts will include application of next generation sequencing technologies and development of advanced comparative genomic tools for the analysis of bacterial pathogens. The successful candidate will be independent and motivated with a track record of excellent research in genomics, evolutionary microbiology or a related field. Strong quantitative and/or programming skills are required and experience in bioinformatics is expected. The fellow will work closely with Dr. Hanage and staff in the multidisciplinary research team based in the Center for Communicable Disease Dynamics where they will have the opportunity for professional development through interaction with other scientists applying bioinformatic, epidemiological and epidemic modeling approaches to viral, bacterial, and protozoan pathogens. They will also have opportunities to interact with leaders of bacterial evolution and infectious disease epidemiology at this institution and abroad. The fellow will have access to a wealth of resources including high-quality genomic and epidemiological data, a cutting-edge computing facility, robust analytical pipelines, the most recent sequencing and laboratory technology, and research expertise in genomics, mathematics, and computer science. The position is available immediately and is funded through June 2018.

Postdoctoral Research Fellow Studying Rapid Detection of Antibiotic Resistance: The Center for Communicable Disease Dynamics at the Harvard T.H. Chan School of Public Health is seeking an exceptional and creative scientist for a post-doctoral fellowship to develop innovative approaches that can rapidly identify drug resistant pathogens, in a project funded by the Bill and Melinda Gates Foundation. The successful candidate will be independent and motivated, with a record of excellent research in statistical genetics, computational biology or a related field. Strong programming skills are essential, and experience with bacterial systems is expected. Specific expertise in microbial sequence analysis is welcome, but not essential. The fellow will work closely with Dr. Bill Hanage in the Center for Communicable Disease Dynamics

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CalAcademy 4 CoralReefEvolution

FOUR POST-DOCTORAL FELLOWSHIPS IN CORAL REEF STUDIES

The Institute of Biodiversity Science and Sustainability and the Steinhart Aquarium, California Academy of Sciences, are recruiting four post-doctoral fellows to be a part of our new 5-year Coral Reefs Initiative. Positions are for 2 years (renewable), have several potential start dates (2016-2018), and come with generous support for laboratory and field work.

The post-doctoral fellows will work closely with Dr. Luiz Rocha (reef fish taxonomy, ecology, and evolution), Dr. Rebecca Albright (global coral reef ecology), Dr. Pim Bongaerts (reef coral taxonomy, ecology, and evolution), and Steinhart Aquarium Director Bart Shepherd (coral restoration), as well as our other coral reef curators Dr. Terry Gosliner (nudibranchs), Dr. Gary Williams (soft corals) and Dr. Rich Mooi (echinoderms). Desired research expertise include mesophotic reef biology, genomics, bioinformatics, coral reef conservation, and ecological data analyses, but applicants with expertise in any area of coral reef evolution, ecology, and conservation will be given full consideration. The California Academy of Sciences is also a public facing institution that receives ˜1.5 million visitors every year, so public outreach through in person and online interactions will be encouraged.

Applicants should possess a PhD in a relevant discipline at the time of hiring, be able to work collaboratively across the different laboratories and departments involved, and have strong academic publication and outreach records. California Academy of Sciences post-docs are expected to participate in a wide variety of outreach programs, both online and in our public museum.

To apply please submit a letter of interest, curriculum vitae, and a 2-page research statement summarizing your research accomplishments and goals to SnapHire (http://calacademy.snaphire.com/-jobdetails?ajid=3DUPxO8) at the CalAcademy website by September 24, 2016. Please specify your desired start date in your letter of interest. General inquiries should be sent to Luiz Rocha (lrocha@calacademy.org).

The California Academy of Sciences is a scientific and educational institution dedicated to exploring, explaining, and sustaining life on Earth. Based in San Francisco's Golden Gate Park, it is home to a world-class natural history museum, aquarium, and planetariumall under one living roof.

Luiz A. Rocha, PhD Associate Curator and Follett Chair of Ichthyology California Academy of Sciences p. 415.379.5370 f. 415.379.5731 LRocha@calacademy.org http://www.luizrocha.com/academic/ 55 Music Concourse Drive Golden Gate Park San Francisco, CA 94118

Luiz Rocha <lrocha@calacademy.org>

ClemsonU ComparativeGenomics

Vince Richards??? lab in the Department of Biological Sciences at Clemson University is accepting applications for a post-doctoral position. The successful candidate will participate in an NIH funded project investigating the human oral microbiome and its role in tooth decay (caries). Specifically, comparative/functional genomics, a rodent model, transcriptomics, and systems biology will be used to investigate the interaction among oral bacteria implicated in caries and health. Information generated will identify bacterial biomarkers for use in risk assessment and design of pro-, pre- and synbiotic therapies.

The candidate should have a strong publication record, a background in microbial genomics, experience analyzing next-generation sequence data, and be well versed in Linux/bash. Strong communication and writing skills are essential.

The position will be available starting August 1st, 2016 and is initially for two years with the possibility of extension. Applicants should contact Vince Richards directly at vpricha@clemson.edu. Please provide a cover letter describing research interests, experience, and career goals, CV, PDFs of representative publications, and contact information for three references. The position is benefits eligible and review of applications will continue until the position is filled.

Clemson University is ranked 21st among national public universities by U.S. News & World Report and is located on Lake Hartwell near the Blue Ridge Mountains in beautiful Upstate South Carolina.

Vincent P. Richards, Ph.D. Assistant Professor Department of Biological Sciences Clemson University Clemson, SC 29634 Email: vpricha@clemson.edu Lab website: http://www.vprichards-lab.com Vincent Paul Richards <vpricha@clemson.edu>

CNAG-CRG Barcelona PopulationGenetics

The Centro Nacional de Analisis Genomico (CNAG-CRG) is seeking:

Population genetics Postdoctoral Fellow

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 seek a postdoctoral researcher to work at the CNAG-CRG on the project Development of new statistical tools for improving the detection of population substructure at individual level with applications in humans, led by the team leader of Population Genomics Dr Oscar Lao.

The position requires a candidate with high experience in algorithm development, statistical modeling and data analysis in the field of population genetics.

The duration of the contract is for two years.

Requirements:

- A doctoral degree in bioinformatics, biostatistics, computer science or a related discipline, with emphasis on algorithm and software development, and population genetics.

- An advanced knowledge of C, C++ or other high-performance language for numerical computation, 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.

Application procedure:

Interested candidates should submit a CV and a brief statement of experience and interests before July 31^st to the recruitment portal through the following link:

http://www.crg.eu/en/content/jobs/cnag-jobs
BFU2015-68759-P (MINECO/FEDER, EU)

Best regards,

Nadezhda Alexandrovich

Talent Management - HR Department

Centre for Genomic Regulation (CRG)

C/ Dr. Aiguader, 88

PRBB Building

08003 Barcelona, Spain

Phone. +34 93 316 01 75 (ext. 1175)

Email: Nadezhda.Alexandrovich@crg.eu

www.crg.eu Follow us on Twitter | Facebook | YouTube

Nadezhda Alexandrovich
<Nadezhda.Alexandrovich@crg.eu>

ColoradoStateU PopulationGenomics

POSTDOC POSITION IN FROG POPULATION GENOMICS AND EVOLUTIONARY ECOLOGY

We are seeking to recruit a highly motivated postdoctoral researcher to work on two research projects focusing on the population genomics and evolutionary ecology of Columbia spotted frogs (Rana luteiventris) and tailed frogs (Ascaphus spp). This postdoctoral position will be based in the laboratory of W. Chris Funk at Colorado State University.

The main duty of this postdoc will be to conduct population genomic analysis of Columbia spotted frogs and tailed frogs to test the effects of landscape features on gene flow and to identify loci under selection across environmental gradients. In addition, this postdoc will lead field work and physiological lab work in the summer.

REQUIRED QUALIFICATIONS AND SKILLS: We are seeking an individual with expertise in population and landscape genomics, excellent writing ability, and strong interpersonal skills. The candidate should have experience in the collection of NGS data (especially RAD seq library prep), bioinformatics pipelines to assemble Illumina reads and call SNPs, GIS, and landscape genetic analysis. The candidate will also ideally have experience with reference genome annotation.

START DATE AND DURATION: The position start date is somewhat flexible, but we hope to employ someone by September 1, 2016. Funding is available for up to 2 years pending satisfactory performance.

APPLICATIONS: Send a 1-page letter describing why you are interested in this job and your relevant experience; your CV; and the names and contact information for three references to Chris Funk at Chris.Funk@colostate.edu. Review of applications will start July 24th and will continue until a strong candidate is hired.

SALARY: $40,000-$44,000 the first year depending on experience.

Colorado State University does not discriminate on the basis of race, age, color, religion, national origin or ancestry, sex, gender, disability, veteran status, genetic information, sexual orientation, or gender identity or expression. Colorado State University is an equal opportunity/equal access/affirmative action employer fully committed to achieving a diverse workforce and complies with all Federal and Colorado State laws, regulations and executive orders regarding non-discrimination and affirmative action. The Office of Equal Opportunity is located in 101 Student Services.

Colorado State University is committed to providing a safe and productive learning and living community. To achieve that goal, we conduct background investigations for all final candidates being considered for employment. Background checks may include, but are not limited to, criminal history, national sex offender search and motor vehicle history.

W. Chris Funk, Associate Professor Department of Biology Colorado State University 1878 Campus Delivery Fort Collins, CO 80523-1878 Tel: 970-491-3289 Fax: 970-491-0649 E-mail: Chris.Funk at colostate.edu URL: http://wp.natsci.colostate.edu/-funklab/ "Chris.Funk@colostate.edu" <Chris.Funk@colostate.edu>

ColumbiaU PopulationGenetics

POSTDOC IN POPULATION GENETICS, COLUMBIA UNIVERSITY

A postdoctoral position is available in Molly Przeworski's group at Columbia University.

Our research focuses on understanding mutation and recombination in humans and other species, and on modeling and detecting the footprints of natural selection in genetic variation data. For more information, see: http://przeworski.c2b2.columbia.edu/ This search is for a postdoc interested in mutation processes and their evolution. The specifics of the project are flexible, but will likely include both data analysis and modeling. Candidates must therefore have a background in bioinformatics, including extensive experience with genomic data analysis, as well as strong quantitative and programming skills. Moreover, they must have demonstrated intellectual independence, notably in the form of lead authorship on at least one substantial, completed project.

Our group is located in a newly renovated computational space on the main (Morningside Heights) campus of Columbia University. The space is contiguous to Guy SellaÕs and we benefit from close ties to that lab, as well as the one led by Joe Pickrell (NYGC), including joint lab meetings and journal clubs.

Postdoctoral fellows at Columbia have access to nice, subsidized housing within walking distance of campus.

Informal inquiries as well as applications (including a CV, copies of relevant publications and two letters of recommendation) should be emailed to Molly Przeworski at <molly.przew@gmail.com>. The target start date is January 2017, but is flexible.

Molly Przeworski Professor Dept. of Biological Sciences Dept. of Systems Biology Columbia University

molly.przew@gmail.com

CornellU EvolutionaryOrnithology

CornellU.Ornithology The Cornell Lab of Ornithology invites applications for our Edward W. Rose Postdoctoral Fellowships. These competitive postdoctoral fellowship awards (www.birds.cornell.edu/postdoc) support innovative, independent research by early career scholars of exceptional promise. Multiple Rose Fellowships are available annually, with applications due on September 8. All Rose Fellows join a vibrant community of more than a dozen concurrent postdocs within the Rose Postdoctoral Program and interact with many other scholars across a wide range of disciplines.

The Rose Postdoctoral Fellowship awards support individuals pursuing cutting-edge scholarship, while fostering intellectual interaction with multiple Lab programs and Cornell scholars. Any area of inquiry related to the Lab's mission "to interpret and conserve the earth's biological diversity through research, education, and citizen science focused on birds" is appropriate. Potential applicants are encouraged to learn more about the Cornell Lab and our formal programs in Bioacoustics, Bird Population Studies (avian ecology), Citizen Science, Conservation Science, Communication, Education, Evolutionary Biology, Information Science, Macaulay Library (animal behavior), Multimedia Productions, and Public Engagement in Science. Activities involving research and/or outreach spanning several of these areas are particularly encouraged, and therefore each postdoctoral scholar may be co-mentored by two senior Cornell scholars. Projects that foster links to people and units from across Cornell University are likewise welcome. Potential applicants are encouraged to contact the most relevant faculty and staff at the Lab to brainstorm about areas of mutual interest and synergistic projects. We are especially interested in supporting the independent research of individuals who can bring new ideas, approaches, and connections to the Lab, while simultaneously leveraging our existing tools, data, and expertise in science, education, and communication.

Each Rose Postdoctoral opportunity spans up to 24 months via two consecutive year-long appointments at the Lab. Located at the Imogene Powers Johnson Center for Birds and Biodiversity in the 220-acre Sapsucker Woods sanctuary, the Cornell Lab of Ornithology is a vibrant unit within Cornell's University's College of Agriculture & Life Sciences. More than 200 faculty and staff work at the Lab within our 10 mission-driven programs. Our management and staff are committed to the highest standards of ethics and excellence in all areas of our work.

These appointments provide a competitive salary, Cornell health and other benefits, and funds to help support the Scholar's research and other professional needs. Start dates are usually flexible within the year following the application. Interested applicants should visit the Annual Rose Postdoctoral Fellowship Competition web site (www.birds.cornell.edu/postdoc) for more information about the overall Program and about the Rose Fellow selection process.

The application package consists of a cover letter, CV, two-page research proposal, pdfs of up to three representative publications, and names and contact information for three references. Applicants must have received their PhD before beginning their postdoctoral appointment at Cornell. Application materials should be sent as a single pdf file to the attention of Sue Taggart (SET2@cornell.edu). Applications for the positions available in 2017 will be accepted until September 8, 2016. The selection committee is chaired by Dr. Irby Lovette (IJL2@cornell.edu), Fuller Professor of Ornithology and Associate Director for Academic Affairs at the Lab.

Edward W. Rose, known by family and friends as "Rusty," joined the Lab's Administrative Board in 1993 and served as its Chairman from 2004 to 2014. Rusty was a brilliant man who inspired everyone at the Lab, not only through his infectious laugh but even more by asking tough questions, expecting excellence, and seeking global impact. Rusty had a deep conservation ethos which he exemplified both in his own actions and through his support of the Cornell Lab and kindred institutions. He was among the Lab's most enthusiastic promoters of early career scientists, and he always relished learning about their discoveries and accomplishments. Rusty passed away in January 2016, but his legacy endures in many contexts, including the Edward W. Rose Postdoctoral Fellowship Program which brings together the Lab's entire postdoctoral community. Through the generosity of Rusty and his wife Deedie, together with that of fellow board members Larry and Nancy Fuller, Russ and Carol Faucett, and Imogene Powers Johnson, the Lab shall award multiple Edward W. Rose Postdoctoral Fellowships annually.

Cornell University is an innovative Ivy League university and a great

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CornellU EvolutionInvasiveSpecies

A postdoctoral research position is available to pursue collaborative research that would inform the management and policy of freshwater and/or marine ecosystems, with a focus on invasive species and their interactions with other drivers of global change. Experience with environmental DNA (eDNA) or related genetic methods and/or coastal marine ecosystems would be especially valuable. The postdoctoral fellow would join an interdisciplinary team of researchers, and lead one or more efforts within an NSF Coastal SEES project that includes a global network of collaborators working in coastal environments. Subprojects might focus on one or more of the following: metagenetic characterization of freshwater and marine communities with eDNA; quantitative analysis to forecast species dispersal and range changes caused by shipping and other vectors, and interactions with climate change; quantification of the ecological and economic impacts of invasions; and management and policy of invasive species at local, national or global scales. Intellectual leadership would be expected, with the choice of topic(s) depending on experience and interests.

Opportunities for collaborations exist with other biologists, big data scientists, economists, and policy experts. The postdoc would assist with the organization and administration of projects, including organizing eDNA sampling with collaborators around the world, and contribute to on-going publication preparation. Funding is available for at least two years. Applicant screening is rolling; the desired start date is as soon as possible (summer/fall 2016) but not later than spring 2017.

Salary and benefits will be competitive. The postdoc would be supervised by David Lodge, who has recently moved to Cornell from Notre Dame (Lodge Lab website in transition). Collaborations with other researchers at Cornell, Notre Dame, and other universities will be encouraged. Applicants should email (in one pdf document) a letter describing prior research experience and current interests, a curriculum vitae, and the names and contact information of three references to David Lodge (dml356@cornell.edu). The subject line of the email should read "Coastal SEES Postdoctoral Application 2016." Additional postdoctoral opportunities at Cornell's Atkinson Center for a Sustainable Future may also interest prospective applicants.:

Dr. Kristy Deiner Cornell University Department of Ecology and Evolutionary Biology Corson Hall A406A, 215 Tower Rd. Ithaca, NY 14850 Ph. 01-408-412-1704

Kristy Deiner <alpinedna@gmail.com>

Edinburgh ViralPhylodynamics

Postdoctoral Research Associate

The Centre for Immunity, Infection & Evolution and Usher Institute at the University of Edinburgh seeks to appoint an excellent Postdoctoral research associate to support the work of Andrew Rambaut and Mark Woolhouse on a broad range of research projects. This could include developing models of molecular evolution for RNA viruses, developing efficient computational techniques to analyse very-large scale phylodynamics data sets of viruses, creating visualization tools using JavaScript/D3, etc. depending on the skills and interests of the applicant.

Candidates will have a PhD (or near completion) in a relevant field (such as molecular evolution, statistics, computational biology, computer science).

Further details and application instructions are here:

https://www.vacancies.ed.ac.uk/pls/corehrrecruit/erq_jobspec_version_4.jobspec?p_id=036657 Informal enquiries to Andrew Rambaut (a.rambaut@ed.ac.uk).

Andrew Rambaut Institute for Evolutionary Biology | Centre for Infection, Immunity & Evolution Ashworth Laboratories, University of Edinburgh, Edinburgh, EH9 3FL, UK

contact a.rambaut@ed.ac.uk | http://tree.bio.ed.ac.uk | tel +44 131 6508624

"a.rambaut@ed.ac.uk" <a.rambaut@ed.ac.uk>

Faro Portugal LandPlantPhylogenetics

Post-Doctoral Research Fellowship Advertisement - 1 vacancy

Ref. Â: CCMAR/BPD/0019/2016 - within the project PTDC/BIA-EVF/1499/2014

The Centre for Marine Sciences (CCMAR) in the Algarve, Portugal, opens a position for a Post-doctoral Researcher fellowship (BPD) in the project with the reference PTDC/BIA-EVF/1499/2014 named "Determining the causes of inter-genomic conflict in the land plant phylogeny" financed by the Portuguese Foundation for Science and Technology - FCT/MCTES (PIDDAC) under the following conditions:

Tasks to perform: The project will determine the causes of the conflict among the current best phylogenies derived from each of the three genomes of land plants and their algal ancestors. Because the substitution process can vary both among sites (data heterogeneity) and among lineages (time heterogeneity), heterogeneous substitution models will be used in a Bayesian phylogenetic context to test the adequacy of model fit through posterior predictive simulations. The fellowship holder will be expected to use bioinformatic tools to determine phylogenetic relationships.

Scientific orientation: Dr. Cymon J. Cox, group leader of Plant Systematics and Bioinformatics, Coordinator Researcher at CCMAR and PI of the PTDC/BIA-EVF/1499/2014 project.

Work place: CCMAR

Requirements: 1. The applicant must speak English fluently and have a high proficiency in written English (the latter will be assessed from a Letter of Motivation submitted with the application); 2. The applicant must have a PhD and publications in an area related to Evolutionary Biology.

Evaluation criteria: 1. Experience and publications in the area of analysis of molecular sequences and knowledge of phylogenetic methodologies - 40% 2. Demonstrable knowledge of the systematics of plants - 30% 3. Competency in bioinformatic techniques including proficiency with Unix-based systems and programming/scripting languages (in particular Python) - 30%

The selection jury will exercise the right to contact and interview candidates should they require further information or clarification about their application. In the event that no applicant has the necessary profile the jury reserves the right to close the call without any recruitment.

During the fellowship, and in the event that the fellowship holder should resign, the jury reserves the right, upon convenience and opportunity, to assign the fellowship to the next applicant in accordance with the ranking position of the selection jury.

Grant conditions: The grant will have an initial duration of 12 months, starting in September 2016. It is anticipated that the grant will be renewed for additional periods until the end of the research project (a total length of 36 months). The fellowship must be undertaken exclusively (full time) according to the Portuguese law 40/2004, of 18 of August (Scientific Research Fellowship holder statutes), Fellowship Regulation of the Portuguese Foundation for Science and Technology in force http://goo.gl/G0RtCU and the rules of CCMAR research grants http://goo.gl/08o1Va .

Monthly maintenance allowance: A maintenance allowance of 1495/net (tax free) will be paid each month through inter-bank transfer in accordance with the grant amounts set by the Portuguese Foundation for Science and Technology (http// www.fct.pt/apoios/bolsas/valores.)

Application period: 8 to 21 of July 2016.

Application documents: The application should include a Letter of Motivation written in English that details the candidates experience in each evaluation criterion, a detailed Curriculum Vitae, a copy of the candidates PhD certificate and the email addresses of 3 academic referees.

Application Submission: Applications should be submitted by email to ccmar@ualg.pt indicating the reference CCMAR/BPD/0019/2016 (note that we can only accept applications sent through this email). You should consider your application as correctly submitted only after receiving an email confirmation from CCMAR.

Results: The judgement of the selection committee will be communicated in writing within 45 working days after the application deadline.

Selection Committee: Dr. Cymon J. Cox, group leader of Plant Systematics and Bioinformatics, Coordinator Researcher at CCMAR and PI of the PTDC/BIA-EVF/1499/2014 project (President of the jury), Dr. Gareth Pearson, researcher at CCMAR (member) and Dr. Gianluca De Moro, researcher at CCMAR (member).

CCMAR's non-discrimination and equal access opportunities policy - No candidate can be privileged, benefited, jeopardised or deprived of any right or exempt of any claim in regards to descendent, age, gender, sexual orientation, marital status, economic situation, origin, social economy, genetic heritage, disability, chronic disease, nationality, ethnicity, territory of origin, language, religion, politics and ideological beliefs

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Finland AdaptiveFescueTraits

INTERESTED IN EVOLUTIONARY ECOLOGY OF PLANT-MICROBE INTERACTIONS?

POSTDOCTORAL POSITION

We are looking for an enthusiastic and highly motivated postdoctoral scientist to work on a four-year research project "Heritability of adaptive fescue traits in changing climate" funded by Academy of Finland. The work continues our long-term research on the ecology and evolution of interactions between plants, microbes and herbivores. Strong collaboration with several national and international research groups, and the previously collected extensive plant material across Europe provide a solid basis for this work.

The present project aims to understand the mechanisms underlying phenotypic variation of ecologically relevant traits in red fescue (Festuca rubra) and its symbiotic fungal Epichloë endophyte. The closely linked fitness of the Epichloë symbiont and the host grass is presumed to align the coevolution of the species towards specialization and mutually beneficial cooperation. Here we will examine what is the relative importance of phenotypic plasticity, endophyte presence, and heritable variation including changes in DNA sequence and epigenetic modifications in red fescue adaptations across different latitudes. The approach includes rigorous, manipulative field experiments and lab work on genes that are responsible of traits that are ecologically important. The research will be conducted at Natural Resources Institute Finland (Luke) in Turku and/or Helsinki.

