EvolDir

March 1, 2018

Month in Review

Foreword

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

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

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

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Conferences

Ankara ArchaeologyOfHumanImpact Sep2-7

Dear colleagues,

This email to raise your attention about the session we are organizing during the next International Congress of Zooarchaeology in Ankara (http://www.icaz2018ankara.com), concerning “*The archaeology of human impact on faunas”*. The aim of this session is to bring together researchers exploring the question of the environmental impact of past societies thought the studies of faunas. We are welcoming people working on every taxa and geographic areas, and using all kind of methodologies.

*Abstract:** Archaeological sciences and especially zooarchaeology have demonstrated their relevance to address the impact of humans on past aquatic and terrestrial faunas. This impact leads to the modification of faunal communities which is driven by a wide diversity of phenomena like introduction or extinction/extirpation of species, and erosion of the genetic or morphological diversity of taxa. The archaeological record is crucial to understand the slow mechanisms leading to the alteration of faunas as well as the environmental impact of past human populations in the light of the archaeological record. This kind of research is of special interest in the context of the current sixth mass extinction crisis, and is a good opportunity to generate exchange between zooarchaeology and other scientific fields like ecology and evolution sciences. *

This session seeks to discuss methodological questions and to present study case concerning every aspect of human impact on past wild fauna.

Communicants working on all taxa and regions of interest for these questions are welcome in order to generate fruitful discussions about global trends observed in the archaeological record as well as current and future evolution of this field of research. Transdisciplinary approaches are especially welcome. Studies of modern faunas that can be used as model for the study of past assemblages are also relevant.

The meeting will take place between the *2nd to the 7th of September*. The deadline for abstract submission is the *30th of March*. Do not hesitate to get in touch with us for any information. Of course, feel free to forward this message to any potentially interested colleague.

We hope to see you in Ankara,

Best regards,

Corentin Bochaton

Arnaud Lenoble

Anne Tresset

– Corentin Bochaton Postdoctoral Researcher - FYSSEN Fundation fellow

Max Planck Institute for the Science of Human History - Department of Archaeology 10 Kahlaische Straáo̲e 07745 Jena, Germany

Institutional email: bochaton@shh.mpg.de Phone: +49 3641 686 747

ResearchGate: https://www.researchgate.net/-profile/Corentin_Bochaton Corentin Bochaton <corenboch@gmail.com> Corentin Bochaton <corenboch@gmail.com>

Barcelona Hennig2018 Sep16-20

Dear Colleagues

It is our great pleasure to invite you all to the XXXVII Annual Meeting of the Willi Hennig Society that will be held in Barcelona, from September 16th to 20th, 2018. Please, save the dates.

To honour Barcelona'Âs long tradition of open-mindedness and eclecticism, we propose a meeting where all perspectives and approaches to modern systematic research could be presented and discussed. The Willi Hennig Society meeting in Barcelona will provide an arena for exchanging ideas, sparking collaborations, developing new vocations and training the next generation of systematic biologists.

We especially would like to encourage the participation of women in a plea for a most needed gender equality.

We would also like to remind you that the society awards three student prizes: The Rosen Prize for $1000, which is given to the best poster presentation; The Brundin Prize for $1500 for an outstanding oral presentation; and the Hennig Prize for $3000 for the presentation of highest scientific content. In addition, students who register for the meetings are admitted to the banquet for free.

The meeting will be structured around 4 main symposia: “Understanding diversity through space”, “Understanding diversity through time”, “The rhythms of Life” and “Big questions, big data”. Additional contributions on any other filed of Biological systematics are also welcome.

Confirmed plenary speakers are:

Christophe Dessimoz, University of Lausanne, Switzerland Greg Edgecombe, The Natural History Museum, London, UK Dan Rabosky, University of Michigan, USA Isabel SanmartÂÂn, Real JardÂÂn BotÂ'nico de Madrid, Spain

On line registration and abstract submission will open in the next days (mid-February 2018). Deadline for abstract submission and Early bird registration is April 30th 2018.

For any further information please contact us directly at hennig2018bcn@gmail.com or check the congress website at http://www.hennig2018bcn.org We look forward to seeing you in September!