Candidates who are self-motivated and career-oriented are welcome to join an exciting and highly interactive research team. The candidate should enjoy working both in the field and in the lab. The ideal applicant will have a background in evolutionary ecology, molecular biology or other relevant biological sciences, show scientific curiosity and be capable of working independently. Strong demonstrated communication and writing skills are essential.

Applications should consist of a short cover letter, a curriculum vitae, a publication list, and the names and contact information of two referees. Applications should be addressed to Kari Saikkonen preferably by e-mail (kari.saikkonen@luke.fi). Review of applications will begin 15 August 2016 and continue until position is filled.

Kari Saikkonen Professor

Natural Resources Institute Finland (Luke) Itäinen Pitkäkatu 3 20520 Turku FINLAND

Tel. +358 29 532 6510 kari.saikkonen@luke.fi

https://www.luke.fi/en/personnel/kari-saikkonen/ http://scholar.google.fi/-citations?user=USjTDCoAAAAJ&hl=en https:/-/www.researchgate.net/profile/Kari_Saikkonen
"Saikkonen Kari (Luke)" <kari.saikkonen@luke.fi>

FloridaIntlU MarineEvolutionaryGenomics

PostDoc: Evolution of Bioluminescence and Light Detection in the Deep Sea

The Bracken-Grissom Lab at Florida International University in the Department of Biology and Marine Sciences Program is looking for a postdoctoral fellow to work on a NSF-funded project to study the evolution of bioluminescence and vision in deep-sea shrimp. This position is for 1-year with possible extension dependent on performance.

The CRUSTOMICS Lab is fundamentally interested in using genomic techniques to study the evolution and adaptation of marine invertebrates with a focus on crustaceans. We are searching for a postdoc to lead a recently funded NSF project aimed to test several hypotheses addressing the evolution of bioluminescence and light detection in the deep sea. As part of this project the postdoctoral fellow will use phylogenomic methods to trace the evolution of different bioluminescence modes across deep-sea shrimp. In addition, RNA-Seq will be used to characterize the visual systems and bioluminescence organs within a comparative framework. Experience with wet-lab molecular techniques, phylogenomics, transcriptomics (RNA-Seq), large data matrices, associated analyses and software, and bioinformatics is required. Additional experience with visual system ecology and opsin evolution is a plus. In addition to research, mentoring of graduate and undergraduate students and lab manager duties are expected as part of this position. The successful candidate must have completed her/his doctoral degree before taking the position. Our work requires good organizational and computational skills and the ability to work collaboratively as part of a team. Occasional physically demanding fieldwork (research cruises) may also be required to support research.

Additional information on the lab's research, the biology department, and marine sciences program can be found here: and *www.brackengrissomlab.com, http://-biology.fiu.edu/ and www.fiu.edu/˜marine . *Requirements*: As a *single PDF*, applications must include a 1) cover letter briefly outlining the candidate's fit to the position 2) curriculum vitae 3) research statement, 4) contact information (email and phone) for three references, preferably including doctoral advisor and/or postdoctoral advisor (if relevant) and 5) three relevant PDFs and 5) All information may be sent directly to Dr. Heather Bracken-Grissom at hbracken@fiu.edu. If you attending SMBE 2016 and are interested and qualified for the position please contact me so that we can meet.

Due Date: To receive full consideration, applications and required materials should be received by July 5th, 2016. Review will continue until position is filled. The position may be taken as early as late August 2016 (if search is complete), but start date is flexible (+ a few months). A competitive salary and benefits package will be included. This position will be based on the Biscayne Bay Campus.

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

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

INRAFrance EvolQuantGenetics

Post doc position in Evolutionary Quantitative Genetics, INRA, Bordeaux, France

Job description: The general goal of the research is to predict evolutionary changes of trees, particularly European white oaks, to environmental changes using diachronic approaches. These predictions will be based on observations conducted in situ in age structured cohorts of different ages (from 360 to 5 years), and in common garden experiments. Populations that have experienced the little ice age (360 years ago) will be compared with more recent and modern populations. A major goal of the project will be to estimate components of evolutionary change (selection gradients, heritability, elements of the G matrix), by analyzing existing genomic, genetic and phenotypic data in wild populations.

Scientific environment: The post doc position is part of the ERC project Treepeace (http://www.treepeace.fr/). The working location will be at the BIOGECO research unit (20 km south-west of Bordeaux, France: https://www4.bordeaux-aquitaine.inra.fr/biogeco_eng/). BIOGECO is a joint research unit between INRA and the University of Bordeaux and has long standing experience in studying evolution of forest trees by assembling contributions of different disciplines (ecology, genetics, genomics and evolution).

Expected profile: We seek for a scientist with a PhD degree and experience in the field of evolutionary quantitative genetics and/or proficiency in statistical modeling. Knowledge of tree ecology and practice of computer programming will be helpful. Candidates should be fluent in English.

Application: Application with CV, a brief statement of research interests, contact information for two professional references and publication list should be submitted in an electronic form to Dr. Antoine Kremer (antoine.kremer@pierroton.inra.fr). Review of applications will begin on August 1st 2016 and continue until the position is filled. Do not hesitate to contact us for further details or questions. The position is open for 2 years.

Examples of recent publications: Alberto F., J.Derory J, et al. (2013). "Imprints of natural selection along environmental gradients in phenology-related genes of Quercus petraea". Genetics 195, 495-512.

Kremer, A., B. M. Potts, et al. (2014). "Genetic divergence in forest trees: understanding the consequences of climate change." Functional Ecology 28(1): 22-36.

Kremer, A., O. Ronce, et al. (2012). "Long-distance gene flow and adaptation of forest trees to rapid climate change." Ecology Letters 15(4): 378-392.

Soularue, J. P. and A. Kremer (2014). "Evolutionary responses of tree phenology to the combined effects of assortative mating, gene flow and divergent selection." Heredity 113(6): 485-494.

cyril.firmat@pierroton.inra.fr

KarisokeResCenter Rwanda Biodiversity

The Dian Fossey Gorilla Fund is seeking a talented scientist to join our biodiversity research program. The position is based out of the Karisoke Research Center, located in Musanze, Rwanda, and is an opportunity to work in the biodiversity-rich forests of Rwanda and eastern DR Congo. The successful applicant will join a team of over 100 field workers and three PhD scientists working at the Fossey Fund's three field sites in Rwanda and in DR Congo. It is anticipated to be a two year position with potential for extension and/or long-term collaboration.

The successful candidate will work on applied projects relating to biodiversity (excluding gorillas) assessment and monitoring and there is also the potential to work in areas related to ecosystem restoration, water management, land use planning and climate-change adaptation planning. Primary position responsibilities will include evaluating current biodiversity monitoring and other research programs for key indicator species and adapting as appropriate; evaluating threats to biodiversity conservation; identifying and coordinating collaborative research opportunities; identifying and applying for grant funding to support programs; mentoring staff and students in biodiversity research; publishing and presenting results of studies to variety of audiences (management, scientists, tourists).

Qualifications We are looking for a motivated individual with a strong science background and excellent communication skills to join our team. A PhD in a biology, wildlife ecology, or related field and experience working in a field setting is required. Important skills include proficiencies with GIS and spatial analysis; database use and management; data analysis and modelling platforms such as R or Python; publishing in peer-reviewed journals. The candidate must be able to synthesize information from a variety of sources and communicate findings clearly in technical reports, scientific publications and presentations. The ideal candidate will have experience in some of the following areas:

. Strong field identification skills for wildlife and plants (desirable) . Setting up long-term biodiversity monitoring programs through direct and indirect (e.g. camera traps) assessment; . Assessing landscape physical and ecological change over time using contemporary and historical data sources; . Applying original research to develop management strategies; . Sophisticated statistical analysis, including population modeling; . Project or task management, including overseeing staff, budgets, schedules, and deliverables . Establishing collaborations and leading partnerships; . Scientific mentoring of staff and students;

To apply, please send a cover letter, resume and a list of three references by August 15th to hlaw@gorillafund.org. Please include “biodiversity research position” in the subject line of your email. No phone calls please.

About the Dian Fossey Gorilla Fund: The Dian Fossey Gorilla Fund is dedicated to the conservation and protection of gorillas and their habitats in Africa, through research, conservation action, education and partnerships. Founded by Dian Fossey as the Digit Fund and renamed after her death, the Fossey Fund operates the Karisoke Research Center in Rwanda, and maintains a staff of 120 who work in and around the Volcanoes National Park. DFGFI also employs a staff of 30 individuals operating at two field sites in eastern DR Congo and participates in critical conservation, health, and community development projects in both Rwanda and DRC. For more information about DFGFI, visit www.gorillafund.org . Helen Law Special Projects Assistant The Dian Fossey Gorilla Fund International 800 Cherokee Avenue, SE Atlanta, GA 30315 Main Line: 404-624-5881 Email: hlaw@gorillafund.org Web: gorillafund.org

Helen Law <hlaw@gorillafund.org>

Kew London HazelPopulationGenomics

A postdoc position is available for 15 months at RBG Kew working on population genomics of hazel nut trees. Closing Date 31/07/2016.

https://careers.kew.org/vacancy/post-doctoral-research-fellow-pdrf-in-plant-genomics-270154.html
You will be based in the Jodrell Laboratory at RBG Kew (London). Your project will involve deep transcriptome sequencing and surveying of genome-wide variation in over 100 wild and commercial varieties of hazel (Corylus avellana). You will manage the collection and sequencing of samples in collaboration with researchers in Turkey. You will assemble, map and annotate transcriptome and RAD-seq data and analyse genomic diversity using population genetic and phylogenomic methods. You will provide training to Turkish researchers on these methods. You may make occasional visits to Turkey (Istanbul and/or Giresun). Your work is intended to lay foundations for enhanced breeding of hazel trees with tolerance of spring frosts, summer droughts, and an emerging powdery mildew threat. Turkey produces 70-80% of the world’s hazelnut market and 61% of the rural Black Sea region population rely on hazelnut for their primary income.

Your project is in collaboration with Sabanci University and the Giresun Hazel Research Centre and is funded by a Newton Fund Institutional Links Grant. You will be based in the Kew plant health team, reporting to Dr Richard Buggs, Senior Research Leader at Kew and Reader in Evolutionary Genomics at Queen Mary University of London. The post will last for 15 months and you will be trained and encouraged to write a career development fellowship to continue the project beyond the current grant.

You must already hold PhD or D.Phil in genomics, and have specialist knowledge in genomics, transcriptomics and bioinformatics, including coding in python, perl or ruby. You must have experience of contributing to publications/presentations (at least one a first-named author paper in a journal of CIF >3). We are seeking excellent communication skills, including the ability to write for publication, present research proposals and results, and represent the research group at meetings. You need experience of independently managing a discrete area of a research project and experience of assembly and analysis of high-throughput sequence data.

We are committed to equality of opportunity and welcome applications from all sections of the community. We guarantee to interview all disabled applicants who meet the essential criteria for the post.

Richard Buggs <R.Buggs@kew.org>

LinkopingU Sweden GenomicsSexDifferences

Postdoc opportunity for 2 years in the research group of Dr Urban Friberg at IFM Biology, Linkoping University Sweden. Our research group has a broad general interest in the area of evolutionary biology/genetics/genomics, and ongoing projects focus on the evolution of ageing and the genetics/genomics of sexual dimorphism (see https://www.liu.se/forskning/foass/urban-friberg?l=en for more information).

Most sexual species exhibit distinct differences between the sexes, despite males and females sharing the same genome. How this is accomplished is yet not fully understood. We use the model organism Drosophila melanogaster to learn more about this phenomenon. The successful applicant is expected to primarily work on two projects: one which aims to molecularly characterize the genetics of a recent reversal in male and female body size, and a second aimed to enhance our understanding of the genomics of condition dependent sexual dimorphism. The successful applicant will also have the opportunity to develop own ideas related to these questions.

We seek a bright, highly motivated and enthusiastic person able to work both as part of a team and independently, having a PhD in evolutionary biology/genetics/genomics. Documented experience in one or several of the following topics is highly beneficial: statistics, quantitative genetics, Drosophila genetics/lab work, bioinformatics, and in particular analyses of RNAseq data. The working language at the department and in the lab is English. A high standard of spoken and written English is required. For further inquiries about the position, please contact Urban Friberg (urban.friberg@liu.se).

Linköping University is a modern university with a vibrant and growing biology division. The university attracts some 27 000 students from all over the world, creating an international and stimulating research environment as well as providing a multitude of opportunities for collaboration and socializing. Linköping is located in central Sweden only a couple of hours by train/car from Stockholm, and have beautiful and easily accessible surroundings.

Applications should be written in English and include i) a cover letter with information on your background, research interests and experiences, and your motivation to work on this project (max 3 pages), ii) complete CV, and iii) the names and email addresses of 2-3 independent referees. Applications should be sent as one PDF to urban.friberg@liu.se. The position is open until filled. Applications will be reviewed continuously, but for full consideration please apply by August 31. Suggested starting date is end of 2016 - early 2017.

"urban.friberg@liu.se" <urban.friberg@liu.se>

LundU SocialEvolution

A postdoctoral fellowship is available for 3 years to work on the evolution of multicellularity

The fellow will work with researchers in the molecular ecology and evolution lab and the aquatic ecology group at the Department of Biology, Lund University.

The position will focus on understanding what predisposes some species to undergo a major evolutionary transition, with particular focus on predicting why species go from being unicellular to multicellular.

Over evolutionary time there have been several major transitions that have shaped contemporary patterns of organismal complexity. In each of these transitions a group of individuals that previously replicated independently joined together to form a new, more complex life form. For example, unicells joined together to form multicellular bodies, asexual organisms combined to reproduce sexually and individual organisms have foregone independence to live in groups.

The project will use a combination of experimental evolution on target groups (e.g. green algae), and comparative analyses of the independent transitions to multicelluarity across the tree of life using genomic, ecological and life-history data. This position will provide the opportunity to explore social evolutionary theory and develop skills in experimental design, bioinformatics, phylogenetic comparative methods and meta-analysis. The post-doc will also be supported by a technician.

The Department of Biology at Lund has a number of research units studying a range of ecological and evolutionary topics including aquatic ecology, microbial evolution, speciation, sexual selection, and host-parasite coevolution, and the post-doctoral fellow will be integrated across these different units.

Description of the qualifications that are required of the candidate

Applicants should have completed a PhD within the fields of Evolution, Ecology or Molecular Biology within four years from application deadline. Candidates should have a keen interest in general evolutionary theory and demonstrate an ability to be work both independently and in teams with other researchers, including co-supervising PhD and MSc students. Experience and skills in the following areas is essential: experimentation using algal and/or other microorganisms, molecular genetic analyses and laboratory work. Experience and skills in the following areas is desirable: bioinformatics, experimental evolution, linear mixed modeling and phylogenetic comparative analysis. Complementary training will be provided where needed.

Fluent written and spoken English is essential with a strong record of publishing in internationally recognized scientific journals. The scientific aptitude and the ability to develop and carry out high-quality research within the subject area will be given special attention in the assessment of the candidate. Importance will be attached to the potential of the candidate to develop as an independent researcher.

Salary will be set according to the general regulations for postdoctoral positions at Lund University in relation to the number of years research experience and achievements. Applicants should send a cover letter explaining their background, research interests and motivation for applying to this position, and a CV that includes publications and the contact information for two referees.

Additional Information

Deadline 15th July 2016

For more information and informal discussion about the position candidates can contact Charlie Cornwallis (charlie.cornwallis@biol.lu.se). Link to position and information about application procedure: https://lu.mynetworkglobal.com/en/what:job/jobID:103762/
Charlie Cornwallis <charlie.cornwallis@biol.lu.se>

MNHN Paris Biogeography

Postdoctoral position in macroecology and biogeography at the MNHN, Paris, France

The Muséum national d'Histoire Naturelle (MNHN, Paris) invites applications for a full-time 2-year postdoctoral position in macroecology and biogeography of phytophagous insects.

The MNHN is a world-class research institution that aims to document and understand global and local biological and ecological diversity, disseminate the results of these studies to a broad academic and non-academic audience, and contribute to high-level education at all stages of the curriculum. The position will be based within the Institute for Systematics, Evolution and Biodiversity (ISYEB UMR 7205 CNRS, MNHN), a research unit hosting more than 90 researchers whose investigations address questions in systematics, evolutionary biology and ecology, biogeography and macroecology on a variety of non-model organisms in all kingdoms of Life.

The successful applicant will work under the supervision of Dr. Rodolphe Rougerie as part of the research program ACTIAS (http://www.cesab.org/index.php/en/projets-en-cours/projets-2014/130-actias), funded by the Center for Synthesis and Analysis of Biodiversity (CESAB). One of the main objectives of the ACTIAS project is to carry out a global-scale macroecological analysis of two of the best-documented families of moths (Sphingidae & Saturniidae), highlighting areas where species diversity and evolutionary distinctness are concentrated and most threatened. It will represent the first such analysis on a global scale for a diverse group of invertebrates (>4500 species; see Ballesteros et al., 2016 [doi: 10.1111/ecog.02438] for an example of what has recently been achieved by members of our consortium on Old-World Sphingidae species), made possible by the wealth of existing diversity, distributional, ecological and phylogenetic information available for these moths, including an almost comprehensive species-level DNA barcode database.

The ACTIAS program is run by an international consortium of 12 researchers (see link above for a list) from five countries. Working under Dr. Rougerie at the MNHN, but in close collaboration with the other members of the ACTIAS consortium, the postdoc will: (1) develop and implement the pipeline for the construction of Species Distribution Models (SDMs) for all databased species; (2) carry out macroecological analyses of relevant measures of diversity (e.g., species richness, evolutionary distinctness, phylogenetic diversity); (3) compare these patterns with those already existing for plants and vertebrates; (4) analyze their fit to current conservation measures, rarely critically examined for invertebrates; and (5) contribute to a synthesis of macroecological patterns and eco-evolutionary analysis of diversification in these moths. The postdoc will lead the assembly of manuscripts in collaboration with members of the consortium and also participate in and contribute to the organization of four consortium meetings (two in 2017 and two in 2018) at the CESAB headquarters in Aix-en-Provence.

Qualifications

We are seeking applicants holding a PhD degree in ecology, macroecology, biogeography or related discipline (e.g., conservation biology, evolutionary ecology), with a solid theoretical background and a strong publication record in these fields, proven expertise in applied and spatial statistics, and with a keen interest in global patterns of insect diversity and in ecological modeling. The ACTIAS database will collate distribution records that have or lack DNA barcodes and will be hosted within the Barcode of Life Datasystems (BOLD; www.boldsystems.org). The postdoc will develop R scripts and pipelines that can be implemented within the BOLD API system. We thus expect applicants to have demonstrable skills in writing R scripts.

In addition, applicants should have: §Expertise in the use of GIS for analysis and visualization; §Fluency in English, excellent communication skills and a willingness to organize and lead workshops/meetings; §Experience in presenting and communicating results at international conferences and through publications in high-quality peer-reviewed journals; §An excellent understanding of biodiversity data management.

Desirable skills include an interest in insect diversity, experience in participating in research programs that analyze large datasets, and a broader coding aptitude (e.g., Python) that would facilitate the integration of analytical pipelines in the BOLD API system.

Conditions of employment

We offer a fully funded, two-year fellowship of 2500 euros/month (gross salary, health insurance included).

Application procedure

Send applications to rodolphe.rougerie@mnhn.fr, as a single searchable

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Montpellier ExptEvolutionaryMicrobiology

A funded postdoctoral position in experimental evolutionary microbiology is open at the CEFE (Centre for Functional and Evolutionary Ecology) in Montpellier, France.

Project: The recruited postdoc will conduct research in the framework of the ERC CoG HGTCODONUSE project. The main goal is to investigate the impact of codon usage preferences on the success of horizontal gene transfer and on post-transfer evolution. The results gathered will in particular help understand the role of codon usage preferences in shaping the routes of antibiotic resistance gene propagation. The project has a strong experimental component, including mutant collection characterization, experimental evaluation of diverse post-HGT compensatory mechanisms, experimental horizontal transfer and experimental evolution of the resulting populations, and will include exhaustive phenotypic and genomic bacterial characterisation. The experimental parts will be conducted on several bacteria species. The experimental core of the project will be completed by modelling and comparative approaches.

Scientific environment: The postdoc will work in the “Evolutionary Genetics and Ecology” team within the Centre for Functional and Evolutionary Ecology (CEFE), Montpellier, France. http://www.cefe.cnrs.fr/-fr/recherche/ee/gee The CEFE is the largest French institute for ecology and evolution. It gathers numerous recognized research groups, particularly in experimental evolution. It also hosts shared platforms with high-level equipment in microbiology, rearing facilities, molecular biology and ecological chemistry. The "Evolutionary Genetics and Ecology" team is a lively, dynamic and stimulating working environment. The group is composed of 10 permanent researchers and 10 to 15 PhD students and postdocs working on a diversity of topics: reproduction system evolution, life-history trait evolution, mechanisms of adaptation, community evolution and antibiotic resistance evolution. Finally, Montpellier is a medium-size lively student city in the south of France, close to the Mediterranean Sea and to the Cevennes (medium mountain with lots of hiking and climbing opportunities).

Profile: We seek a motivated and enthusiastic scientist with a PhD degree in Evolutionary Biology and with knowledge and experience in experimental evolutionary microbiology and bacterial genetics, ready to perform large scale and long-term experiments involving different bacteria species. Experience in experimental evolution and bacterial genomics will be appreciated. Candidates should be fluent in written and oral English.

Application: Application with CV (including a publication list), a brief statement of research interests and contact information for two professional references should be submitted in an electronic form to Stéphanie Bedhomme (stephanie.bedhomme@cefe.cnrs.fr) before August 26th. The expected starting date is January 1st, 2017. The position is open for 2 years, renewable. The salary will depend on past experience with a minimum net salary of 2040 euros/month. Do not hesitate to contact me for further details or questions.

Stéphanie Bedhomme CR CNRS Equipe "Génétique et Ecologie Evolutive" Centre d'Ecologie Fonctionnelle et Evolutive Montpellier

Tel: 00 33 (0)4 67 61 32 11

BEDHOMME Stéphanie <Stephanie.BEDHOMME@cefe.cnrs.fr>

MuseedelHomme Paris HumanPopGenetics

Post-doc in Human Population Genetics, Eco-Anthropology, Paris

A one-year post-doctoral position starting in Fall 2016 is available in the human population genetics group at the Musée de l'Homme (Unit of Eco-Anthropology and Ethnobiology), 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 size 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. The start date is flexible, but should be between October 2016 and January 2017.

To apply, please send a cover letter detailing experience and research interests, a current CV, and contact information for three professional references to chaix@mnhn.fr, romain.laurent.bioinfo@gmail.com and toupance@mnhn.fr before the 20th of August 2016.

Contact: Raphaëlle Chaix, Bruno Toupance, Romain Laurent UMR7206 - Unit of Eco-Anthropology and Ethnobiology Human Population Genetics group Musée de l'Homme 17, place du Trocadéro 75016 Paris France Email: chaix@mnhn.fr, romain.laurent.bioinfo@gmail.com, toupance@mnhn.fr

References

Chaix, R., C. Cao, et al. (2008). "Is mate choice in humans MHC-dependent?" PLoS Genet 4(9): e1000184.

Laurent, R. and R. Chaix (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 R. Chaix (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., B. Toupance, et al. (2012). "Non-random mate choice in humans: insights from a genome scan." Mol Ecol 21(3): 587-596.

Raphaelle Chaix <chaix@mnhn.fr>

Norwich UK EvolutionaryGeneticsGenomics

Genome duplication, gene flow, and adaptation at the John Innes Centre

We seek big-question-oriented postdocs to join us to work on fundamental problems in evolutionary genomics. We offer a highly interdisciplinary environment with outstanding institutional support and funding.

Two ERC grants have just been won by the Yant lab and our very close collaborators, the Bomblies lab (also at JIC). This greatly enhances an ambitious programme in evolutionary genomics in Norwich. Additionally, we have many collaborations with diverse European groups, offering you outstanding potential for professional development. Current projects have an explicitly phenotype-first orientation, aiming to determine the genetic basis and evolutionary repeatability of adaptation to intense, quantifiable selection pressures, both environmental and intracellular. We do this by applying large-scale population genomics to wild plant populations that have evolved to overcome demonstrable hazards. We currently focus on adaptation to genome duplication as well as adaptation to highly challenging, quantifiable environmental stressors in species ranging from Arabidopsis arenosa, to Chamerion angustifolium, to Mimulus guttatus and back throughout the Brassicaceae to A. lyrata and A. thaliana. See http://yant.jic.ac.uk for more.

We strongly encourage applicants suggest project ideas that fit with these general aims and we are fully committed to helping successful applicants develop their ideas for the eventual formation their own independent research groups. Applicants with evolutionary genetic, computational, or molecular interests in adaptation are encouraged to apply. We seek candidates with initiative, analytical skills, and a drive to push forward on new problems in evolutionary genomics. Successful candidates will perform independent, novel analyses and will have demonstrated clear innovation during or following their PhD.

To begin a meaningful conversation, we ask that you include a cover letter and a statement that indicates which research topics in the lab you are particularly interested in, and why your qualifications make you a good fit with our research. This is an essential part of our shortlisting process and as such we are unable to progress applications without this element.

For further information and details of how to apply, please visit our web site, https://www.jic.ac.uk/-training-careers/vacancies/2016/07/postdoctoral-researcher1003083/ Salary on appointment will be within the range 30,500 to 37,500 per annum depending on qualifications and experience. This post is for a contract of 36 months.

Early application is encouraged, but the deadline for application is 30 August 2016.

If interested but wish to apply later, please contact levi.yant@jic.ac.uk

Levi Yant Project Leader John Innes Centre Norwich Research Park Colney Lane Norwich NR4 7UH United Kingdom

http://yant.jic.ac.uk "Levi Yant (JIC)" <Levi.Yant@jic.ac.uk>

OregonStateU MarineEvolBiol

A postdoctoral position is available for a motivated investigator in the lab of Felipe Barreto in the Department of Integrative Biology at Oregon State University, Corvallis, Oregon. Work in our lab examines broad questions in evolutionary biology in marine animals, integrating physiological, behavioral, and biochemical assays with molecular genetics and genomics/transcriptomics approaches. The successful candidate will have the opportunity to participate in work examining the genetics of physiological adaptations and reproductive isolation in the lab's primary study system, the intertidal copepod *Tigriopus californicus*, and will also be encouraged to develop additional projects on new questions and/or new study species within the general area of evolutionary genetics.

Please visit the P.I.'s homepage for more details on the lab's research: http://www.science.oregonstate.edu/~barretof/ The candidate must have a Ph.D. in evolutionary biology or related fields.

Preferred qualifications:

- experience with basic molecular genetic approaches;

- experience analyzing Next-Generation sequencing data, and willingness to learn additional bioinformatic approaches;

- interest in computational analyzes of population genetic and molecular evolution processes.

For a complete description of the position and required/preferred qualifications, visit the job posting at

https://jobs.oregonstate.edu/postings/28258 Corvallis is located in Western Oregon, within the lush Willamette Valley, and close to a multitude of wilderness areas that satisfy all outdoor enthusiasts. The university is also less than 60 miles from outstanding coastal habitats, such as estuaries, bays, marshes, and rocky shores. The Department of Integrative Biology comprises a vibrant mix of evolutionary biologists, ecologists, and organismal biologists, and the university's Center for Genome Research and Biocomputing provides top-notch training and infrastructure resources for genomic and computational analyzes.

Additional information:

Dept. of Integrative Biology: http://ib.oregonstate.edu/ Center for Genome Research and Biocomputing: http://cgrb.oregonstate.edu/ For application instructions, visit https://jobs.oregonstate.edu/postings/28258 For inquiries about the position, please contact Felipe Barreto (felipe.barreto@oregonstate.edu)

Application deadline is July 31, 2016. Start date is flexible, but could begin as early as September 1, 2016.

Felipe S. Barreto

Assistant Professor

Department of Integrative Biology

3029 Cordley Hall

Oregon State University

Corvallis, OR 97331

Felipe Barreto <felipe.barreto@oregonstate.edu>

Paris CaenorhabditisEvolution

Dearall,

Apostdoctoral position for 3 years is available from 1 December 2016 to studythe robustness and evolution of QR neuroblast migration in /C. elegans/and related species, in the laboratory of Marie-Anne Félix at theEcole Normale Supérieure, Paris, France. This position is funded througha HFSP collaborative project, based on the recent finding by the Korswagengroup that QR cell migration is controlled through the timed expressionof a Wnt receptor (see Mentink et al. Dev Cell 2014 < http://www.ncbi.nlm.nih.gov/pubmed/25373777 > for more information).

Ifyou are interested, please send a CV, a statement of research accomplishmentsand interests, and the contact information of three referencesto

< http://www.hubrecht.eu/onderzoekers/korswagen-group/#research >

Marie-AnneFélixâ€

e-mail:felix@biologie.ens.fr

http://www.ibens.ens.fr/?rubrique29&lang=enMicrosporidia-nematode associationsin methane seeps reveal basal fungal parasitism in the deep sea

– Marie-AnneFelix Instituteof Biology of the Ecole Normale Supérieure (IBENS) 46rue d'Ulm, 75230 Paris cedex 05, France 8thfloor. Office: Room 801. Lab: Room 817. mail:felix@biologie.ens.fr Tel:+33-1-44-32-39-44 http://www.ibens.ens.fr/?rubrique29&lang=en STRAINS:http://www.justbio.com/worms/index.php felix@biologie.ens.fr

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Paris EvolutionaryPhylogenetics

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 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 very diverse backgrounds are encouraged to apply (e.g. mathematics, physics, ecology, evolutionary biology, genomics, bioinformatics). Interest/experience in advancing phylogenetic comparative methods, understanding the role of species interactions on (macro)evolutionary dynamics, 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 Institute of Biology of the Ecole Normale Supérieure. The IBENS is a multidisciplinary research centre in Biology with more than 300 staff members, 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>

Pittsburgh EcologyEvolution

The Department of Biological Sciences at the University of Pittsburgh invites applications for a 2-year Postdoctoral Fellowship in Ecology and Evolution– broadly defined–and including the study of biodiversity, community assembly, species interactions, population and landscape genetics, sexual systems, speciation and reproductive isolation, phenotypic, behavioral and molecular evolution. The goal of the EE Postdoctoral Fellowship is to broaden expertise, diversify perspectives, and stimulate synergistic interactions between faculty interested in these fields. The successful candidate will be expected to conduct original independent research that bridges the interests of two or more faculty members in the Ecology and Evolution section of Biological Sciences and to lead a graduate seminar or workshop in their area of expertise each year.

The Ecology and Evolution group is a collaborative environment within the Department of Biological Sciences at the University of Pittsburgh (www.biology.pitt.edu). Pittsburgh, PA is often voted the most livable city in the US featuring eclectic neighborhoods, diverse culinary and entertainment opportunities as well as easy access to natural areas.

Qualified candidates should submit a 2-4 page coherent research proposal to be completed in 2 years and under the guidance of faculty member(s) and a brief description of the proposed course or workshop. The position does not include research funds so the extent of contributions from the faculty sponsors should be addressed in the proposal. We strongly encourage candidates to contact appropriate faculty sponsors before applying. Preference will be given to candidates with novel ideas, demonstrated research ability, and strong communication skills. Along with the research proposal, applications must include a CV, a short description of research accomplishments and a description of how your research, teaching or service demonstrates a commitment to diversity and inclusion. Two recommendation letters from non-UPitt faculty, and letters from the UPitt faculty sponsor(s) should be emailed to the address below. The salary will depend on experience but is expected to be $44,000 per year with a start date as early as October 2016.

Application materials should be emailed to Dr. Tia-Lynn Ashman at: tia1@pitt.edu, and be received by September 1. The subject line should read "EE Postdoctoral application".

Tia-Lynn Ashman Professor Department of Biological Sciences University of Pittsburgh Pittsburgh, PA 15260 (412) 624-0984

"tia1@pitt.edu" <tia1@pitt.edu>

Pittsburgh EvolutionFloralMicrobes

Postdoc in Floral Microbial Ecology at the University of Pittsburgh

A Postdoctoral fellow position characterizing the floral microbiome in diverse flowering plant communities is available in the laboratory of Tia-Lynn Ashman, Department of Biological Sciences at the University of Pittsburgh. Field work will be conducted in various natural and urban settings including Pennsylvania, California, Hawaii, and Germany.

The work will seek to understand the dominant ecological and evolutionary drivers of floral microbiome diversity by linking plant floral traits, biotic community characteristics (plant-pollinator interactions), abiotic habitat, geographic origin and phylogenetic history. Responsibilities include characterizing plant-pollinator interactions; chemical analyses of flower tissues; culture-independent characterization microbial diversity and function (e.g., amplicon sequencing; metagenomics); phylogenetically-controlled and community-level statistical analyses; and preparation of manuscripts for publication. There is also the ample opportunity to design and implement additional projects of mutual interest.

The postdoc position is for two years. Start date is negotiable, but September 2016 is preferred.

QUALIFICATIONS: PhD in biology, ecology, evolution, microbiology or related disciplines conferred by the time of appointment. Record of publication in the peer-reviewed literature; skills and experience in statistics, bioinformatics, microbial ecology, molecular biology and/or pollination biology; demonstrated verbal and written communication skills; self-motivation, critical thinking and problem solving skills; innovative ideas and vision for collaborative research.

TO APPLY: Please send a CV and a description of your experience and interests as relevant to the position to tia1@pitt.edu, along with the names and contact information for three referees. In a covering letter clearly highlight skills and experience related to key responsibilities. Informal enquiries are also welcome!

Review of application materials will begin immediately and continue until position is filled.

Dr. Tia-Lynn Ashman Professor Department of Biological Sciences University of Pittsburgh Pittsburgh, PA 15260-3929 412-624-0984 http://www.pitt.edu/~tia1/ “Ashman, Tia-Lynn” <tia1@pitt.edu>

Portugal EnvironmentalDNAbarcoding

Postdoctoral Fellowship Reference: ICETA 2016-62

Link to the call <Link%20to%20the%20call>: http://www.eracareers.pt/opportunities/index.aspx?task=global&jobId=78023 Main research field: Biological sciences

Scientific area: Entomology and Environmental DNA

Job summary:

One Postdoctoral Fellowship is available at ICETA (CIBIO-InBIO (http://cibio.up.pt)), Portugal, in the field of Applied Ecology, with reference ICETA 2016-62 - Entomology BPD 2016 funded by Catedra EDP.

Admission requirements:

We expect to recruit an enthusiastic and highly motivated researcher with a PhD in biology, experience and solid background in entomology, phylogeography and DNA-barcoding. Candidates should have a solid experience in the taxonomy of insects, mainly freshwater species. Candidates should also master molecular biology techniques including sequencing, using both Sanger and Next Generation Sequencing procedures, and in phylogenetic and species delimitation analysis. Extensive experience in managing databases and in fieldwork is expected. Candidates should have a good publication record in SCI journals in this area, strong networking skills, be good communicators, and speak and write English fluently.

Work plan:

The Post-doc will be dedicated for developing a DNA barcoding reference collection, covering invertebrate taxa occurring in Portugal. The Post-doc will carry out field sampling for collection of specimens, perform the species identification and barcoding, networking with other expert taxonomists and managing this reference database.

Legislation applicable:

Lei nÂº40/2004, de 18 de Agosto (Estatuto do Bolseiro de Investigação Científica) e Regulamento de Bolsas e Investigação da Fundação para a Ciência e a Tecnologia em vigor (www.fct.pt/apoios/bolsas/docs/RegulamentoBolsasFCT2015.pdf) e de acordo com os Estatutos de Bolsa do ICETA aprovados pela FCT.

Work place:

Work will be conducted at mainly in CIBIO-InBIO headquarters, Vairão, Vila do Conde, Portugal.

Duration of the fellowship:

The fellowship will have a duration of 12 months, starting in September 15th, 2016, renewable for similar periods.

Salary:

Monthly stipend is 1.495 according to the stipends established by FCT, I.P. in Portugal(www.fct.pt/apoios/-bolsas/valores). Payment will be made by bank transfer on a monthly basis.

Selection criteria:

The ranking of candidates will result from a global appreciation of the Curriculum vitae, possibly followed by an interview.

Composition of the Selection Jury: Dr. Pedro Beja (president of the selection jury) Dr. Paulo Célio Alves (vowel) Dr. Joana Paupério (vowel) Dr. Simon Jarman (substitute vowel)

Publicity and communication of results:

The ranking of the candidates will be published at a visible and public area of ICETA facilities, and all candidates will be informed about the result of their application by email.

Application deadline:

This call is open between the 19th of July and the 2st of August 2016.

Applications should be sent to bolsas.cibio@cibio.up.pt and will include a motivation letter, a detailed CV, a copy of your degree certificate (or other proof) and the email contact of three referees.

CIBIO-InBIO Divulgação

RBGV Australia AsparagalesSystematics

Postdoctoral Fellow (Asparagales Systematics) - Royal Botanic Gardens Victoria, Australia

An outstanding opportunity exists to fill the role of Postdoctoral Fellow within the Plant Sciences and Biodiversity Division of the Royal Botanic Gardens Victoria, one of Victoria's premier scientific and cultural organisations. The National Herbarium of Victoria is the major centre for taxonomic and systematic botanical studies in Victoria and the collection of approximately 1.2 million plant specimens is one of the largest and most important in Australia.

This exciting project is focused on non-orchid Asparagales systematics and will investigate the evolution and historical biogeography of Australian lineages; examine interspecific relationships in species complexes of Lomandra; and revise the taxonomy of these groups. The project will be based at the Royal Botanic Gardens Victoria (RBGV) and will be co-supervised by Dr D. Murphy (RBGV) and Dr J. Birch (The University of Melbourne) in collaboration with Dr J. Conran (The University of Adelaide) and Dr J.C. Pires (University of Missouri). The project is supported by an ABRS (Australian Biological Resources Study) grant for an initial period of 2 years.

The successful candidate will have a PhD in Botany (or equivalent field) and demonstrated experience studying the evolution of large and complex lineages drawing on molecular, morphological, and geographic data. It is essential to have research experience generating DNA sequence data, including the application of Next-Generation Sequencing techniques, and demonstrated proficiency in conducting evolutionary analyses.

Excellent written and oral communication skills are also essential in order to communicate effectively with colleagues, the public, international and national researchers, and successfully prepare results of research for publication.

How to Apply

If you are interested in this role please send your resume and letter, addressing the key selection criteria, to the Royal Botanic Gardens Victoria's website at http://www.rbg.vic.gov.au/about-us/job-opportunities or http://jobs.careers.vic.gov.au (Position reference number: VG/N0263D1) and press the 'Apply Now' button.

Applications required by COB Monday 8th August, 2016. For any enquiries about this opportunity or to find out more about the role please contact Daniel Murphy, Molecular Systematist, Plant Sciences and Biodiversity, Royal Botanic Gardens Victoria, at: email daniel.murphy@rbg.vic.gov.au, or Joanne Birch, Herbarium Curator, School of BioSciences, The University of Melbourne at: email joanne.birch@unimelb.edu.au; ph +613 8344 5040.

Applications will only be accepted through the Victorian Government website.

For a copy of the Position Description please visit: http://www.rbg.vic.gov.au/about-us/job-opportunities Jo Birch <joanne.birch@unimelb.edu.au>

RiceU HuxleyFellowship

Dear colleagues– Please circulate this opportunity among early-career (finishing PhD and early postdoc) ecologists and evolutionary biologists.

The application page isn't live yet. Folks can contact me for more info.

Tom

HUXLEY FELLOW in ECOLOGY & EVOLUTION: BioSciences at Rice University seeks to fill two positions in the prestigious Huxley Fellow Program in Ecology and Evolutionary Biology

(http://biosciences.rice.edu/Content.aspx?id=-2147484167) starting in January 2017. Huxley Fellows are outstanding early-career scientists who pursue their own independent research programs in ecology and/or evolution while teaching at the graduate and undergraduate levels.

Huxley Fellow appointments are for two years with a third year extension possible. We seek candidates with a Ph.D. and outstanding potential in research and teaching, who can contribute through their research and teaching to the inclusive excellence of the Rice academic community.

Huxley Fellows receive non-tenure track faculty status, benefits, competitive salary, and research funds. Application instructions are under the employment section on the department website, http://biosciences.rice.edu. Application review will begin August 22, 2016.

For informal inquiries, contact Dr. Tom Miller (Tom.Miller@rice.edu), Huxley Fellow Search Committee Chair.

Rice is a private university with a strong commitment to the highest standards of research and undergraduate and graduate education. Rice University is an Equal Opportunity/Affirmative Action employer, committed to excellence through diversity and inclusion. In this spirit, we particularly welcome applications from women and members of historically underrepresented groups who bring diverse cultural experiences and who are especially qualified to mentor and advise all members of our diverse student population. The university will provide reasonable accommodations to individuals with a disability.

Tom E.X. Miller, Ph.D.

Godwin Assistant Professor

Program in Ecology and Evolutionary Biology

Department of BioSciences

Rice University

Tom Miller <tom.miller@rice.edu>

RutgersU EcolEvolAutomaticID

Title: RutgersU.EcolEvolAutomaticIDPostdoc

Postdoctoral position. Evolutionary ecology & biodiversity informatics

Dept. Biological Sciences, Rutgers University, Newark, New Jersey

One two-year postdoctoral position is available as part of an NSF grant (no. 1564386). This is a collaborative project between the University of Alabama, University of Tennessee, and Rutgers University-Newark, but the postdoc will work primarily in Jessica Ware's Lab at Rutgers. Ware and her affiliates work on insect evolution and systematics, with additional ecology-focused projects ongoing. The project at hand focuses on automatic species identification of dragonflies and damselflies. The postdoc will design and implement comparative studies of Odonata (dragonflies and damselflies) using morphological data, while supervising a multi-person team, and utilizing in-house software for automatic species identification and automatic phenotyping. There is a possibility of (optional) travel to University of Alabama and University of Tennessee.

Required qualifications:

* a PhD in any biological field,

* a strong interest in and enthusiasm for organismal biology,

* good skills in technical writing and communication,

* experience working in a collaborative environment,

* experience with statistical analysis,

* familiarity with programming (R, Python, etc.) or an interest in learning these skills.

Encouraged, but not required, qualifications:

* a background in morphological systematics,

* skills in Python coding,

* an interest in Odonata and/or other arthropod taxa, and

* a familiarity with methods in machine learning and computer vision.

Review of applications begins immediately and will continue until the positions are filled. Starting dates are flexible and salary is $44,000 with a cost-of-living increase the 2^nd year.

To apply, please submit:

i) a cover letter summarizing your research interests and expertise,

ii) your Curriculum Vitae (including publications), and

iii) names and contact information for at least two references.

Questions and application should be sent to Jessica Ware (jware42@andromeda.rutgers.edu).

Jessica Ware <jware42@andromeda.rutgers.edu>

Dr. Jessica L. Ware Associate Professor Rutgers, the State University of New Jersey Boyden Hall, room 406 195 University Ave, Newark, NJ, 07102, 973.353.5531 A word after a word after a word is power." -Margaret Atwood

Jessica Ware <jware42@andromeda.rutgers.edu>

RutgersU EvolutionOfGeneExpression

We are looking for two brilliant, motivated, and adventurous individuals to join the Shah Lab (theshahlab.org) at Rutgers University as postdoctoral researchers.

What we do:

We generate high-throughput genomic datasets and use computational models to study 1. How patterns of gene expressions evolve and how various factors influence the dynamics of protein synthesis in cells. 2. How epistatic interactions between mutations affect protein evolution.

What will you get to do:

We are not looking for someone to work on specific projects ongoing in the lab. Rather,

you will have the freedom to work on your best ideas that are aligned with the lab's research focus. You will also have several opportunities to collaborate with researchers both at Rutgers and elsewhere on your ideas and other projects of mutual interests. In addition, you will have opportunities to mentor students and co-teach classes, if you so desire.

Finally, you will get the resources and support to develop your own research program as you plan to move to the next stage of your career.

What is expected of you:

Good writing and speaking skills to communicate and convince others of your research ideas, and a drive to see them to completion. You should be willing to collaborate freely and be open to give/take constructive criticism. You should also be willing to teach/share tricks and tools you picked up in grad school with the rest of the group.

What to expect:

Environment:

A fun, supportive environment - both in the lab and the Genetics department. Lab and office space in a fancy new-ish building and quiet workspaces when needed.

Coffee:

Coffee is serious business in the lab. You will have access to the finest beans from micro-roasters across the country for amazing espressos, lattes and pour-overs. Because we are an inclusive bunch, tea drinkers will also be tolerated.

Compensation:

Let's face it, postdoc pay sucks. Salaries will be based on NIH scales with some flexibility depending on the funding level of the lab at the time. In addition to medical and life insurance, Rutgers offers not-too-shabby retirement benefits.

Advice/Mentoring/Support:

In addition to being your scientific mentor, my primary responsibilities would be towards your personal and professional growth. You will always find an audience to discuss opportunities and challenges, and a strong advocate for your interests.

Desired Qualifications:

A Ph.D. in evolution, genetics, or statistics. In rare cases we will also consider individuals with a Ph.D. in mathematics or physics.

How to apply:

Fill out the form here - https://goo.gl/sNO5pq Thanks, Premal

Premal Shah Assistant Professor Department of Genetics Rutgers University http://theshahlab.org Premal Shah <premal.shah@rutgers.edu>

TelAvivU IrisFlowerColorEvolution

The Sapir Lab at Tel Aviv University, Israel, is looking to hire a postdoctoral fellow to join an ISF-funded project on the evolution of flower color in the irises of section Oncocyclus. Research in the lab encompasses plant ecology, conservation, molecular ecology and some crazy ideas about plant-pollinator interactions. Our questions are centered on understanding ecological determinants of floral trait evolution and identifying the mechanisms that underlie changes in floral traits (see lab research page).

The postdoc will lead research aimed at linking genotype and phenotype of pigment synthesis genes and their associated floral color, and estimating natural selection on floral color in natural and artificial settings. The study is in the Middle-Eastern endemic Oncocyclus species of the genus Iris. These plants are unique by their highly diverse floral color, from white and light pink to purple and black. Also distinctive is the extreme dark colors of the flowers, shown to be associated with heat reward to the pollinators (See Sapir et al., 2005, 2006).