Organizers: Miquel A. Arnedo, Universitat de Barcelona (chair) Carles Ribera, Universitat de Barcelona Marta Riutort, Universitat de Barcelona Julio Rozas, Universitat de Barcelona Salvador Carranza, Institut de Biologia Evolutiva (CSIC-UPF) Ignacio Ribera, Institut de Biologia Evolutiva (CSIC-UPF) Rosa FernÂ'ndez, Centre de RegulaciÂÂ GenÂÂmica Dacha Atienza, Museu de CiÂÂncies Naturals de Barcelona Francesc Uribe, Museu de CiÂÂncies Naturals de Barcelona

marnedo@gmail.com

Bordeaux SMEF10Morphometrics Jun18-20

Dear colleagues,

We are pleased to announce the 10th SMEF “Symposium de Morphométrie et Ãvolution des Formes” which will be held in Bordeaux (France), June 18th to 20th, 2018.

The SMEF meetings aim to foster exchanges among users of morphometric approaches in different fields of research, such as evolutionary biology, developmental biology, systematics, paleontology, bioarchaeology and ecology. This approach is traditionally targeted at researchers interested in the morphological quantification of biological form. This year, the symposium will also include a special focus on the material culture in archeology.

More information, registration, and abstract submission will be available soon on the SMEF10 website:

https://smef-2018.sciencesconf.org/ This year we are very glad to welcome Dr. Philipp Mitteröcker (University of Vienna) as keynote speaker.

For anyone interested in visiting the historical center of Bordeaux, a mid-congress guided visit will be organized.

The deadline for abstract submission is March 30^th 2018.

We look forward to seeing you in Bordeaux!

The organizing committee of the 10^th SMEF

Nicolas Navarro <nicolas.navarro@u-bourgogne.fr>

Galway Ireland AmphioxusEuroEvoDevo Jun25-26

Dear colleagues,

We are very pleased to announce that the third Amphioxus Satellite Meeting will be held ahead of the 2018 EuroEvoDevo Meeting in Galway, Ireland, on Monday, June 25, and Tuesday, June 26, 2018 (http://www.evodevo2018.eu/ehome/evodevo2018/Satellitesessions).

Everybody working on amphioxus and/or interested in evolutionary developmental biology questions related to this model are cordially invited to participate!

If you are interested in giving a talk or in presenting a poster at the Amphioxus Satellite Meeting, please submit your abstract directly to one of the organizers: Michael Schubert (michael.schubert@obs-vlfr.fr), Hector Escriva (hescriva@obs-banyuls.fr) or Jr-Kai Sky Yu (jkyu@gate.sinica.edu.tw).

Importantly, please note that the abstract submission deadline for the main EuroEvoDevo Meeting (i.e. February 16, 2018) does NOT apply to the Amphioxus Satellite Meeting!

Instead, we request to receive your abstracts by April 13, 2018, which is the early bird registration deadline. For registration, please use the website of the main EuroEvoDevo Meeting (http://www.evodevo2018.eu/ehome/evodevo2018/Registration < http://www.evodevo2018.eu/ehome/evodevo2018/Registration >).

We are very much looking forward to seeing you in Galway, Ireland, this coming June!

Sincerely Yours Michael, Hector, and Sky

Michael Schubert Evolution of Intercellular Signaling in Development (EvoInSiDe) Group Laboratoire de Biologie du Développement de Villefranche-sur-Mer (UMR 7009 - CNRS/Sorbonne Université) Observatoire Océanologique de Villefranche-sur-Mer 181 Chemin du Lazaret 06230 Villefranche-sur-Mer France Tel: + 33 (0) 4 93 76 37 91 Fax: + 33 (0) 4 93 76 37 92 Web: http://lbdv.obs-vlfr.fr/en/evoinside.html Michael Schubert <michael.schubert@obs-vlfr.fr>

Hungary SocialEvolution Apr19-22

SOCIAL EVOLUTION - conference in Hungary, 19-22 April 2018

To celebrate the launch of an ELVONAL cutting edge research project on breeding system evolution, we are organising a conference in Hungary 19-22 April 2018. ELVONAL is a new funding stream by the Hungarian government to support top science across all disciplines, and our team was one of the 12 winners (see Nature 2017, 551: 425). This will be a 5 year project that will test key hypotheses of breeding system evolution using genomic, immunologic and demographic approaches using shorebirds (plovers, sandpipers and allies) that exhibit an unusual diversity of mating systems and parental care as a model.