This project builds on previous contrasting studies, one suggesting that dark-colored flowers are favored by the pollinators of the irises (Sapir et al., 2006), while the other (Lavi & Sapir, 2015) showed no pollinator-mediated selection on flower color in two species. In order to solve this puzzling contradiction, we will employ a series of tests, including accurate measure of color variation, measuring both male and female fitness, and by stretching the natural variation by (a) using the large Iris collection in the botanical garden, (b) measuring natural selection on color in the two most diverse populations, one coastal and one in the desert, and (c) building artificial flowers of irises and printing 3-D flowers in the shape of irises in various colors.

The project includes also the identification of genes underlying anthocyanin pigment synthesis, verification of their biochemical activity and measure their expression in natural population. this will enable to connect the molecular level with ecological effects, to understand the evolutionary process governing color evolution in flowers. Till now, this was done in model plants with discrete color morphs (Petunia, Mimulus...). This project will be the first to use CONTINUOUS flower color, which gets to extreme dark (black) flowers.

Qualified candidates will have a PhD in biology or related disciplines and a strong publication record. Experience in plant biochemistry/ development/ molecular biology and/or analysis of next-generation sequence data is a plus. To apply for the positions, please send a brief letter of interest (1-2 paragraphs), a CV, and the names and contact information for three references to Yuval Sapir, sapiry@post.tau.ac.il. The position is available for 1 year with the possibility of renewal for up to two additional years depending on research progress. The start date is flexible, but could be as early as November 1st, 2016. Review of applications will begin on August 24, 2016 and will continue until the position is filled.

Yuval Sapir, PhD Director, The Botanical Garden Senior lecturer Dept. of Molecular Biology and Ecology of Plants Tel-Aviv University, Tel Aviv, 69978 Israel Tl: +972(0)3-6407354 (lab); +972(0)54-7203140 (mobile)http://botanic.tau.ac.il/http://labsapir.wix.com/labsapir Stop population growth for a sustainable future http://www.populationmatters.org/ sapiryuval@gmail.com

TempleU TheoreticalEvolutionaryGenomics

Postdoctoral opportunity available in the brand new research of group of Dr. Joshua Schraiber at Temple University. Work in the group covers the full stack of computational genomics: pen and paper theory, statistical methods development, and application to data. An ideal candidate would be well versed in population genetics, statistics and/or programming, as well being independent and comfortable directing their own research. Possible research projects include development of methods to take advantage of ancient DNA for demographic inference and detection of natural selection or development and application of models of evolution of molecular phenotypes (e.g. gene expression, chromatin accessibility, DNA-protein interactions). Several long-standing collaborations with empirical groups will provide first-chance access to high quality, interesting datasets. The group is embedded in the Center for Genetics and Genomics (CCGG) as well as the Institute for Genomics and Evolutionary Medicine (iGEM). Between iGEM and CCGG, a postdoc would be able to interact with a variety of people at the forefront of computational evolutionary genomics, including Sudhir Kumar, Jody Hey, Blair Hedges, Ananias Escalante, Masatoshi Nei, Sergei Pond, David Liberles, Rachel Spigler and Rob Kulathinal. CCGG offers training opportunities for postdocs intersted in careers in both academia and industry. Temple University is also well situated near other campuses with exciting work going on in evolutionary genomics, making it an ideal location for a postdoc to forge connections and collaborations. Interested applicants should send a CV and a brief (i.e. one paragraph) statement of interest to Joshua Schraiber (joshua.schraiber@temple.edu).

"tug85527@temple.edu" <tug85527@temple.edu>

TrentU 2 EvolBiol

PhD position or Post-Doctoral Fellowship investigating carnivore responses to landscape heterogeneity - Trent University

We are currently seeking a highly motivated PhD student or Post-Doctoral Fellow to examine relationships between landscape heterogeneity and physiological, genetic, and genome-level variation in carnivores. Building on our 35,000+ repository of wolf, coyote, fox, lynx and bobcat fur and tissue samples, we aim to determine how carnivore stress levels, diet breadth, and genetics vary according to environmental factors like climate, habitat, or anthropogenic activity. There is further opportunity to investigate processes underlying spatio-temporal variation in patterns of dispersal and population connectivity, and the contribution of environmental variability and intrinsic features of the individual animal to such processes. Of particular interest is the role of climate change on stress levels and diet breadth, as well as potential variation in functional genes especially in environments undergoing rapid change. Our recent work (mostly on lynx and coyotes) sets the foundation for this work, and our next challenge is to develop a more comprehensive understanding of physiological-dietary-genetic linkages across carnivore species and through space and time. Our team has access to abundant samples and state-of-the-art analytical facilities and equipment to address these research questions, and the successful candidate will have the opportunity to develop his/her own research interests within the scope of the broader program.

Applicants must have a strong academic record and graduate degree(s) in Biology, Physiology, Ecology, Genetics or a related field. Candidates with an interest in and/or knowledge of hormone assays, stable isotope analysis, DNA extraction, bioinformatics, or other relevant procedures, will be highly sought. Candidates should demonstrate evidence of research potential (including scientific publications), a strong work ethic, and willingness to work in a large, dynamic, and collaborative research environment. The funding package is competitive and will include a foreign tuition waiver, if the successful applicant is an international PhD student.

The position will be offered through an NSERC CREATE program in Environmental Monitoring and Assessment (www.create-enviro.ca). The position will be closed as soon as a suitable candidate is found, so apply early! To apply, please submit: cover letter, unofficial transcripts, curriculum vitae, and names of three references to: Dennis Murray (dennismurray@trentu,ca; www.dennismurray.ca).

PhD position or Post-Doctoral Fellowship investigating mechanisms underlying the plasticity of amphibian responses to environmental stressors - Trent University

We are currently seeking a highly motivated PhD student or Post-Doctoral Fellow who will examine mechanisms governing the effects of environmental stressors on phenotypic and behavioural plasticity in amphibian models. Building on our longstanding research on amphibian responses to environmental stressors (including disease, predation risk, and contaminants), we aim to further establish a mechanistic link among ecological, physiological, and genome-level responses in amphibian tadpoles to natural or human-caused stressors. We are especially interested in building a bioinformatics approach to help identify the mechanisms involved in stressor-induced phenotypic and behavioural plasticity. Our preliminary work indicates differences in gene expression that are related to tadpole exposure to different stressors, and our next challenge is to establish the functional link between expressed genes and type of stressor. Our team has access to state-of-the-art facilities and equipment allowing us to address these cutting-edge research questions, and the successful candidate will have the opportunity to develop his/her own research interests within the scope of the broader program.

Applicants must have a strong academic record and graduate degree(s) in Biology, Physiology, Ecology, Genetics or a related field. Candidates with an interest in and/or knowledge of bioinformatics platforms/resources, experience in extracting genetic material or other relevant lab procedures, and conducting lab experiments with larval amphibians, will be highly sought. Candidates should demonstrate evidence of research potential (including scientific publications), a strong work ethic, and willingness to work in a large, dynamic, and collaborative research environment. The funding package is competitive and will include a foreign tuition waiver, if the successful applicant is an international PhD student.

The position will be closed as soon as a suitable candidate is found, so apply early! To apply, please submit: cover letter, unofficial transcripts, curriculum vitae, and names of three references to:

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Tuebingen Germany GenomicsBehavior

Postdoc Position in evolutionary genomics of behaviour

The application deadline for below postdoctoral position has been extended till July 8, 2016

University of Tübingen, Institute of Evolution and Ecology, Group of Comparative Zoology

We have an open position (2 years) for a PostDoc with a strong interest in the genetic/genomic basis of phenotypic traits. In a project related to the genetic basis of behavior, we will use already available phenotypic data on personality and cognitive traits from a captive population of European harvest mice to search for genetic variation that correlates with behavioral profiles. We seek a candidate with strong molecular lab skills, including Sanger and next generation sequencing, and strong bioinformatics skills, preferably with training in genome wide association studies. A theoretical background in the evolutionary genetics of behaviour would be an asset.

Tübingen University offers a large community of researchers working in the field of evolution and ecology of model and non-model systems, joined together in the Institute for Evolution and Ecology (https://www.uni-tuebingen.de/en/faculties/faculty-of-science/departments/bi ologie/institute/evolutionecology.html). The successful candidate will join the Comparative Zoology group of Katharina Foerster. We offer molecular lab facilities within the group and through collaborations with the Max Planck Institute Tübingen. Further lab support and computational facilities are available through the Quantitative Biology Center on campus (http://www.uni-tuebingen.de/en/facilities/zentrale-einrichtungen/quantitati ve-biology-center-qbic.html).

The working language in the group is English. However, for teaching and everyday life at the University and in Tübingen, some knowledge of German or the willingness to learn the language will be advantageous.

Founded in 1477, Tübingen University has influenced the historical town significantly. Tübingen today remains a place of research and teaching. In addition to the 85.500 inhabitants, there are some 28.300 German and international students. 450 professors and 4.400 other academic staff teach at the University's seven faculties. Tübingen offers a lively mix of shops, bars, and restaurants. Urban parks, nearby nature reserves, as well as the Swabian Jura and the Black Forest offer outdoor recreation. Tübingen is well connected via bus and local trains to Stuttgart and its airport. The Welcome Center of the university provides service and support for international researchers: https://www.uni-tuebingen.de/en/international/international-scholars.html Applications are being accepted immediately. Review of applications submitted before the initial deadline has started; the extended deadline for applications is July 8, 2016. Intended starting date is September 1, 2016. Applications should include a current CV (specifying training in relevant methods and applications), along with a cover letter that provides a short statement of research interests (maximum three pages) and contact information for three references. Applications should be submitted by email as a single file attachment to henri.thomassen@uni-tuebingen.de, with the subject line: Postdoc. Informal inquiries can be sent to katharina.foerster@uni-tuebingen.de.

Henri Thomassen <henri.thomassen@uni-tuebingen.de>

UAarhus Denmark MegafaunaEvolutionFunction

Open 2-yr postdoc at Section for Ecoinformatics & Biodiversity, Department of Bioscience, Aarhus University < http://bit.ly/ecoinfAU > on evolution of megafauna functional diversity in mammals. Experience in ecoinformatics and advanced analyses of large macroevolutionary data sets as well as with paleobiology is expected. See additional details and application procedure here: <

http://bit.ly/mamevoPD >. Information about Aarhus can be found here: < http://bit.ly/AarhusES >.

The main supervisor will be Prof. Jens-Christian Svenning. Other collaborators include: prof. Felisa A. Smith (University of New Mexico, US), prof. Chris E. Doughty (Northern Arizona University, US) and postdoc Søren Faurby (National Museum of Natural History, Spain).

Contact Jens-Christian Svenning <svenning@bios.au.dk> with questions.

bob.muscarella@gmail.com

UBirmingham 2 EnvironmentalOmics

Two JOBS: Research Fellows in Environmental Omics

Two 36-month postdoctoral research fellowships (bioinformatics, computer scientist) in Environmental Omics are available within the School of Biosciences and the Centre for Computational Biology at the University of Birmingham, UK.

"Cracking the Code of Adaptive Evolution" (dCODE) is a multidisciplinary collaboration among seven investigators at the University of Birmingham who form a vibrant research community to advance the field of environmental omics. We pursue foundational science using natural populations of the ecologically relevant model species Daphnia. This project seeks to discover the relative contributions of phenotypic plasticity, the epigenome, and of molecular evolution to the process of adaptation, by experimenting on an historical Daphnia population that is "resurrected" from dormancy spanning 100 years of evolution.

1. The bioinformatics candidate will contribute to the planned research by (1) locating loci under selection in the sequenced genomes from >100 natural isolates, (2) identifying regulatory elements affected by the changing environmental conditions; and (3) discovering Quantitative Trait Loci (QTL) that control variation in global mRNA and metabolic products (eQTLs and veQTLs) that co-associate with adapted traits and condition-dependent expression. The ideal candidate will: (i) understand theoretical underpinnings of sequence alignment algorithms for next generation sequencing (NGS) data; (ii) have proven experience in NGS analysis in genome re-sequencing, RNA-seq, Chip-seq, metabolomics or related data; (iii) have knowledge of data visualization methods and of bioinformatics resources such as annotation tools and databases; (iv) have knowledge of methods and approaches at data integration; and have a strong statistical genetics background and experience at discovering QTLs.

2. The computer scientist candidate will work at (1) integrating the muti-omics data to identify co-regulated genes and co-responsive genes and other elements, and (2) predicting candidate networks and pathways relevant to adaptive change. The ideal candidate will: (i) have experience in applying statistical machine learning algorithms (Random Forests, Deep Learners, MARS, etc.) and to large, high-dimensional datasets and be familiar with complex (including multi-layer / tensor) network analysis; (ii) be proficient in R/BioConductor and High level (e.g. python) programming (low / mid level C, C++, JAVA programming is considered an advantage); (iii) have experience at database (SQL, PostgreSQL, or similar) development and at maintaining code repositories (version control, GitHub); (iv) have UNIX expertise including file systems, shell, hardware/software monitoring etc., with working knowledge of batch processing in a high performance computing environment.

Applicants must hold a PhD-degree with substantial experience in Bioinformatics, Mathematics, Statistics and/or Computer Sciences. Some background in molecular biology, omics technologies and/or quantitative genetics, evolutionary ecology and/or evolutionary biology is considered an advantage.

Pay Grade 7: 28,982 to 37,768. With potential progression once in post to 40,082 a year.

The application must include:

* Application letter including a statement of interest, summarizing your scientific work and how well you fit with the project * CV * Complete list of publications, and copies of 2 best peer-reviewed publications * Names and contact details of 3 references

Applications are made at the University of Birmingham jobs webpage: Research Fellow - 55534

Informal enquiries about this post can be addressed to Professor John Colbourne by email (J.K.Colbourne@bham.ac.uk) or Dr Luisa Orsini (L.Orsini@bham.ac.uk).

Dr Luisa Orsini Lecturer in BioSystems and Environmental Change Environmental Genomics Group, School of Biosciences, University of Birmingham Birmingham, B15 2TT, United Kingdom T: +44 (0)121 4145894 F: +44 (0)121 414 5925 Email: l.orsini[at]bham.ac.uk

http://www.birmingham.ac.uk/schools/biosciences/-staff/profile.aspx?ReferenceId=63090&Name=dr-luisa-orsini https://www.researchgate.net/profile/-

Luisa_Orsini Luisa Orsini <l.orsini@bham.ac.uk>

UBourgogne QuantGenetics

Postdoc position for a year in quantitative genetics and geometric morphometrics to participate in an ongoing research project on the identification of loci implied in shape variation using outbred mice.

Project-

Two age cohorts (weaning and sexual maturity) from a population of 500 mice having experienced different uterine environments have been genotyped at 150 000 SNPs. The skull morphology is being acquired using X-ray microtomography and will be analyzed using geometric morphometrics. The project aims at identifying the loci controlling the variation in this population and their interaction with the uterine environment.

The postdoc will work in the Biome team of the Biogeosciences laboratory in Dijon, France.

Starting date should be before December 31, 2016.

Feel free to contact me for more information.

Nicolas Navarro

Nicolas Navarro Biogeosciences, UMR CNRS 6282 Univ Bourgogne Franche-Comte EPHE, PSL Research University F-21000 Dijon, France

tel - +33 (0)380 39 64 48 fax - +33 (0)380 39 63 87

"nicolas.navarro@u-bourgogne.fr" <nicolas.navarro@u-bourgogne.fr>

UCalgary GenomicsAdaptation RESEND

Dear Evoldir:

I have posted two ads for postdoc positions over the past few months. Unfortunately, there was a hacking incident here at University of Calgary and as a result I have lost all my old emails, including some applications for the positions. If you previously applied for one of these positions and haven't heard from me, please contact me to double check that I still have your application. Otherwise, I am currently reviewing applications, so please contact me if you're interested!

My apologies for the problems this has caused,

Sam Yeaman

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Postdoctoral positions: Genomics of local adaptation Yeaman Lab

Department of Biological Sciences, University of Calgary

I am looking to hire two postdoctoral fellows to collaborate on projects studying how patterns in the genome evolve during local adaptation:

1. Genomic rearrangements and local adaptation: This project will develop and use comparative genomic approaches to study whether rearrangements have contributed to the evolution of clusters of functionally related genes (genomic islands, metabolic clusters, etc.). We are currently working on an assembly of the tubesnout genome (a relative of stickleback) as a means of studying if/where/when rearrangements have contributed to the evolution of clustered architectures observed in the stickleback. We will also be exploring patterns in a range of already-assembled genomes, and there is some budget flexibility to play around with new ideas. Good bioinformatics and R-scripting skills will be very important, ideally with experience in comparative genomics.

2. Genomics of local adaptation to abiotic stress in sunflower: For this project, we will be studying whole genome sequence data from over 600 individuals, searching for associations with environment and signatures of selection, and developing new methods for data analysis. It is a large-scale collaboration with Loren Rieseberg and John Burke, funded by Genome Canada. Experience managing and analyzing NGS data, GWAS, and related approaches would be ideal, coupled with strong R & unix skills.

Positions will run for 2+ years (CAD $50k salary).

TO APPLY: Please send a CV and a short description of your interest in the position to samuel.yeaman at ucalgary.ca, along with the names and emails of three people I could contact for reference letters. I will begin reviewing applications on July 1st, 2016, but please contact me to check in if you need to make a quick decision. I will be at SSE and CSEE this summer, so please get in touch if you'd like to chat with me about it then!

Samuel Yeaman <samuel.yeaman@ucalgary.ca>

UCalifornia LosAngeles OakGenomics

Post doc opening: UCLA Adaptation genomics of oaks We have a post-doc opening to join a research team studying the genomics of valley oak through a project funded by the NSF Plant Genome Research Program. The overall goal of the project is to provide a complete, high-quality sequence of the valley oak genome with structural and functional annotations of genic regions and repetitive elements. The postdoc for this position will play a major role in the annotation component of the project by focusing on genes associated with local adaptation and response to climate change. In particular, the post-doc will design gene expression experiments that utilize to greenhouse, growth chambers, and two common gardens of ca.7000 trees planted at two sites maintained by the US Forest Service. The post-doc should be willing to assist in outreach projects and/or student training.

The post-doc will work in the laboratory of Victoria Sork at UCLA and join a collaborative multi-institutional team that includes Steven Salzberg (Johns Hopkins University Center for Computational Biology), Matteo Pellegrini (UCLA Institute of Quantitative and Computational Biosciences), and Paul Gugger (University of Maryland Center for Environmental Sciences, Appalachian Laboratory). For more details of the project see the valley oak genome project website: valleyoak.ucla.edu.

The applicant should possess a PhD or equivalent in the biological sciences, preferably with empirical, analytical or bioinformatics training in molecular or evolutionary genetics. Previous experience in molecular techniques, next-gen sequence analysis, and variant calling are preferable. Candidate should have a research track record with relevant publications in peer-reviewed journals. Interest in plant evolutionary biology or evolutionary genomics of local adaptation is desirable.

This position will begin January 2017 (flexible), and with possibility of renewal, based on performance. Applicants should email their CV, pdf's of 3 publications, statement of research interests, and email information for three referees to sorklab@gmail.com. Cover letter should include a short personal statement describing your research experience and interests that would match this project. Please also include any outreach activities or other broader impacts associated with your previous research or education.

Review of applications will begin September 1, 2016 and continue until position is filled. For informal queries, please contact Victoria Sork by email, vlsork@ucla.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.

"Sork, Victoria" <vsork@college.ucla.edu>

UCalifornia SanDiego EvolutionDevelNetworks

A postdoctoral position on the evolution of genetic networks and development is available starting as soon as Sept 1 2016 in the lab of Scott Rifkin at UC, San Diego.

There are two potential research projects:

The first uses the Caenorhabditis genus as a model system for studying the phenomenon of morphological stasis or robustness.Caenorhabditis worms are famous for their highly stereotyped and invariant pattern of development, but beneath this is a substantial amount of genetic change.The project would focus on the mechanics and evolution of developmental decisions in early embryogenesis and involve single molecule resolution measurements of gene expression, 4-D microscopy, and, potentially, mathematical modeling.

The second project investigates how genetic networks are organized so as to buffer or amplify stochastic, genetic, and environmental variation.The focus will be on the evolution of the dauer decision, a ecologically and evolutionarily crucial life-history decision in Caenorhabditis where all three types of variation of variation play a role. Techniques would involve microfluidics, microscopy, image processing, and genetic engineering, and, potentially, mathematical modeling and experimental evolution.

Candidates must have an experimental background, ideally with worms. As both projects involve substantial analysis of microscopy images and variation, experience in programming, image analysis, and/or statistics are preferred.Only candidates with lead authorship on at least one substantial published project will be considered.

Our group is located on the campus of University of

California, San Diego, in the Division of Biology, Section of Ecology, Behavior, and Evolution (EBE).UCSD has a strong reputation for quantitative biology and a thriving worm research community, and EBE has a particular strength in experimental evolution.

If you are interested, please send a CV, a statement of research interests, copies of relevant publications, and the names and contact information of at least two references to Scott Rifkin at <sarifkin@ucsd.edu>.The position has a target start date of September 1, 2016, but is flexible.

"sarifkin@ucsd.edu" <sarifkin@ucsd.edu>

UChicago Marcoevolution

Postdoc in Macroecology/Macroevolution, University of Chicago

Seeking a postdoctoral scholar to participate in an ongoing collaborative research project (D. Jablonski-K. Roy-J. W. Valentine) on the origin and maintenance of trait and functional diversity in time & space. Marine bivalves will be used as a model system due to their excellent fossil record, ecological diversity, highly resolved taxonomy and increasingly refined phylogenies. Research involves quantifying biogeographic and morphological patterns of fossil and modern taxa, quantifying the Cenozoic spatial and evolutionary dynamics underlying them, and relating these patterns to environmental change, past, present, and future.

Postdoctoral scholar will assist in data collection (literature and museums), analysis, and modeling of diversity dynamics, and will take the lead on some new research projects. Experience in some combination of modeling, statistical, morphometric, and spatial (GIS) analyses and/or database management required.

One-year appointment renewable for one or more additional years. Starting date negotiable but prefer early fall 2016. Requires either Ph.D. in hand or dissertation submitted and approved for degree.

Please email a letter documenting research interests and experience, a CV, and the email addresses of two references to Dr. David Jablonski (djpostdoc@geosci.uchicago.edu) at the University of Chicago. Applications required by August 31, 2016 for full consideration.

All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, age, protected veteran status or status as an individual with disability.

The University of Chicago is an Affirmative Action/Equal Opportunity/Disabled/Veterans Employer.

Kaustuv Roy <kroy@ucsd.edu>

UConnecticut HorizontalGeneTransfer

University Postdoctoral Fellow

The Noll Lab in the Department of Molecular and Cell Biology of the University of Connecticut is seeking a talented, motivated and hard-working University Postdoctoral Fellow to participate in a 1-year NASA-funded project to examine the process of bacterial gene acquisition by horizontal gene transfer in laboratory evolution experiments.

Minimum Qualifications: A Ph.D. degree in Microbiology or related field with previous experience in bacterial or archaeal molecular genetics research, including constructing chromosomal mutants of bacteria or archaea, designing genetic selections and screens, genomic sequencing and data analysis, and constructing sequence-based evolutionary phylogenies. Experience with cultivation of strictly anaerobic microbes is highly desirable. A demonstrated ability to work independently is essential and the successful applicant will be expected to take the lead role on the assigned projects under the supervision of the P.I. Excellent English writing and oral communication skills are required and the postdoc will be expected to participate in efforts to secure future funding for the project.

To Apply: Interested applicants must apply by sending a single PDF file containing a (1) cover letter, (2) CV, (3) one-page statement of research accomplishments and demonstration of the minimal qualifications described above, and (4) contact information for three references via the UConn Careers Website (www.jobs.uconn.edu). Review of applications will begin immediately and continue until the position is filled. Employment of the successful candidate will be contingent upon the successful completion of a pre-employment criminal background check. Anticipated start date is September 1, 2016 or shortly thereafter.

All employees are subject to adherence to the State Code of Ethics which may be found at http://www.ct.gov/-ethics/site/default.asp . The University of Connecticut is committed to building and supporting a multicultural and diverse community of students, faculty and staff. The diversity of students, faculty and staff continues to increase, as does the number of honors students, valedictorians and salutatorians who consistently make UConn their top choice. More than 100 research centers and institutes serve the University's teaching, research, diversity, and outreach missions, leading to UConn's ranking as one of the nation's top research universities. UConn's faculty and staff are the critical link to fostering and expanding our vibrant, multicultural and diverse University community. As an Affirmative Action/Equal Employment Opportunity employer, UConn encourages applications from women, veterans, people with disabilities and members of traditionally underrepresented populations.

"Noll, Kenneth" <kenneth.noll@uconn.edu>

UEasternFinland EvolutionarySalmonidEcol

Link to full job ad: http://www.uef.fi/en/uef/en-open-positions We are now inviting applications for the position of a

Postdoctoral Researcher in Evolutionary Fish Ecology

A postdoctoral position for 2 years (2017-2018) is available at the University of Eastern Finland, Department of Environmental and Biological Sciences (Joensuu campus).

We announce a post doc position in the project "Evolutionary restoration of trout populations impacted by human-induced selection", funded by the Academy of Finland. The project aims to reveal the genetic basis of vulnerability to angling and pace-of-life syndromes especially with respect to migration behaviour in endangered brown trout through artificial breeding, behavioural experiments and RAD-sequencing. The project ultimately aims to provide tools to mitigate harmful fishing- and hatchery-rearing induced evolutionary changes.

We encourage applications from highly motivated, mobile international candidates with demonstrated publishing skills and interest on evolutionary genetics, animal personality research and fishing/hatchery- induced evolution. We expect the successful candidate to be fluent in English. The chosen person must be able to participate in teaching courses relating to evolutionary ecology, genetics or fish ecology. The teaching takes at maximum 5-10% of the annual 1600 hour working time.

The main duties of the Postdoctoral Researcher will be to:

- Develop experimental (and / or genetic) research on artificially selected experimental brown trout strains

- Take responsibility in conducting experimental work together with PhD and MSc students

- Publish the results as high-quality articles in leading international scientific journals.

Candidates are expected to have a strong background in evolutionary and behavioural ecology or in bioinformatics and genetics. At minimum basic knowledge of fishing and hatchery induced evolution is a necessity. The focus area (genomics or conservation-oriented evolutionary ecology) will be tailored for the chosen person, and there is flexibility to modify the research plan according to personal interests. The work will require a 1-3 month stay in Professor Robert Arlinghaus' lab at Humboldt University of Berlin / Leibniz-Institute of Freshwater Ecology in 2017. Genetic work is conducted mainly at the University of Turku, and experimental work takes place at the Kainuu Fisheries Research station in Paltamo (www.kfrs.fi), located 270 km north from Joensuu.

The salary of the position is determined in accordance with the salary system of Finnish universities and is based on level 5 of the job requirement level chart for teaching and research staff (euro 2.865,30/month). In addition to the job requirement component, the salary will include a personal performance component, which may be a maximum of 46.3% of the job requirement component.

The electronic application should contain the following appendices:

- a résumé or CV < http://www.tenk.fi/en/-template-researchers-curriculum-vitae > - a list of publications <http://www.aka.fi/en/funding/how-to-apply/appendices- required/guidelines-for-list-of-publications/> - a motivation letter (two pages describing in English, why would you be a suitable person for the work, how do you see research on fish genetics could help to solve conservation issues and what are your personal ambitions in science. Please also analyse your strengths and weaknesses) - copies of the applicant's academic degree certificates/ diplomas, and copies of certificates / diplomas relating to the applicant's language proficiency, if not indicated in the academic degree certificates/diplomas - five of your publications demonstrating required skills as a single pdf file

The application needs to be submitted no later than August 31, 2016 (by 24.00 hours Finnish time) by using the electronic application form.

Link to full ad and electronic application form:

http://www.uef.fi/en/uef/en-open-positions Direct link to full ad:

https://www.saimanet.com/-certiahome/open_job_view.html?id=-3D00002538&did=3D5600&lang=en&jc=-16&nav_from_open_jobs_view_new=true Anssi Vainikka, associate professor, PhD, docent Department of Environmental and Biological Sciences University of Eastern Finland P.O. Box 111 FI-80101 Joensuu, Finland Phone: +358 500 443290, Fax: +358 13 318 039: Skype: ansvain http://www.kotikone.fi/ansvain/official.html

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UEasternFinland HymenopteranEvolution

Link to full job ad: www.uef.fi/en/envbio We are now inviting applications for the position of a

Postdoctoral Researcher in Hymenopteran Phylogenomics and Diversification

A postdoctoral position for 1+2 years is available at the University of Eastern Finland, Department of Environmental and Biological Sciences (Joensuu campus).

We are looking for a highly motivated person to conduct research on the macroevolutionary history of the hyperdiverse insect order Hymenoptera (sawflies, bees, wasps, ants, and parasitoids) in a new research project funded by the Academy of Finland.

The main duties of the Postdoctoral Researcher will be to:

- Develop protocols for successful DNA extraction and next-generation sequencing from insect museum specimens.

- Perform large-scale phylogenomic analyses of diverse hymenopteran groups using data collected by targeted capture and sequencing of ultraconserved elements (UCE's).

- Conduct statistical analyses of ecological trait evolution, phylogeography, and factors influencing diversification rates within the Hymenoptera, with a focus on the ancestrally plant-feeding (sawfly) lineages.

- Publish the results as high-quality articles in leading international scientific journals.

In addition to a suitable doctoral degree, the ideal candidate has a promising publication record and experience with the aforementioned laboratory and data-analysis techniques, but applicants possessing related skills and a proven ability to learn quickly will also be considered.

The work will be performed mainly in the Joensuu Molecular Ecology Group (www.jmeg.fi), which operates at the Department of Environmental and Biological Sciences of the University of Eastern Finland (www.uef.fi/en/envbio). Part of the laboratory work will be done during extended research visits to the laboratories of Brant Faircloth (Louisiana State University; www.faircloth-lab.org) and Niklas Wahlberg (Lund University; www.biology.lu.se/niklas-wahlberg). The project also includes extensive collaboration with an international network of experts on hymenopteran taxonomy, biogeography, and ecology.

The position will first be filled for one year, with a possibility for prolongation for two more years. The continuation of the position will be agreed separately. The start date of the position is 1 September 2016 or as agreed.

The salary of the position is determined in accordance with the salary system of Finnish universities and is based on level 5 of the job requirement level chart for teaching and research staff (euro2.865,30/ month). In addition to the job requirement component, the salary will include a personal performance component, which may be a maximum of 46.3% of the job requirement component.

The electronic application should contain the following appendices:

- Full CV, including names and contact details of two references

- list of publications

- copies of the applicant's academic degree certificates, and copies of certificates relating to the applicant's language proficiency, if not indicated in the academic degree certificates

- cover letter explaining past research, future interests, and motivation for applying for the position (max. 2

pages).

The application needs to be submitted no later than August 15, 2016 (by 24.00 hours Finnish time) by using the electronic application form (link below).

Link to full ad and electronic application form:

http://www.uef.fi/en/uef/en-open-positions Direct link to full ad:

https://www.saimanet.com/certiahome/-open_job_view.html?id=00002551&did=5600&lang=-en&jc=16&nav_from_open_jobs_view_new=true Tommi Nyman

Department of Environmental and Biological Sciences

University of Eastern Finland

P.O. Box 111

FI-80101 Joensuu

Finland

Phone: +358 40 520 6540 (mobile)

E-mail: Tommi.Nyman@uef.fi

Homepage: www.jmeg.fi Tommi Nyman <tommi.nyman@uef.fi>

UGdansk Bioinformatics

36-MONTH POSTDOC POSITION AT THE UNIVERSITY OF GDANSK (POLAND)

Bioinformatician in a large project on orchid symbiosis and metabolism

Fields of interest and research objective: Prof. M.-A. Selosse's team is based in Brazil (ViÃÂ), France (National Museum of Natural History, MNHN-Paris) and Poland (Gdansk) and studies the ecology and evolution of mycorrhizal symbiosis, i.e. the association of plant roots with soil fungi, in tropical and temperate regions. The current project focuses on our special interest in mycorrhizae of temperate orchids and their role in plant physiology. In most cases, fungi provide soil minerals to the plant, in exchange for photosynthetic sugar. Yet, during orchid germination, the fungi provide carbon to germinating seedlings that have no reserve. Moreover, in some orchid species, adult plants also recover carbon from their fungi: some are achlorophyllous and non-photosynthetic (mycoheterotrophic species) while others are green and mix photosynthesis with exploitation of fungal carbon (mixotrophic species). We aim to study these various nutritional strategies (germination, adult autotrophy, mycoheterotrophy and mixotrophy) within several evolutionary and ecological frameworks, using metabolomic and transcriptomic approaches in situ. These original approaches open the way to a fully new integrated vision of plant biology.

Research environment: The research is funded by the National Science Centre (Maestro7-NZ project entitled Orchidomics to M.-A. Selosse) at the University of Gdansk (UG, Poland) from 2016 to 2020. The position will be based in the Department of Plant Taxonomy and Nature Conservation, within which a team of 4 full researchers and 2 PhDs will focus on Orchidomics. The team will access various facilities of UG according to project needs. The candidate will be part of the international network of renowned European scientific institutions involved in Orchidomics. This includes Adam Mickiewicz University in PoznaÄ¹â€(Prof. I. MakaÄ¹â), the Faculty of Biotechnology of UG and the Medical University of GdaÄ¹â(Prof. E. Ä¹ï¿½ojkowska), MNHN in Paris (Prof. M.-A. Selosse) and its Molecular Facilities (Dr. R. Debruyne), and the University of Fribourg (P.-E. Courty). He/She may contribute as a co-author to other projects, started or yet to be launched, within this network and in Brazil. He/She will also help organise an international congress on mycorrhizal ecology and physiology in 2019.

Responsibilities and required skills: The ambitious Orchidomics project needs candidates with strong bioinformatics skills. The selected candidate will assume responsibility for bioinformatics throughout the project. He/She should have a background (PhD or previous post-doc) in computational biology and bioinformatics. With initial help from his/her collaborators at Adam Mickiewicz University (PoznaÄ¹â€) and MNHN (Paris), the candidate will handle, assemble and integrate large amounts of data generated by the project, in order to help plant biologists to draw relevant conclusions. A strong background with perl or python as well as in RNA-seq analyses (de novo assembly, annotation, homology, mapping;) is required. A solid grounding in SQL and R will be welcome. We also value, but do not require, an interest in plant biology. The postdoc will be free to join the team during field sampling sessions. A good level of spoken and written English is necessary.

Duration: This 36-month (full-time) position would ideally start between November 2016 and January 2017.

Salary and other conditions: Competitive salary, especially on the basis of local standards, including health insurance and social advantages. In the 5 first months of the position, the successful candidate will be allowed to devote 20% of his/her working time to finishing previous papers.

How to apply: Prepare a cover letter explaining your interest in the position and how it makes sense at this stage of your career. Give the names and email addresses of one to two people(s) with first-hand knowledge of your skills and past research experience. Add a curriculum vitae including a publication list (3 pages maximum). Send your completed application in a single pdf file to the principal investigator (ma.selosse@wanadoo.fr).

Please include in your application the following statement: "In accordance with the personal data protection act from the 29th of August 1997, I hereby agree to process and to store my personal data by the Institution for recruitment purposes'. Call for applications open until the position is filled. For full consideration, apply by September 30^th, 2016. After pre-selection, an interview will be organized, if necessary by Internet.

Marc-André SELOSSE <ma.selosse@wanadoo.fr>

UHaifa Evolution

Biology, mathematics, computer science and bioinformatics students/researchers are needed

Dr. Livnat's new lab for the study of evolution at the University of Haifa in Israel is seeking applications for Ph.D, postdoc and other positions from individuals with a background in biology, mathematics, computer science or bioinformatics and a record of past excellence.

We study the deep principles of how evolution works both theoretically and experimentally. 1) Students with a background in theoretical computer science or other branches of mathematics may participate in work at the interface of evolutionary biology and theoretical computer science whose goal is to form a new mathematical framework for evolution. Our lab works in collaboration with leading computer scientists abroad and in Israel. 2) Students with a background in bioinformatics and students with molecular biology lab skills may participate in evolutionary research involving cutting-edge sequencing methods. 3) Students interested in the evolution of behavior are also encouraged to apply.

Applicants should send a cover letter and a CV to alivnat@univ.haifa.ac.il, including the names of 2-3 references. More info at http://sci3.haifa.ac.il/˜alivnat/ adi.livnat@gmail.com

UHeidelberg 2 EvolutionaryGenomics

TWO POSTDOC POSITIONS IN EVOLUTIONARY SINGLE-CELL GENOMICS (experimental and computational)

Joint interdisciplinary postdoctoral positions in the research groups of:

Detlev Arendt, European Molecular Biology Laboratory (EMBL), Heidelberg Wolfgang Huber, European Molecular Biology Laboratory (EMBL), Heidelberg Henrik Kaessmann, Center for Molecular Biology (ZMBH), Heidelberg University

Overall topic: Cell types are the fundamental units of multicellular life. They make up distinct tissues and organs in vertebrates and invertebrates. However, the cellular origins and diversification events underlying the emergence of new animal tissues during evolution remain poorly understood. The recent revolution in single-cell genomics technologies now allows for detailed investigations of the evolutionary and cellular origins of tissues and organ systems as well as the underlying gene regulatory networks. We are particularly interested in the origin and evolution of the vertebrate/bilaterian nervous system.

The host labs: The three labs combine complementary expertise in cell type and nervous tissue evolution (Arendt group), statistical computing (Huber group), and vertebrate evolutionary (functional) genomics (Kaessmann group). This setting provides a unique framework for carrying out groundbreaking interdisciplinary postdoctoral projects in evolutionary single-cell biology.

Projects: We call for proposals of specific biological projects, to be developed by you with feedback from the three mentors, within the overall frame outlined above. We envisage that one of the projects will focus on the development and application of single-cell sequencing protocols for profiling transcriptomes and epigenomes across tissues and developmental stages from multiple, carefully selected species. This project will also include follow-up experiments (e.g., FISH to assess the distribution and abundance of cell types using markers predicted from whole transcriptome analyses). The other project will focus on the development of statistical and bioinformatics approaches for detailed analyses and understanding of single-cell sequencing data in the evolutionary context. Particular challenges include spatio-temporal registration and modelling of cells and the identification of functional homologies and divergences of cells and their gene regulatory programs. We expect both projects to take a highly collaborative approach between each other and with the other members of the host labs. We also expect candidates to acquire interdisciplinary skills in the course of the project (i.e., a wet lab postdoc will learn and perform bioinformatics approaches; a bioinformatics postdoc will perform targeted experiments).

The candidates: The ideal experimentally oriented candidate has experience and strong experimental skills in molecular and cell biology. Expertise in developmental biology, the biology of specific organs (e.g., the brain), and/or genome-scale work is a plus. For computational candidates, we expect outstanding quantitative and analytical skills. We are looking for candidates with PhD level education in molecular biology, bioinformatics, statistics, mathematics or a related field, who aim to make an impact on our understanding of fundamental aspects of cellular evolutionary biology. Experience in the analysis of high-throughput sequencing data and/or the development and optimization of statistical approaches is desired. Experience in the analysis of single-cell genomic or transcriptomic data is a plus.

Both candidates should ideally be driven by a passion for evolutionary biology, and both positions require the ability to independently take responsibility for their projects, as well as strong teamwork and communication skills, problem-solving abilities, reliability, attention to detail and effective time management.

Funding: The selected candidates will be encouraged to apply for independent funding, including the EMBL Interdisciplinary Postdocs (EIPOD) fellowship program (http://www.embl.de/training/postdocs/08-eipod/).

Research environment and location: The language of our institutes (EMBL and ZMBH) is English and host scientists from around the world. The institutes are located in Heidelberg, a picturesque cosmopolitan city that offers a very stimulating, diverse and collaborative research environment also thanks to nearby cutting-edge institutions, such as the German Cancer Research Center (DKFZ) and the Center for Organismal Studies (COS).

For more information, please refer to our websites at www.embl.de/research/units/dev_biology/arendt/ and www.huber.embl.de and http://www.zmbh.uni-heidelberg.de/Kaessmann/ Please submit a CV, statement of research interest, references,

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UJyvaskyla QuantEvolution

Postdoctoral Researcher in Quantitative Ecology: Effects of rapid evolution on ecosystems.

The Department of Biological and Environmental Science at the University of Jyvaskyla is currently seeking to recruit a qualified candidate to the position of Postdoctoral Researcher in Quantitative Ecology The postdoctoral researcher will work in the project “The ecosystem effects of a rapidly evolving invader” (http://tinyurl.com/jy6uojx) led by Dr. Andres Lopez-Sepulcre and funded by the Academy of Finland. In this project we develop a novel mathematical framework to study the effects of consumer invasion and evolution on nutrient cycling, and apply it to isotope tracer data from an ongoing long-term evolutionary experiment using introduced guppies (Poecilia reticulata) in Trinidadian headwater streams. While the researcher is expected to contribute to the development of the mathematical tools, there is considerable freedom to develop their own research questions.

The project is co-directed with experts in ecosystem science (Prof. Steven Thomas, Prof. Rana El-Sabaawi, and Dr. Sarah Collins). It forms part of an international network of researchers from France, Canada, USA, and the UK, including collaborations with evolutionary biologists (e.g. Profs. David Reznick, Joseph Travis, and Tim Coulson).

The postdoctoral researcher is expected to focus on scientific research and the task may also include teaching within his/her own area of expertise.

The duties, qualification requirements and language skills of postdoctoral researcher are stipulated by the University of Jyvaskyla Regulations and language skills guidelines. While the University may grant exemption from some of the requirements, a good command of English is imperative.

For this position we will recruit a person with a PhD in Ecology, Evolution, Statistics or related fields. Expertise in statistical and ecological modeling is necessary, including the ability to work with large data sets. Experience in Bayesian methods and the ability to create and optimize R packages are strongly desirable. Experience in ecosystem science, limnology, or food web ecology is not necessary but will be considered an asset.

The job-specific salary component of a postdoctoral researcher is based on the job demands level 5-6 (EUR 2865,30-3340,77/month) according to the salary system concerning teaching and research staff at universities. In addition, a personal performance-based salary component amounting to the maximum of 46,3% of the job-specific salary component is also paid. Health care is included.

The position may be renewed annually for a maximum of 4 years with an initial trial period of four months. The position is available from September 15th 2016 but the starting date is negotiable.

For further information, please contact: Dr. Andres Lopez-Sepulcre (alopez@biologie.ens.fr, http://ecoevo.pagecloud.com).

The application (in English) should include (as pdf files): 1) A brief letter of interest (maximum 2 pages), detailing your research and career goals, qualifications and skills that are applicable to this project.

2) Curriculum vitae (CV) containing a publication list and contact details of two academics available for reference.

Application will be open until September 1st 2016. Please submit your application using the online application form at:http://tinyurl.com/jnvlko9 Andrés López-Sepulcre <lopezsepulcre@gmail.com>

UKonstanz 2 Bioinformatics

TWO POSTDOC POSITIONS

in molecular ecological/evolutionary genomics/bioinformatics

in Axel Meyer's lab at the University of Konstanz in Germany

Two positions as Postdoc in the lab of Axel Meyer at the Department of Biology of the University of Konstanz in Germany are available immediately. The initial contract period would be for two years with the potential for extension. Funding is provided through the ERC advanced grant GenAdap that focuses on the repeated adaptive radiations of cichlid fish species flocks in Nicaragua. We have large population genomics and comparative genomic data sets (ddRADseq, RNA-Seq, more than 200 re-sequenced complete genomes) and are planning to collect more comparative ecological genomic and genetic data (e.g. CHiP-Seq, GWAS and QTLs) to understand the repeated evolution of adaptations and speciation. Also, more field work in Nicaragua will be conducted. http://www.evolutionsbiologie-uni-konstanz.com/original-articles.html The overall aims of this project are to understand the genomic basis of parallel evolution and sympatric speciation in these very young (some species are less than 2000 years old) radiations. Further information on our research and about the members of the Meyerlab (English is, of course, the language of the lab) and their publications can be obtained from our web page: http://www.evolutionsbiologie-uni-konstanz.com/ . Talented and highly motivated candidates should have a background in molecular evolutionary biology, comparative genomics or bioinformatics. We would also be interested in a wet-bench postdoc with strong expertise in molecular biology, with a genomics or molecular evolution background and knowledge in programming languages (such as Python, Perl, Java, etc.).

Please contact me if you need more information. Applications should be send to Axel Meyer directly (axel.meyer@uni-konstanz.de) and should include 1) a cover letter explaining your background and motivation, 2) a CV, and 3) email addresses of two references.

Review of applications will commence immediately and applications should be received by July 31st at the latest. Starting dates are flexible, but we are looking to fill these posts quickly. This search will remain open until the positions are filled. Konstanz is a very beautiful and pleasant place to live. The University of Konstanz is an equal opportunity employer and rated as one of the best universities in Germany.

Prof. Axel Meyer, Ph.D.

Department of Biology

University of Konstanz

78457 Konstanz, Germany

fon + 49 (0)7531 88 4163

secretary: Christiane.Weber@uni-konstanz.de tel. + 49 (0)7531 88 3069

https://cms.uni-konstanz.de/evolutionsbiologie/ Axel Meyer <a.meyer@uni-konstanz.de>

ULausanne ComputationalBiology OpenCall

Postdoctoral associate positions University of Lausanne & Swiss Institute of Bioinformatics Start date: 1 January 2017 or later

We are looking for postdocs to participate in the vibrant community of computational evolutionary biology at University of Lausanne and Swiss Institute of Bioinformatics.

This call is common to four groups: Jérôme Goudet, Christophe Dessimoz, Nicolas Salamin and Marc Robinson-Rechavi. Our interests span population genomics, phylogenetics, gene expression, evo-devo, databases, ontologies, evolutionary models, and orthology.

We welcome applications from postdoc candidates either for one of these groups, or for a collaboration between two groups.

This is an open call: the candidates should propose a project, to be refined in discussion with the group leaders.

The postdocs will work in the Department of Ecology of Evolution, or in the new Department of Computational Biology, and also be a full member of the Swiss Institute of Bioinformatics. The postdocs will participate in the life of the Department of Ecology and Evolution (internal and external seminars, journal clubs, etc.), one of the largest and most active of Europe.

The initial contract will be for 1 year, but is renewable twice for 2 years, depending on funding and job satisfaction. The postdoc will participate in some undergraduate and/or masters teaching, in English or in French.

Working conditions in Lausanne are extremely competitive, and include access to state-of-the-art computing and sequencing facilities. The Department is highly international, and all research activities are conducted in English.

For background, please see our group webpages. If you cannot find them, you don't qualify. :-)

Profile requirements

- Doctorate degree in bioinformatics, computational biology, biostatistics, or a related field, necessary. - Basic competence in programming necessary. - Track record of publication necessary. - Proven experience in interdisciplinary work necessary. - Strong interest in evolutionary biology necessary. - Published methods, software or databases would be a plus. - Published biology papers using bioinformatics would be a plus. - Experience with genomics or transcriptomics data would be a plus. - Good oral and written English communication skills in would be a plus.

Please send your application to

One page project that you would like to conduct, including target groups (max 2); CV and publication list; the contact information of 3 referees; all documents in English.

Informal enquiries and full applications should be sent to the main group leader concerned.

Deadline for applications: 31 August 2016

SNSF Prof, UNIL Dept of Ecol. and Evol. & UNIL Centre for Integrative Genomics Reader, UCL Genetics Evolution and Environment & UCL Computer Science Group Leader, Swiss Institute of Bioinformatics

http://lab.dessimoz.org - Tel: +41 21 692 4155 - Twitter: @cdessimoz

"Christophe.Dessimoz@unil.ch"
<Christophe.Dessimoz@unil.ch>

ULausanne EvolutionAndFunctionOfLncRNA

Postdoctoral associate University of Lausanne & Swiss Institute of Bioinformatics Start date: 01.10.2016 (or as soon as possible thereafter)

The postdoc will take part in an interdisciplinary collaboration between the labs of Christophe Dessimoz, Ana Claudia Marques and Sven Bergmann. The project aims to better understand the role of long non-coding RNA birth and death on gene expression network remodeling. To this end we will leverage the expertise in ACM's lab on the functional genomics of lncRNAs, particularly in the context of embryonic stem cell biology, the expertise in CD's lab on fineÂ'grained orthology inference and evolutionary genomics; and the recent advances by the group of SB on the reconstruction of cellÂ'type specific regulatory networks.

The successful candidate will also have the opportunity to gain teaching experience (e.g. via student project supervision and contribution to undergraduate or graduate teaching) and to contribute to other ongoing projects in the host labs.

Working conditions in Lausanne are extremely competitive, and include access to state-of-the-art computing and sequencing facilities. The environment is highly international, and all activities are conducted in English.

Qualifications sought:

Essential:

- Doctorate degree in bioinformatics or biology with solid quantitative component - Solid statistical knowledge - Excellent spoken and written English proficiency - Demonstrated programming skills - High level of motivation - Publications in peer-reviewed journals - Ability to collaborate in an interdisciplinary environment

Desirable:

- Experience in comparative genomics and molecular evolution - Experience in the analysis of transcriptomics data - Experience in functional genomics analysis and integration of different omics data.

How to apply:

The application should consist of a single PDF file containing the following elements

- Motivation letter - Curriculum vitae including list of publications - Copy of university diplomas - Reference to best paper accompanied by a brief supporting statement (approx. 200 words) - One page statement on research and career objectives

Applications should be sent to Prof. Christophe Dessimoz (Christophe.Dessimoz@unil.ch).

For informal information, please contact Prof. Dessimoz, Prof Marques (Anaclaudia.Marques@unil.ch), or Prof. Bergmann (Sven.Bergmann@unil.ch).

Deadline for applications: 31 July 2016

More info:

Dessimoz lab: http://lab.dessimoz.org Marques lab: https://wwwfbm.unil.ch/physiol/marques_pres_en.html Bergmann Lab: http://www2.unil.ch/cbg SNSF Prof, UNIL Dept of Ecol. and Evol. & UNIL Centre for Integrative Genomics Reader, UCL Genetics Evolution and Environment & UCL Computer Science Group Leader, Swiss Institute of Bioinformatics

http://lab.dessimoz.org - Tel: +41 21 692 4155 - Twitter: @cdessimoz

"c.dessimoz@ucl.ac.uk" <c.dessimoz@ucl.ac.uk>

ULaval FungalAdaptation

Postdoctoral position: Genomics of adaptation in fungi at ULaval, Quebec, Canada

A postdoctoral position is available in the Landry Laboratory at Universite Laval in Quebec City under the Canada Research Chair in Evolutionary Cell and Systems Biology. The PDF will work on a collaborative project looking at the population genomics of plant pathogenic fungi of the genus Ophiostoma, including the species responsible for the Dutch elm disease. The goal of the project is to perform a large genomic and phenotypic survey of North American and world-wide isolates ($n > 500$) to examine the role of natural selection, inter-species hybridization and genome dynamics in the adaptation and range expansion of this pathogen. See our recent work on budding yeast (Leducq et al. Nature Microbiology, doi:10.1038/nmicrobiol.2015.3)

The candidate is expected to have a PhD in biology, bioinformatics or computational biology or a related discipline, with a strong background in bioinformatics and statistics (R, Python) and at least some experience with whole-genome sequencing analysis and population genetics. The candidate should have strong leadership skills, motivation and creativity and be able to work in a team of collaborators within the laboratory and with other laboratories involved in the project.

The Landry lab is located at the Institut de Biologie Intégrative et des Systèmes (IBIS) of Université Laval and is part of the Quebec Network for Research on Protein Function, Engineering, and Applications (PROTEO). IBIS and PROTEO offer a stimulating training environment and cutting edge technologies in genomics and proteomics. The Landry lab is an international team of 15 students, PDFs and research associates from different backgrounds (microbiology, biology, bioinformatics, biochemistry) addressing questions in evolutionary cell and systems biology.

The application package (1 single PDF file) should include a motivation letter demonstrating the interest of the candidate for the field and his/her ability to perform this type of research, reprints of the candidate's most important contributions, a CV and the contact information of three people who can provide letters of reference. The file should be sent to landrylaboratory@gmail.com

Starting date could be as early as January 2017. The competition will remain open until a candidate is selected. The position is initially for 2 years with a possible extension to 3.5 years.

For recent publications from the Landry lab, please visit:

http://landrylab.ibis.ulaval.ca/ Christian Landry

Christian Landry, PhD Professeur agrégé

Chaire de Recherche du Canada en Biologie évolutive des systèmes cellulaires // Canada Research Chair in Evolutionary Cell and Systems Biology

Département de Biologie Institut de Biologie Intégrative et des Systèmes PROTEO Centre de recherche en données massives (CRDM)

Local 3106, Pavillon Charles-Eugène-Marchand 1030, Avenue de la Médecine Université Laval Québec (Québec) G1V 0A6 Canada

http://landrylab.ibis.ulaval.ca/ Téléphone: 418-656-3954 Télécopieur: 418-656-7176

Christian Landry <Christian.Landry@bio.ulaval.ca>

ULyon PhD PDF EvolutionaryGenomics

The Convergenomix project is looking to hire PhD and post-doc positions in Evolutionary Genomics at the University of Lyon, France.

Successful applicants will work within the ANR Convergenomix project, which groups 4 labs all based in Lyon. Convergenomix aims to study convergent evolution at the genome scale by developing and applying bioinformatic methods in 3 different groups of animals.

While evolving in a collaborative project, each PhD student or post-doc will be in charge of her/his own research project.

Position 1 : Convergent genomic evolution in groundwater species with particular interest in regressive evolution and aging

Position 2 : Study of rodent adaptation to arid environment based on transcriptome data.

Position 3 : Development of a computational method to detect genomic convergence taking into account mutation biases and incomplete lineage sorting.

*Your profile

The applicants will have a strong interest for evolutionary biology, and will be willing to work in a collaborative environment including molecular and developmental biologists, ecologists, and computer scientists.

Specific skills:

Position 1 & 2 : either a biologist with interest in genomics and large-scale data analysis or a computer scientist with interest in biology. The project will involve programming in R, Python or Perl, and statistics.

Position 3 : a scientist with skills in programming (C++ or OCaml), statistics and model development

*We offer

PhD fellowships are for 3 years, post-doc positions are for 2 years.

The laboratories involved in the Convergenomix projects have generous resources for genomic analysis (scientific high-performance computing, data management, training and support). They offer a stimulating environment, with a rich spectrum of research activities in life sciences (biodiversity research, evo-devo, evolutionary genomics, ecology). Position 1 will be based in the LEHNA laboratory within a team specialized in subterranean biology. Position 2 will involve two labs: the LBBE and the LBMC specialized in bioinformatics and evo-devo, respectively. Position 3 will be located at the LBBE.

*More information

For more information, contact us at convergenomix@univ-lyon1.fr or

see the following webpage: http://lbbe.univ-lyon1.fr/-convergenomix/ . Websites of the involved labs:

LBBE:

https://lbbe.univ-lyon1.fr/?lang=en LBMC:

http://www.ens-lyon.fr/LBMC/spip/?lang=en LEHNA:

http://umr5023.univ-lyon1.fr/ Lyon is the second largest French city, is very well connected to other European cities, is famous for its food, and offers a broad range of cultural and recreational activities.

*Further information and application

Application packages should include a letter of motivation, a curriculum vitae, and the names and email addresses of two referees. Documents should be submitted as a single PDF file to convergenomix@univ-lyon1.fr. Applications are welcome until the position is filled. We will begin reviewing applications in August 2016.

Marie Sémon, PhD, LBMC

Tristan Lefébure, PhD, LEHNA

Laurent Guéguen, PhD, LBBE

Philippe Veber, PhD, LBBE

Bastien Boussau, PhD. LBBE

Email: convergenomix@univ-lyon1.fr

Web: http://lbbe.univ-lyon1.fr/convergenomix/ boussau@gmail.com

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UMadrid EvolutionaryBiol

The Evolution and Conservation Biology research group at Complutense University of Madrid (Spain, www.ucm.es/bcveng) welcomes proposals of postdoctoral researchers who wish to join the Department of Zoology and Physical Anthropology taking advantage of the excellence programme for attracting talent released by the Regional Government of Madrid.

The successful candidate will demonstrate outstanding research performance in any field that fits to our department (not necesarily our own lines), independence and mobility (at least three years of research activity outside Spain). We offer an opportunity for developing independent research lines and for gaining teaching experience.

The deadline to submit applications is July 21, 2016. Applicants are to submit their proposals directly to UCM, but please be aware that they have to be sent to us in advance in order to be accepted by our Department. There are two parallel funding schemes directed to experienced researchers and young posdocs. Further information available at the following sites:

Trained researchers: http://www.ucm.es/ct40-16/ Young postdocs: http://www.ucm.es/ct41-16/ Prospective applicants should submit a summary of their proposals to Javier Pérez-Tris (jperez@ucm.es) not later than July 19, 2016.

Javier Pérez-Tris

Departamento de Zoología y Antropología Física Facultad de Biología, Universidad Complutense de Madrid E-28040 Madrid, Spain

Tel.: +34 91 394 49 49 Fax: +34 91 394 49 47

email: jperez@ucm.es

http://www.ucm.es/perez-tris jperez@ucm.es

UMassachusetts Amherst EvolutionaryMorphology

POST-DOCTORAL POSITION in Evolutionary Morphology, University of Massachusetts at Amherst

The Dumont Lab at the University of Massachusetts at Amherst (UMass Amherst) seeks a Postdoctoral Research Associate to work collaboratively on projects that focus on the form, function and evolution of the skulls and jaw of vertebrates. This is a fully benefited, full-time Postdoctoral Research Associate position. Initial appointment for one year; reappointment beyond first year is contingent upon availability of funding and job performance. Salary is subject to bargaining unit contract. The postdoctoral associate's primary responsibilities will be to contribute to a Collaborative NSF Dimensions of Biodiversity grant that focuses the evolution of sensory systems in bats (http://www.nsf.gov/awardsearch/showAward?AWD_ID=3D1442278&HistoricalAwards=false), by collecting and analyzing data and contributing to co-authored manuscripts for peer-reviewed publication and to mentor undergraduate and graduate students. Independent projects related the lab's mission and participation in mentored undergraduate teaching experiences are encouraged. For more information on the Dumont Lab visit http://www.bio.umass.edu/biology/dumont and www.biomesh.org.

Minimum requirements include a completed PhD in a related field (e.g., evolutionary biology, zoology, paleontology). Ability to make regular day trips to Cambridge, MA to use ct-scanning facilities.

Preferred requirements include training in some combination of comparative anatomy, comparative methods, geometric morphometrics staining specimens for ct-scanning, 3D visualization of ct-scans, manipulation of 3D images, and mentoring or teaching experience.

Postdoctoral Research Associates at the University of Massachusetts are unionized and receive standard salary and benefits, depending on experience.

Please apply online by submitting a cover letter, CV, summary of research interests, summary of mentoring/teaching experiences, and the contact details of three references to: http://umass.interviewexchange.com/jobofferdetails.jsp?JOBID=3D73899 For information email: bdumont@bio.umass.edu .

Review of applications will begin July 25^th, 2016. Applications received by July 25th will be given priority consideration.

The University of Massachusetts Amherst is an Affirmative Action/Equal Opportunity Employer of women, minorities, protected veterans, and individuals with disabilities and encourages applications from these and other protected group members.

Lisa Barry Biology Department Morrill Science Center South, Room 348 611 North Pleasant Street University of Massachusetts Amherst, MA 01003

Phone: 413-545-2602 Fax: 413-545-3243

Lisa Barry <lisak@bio.umass.edu>

UMontana ClimateChangeAdaptation

POSTDOCTORAL RESEARCHER (Climate change, PVAs, & CCVAs)

University of Montana - Flathead Lake Biological Station Division of Biological Sciences

We are seeking a highly motivated postdoctoral researcher to analyze and use geospatial datasets to conduct Climate Change Vulnerability Assessments and Population Viability Analysis to assess salmonid vulnerability to climate change across the Columbia River Basin. This NASA-funded collaboration aims to support resource managers with a prototype decision support system (software) that includes vulnerability, landscape genetic and demogenetic modeling tools. The successful applicant will have the opportunity to work in collaboration with veteran scientists in NOAA (e.g., Dr. Jeff Hard and Dr. Robin Waples) and in the USGS (e.g., Jen Bayer, Clint Muhlfeld), as well as other state (MFWP, IDFG, WDFG) and tribal agencies (CRITFC). With these collaborations, the successful applicant will identify needs of researchers and mangers regarding novel computational approaches and data products for assessing salmonid viability. These approaches and data products will then be incorporated into the RAP (http://rap.ntsg.umt.edu/) decision support system. Opportunities exist to also participate in other projects on biodiversity conservation and landscape genomics. The position is centered in the labs of Dr. Gordon Luikart, http://flbs.umt.edu/people/-luikart3422/default.aspx?ID=3D3422) at the University of Montana main campus and the Flathead Lake Biological Station (http://flbs.umt.edu/default.aspx), in close collaboration Dr. Brian Hand, Dr. John Kimball, and researchers at the FLBS.

Review of applications will begin on September 1st, 2016 and continue until the position is filled. This position requires a Ph.D. in ecology or a related discipline, and some experience in population viability analysis or climate change vulnerability assessment (and ideally in spatial analysis). Desired qualities also include experience in fisheries or aquatic ecology and management, web programming or website design, and experience working in GIS (ArcGIS). Start date is negotiable, but likely between January and March, 2017. Salary and benefits are competitive. Position is for 1 year, with continuation for an additional year pending satisfactory progress. To apply, please send in pdf format a CV, and names of 3 references (with email and postal address), a research interests statement, and up to 3 representative reprints via email to: Gordon Luikart and Brian Hand (gordon.luikart@umontana.edu and brian.hand@umontana.edu). *UM is an Equal Opportunity/Affirmative Action/ADA educator and employer.*

"Luikart, Gordon" <gordon.luikart@mso.umt.edu>

UMontana RiverBiodiversity

POSTDOCTORAL RESEARCHER (Biodiversity in Rivers)

University of Montana - Flathead Lake Biological Station Division of Biological Sciences

We are seeking a postdoctoral researcher to work on ecology, biodiversity, and evolutionary genomics of river and aquifer microinvertebrates. This NSF-funded collaboration builds on over 30 years of research understanding floodplain ecology and effects of land use and climate change. The successful applicant will have an unprecedented opportunity to analyze thousands of samples from 12 focal species (mainly stoneflies) from six floodplains from the Rocky Mountains of Montana and from western Washington. With collaborators, genotypes from 12 focal species (and hundreds of species from bioblitzs) will be analyzed to quantify and model the effects of environmental change on different dimensions of biodiversity (e.g., phylogenetic, population genetic, and functional diversity). The position is centered in the labs of Dr. Gordon Luikart, http://flbs.umt.edu/people/-

luikart3422/default.aspx?ID=3422) and Flathead Lake Biolgical Station (http://flbs.umt.edu/default.aspx) at the University of Montana, in close collaboration with Dr. Jack Stanford (emeritus), and Dr. Brian Hand. Both FLBS and the main UM campus have facilities for research on taxonomy, physiology, and genomics of invertebrates, including state-of-of-the art equipment, computational facilities and staff support.

Review of applications will begin on September 1st, 2016 and continue until the position is filled. A Ph.D. in Biology or a related discipline, combined with field ecology experience in aquatic insects is required. Desired qualities also include a background in population or community ecology, physiology, stable isotope analysis, and population genomics. Start date is negotiable, but likely between January and March, 2017. Salary and benefits are competitive. Position is for 1 year, with continuation for an additional 3 years pending satisfactory progress. Opportunities exist to also participate in other exciting projects on biodiversity conservation and ecological genomics. To apply, please send in pdf format a CV, and names, addresses and email addresses of 3 references, a research statement, and up to 3 representative reprints via email to: Gordon Luikart and Brian Hand (gordon.luikart@umontana.edu; and brianHand@umontana.edu). *UM is an Equal Opportunity/Affirmative Action/ADA educator and employer.*

"Luikart, Gordon" <gordon.luikart@mso.umt.edu>

UNewHampshire PopulationGenomics

A postdoctoral position in population genomics is available in the Kovach lab at the University of New Hampshire. The postdoctoral scientist will work on collaborative projects that use genomic tools to address questions of both fundamental and applied nature. Primary areas of interest include studying adaptive variation and signatures of selection, identifying environmental correlates of gene flow, and developing high-resolution SNP marker panels from genomic resources.

The postdoctoral researcher will contribute to two primary areas of inquiry: 1) Genomic investigations of adaptation in tidal marsh sparrows, including intra and interspecific patterns of neutral and adaptive gene flow in relation to environmental gradients, the genetic basis of adaptations to tidal marshes, and the development of genomic resources for a study of migratory connectivity; 2) RAD-Sequencing and whole genome resequencing studies of ecotype variation, environmental correlates of adaptive variation, demographic connectivity, stock identification and the spatial scale of gene flow for Atlantic cod in US waters.

Both projects have a strong focus in fundamental questions of evolutionary ecology, as well as applications in conservation genomics. Extensive opportunities for collaboration exist through the Saltmarsh Habitat and Avian Research program (www.tidalmarshbirds.org), faculty, postdocs, and graduate students at UNH and other institutions (UConn, UMaine, UDelaware, SUNY-ESF, Cornell University, UMass-Dartmouth, and Gulf of Maine Research Institute), and conservation partners. Outreach opportunities to the public and stakeholders, including natural resources managers, fisheries scientists, and fisherman are also available.

Funding is available for 2 years; additional grant-writing opportunities will be available. Start date: as soon as position can be filled with appropriate candidate; September 1 the latest.

Qualifications: Applicants should have a PhD and prior research experience with population genetics, genomics, and bioinformatics. Additional qualifications include laboratory bench skills, quantitative skills, excellent writing and communication skills, and a demonstrated interest in working in a highly collaborative environment. A background in evolutionary ecology and interest in conservation science are desirable.

To apply: send a brief research statement (1-2 pages) that includes relevant skills and experiences for the project and future goals, a curriculum vitae, and contact information for three references. Inquiries and application materials should be sent via email to Adrienne Kovach: akovach@unh.edu

Review of applications will begin immediately and continue until the position is filled.

"Kovach, Adrienne" <Adrienne.Kovach@unh.edu>

UNewMexico EvolutionInPlantHybrids

Post-doctoral Research Associate

Role of Hybridization in Adaptive Evolution in Plants

An NSF-funded postdoc in the area of experimental evolution is available to start in fall 2016 or spring 2017.

The postdoctoral associate will collaborate closely with the Whitney Lab (University of New Mexico) and the Rieseberg Lab (University of British Columbia) and will be based at UNM, with fieldwork in Texas. Initial funding will be one year, with renewal for a second year following satisfactory performance.

The associate will have a unique opportunity to capitalize on a long-term field experiment examining whether hybridization increases rates of adaptation, and the degree to which evolution in hybrids is repeatable. The focus is on a set of control and hybrid field populations of wild sunflowers established in 2003. Responsibilities will center on planting and supervising data collection on a large set of field common gardens during the summers of 2017 and 2018; the aim is to assess fitness and trait evolution across 15 generations of the hybrid versus control lineages. The associate will also contribute to tests of microevolutionary hypotheses focusing on changes in quantitative trait locus (QTL) allele frequencies in the hybrid lineages across the generations. There will be opportunity for the associate to develop independent projects related to the main questions.

The ideal candidate will have Ph.D. in evolutionary biology, evolutionary ecology or a related field; will have excellent writing and communication skills; and will have experience in several of the following areas:

- Field work with plants and their associated herbivores, pathogens, and pollinators
- Measurements of natural selection
- Statistical genetics, bioinformatics
- Basic molecular biology techniques (e.g. DNA extraction).

To indicate interest: please send a short letter of interest (including ideal start date), PDFs of 1-2 relevant manuscripts, and a CV to Ken Whitney <whitneyk@unm.edu>.

Ken Whitney

Associate Professor

Department of Biology

University of New Mexico

Albuquerque, NM 87131

whitneyk@unm.edu

http://biology.unm.edu/whitney/ Kenneth Whitney <whitneyk@unm.edu>

UOulu PlantEvolutionaryGenomics

Link to jobposting https://www.saimanet.com/-certiahome/open_job_view.html?did=5600&jc=1&id=-00002550&lang=en Post-doctoral position to study evolutionary genomics of haploid life-stage in conifers in University of Oulu

A postdoctoral position for 20 months is available in the Department of Genetics and Physiology, University of Oulu, Finland to work in Dr Tanja Pyhäjärvi's research group (https://wiki.oulu.fi/x/_DLM).

Environment The Department of Genetics and Physiology has strong expertise and tradition in plant population genetics. Current research topics include genetics of local adaptation both in trees and Arabidopsis, genetics of speciation, conservation genetics and molecular evolution of insects. We offer a scientific environment that is enthusiastic about plant evolutionary genetics, a possibility to develop your genomics and bioinformatics skills and initiate international collaboration. The Pyhäjärvi research group is part of Biocenter Oulu and of the Population and Statistical Genomics Research Consortium which combines different population genomics research groups within the university. Within Europe, we collaborate closely with other forests geneticists via the Horizon 2020 project GenTree.

Finland is one of the most livable countries, with a high quality of life, safety and excellent education system. The successful candidate will receive full benefits provided by the University of Oulu to university employees, including free occupational health care services, and obtain access and high-quality affordable childcare services.

The project This project investigates the evolutionary consequences of haploid selection in plants. For this purpose, we use data from Pinus sylvestris (Scots pine), a widespread coniferous tree. The main objective of the study is to evaluate the effect of haploid phase in gymnosperm evolution using both RNA-seq and genome wide polymorphism data. Gymnosperms are of special interest in understanding evolutionary consequences of different ploidy levels, as they have extensive haploid life stage compared to flowering plants. The project is part of a 5-year Academy Research Fellow project of Dr. Pyhäjärvi funded by the National Research Council of Biosciences and Environment.

Qualifications The applicant should have a doctoral degree, recorded scientific expertise and interest in population and evolutionary genomics. Experience in bioinformatics, gene expression analysis and/or targeted sequencing is an advantage. The successful applicant will contribute to gene expression and population genetic analysis and research questions can be adjusted according to her/his interests and skills. The duties also include a small amount of teaching and supervising students. The work will be conducted in collaboration with Natural Resources Institute Finland (LUKE) and as a part of an international team who are experts in gymnosperm gene expression analysis (Jukka-Pekka Verta, FML of the Max Planck Society) and theoretical plant evolutionary genetics (Yaniv Brandvain, University of Minnesota).

Details Starting time for the position is January 1st 2017. The salary depends on the competence of the applicant, but likely will be level 5 of the national salary scale for teaching and research staff of Finnish universities. In addition, a supplementary remuneration will be given for personal achievement and performance, the sum rising to a maximum of 46.3% of the salary scale. (The total salary is expected to be around 3,200 euro/month).

Applications should consist of (1) a letter of motivation (maximum 2 pages) and (2) a CV that includes a list of publications and the contact details of at least two referees. Applications should be submitted in English using the electronic application form by September 1st, 2016

For further information please contact Academy Researcher Tanja Pyhäjärvi (tanja.pyhajarvi[at]oulu.fi) or Head of Administration Tiina Pääkkönen (tiina.paakkonen[at]oulu.fi).

Tanja_Pyhäjärvi <tanja.pyhajarvi@oulu.fi>

UPittsburgh HostParasiteInteractions

Postdoc: Evolution of host-parasite interactions at the University of Pittsburgh

A postdoctoral position is available in Jon Boyle's lab at the University of Pittsburgh in the Department of Biological Sciences. The position is for a minimum of 3 years. Start date is negotiable.

Toxoplasma gondii is a globally ubiquitous parasite of humans and nearly all warm-blooded animals, and causes severe disease in HIV/AIDS patients and the developing fetus. Work in our lab seeks to understand, on a molecular level, how Toxoplasma manipulates the host cell and host immune response to promote its survival.

Ongoing projects include: 1. Using comparative and functional genomics approaches to understand how virulence has uniquely evolved in Toxoplasma gondii. 2. Understanding how gene duplication and diversification drives the evolution of novel phenotypes. 3. Using cell biological and genetic approaches to understand how Toxoplasma infects the human placenta and ultimately the fetus.

We provide extensive training and perform research using human primary cell culture, bioinformatics, molecular genetics/cloning, QTL mapping, analysis of innate immune responses, and next-generation sequencing. Phenotypes are assessed both in tissue culture and in laboratory animals.

QUALIFICATIONS: Successful candidates will have a PhD in biology or related discipline (including evolutionary biology, molecular evolution and molecular biology). Microbiology experience preferred but by no means required. PhD-level scientists looking to combine in silico analyses with wet lab experiments will be a good fit for this position. Regardless, candidates must be self-motivated and have exhibited strong skills at the bench and/or computer as evidenced by a strong publication and/or research funding record.

TO APPLY: Interested applicants should send the following information in a single PDF file to the email address below: 1. A curriculum vitae 2. The names and addresses of three references 3. A one-page statement of research accomplishments and interests

The Department of Biology has top-notch research facilities, and the University of Pittsburgh consistently ranks in the top 10 nationally for biomedical research funding. The University is also situated in an exciting, livable city. For more information about living in Pittsburgh, see: http://www.coolpgh.pitt.edu/

Jon P. Boyle, PhD. Associate Professor Department of Biological Sciences, Dietrich School of Arts and Sciences University of Pittsburgh Pittsburgh, PA. boylej@pitt.edu http://boylelabresearch.com "Boyle, Jon P" <boylej@pitt.edu>

URochester EvolutionaryGenomics

NIH-fundedpostdoc positionUniversity of Rochester, Department of Biology

Positiondetails: TheLarracuente lab seeks an enthusiastic postdoc to join their team. The lab takes an interdisciplinary approach to study genome evolution, with a focus on the evolutionary and functional genomics of satellite DNA, sex chromosomes and selfish genetic elements. All lab members gain skills in genomics, population genetics, molecular and cytogenetic techniques.

Description: Researchobjectives will be determined according to the interests and career goals of the postdoc. The postdoc will have an opportunity to gain skills in teaching and mentoring, although this is not a requirement of the position. The position is for a minimum of one year, and will be renewable based on performance. The salary is competitive and will be commensurate with experience.

Requirements: Theapplicant must have a PhD in Bioinformatics, Genetics, or a related field, a strong publication record and the ability to conduct independent research. Preference will be given to individuals that are proficient in at least one programming language and experienced in analyzing next generation sequence data, although molecular geneticists eager to learn computational techniques are also encouraged to apply.

ApplicationInstructions: Interestedapplicants should send a CV, a brief description of research accomplishments and interests, and contact information for 3 professional references to alarracu@bio.rochester.edu. Review of applications will begin immediately and continue until the position is filled.

TheDepartment of Biology at the University of Rochester offers an intellectually stimulating, supportive and collaborative environment for postdocs. The Larracuente lab is part of the EEB groupa vibrant group with strengths in evolutionary genetics and genomics. Please visit the following web pages to learn more about the group:

LarracuenteLab: http://blogs.rochester.edu/larracuente UofREEB: http://blogs.rochester.edu/EEB/ UofRBIO: http://www.rochester.edu/college/BIO/ TheUniversity of Rochester is an Equal Opportunity Employer.

AmandaM. Larracuente, Ph.D. AssistantProfessor Universityof Rochester Departmentof Biology 343Hutchison Hall Rochester,NY 14627 alarracu@bio.Rochester.edu 585-273-1693 http://blogs.rochester.edu/larracuente/ alarracu@UR.Rochester.edu

UUtah EvolutionaryGenomics

POSTDOC: EVOLUTIONARY GENOMICS

A postdoctoral position is available in the laboratory of Dr. Mike Shapiro in the Department of Biology, University of Utah. We seek a highly motivated and creative colleague to study evolutionary genomics of adaptive radiations in a classic host-parasite system.

Adaptive radiations of parasites occur as they switch to new host species, yet the genetic mechanisms mediating these events remain poorly understood. Parasites represent a massive component of the earth's biodiversity, so understanding how they adapt to new hosts represents a major problem in evolutionary biology. This project focuses on rapid adaptation of lice to changes in host (pigeon) conditions in an experimental system and is funded by an NSF Dimensions of Biodiversity grant in collaboration with the labs of Dale Clayton and Sarah Bush (Utah) and Kevin Johnson (Illinois).

Please visit our home page for more information about our lab and recent publications: http://biologylabs.utah.edu/shapiro/ < http://biologylabs.utah.edu/shapiro/Shapiro_Lab/Index.html >

REQUIREMENTS 1. Ph.D. in genetics, genomics, developmental biology, evolutionary biology, or a closely related field. Applicants with fewer than 2 years of postdoc experience are strongly preferred. 2. Track record of productivity 3. Demonstrated ability and willingness to work both independently and collaboratively 4. Excellent written and oral English communication skills 5. A strong background in analysis of high-throughput sequencing data

TO APPLY Please submit the following materials:

1. CV, including a list of publications 2. Statement that includes your research experience and interests, as well as your preferred approximate start date 3. Names of three referees who will be willing to submit letters of reference upon request

Please email application materials in PDF format to Dr. Mike Shapiro: shapiro@biology.utah.edu

Informal inquiries are welcome prior to formal application.

SCIENTIFIC AND CULTURAL ENVIRONMENT The Department of Biology comprises a diverse and vibrant group of laboratories, with research interests ranging from environmental biology to biochemistry. The genetics community is strong on the University of Utah main and medical school campuses and offers numerous opportunities for collaboration. The growing interdepartmental evolutionary genetics and genomics community is especially interactive.

The University of Utah is located in beautiful (and affordable) Salt Lake City, with easy access to world-class entertainment and recreation. Salt Lake City and nearby Park City are home to the annual Sundance Film Festival and a year-round cinema and arts scene, as well as outstanding restaurants, coffee houses, and brewpubs. Several national parks are located within a just few hours' drive, and the university is within a 40-minute drive of at least six major alpine skiing and snowboarding resorts, including venues of the 2002 Olympics. Hiking and mountain biking trails begin essentially on campus. Outside Magazine recently called Salt Lake City "one of the nation's most underrated outdoor meccas." The city is also a major airline hub, with non-stop flights throughout North America and Europe (Paris, London, Amsterdam).

NONDISCRIMINATION & ACCESSIBILITY STATEMENT The University of Utah does not discriminate on the basis of race, color, religion, national origin, sex, age, status as a disabled individual, sexual orientation, gender identity/expression, genetic information or protected veteran's status, in employment, treatment, admission, access to educational programs and activities, or other University benefits or services.

Mike Shapiro Associate Professor, Department of Biology Adjunct Associate Professor, Department of Human Genetics University of Utah 257 S 1400 E Salt Lake City, UT 84112 (801) 581-5690, fax (801) 581-4668 http://www.biology.utah.edu/shapiro/ @MikeDShapiro

"shapiro@biology.utah.edu"
<shapiro@biology.utah.edu>

UWashington EvolutionFlowerDevelopment

PostDoc: University of Washington, Seattle

The Di Stilio lab at University of Washington investigates the evolution of flower development and is looking for a post doc to work on the functional characterization of orthologs of the flowering pathway gene LEAFY in the fern Ceratopteris richardii. Desirable qualifications: keen observational skills and a love of plants, sterile plant culture, basic molecular biology skills (nucleic acid extraction, gene expression), characterization of morphology via histology, SEM and confocal microscopy, characterization of gene expression by in situ. Excellent writing and communication skills, proof of publication experience (lead authorship on at least one paper). Start date as soon as Sept 1st or later (negotiable). Funding is available for one year, with possibility of extension (pending additional funding). The project is underway as part of a collaboration with U of Oxford (Langdale lab), so it is expected that results will be ready for publication by the end of year 1. Send CV, statement of research interests, copies of relevant publications, and the names and contact information of at least two references to distilio@uw.edu

The University of Washington is located in vibrant and scenic Seattle, for more information see

http://www.biology.washington.edu/prospective/postdoctoral-fellows http://www.biology.washington.edu/users/veronica-di-stilio Veronica

Veronica S. Di Stilio, PhD Associate Professor Department of Biology University of Washington 506 Hitchcock Hall Seattle, WA 98195-1800

(206) 616-5567 off (206) 685-4755 lab FAX (206) 685-1728 http://www.biology.washington.edu/users/veronica-di-stilio "distilio@uw.edu" <distilio@uw.edu>

UWashington GlobalChange

Mainly, I'm looking for a person with broad interests and expertise. The skill set that the position requires molecular work and bioinformatics is very likely to be found among people with PhDs in evolution (as I myself have).

Postdoc in Molecular Ecology and Global Change, University of Washington

Seeking an enterprising and talented person to join the Kelly Lab (http://kellyresearchlab.com/) for a full-time position as a postdoctoral fellow (Research Associate; job class code 0148) at the School of Marine & Environmental Affairs, University of Washington. The postdoc will lead day-to-day work on a project to measure the effects of locally intensified ocean acidification on nearshore ecological communities using molecular techniques (eDNA, metabarcoding). The position will be located in Seattle and will entail occasional travel for fieldwork and related activities.

The ideal candidate will combine significant molecular ecological experience with knowledge of nearshore ecology, ocean acidification, and global change. A PhD or foreign equivalent is required, and required skills include (1) facility with PCR (and related skills) and high-throughput sequencing, (2) coding in R, (3) general familiarity with bioinformatics methods and statistics, (4) a strong interest in nearshore ecology and global change, and (5) the ability to find and integrate data across a diverse spectrum of disciplines. Desirable skills include broader computer coding aptitude (e.g., Python, Perl, bash) and familiarity with the basics of carbonate chemistry. The postdoc will have an opportunity to work at the science/policy interface in this applied project-and therefore communications and outreach skills are a significant plus-but core quantitative and molecular skills will be the foundation of any successful application.

The University of Washington (UW) and the School of Marine and Environmental Affairs (SMEA) promote diversity and inclusivity among our students, faculty, staff, and public. Thus, we are strongly seeking candidates whose experiences have prepared them to fulfill our commitment to inclusion and have given them the confidence to fully engage audiences from a wide spectrum of backgrounds. The UW is located in the greater Seattle metropolitan area, with a dynamic, multicultural community of 3.7 million people and a range of ecosystems from mountains to ocean. The UW serves a diverse population of 80,000 students, faculty and staff, including 25% first-generation college students, over 25% Pell Grant students, and faculty from over 70 countries.

This is a full-time (12-month, 100%FTE), appointment for one year with the possibility of extension. Applicants may apply electronically by sending applications to Ryan Kelly (rpkelly@uw.edu). Applications should consist of an email with the subject line “Application: eDNA - OA postdoc,” and the following application materials should be attached:

1. Cover letter, 2. Curriculum vitae, 3. 1-page statement of research interests and experiences, 4. If available, one or more publications that best represent work relevant to the position, and 5. Names and full contact information for three professional references.

Items 1-5 should be merged into a single searchable PDF document attached to your email. Consideration of applications will begin immediately and continue until the position is filled. Priority will be given to applications received by September 1, 2016.

The UW and SMEA are committed to building a culturally diverse workforce. More details can be found at https://smea.uw.edu/about/diversity/. UW is an affirmative action and equal opportunity employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, gender expression, national origin, age, protected veteran or disabled status, or genetic information. All UW faculty engage in research, teaching, and service.

Ryan Kelly <rpkelly@uw.edu>

UWisconsinMadison NetworkEvolution

A postdoctoral position in regulatory network evolution is available in the lab of Dr. Sushmita Roy at the Wisconsin Institute for Discovery University of Wisconsin, Madison. Our lab develops and applies computational methods, based on statistical machine learning, to identify regulatory networks, how they change across developmental and/or evolutionary time scales, and construct predictive models of global phenotypes. Our methods integrate regulatory genomics datasets from diverse species to infer and analyze these networks. The WID is a highly interdisciplinary research institute with state-of-the-art research and computing facilities that brings together researchers from the mathematical, computational and biological sciences.

Requirements: PhD in computer science, statistics, bioinformatics, or computational biology, with a strong interest in graph theory and biological network analysis. Ability to develop, implement and apply statistical machine learning algorithms for analysis of genomic datasets.

How to apply: Please send (1) CV with publications, (2) statement of current and future research interests, (3) career goals, (4) contact information of two references to sroy@biostat.wisc.edu.

Relevant websites: WID: http://wid.wisc.edu Roy lab: http://pages.discovery.wisc.edu/ ˜ sroy
“sroy@biostat.wisc.edu” <sroy@biostat.wisc.edu>

WorkshopsCourses

Asilomar California ConservationAndGeneExpression Sep19-23 2

DEADLINE EXTENDED

Genomic variation has been a recent focus in conservation of rare and endangered species. However, the immediate response to environmental challenges will likely be determined by gene expression, which will constrain the efficacy of response and the likelihood of population persistence. Nonetheless, gene expression has been poorly studied in natural populations facing environmental and anthropogenic threats. This 5-day workshop at Asilomar, a resort on the central California coast, will focus on providing an overview of the general approaches to studying gene expression as well as the molecular and analytical tools needed to initiate and complete a field study. We will be oriented toward questions regarding the conservation of biodiversity, but the tools and approaches can be applied to a wide variety of questions. The topics covered will include: 1) RNA sampling, preservation, extraction and quantification; 2) library construction and sequencing (RNA-Seq and reduced representation bisulphite sequencing (RRBS)); 3) filtering, quality control, mapping of reads to transcriptomes and genomes; and 4) statistical analysis, mixed linear model, WGCNA, GO analysis, TOA and TCA (for whole blood samples) and other inference techniques; and 5) interpretation of results and functional analysis. The workshop will not be restricted to taxonomic groups; it will include examples from plants, invertebrates, and vertebrates. Applications from University of California graduate and post-graduate community will receive higher priority as funding is partly due to a UC president's office catalyst award. However, all applications will be considered. *There will be some special fellowship support for UC students. The $600 registration includes housing and all meals. Please apply online below. Space will be limited to 25 students. Applications will be rolling and accepted until July 15th, 2016.*

Lecturers Robert Wayne, Matteo Pellegrini, Steve Cole (UCLA), Beth Shapiro (UCSC), Jenny Tung (Duke U), Steve Palumbi (Stanford U), Bridgett vonHoldt (Princeton U), Zac Cheveron (U Montana) and Christina Richards (U South Florida).

Workshop Instructors Rachel Johnson, Tiffany Armenta, Alice Mouton, Devaughn Fraser, Gabriela Pinto, Annabel Beichman, Adam Freedman, and Amanda Lee.

Apply here: https://ucconservationgenomics.eeb.ucla.edu/workshops/
Rachel Meyer <rm181@nyu.edu>

Banff IntroToGeometricMorphometrics Jan9-13

Dear colleagues,

Registration is open for the course “INTRODUCTION TO GEOMETRIC MORPHOMETRICS- 8th edition”.

INSTRUCTORS: Prof. Chris Klingenberg (University of Manchester, UK) and Dr. JesÃºs Marugán (UAM, Spain).

Dates: January 9th-13th, 2017.

Place: Banff Center, Alberta, Canada (https://www.banffcentre.ca/)

More information and registration: http://www.transmittingscience.org/courses/geometric-morphometrics/introduction-geometric-morphometrics-canada/ This course is entitled to teach the main concepts of shape analysis based on landmark coordinates and its multivariate procedures, and how they can be put into practice across any biological discipline in which the phenotype (form) and its variation are the principal sources of information.

Program:

1. Introduction: Shape, size and biological morphology. 2. Morphometric data: Equipment, landmarks, outlines and surfaces. 3. Visualizing shapes and shape changes. 4. Looking at variation: PCA. 5. Distinguishing groups: CVA and discriminant analysis. 6. Symmetry and asymmetry. 7. Morphometrics in a messy world: outliers and measurement error. 8. Regression and allometry. 9. Covariation between things: PLS. 10. Morphological integration. 11. Modularity. 12. Phylogeny and comparative methods. 13. Putting things together: Combining analyses to solve biological questions. 14. Presentation of group work by participants.

Please feel free to distribute this information between your colleagues if you consider it appropriate.

With best regards

Sole

Soledad De Esteban-Trivigno, PhD. Scientific Director Transmitting Science www.transmittingscience.org soledad.esteban@transmittingscience.org

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Berlin BioinformaticsWithLinux Nov14-18 txt

Course: Introduction to Linux and workflows for biologists >From Monday 14th to Friday 18th November 2016 in Berlin, Germany

Instructor: Dr Martin Jones

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 genome assemblers, read mappers, and annotation tools 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.

Intended audience This workshop is aimed at researchers and technical workers with a background in biology who want to learn to use the Linux operating system and the command line environment. No previous experience of Linux is required.

Course Programme

Monday 14th - Classes from 09:30 to 17:30

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 15th - Classes from 09:30 to 17:30

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 16th - Classes from 09:30 to 17:30

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 computer 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 17th - Classes from 09:30 to 17:30

Session 7 - Combining methods

In the next two sessions i.e. one full day 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.

Session 8 - Combining methods

The second part of the next-gen workflow is to call variants to identify SNPs between our two samples and the reference genome. We'll look at the VCF file format and figure out how to filter SNPs for read coverage and quality. By counting the number of SNPs between each sample and the

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Berlin PythonIntroForBiologists Dec5-9

Introduction to Python for biologists

Monday 5^th to Friday 9^th December 2016 in Berlin, Germany

Instructor: Dr Martin Jones

Overview:

Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. This workshop is aimed at complete beginners and assumes no prior programming experience. It gives an overview of the language with an emphasis on practical problem-solving, using examples and exercises drawn from various aspects of bioinformatics work. After completing the workshop, students should be in a position to (1) apply the skills they have learned to tackling problems in their own research and (2) continue their Python education in a self-directed way. All course materials (including copies of presentations, practical exercises, data files, and example scripts prepared by the instructing team) will be provided electronically to participants.

Intended audience:

This workshop is aimed at all researchers and technical workers with a background in biology who want to learn programming. The syllabus has been planned with complete beginners in mind; people with previous programming experience are welcome to attend as a refresher but may find the pace a bit slow. If in doubt, take a look at the detailed session content below or drop Martin Jones (martin@pythonforbiologists.com) an email.

Teaching format:

The workshop is delivered over ten half-day sessions (see the detailed curriculum below). Each session consists of roughly a one hour lecture followed by two hours of practical exercises, with breaks at the organizer's discretion. There will also be plenty of time for students to discuss their own problems and data.

Assumed background:

Students should have enough biological background to appreciate the examples and exercise problems (i.e. they should know about DNA and protein sequences, what translation is, and what introns and exons are). No previous programming experience or computer skills (beyond the ability to use a text editor) are necessary, but you'll need to have a laptop with Python installed.

Course programme:

Monday 5^th - Classes from 09:30 to 17:30

Session 1-. Introduction

In this session I introduce the students to Python and explain what we expect them to get out of it and how learning to program can benefit their research. I explain the format of the course and take care of any housekeeping details (like coffee breaks and catering arrangements). I outline the edit-run-fix cycle of software development and talk about how to avoid common text editing errors. In this session, we also check that the computing infrastructure for the rest of the course is in place (e.g. making sure that everybody has an appropriate version of Python installed). Core concepts introduced: source code, text editors, whitespace, syntax and syntax errors, Python versions

Session 2-Output and text manipulation

In this session students learn to write very simple programs that produce output to the terminal, and in doing so become comfortable with editing and running Python code. This session also introduces many of the technical terms that we'll rely on in future sessions. I run through some examples of tools for working with text and show how they work in the context of biological sequence manipulation. We also cover different types of errors and error messages, and learn how to go about fixing them methodically. Core concepts introduced: terminals, standard output, variables and naming, strings and characters, special characters, output formatting, statements, functions, methods, arguments, comments.

Tuesday 6^th - Classes from 09:30 to 17:30

Session 3-File IO and user interfaces

I introduce this session by talking about the importance of files in bioinformatics pipelines and workflows, and we then explore the Python interfaces for reading from and writing to files. This involves introducing the idea of types and objects, and a bit of discussion about how Python interacts with the operating system. The practical session is spent combining the techniques from session 2 with the file IO tools to create basic file-processing scripts. Core concepts introduced: objects and classes, paths and folders, relationships between variables and values, text and binary files, newlines.

Session 4. Flow control 1 : loops

A discussion of the limitations of the techniques learned in session 3 quickly reveals that flow control is required to write more sophisticated file-processing programs, and I introduce the concept of loops. We look at the way in which Python loops work, and how they can be used in a variety of contexts. We explore the use of loops and lists together to tackle some more difficult problems. Core concepts introduced: lists and arrays, blocks and indentation, variable scoping, iteration and the iteration interface, ranges.

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CatalinaIsland California 2bRAD Genotyping Sep3-11

This year's workshop will be held September 3rd to 11th on at the USC

khufford@uwyo.edu

Chicago FuturePhy Oct RequestForProposals

FuturePhy | OpenTree | Arbor *Request for Workshop Proposals: Clade Focused Tree-Data Integration Challenges*

RFP: Two page proposals to fund small workshops and/or hackathons on completing the tree of life and integrating data layers for specific clades. This is the second set of clade workshops - you can see a summary from the first workshop on the *Open Tree of Life blog* < https://blog.opentreeoflife.org/2016/03/09/futurephy-clade-workshops/ >. In this round, we particularly encourage proposals focused on microbes, plants and fungi. *Proposal deadline:* Aug. 1, 2016 *Meeting dates:* Oct. 2016 *Location:* Chicago, IL *Participants per workshop:* 10 maximum funded (virtual attendees possible) *Contacts:* mwestneat@uchicago.edu (FuturePhy), karen.cranston@gmail.com (OpenTree), lukejharmon@gmail.com (Arbor)

The challenges to completing the Tree of Life and integrating data layers (NSF GoLife goals) are huge and vary across clades. Some groups have a nearly-complete tree but lack publicly available data layers, whereas other groups lack phylogenetic resolution or the resources to support tree / data integration. Partnering with Open Tree of Life and Arbor Workflows, FuturePhy will support a series of clade-based workshops to identify and solve specific challenges in tree of life synthesis and data layer integration.

Proposals should focus on challenges in completing the tree of life and integrating data layers for a clade or clades of interest. Cross-fertilization among systematists and other fields is desired, with focus on phylogenetic challenges, data layer development, and/or tree-data integration and analyses. How can developers of Arbor, OpenTree and other resources develop tools to help solve these challenges? What tools and infrastructure are needed for others to solve similar problems?

Proposals (using the *proposal template* < https://docs.google.com/document/d/-1SJbzT2h1oPGOCGDsETfPjAI8ZKDhrgIS9odZPuxySPw/-edit >) should include (1) the status of the phylogeny for your group, including availability of trees in Dryad, TreeBASE or Open Tree of Life, (2) target data layers for the workshops, indicating the locations and accessibility of the data, (3) key biological questions that you would like to ask, given availability of trees and data layers, (4) roadmap to tangible products, with a clear timeline, (5) the challenges to phylogeny and data synthesis in your clade, with specific targets scoped for progress towards a solution during the workshop, (6) evidence that public data exist as a starting point or access to data that can be made public.

General plans & logistics. Each workshop may involve up to 10 funded attending participants, with the first set of workshops to happen in parallel at the same time and location. Open Tree of Life, FuturePhy and Arbor personnel will be there to demo, discuss and plan implementation. Each group should involve participants familiar with data analysis / integration / use of web services (e.g., in R, python). Groups can focus anywhere on the spectrum of completing phylogeny to integrating data layers. Groups agree to make assembled data or tools publicly available and to provide a post-workshop report after the event. Phylogenetic data will be incorporated into Open Tree of Life.

Evaluation. Proposals will be evaluated on (1) the feasibility of solving the specific challenges, including evidence for publicly-available data; (2) participant diversity (discipline, career stages, gender, ethnicity), (3) participant expertise, (4) how solving these challenges will benefit researchers in other clades, (5) potential for increasing public data, tools, products, and contributing trees to Open Tree of Life and related initiatives.

– Mark W. Westneat Professor, Department of Organismal Biology and Anatomy Director of Graduate Studies, Integrative Biology University of Chicago 1027 E. 57th Street, Chicago IL 60637 (773) 702-2412 Lab Web site: http://westneatlab.uchicago.edu email: mwestneat@uchicago.edu

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mwestneat@gmail.com

CollegePark MD Bioinformatics Sep15-18

Hi Everyone-

We are offering a Fall Workshop in Introductory Bioinformatics

Where/when: University of Maryland College Park, Maryland September 15-18, 2016

The handling of large datasets has become intractable without some level of bioinformatic literacy. Many biologists find that there is a steep learning curve to develop the confidence required to explore their genomics datasets effectively. This bioinformatics short course includes a rich collection of hands-on instruction and lectures specifically intended to help novice users become comfortable with a range of tools currently used to analyze deep sequencing data. There is no prerequisite for this course other than a willingness to learn and to work hard throughout the week. All workshop exercises will be implemented via VirtualBox and focus primarily on Illumina data; however, we will also include PacBio data during the genome assembly tutorial. Course participation is limited to 25 students to ensure an intimate learning environment. Course tuition is $800 and is open to graduate students, postdocs, staff, faculty, and industry researchers on a first come basis.

Full course information, contact, instructor info and application instructions at https://biodatatraining.wordpress.com Please contact us if you have any questions or need additional info. Hope to see you in College Park.

Nic and Ian

biodatatraining@gmail.com

Faro Portugal StatisticalGenetics

We still have a few places available... please apply to ccmaratt@ualg.pt

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ADVERTISEMENT WEBSITE: http://att.ccmar.ualg.pt/statistical_genetics_2016 WORKSHOP IN STATISTICAL GENETICS - taught by *BRUCE WEIR* - Professor of Biostatistics, and Director of the Institute of Public Health Genetics at the University of Washington. Bruce Weir is the author of the textbook “Genetic Data Analysis” (3rd edition in preparation) and he has directed the Summer Institute in Statistical Genetics since 1996. http://www.gs.washington.edu/faculty/weir.htm, http://www.ncbi.nlm.nih.gov/pubmed/?term=Bruce+Weir DESCRIPTION: A unified treatment for the analysis of discrete genetic data, starting with estimates and sample variances of allele frequencies to illustrate genetic vs statistical sampling and Bayesian approaches. A detailed look at Hardy-Weinberg and linkage disequilibrium, including the use of exact tests with mid-p-values and a new look at X-chromosome Hardy-Weinberg testing. A new characterization of population structure with F-statistics, based on allelic matching within and between populations with individual relationship estimation as a special case. Analyses illustrated with applications to forensic science and association mapping, with particular reference to rare variants.

VENUE: Centre of Marine Sciences, University of the Algarve, Faro, Portugal. http://ccmar.ualg.pt - Google maps: https://goo.gl/cM78fp

DATE: 8th-9th September 2016

FORMAT: 2-day workshop, lectures and hands-on practical sessions (attendees will need to bring laptops). The course is equivalent to 3 European ECTS credits.

INTENDED AUDIENCE: PhD students, post-doctoral and advanced researchers (but no formal restriction)

REGISTRATION FEE: 240

Registration does not include travel and lodging. Faro has an international airport located 4 km from the Gambelas Campus of the University of Algarve where the course will take place.

HOW TO APPLY: Applications in the form of a CV and motivational letter should be sent to ccmaratt@ualg.pt .

SCHOLARSHIPS: At least 2 scholarships to cover registration fees will be awarded to PhD students; applicants should indicate if they would like to be considered and must send proof of student status.

ACCOMMODATION: Recommended: Hotel Aeromar at Faro beach (http://www.aeromar.net/en) has temporarily reserved (until 31st May) and discounted 8 double rooms, priced 62.5 and 80, double and single occupancy, respectively (mention CCMAR reservation when booking). Additional accommodation at the beach and in Faro centre: http://goo.gl/mgG85g. A minibus service will run between the beach, town centre, and campus.

CONTACTS: Ester Serrão - Assistant Professor, UALG/CCMAR - eserrao@ualg.pt Rita Castilo - Assistant Professor, UALG/CCMAR - rcastil@ualg.pt

Advanced Technologies and Training programme @ CCMAR 2016 ccmaratt@ualg.pt <ccmaratt@ccmar.ualg.pt>, att.ccmar.ualg.pt/statistical_genetics_2016

The Centre of Marine Sciences (Centro de Ciências do Mar, CCMAR) is an independent multidisciplinary, non-profit institute located on the Gambelas campus of the University of the Algarve in Faro with ˜250 members and a mission to promote research and education in the marine sciences. Faro (http://www.algarve-tourist.com/Faro-portugal-guide.html) is the capital city of the Algarve region of southern Portugal and borders the Ria Formosa National Park (http://www.formosamar.com/en). The Algarve (http://www.visitalgarve.pt/?idioma=uk) boasts > 300 days of sun per year, stunning beaches and mountain vistas, opportunities for diving, golf, and other sporting activities, and a unique traditional regional cuisine (esp. seafood). A variety of optional social activities will be organised to coincide with the course and special events can be organised upon request for participants and/or accompanying persons (diving, surf, stand-up paddle, windsurf, kayaking, horse-riding, tennis, birdwatching, nature walks, boat guided tours, fishing, etc). < http://orcid.org/0000-0002-4927-979X >

Cymon Cox <cymon.cox@googlemail.com>

Ferrara Italy NaturalSelection Dec16-18

We are pleased to announce the workshop "Inferring natural selection from genomic data", which will be held in Ferrara, Italy, December 16-18, 2016.

Preliminary information is available at www.sibe2016.it. Confirmed speakers include Andrea Betancourt, Dan Graur, Rasmus Nielsen, Ludovic Orlando, and Pavlos Pavlidis. Three round tables based on general themes or specific papers are planned to stimulate the discussion among participants. Selected participants will be asked to present their contributions.

Registration opens on September, 15.

The workshop is supported by the Italian Society of Evolutionary Biology (http://www.sibe-iseb.it/), in collaboration with the University of Ferrara.

Giorgio Bertorelle Department of Life Sciences and Biotechnology University of Ferrara

"ggb@unife.it" <ggb@unife.it>

Knoxville ImprovingGeneticStatistics Nov7-9

The National Institute for Mathematical and Biological Synthesis (NIMBioS), an NSF funded synthesis center located at the University of Tennessee, is seeking applicants for a workshop on improving analytical approaches in conservation and population genetics. The workshop will be Nov 7-9. A brief summary is below and more information and a link to apply can be found here: http://www.nimbios.org/workshops/WS_nextgen DEADLINE TO APPLY IS VERY SOON- JULY 24. Financial support for travel, meals, and lodging (typically full funding) is available for workshop attendees.

As biodiversity loss accelerates and environmental challenges mount, there is need for quantitative evaluation of the status and trends of genetic biodiversity. However, appropriate mathematical tools for this evaluation are lacking. Despite major recent advances in obtaining genetic data, current genetic metrics are piecemeal, may be incomparable across studies and data types, and are often collected and presented in an ad hoc manner.

There is urgent need to conceive and develop standard, summary-level genetic indices that are robust, easily interpretable and tractable across diverse datasets. In this workshop we will develop a framework for constructing these mathematical tools. Specifically, we will: identify key attributes of successful indices in biodiversity science, survey and critique existing genetic metrics, and identify potential statistical approaches suitable for summarizing the highly dimensional nature of genetic data. We hope the workshop will inspire synthesis papers, new collaborations, and research funding proposals for developing, evaluating and distributing new genetic indices. The inherent challenges of our aims require participants from diverse fields: statistics, mathematics, ecology, evolutionary biology, conservation science, complexity, genetics, network and biodiversity science. Please apply if you have interest in these fields and appreciate broad collaboration and cross-disciplinary work.

Sean Hoban <shoban@alumni.nd.edu>

LeipzigU EvolutionEcol Nov18-20

Dear colleagues,

it is our pleasure to announce the 58th Phylogenetic Symposium "Evolution meets Ecology" which will take place in Leipzig, November 18-20, 2016. (https://conference.uni-leipzig.de/phylosym2016/)

Both ecology and evolution try to understand the diversity of life, including the diversity of species, their genetic inventory, the diversity of functions, interactions and communities; how species and communities evolve, expand, and demise. We aim at highlighting recent achievements in evolutionary ecology, their impact on phylogenetics and biodiversity research, and vice versa.

Confirmed invited speakers are:

Erica Edwards (Providence, Rhode Island): The megaphylogeny approach to big evolutionary questions: are we ready for an 'automated natural history'?

Catherine Graham (Swiss Federal Institute for Forest, Snow and Landscape Research WSL): Linking patterns and processes across scales: a case study with Neotropical hummingbirds

Susanne Fritz (Frankfurt): Macroevolution meets macroecology: diversification, biogeography, and the evolution of ecological niches in birds

Alexandre Antonelli (Göteborg): Teasing apart the ecological and environmental drivers of diversification

Susanne Renner (Munich): Do trees and shrubs of North America, Europe, and Asia have different winter chilling and spring warming requirements? Insights from experiments, monitoring, and phylogenies

Marten Winter (Leipzig/Halle): Phylogenetic diversity: A biodiversity facet under threat - insights from invasion ecology and nature conservation

Christoph Bleidorn (Madrid): Understanding Wolbachia-arthropod symbiosis using comparative genomic analyses

Christian Lexer (Vienna): Plant evolutionary genomics: speciation continuum and beyond

Poster presentations by students and postdocs are welcome. The deadline for abstract submission is September 15, 2016. Please submit your abstracts directly to Martin Schlegel: schlegel@rz.uni-leipzig.de

Registration can be done online, and is free of charge.

We hope to see you soon here in Leipzig!

Kind regards

Alexandra Muellner-Riehl and Martin Schlegel Leipzig University

muellner_alexandra@yahoo.de

Montana ConservationGenetics Sep5-10 3

Course/workshop announcement:

Last chance to participate in the ConGen 2.0 Course and Workshop (3 spaces left)

Theme: Applications of Next Gen Sequencing Data to Understand Population Connectivity, Local Adaptation, and Environmental Influences on Genomic Variation.

Instructors include: Fred Allendorf, Tiago Antao, Brian Hand, Paul Hohenlohe, Marty Kardos, Tabatha Graves, Jeff Good, Gordon Luikart, Garret McKinney, Mike Miller, Brice Sarver, Mike Schwartz, David Tallmon, Robin Waples, Diane Whited, and more.

When: September 5-10, 2016, Flathead Lake Biological Station, Montana

For details on ConGen-2.0: see http://www.umt.edu/-sell/cps/congen/ Past courses: see http://-onlinelibrary.wiley.com/doi/10.1111/mec.13647/full ; and see: Andrews and Luikart 2014, Molecular Ecology, 23:1661-7. doi: 10.1111/mec.12686.

ConGen 2013 - dinner by the lake

Objective: To provide training in conceptual and practical aspects of data analysis for the population and evolutionary genomics of natural and managed populations. Emphasis will be on next generation sequence data analysis (RADs, exon capture, and whole genome sequence analyses) and interpretation of output from recent novel statistical approaches and software programs. The course include discussions (in a workshop like format) among young researchers (student participants) and >12 leaders in population genomics (instructors) to help develop the next generation of conservation and evolutionary geneticists.

Who should apply: Advanced Undergrads, Ph.D. students, post-docs, faculty, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. Participation will be limited to 25-30 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own data to analyze.

gordon.luikart@mso.umt.edu

Scotland GeneticDataAnalysis Aug16-20 Part funded scholarships

"Genetic data analysis/exploration using R" - FUNDING AVAILABLE!

PR STATISTICS ARE PLEASED TO ANNOUNCE THAT THEY HAVE SECURED SOME FUNDING TO CONTRIBUTE TOWARDS TUITION FEES AND ACCOMMODATION WITH A LIMITED NUMBER OF 'COURSE ONLY PLACES' AT 240.00 (inc VAT) or 'ALL INCLUSIVE PLACES' AVAILABLE AT 480.00 (inc VAT).

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 August 1st, successful applicants will be notified by the 3rd August.

Full course details are given below

Delivered by Dr. Thibaut Jombart

http://prstatistics.com/course/genetic-data-analysis-using-r-gdar/ This course will run from 16th - 20th August, Millport Field Station, Ilse of Cumbrae, Scotland This course will provide an extensive overview of exploratory methods for the analysis of genetic data using the R software and aim to equip participants with powerful resources for tackling increasingly common challenges in genetic data analysis.

The course is aimed at PhD students, research postgraduates, and practicing academics as well as persons in industry working with genetic data in fields such as molecular ecology, evolutionary biology, and phylogenetics. This course will provide a comprehensive introduction to various statistical approaches for the analysis of genetic data.

Course content is as follows Day 1 Introduction to phylogenetic reconstruction - Lecture 1a: Reconstructing phylogenies from genetic sequence data. Three main approaches covered: distance-based phylogenies; maximum parsimony; and likelihood-based approaches. - Lecture 1b: Short R refresher. - Practical 1: Phylogenetic reconstruction using R. Three main approaches plus rooting a tree; assessing/testing for a molecular clock; and bootstrapping. Main packages: ape, phangorn.

Day 2 Introduction to multivariate analysis of genetic data - Lecture 2: Key concepts in multivariate analysis. Focus on using factorial methods for genetic data analysis. - Practical 2: Basics of multivariate analysis of genetic data in R. Topics include: data handling, population genetic tests of population structure (PCA, PCoA). Main packages: adegenet, ade4, ape.

Day 3 Exploring group diversity - Lecture 3: Approaches to identifying and describing genetic clusters. Topics include: hierarchical clustering, K-means, population-level multivariate analysis (between-group-PCA, DA, DAPC). - Practical 3: Applying the approaches covered in morning lecture and emphasising their strengths and weaknesses. Main packages: adegenet, ade4.

Day 4 Spatial genetic structure - Lecture 4: Discussing the origin and significance of spatial genetic patterns, and how to test or them. - Practical 4: Visualising and analysing spatial genetic data. Topics: spatial density estimates, Moran/Mantel tests, mapping principal components in PCA, spatial PCA. - Main packages: adegenet, glmnet. Main packages: adegenet, glmnet.

Day 5 Using R for reproducible science - Lecture 5: Using R for reproducible science. - Practical 5: Practical session based on morning lecture - Main packages: knitr, Sweave, rmarkdown - Option to discuss own data (time permitting)

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

Upcoming courses - email for details oliverhooker@prstatistics.com 1. INTRODUCTION TO BIOINFORMATICS USING LINUX (August) 2. INTRODUCTION TO BAYESIAN HIERARCHICAL MODELLING (August) 3. INTRODUCTION TO PYTHON FOR BIOLOGISTS (October) 4. LANDSCAPE (POPULATION) GENETIC DATA ANALYSIS USING R (October) 5. APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS (October) 6. PHYLOGENETIC DATA ANALYSIS USING R (October/November) 7. SPATIAL ANALYSIS OF ECOLOGIC AL DATA USING R (November) 8. ADVANCING IN STATISTICAL MODELLING USING R (December) 9. MODEL BASED MULTIVARIATE ANALYSIS OF ECOLOGICAL DATA USING R (January) 10. NETWORK ANAYLSIS FOR ECOLOGISTS USING R (March) 11. INTRODUCTION TO GEOMETRIC MORPHOMETRICS USING R (June)

Dates still to be confirmed - email for details oliverhooker@prstatistics.com - STABLE ISOTOPE MIXING MODELS USING SIAR, SIBER AND MIXSIAR USING R - INTRODUCTION TO R AND STATISTICS FOR BIOLOGISTS - BIOINFORMATICS FOR GENETICISTS AND BIOLOGISTS Oliver Hooker PR Statistics

– Oliver Hooker PR statistics

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www.prstatistics.com www.prstatistics.com/organiser/oliver-hooker/

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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

Scotland LandscapeGeneticDataAnalysis Oct17-21

"Landscape (population) genetic data analysis using R"

Delivered by Dr. Rodney Dyer

http://prstatistics.com/course/landscape-genetic-data-analysis-using-r-lndg/ This course will run from 17th - 21st October 2016 at SCENE Field Station, Loch Lomond, Glasgow, Scotland 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

Upcoming courses - email for details oliverhooker@prstatistics.com 1. ADVANCES IN SPATIAL ANALYSIS OF MULTIVARIATE ECOLOGICAL DATA (July) 2. INTRODUCTION TO BIOINFORMATICS USING LINUX (August) 3. GENETIC DATA ANALYSIS / EXPLORATION USING R (August) 4. INTRODUCTION TO BAYESIAN HIERARCHICAL MODELLING (August) 5. INTRODUCTION TO PYTHON FOR BIOLOGISTS (October) 6. APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS (October) 7. PHYLOGENETIC DATA ANALYSIS USING R (Octobe/November) 8. SPATIAL ANALYSIS OF ECOLOGIC AL DATA USING R (November) 9. ADVANCING IN STATISTICAL MODELLING USING R (December) 10. MODEL BASED MULTIVARIATE ANALYSIS OF ECOLOGICAL DATA USING R (January) 11. ADVANCED PYTHON FOR BIOLOGISTS (February) 12. NETWORK ANALYSIS FOR ECOLOGISTS USING R (March) 13. INTRODUCTION TO GEOMETRIC MORPHOMETRICS USING R (June)

Dates still to be confirmed - email for details oliverhooker@prstatistics.com - STABLE ISOTOPE MIXING MODELS USING SIAR, SIBER AND MIXSIAR USING R - INTRODUCTION TO R AND STATISTICS FOR BIOLOGISTS - BIOINFORMATICS FOR GENETICISTS AND BIOLOGISTS

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Teaching QuantBiol

Apply by July 15, 2016 at: https://qubeshub.org/groups/mathattitudes/application Quantitative Undergraduate Biology Education Synthesis (QUBES) is pleased to offer a unique networking and professional development opportunity from September - December 2016 for faculty interested in alleviating math anxiety in undergraduate biology students. Quantitative skills are essential for student success in biology, and math attitudes and anxiety can have strong effects on both persistence and performance. This mentoring network will familiarize faculty with background on how math attitudes can impact Biology students, and help participants explore a range of tools to address math attitudes and anxiety in their Biology courses. QUBES (https://qubeshub.org) is an NSF-funded virtual center that supports collaboration to promote quantitative biology education at the undergraduate level.

Benefits of Participation

If you are selected, you will receive:

-Access to strategies to affect math attitudes and anxiety across general themes such as metacognition, growth mindset, learning progressions, model thinking, and data visualization, as well as specific ready-to-use teaching materials in each of these areas. Participants will choose a focal type of intervention, and work to modify, develop, and implement the materials in their own courses in Fall 2016.

-Access to peer mentors on lecture/classroom/lab effective tips and strategies in small group virtual meetings every two weeks

-Support during a half-day workshop at the NABT meeting on November 3, 2016 in Denver, CO, and a reduced registration fee for the meeting

-Opportunity to develop and publish new math attitude materials on qubeshub.org

Commitments

To qualify for this network, participants must commit to:

-Teaching a biology course in Fall 2016

-Incorporating at least one type of math attitude intervention in their fall course

-Attending 30-min online meetings every other week

-Attending the workshop at NABT < http://www.nabt.org/websites/institution/index.php?p=10 > on Nov 3, 2016 and participate in the NABT conference

-Participating in active discussions on QUBESHub

-Sharing materials with the FMN community

-Participating in reporting and evaluation of the Faculty Mentoring Network

Visit https://qubeshub.org/groups/mathattitudes for more information. Apply by July 15, 2016! Questions? Contact Arietta Fleming-Davies at ariettaflemingdavies "at" gmail "dot" com

"anm116@pitt.edu" <anm116@pitt.edu>

UComahueBariloche PhylogeneticMethodsInR Dec12-16

Una introducción a los métodos comparativos filogenéticos en R (An introduction to comparative phylogenetic methods in R) December 12-16 2016 San Carlos de Bariloche, Río Negro, Argentina Instructor:Dr. Liam Revell More info: Lina Moreno Azócar (morenoal@comahue-conicet.gob.ar)

Thank you so much,

kind regards,

Dra. Lina Moreno Azócar Becaria posdoctoral CONICET Laboratorio de Fotobiología Instituto de Investigaciones en biodiversidad y medio ambiente Quintral 1250 TE: +54 (9 294) 4344642 http://www.researchgate.net/profile/Debora_Moreno_Azocar/ Lina Moreno Azócar <morenoal@comahue-conicet.gob.ar>

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.