The topic of the 1st ELVONAL conference is SOCIAL EVOLUTION and we have the following keynote speakers:

Dr Veronika Bokony, Hungarian Academy of Sciences: sex determination and sex ratios Professor John McNamara, University of Bristol: social behaviour and life-history evolution Prof Eors Szathmary, Hungarian Academy of Sciences: social evolution and major transitions Dr Ferenc Jordan, Hungarian Academy of Sciences: social networks and social interactions Dr Araxi Urrutia, University of Bath: genomic basis of evolution of social behaviour

The provisional programme is as follows: Thursday 19 April 2018: Arrival, Welcome reception

Friday 20 April 2018: Full day scientific programme: presentations by senior speakers, and contributions by students and young academics

Saturday 21 April: Full day scientific programme: presentations by senior speakers, and contributions by students and young academics

Sunday 22 April: Bird watching and/or departure

The conference will provide opportunities to discuss results and future plans in a friendly but productive environment. There are opportunities for poster presentation and talks for those academics, postdocs and students interested in presenting their work. Presentation offers from women and minority candidates are especially welcome. Each evening there will be a social event that will include slide shows, round table discussions and/or Hungarian folk dancing.

The event will take place in the Visitor Centre of Hortobagy National Park http://www.hnp.hu/hu/szervezeti-egyseg/turizmus/oldal/hnp-latogatokozpont The Visitor Centre is the hub for the National Park that is a renowned protected area recognised as a UNESCO World Heritage site https://en.wikipedia.org/-wiki/Hortob%C3%A1gy_National_Park To make the Conference accessible to students, we have two types of registration:

(i) 150 EUR - includes accommodation for 3 nights in shared rooms, and breakfast, lunch and dinner for 3 days, and registration

(ii) 20 EUR - includes only registration.

For more information and registration form please contact workshop2018.hortobagy@gmail.com

Registration deadline is 1 March 2018. We have limited places that will be filled by first-come first-served basis.

Professor Tamas Szekely Karola Szemán University of Bath & Debrecen University of Debrecen

Tamas Szekely <T.Szekely@bath.ac.uk>

Izmir Turkey EcolEvolution Jul18-20

We would like to announce the Ecology and Evolutionary Biology Symposium in Turkey (EEBST), which will take place this year on 18-20 July 2018 at Dokuz Eylul University, Continuing Education Center (DESEM), in Izmir, Turkey. EEBST'18 will be the fifth in a series of symposia organized yearly by the Ecology and Evolutionary Biology Society of Turkey. The language of the symposium is English, and is well attended by diverse international faculty and students from Europe, Middle East, West Asia, and North America. The symposium also aims to stimulate international collaborations.

This year's keynote speakers will be Beatriz Vicoso (Institute of Science and Technology, Austria), Robert Ptacnik (University of Vienna, WasserCluster Lunz, Austria) and Virginie Courtier-Orgogozo (Institute of Jacques Monod, Paris).

We are pleased to invite oral and poster presentations in all areas of Ecology and Evolutinary Biology. Registration and abstract submissions are now open and the deadline for abstract submission is April 1st, 2018. Early registration closes May 15th, 2018. For any additional information please visit https://eebst.org/registration/ . We look forward to see you in Ãzmir.

On behalf of the EEBST'18 Organizing Committee.

Efe Sezgin <efeszgn0@gmail.com>

Marseilles EvolBiol Sep25-28 DeadlineJun30

Dear all The dead line for the next evolutionary biology meeting at Marseilles

is June 30

the meeting Will take place on September 25-28 2018 in Marseilles (South of France)

more info : aeeb.fr

The following subjects will be discussed:

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

contact Marie-Hélène Rome marie-helene-rome@univ-amu.fr

Pierre Pontarotti

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

Montana EvolutionaryGenomics Adaptation Jun1-3

The first annual symposium on the Evolutionary Genomics of Adaptation will be held on June 1-3, 2018 at Flathead Lake Biological Station near Polson Montana.

This symposium is linked to a new NSF-funded research and training network (www.unveilnetwork.org). The aim of this network is to both advance the science of genome-to-phenome connections in natural populations, and use these insights to inform effective conservation and resource management strategies and the use of emerging biotechnologies in conservation biology. As a result, both the network and the symposium are interdisciplinary, involving evolutionary geneticists, ecologists, conservation biologists, and resource managers, as well as ethicists and social scientists.

This year'Âs symposium will feature talks by keynote speakers, Sally Aitkin (University of British Columbia), Benjamin Blackman (UC Berkeley), Nancy Chen (University of Rochester), and Mike Shapiro (University of Utah), as well as talks by symposium organizers and other invited talks selected from submitted abstracts, and poster sessions. Talks will feature cutting-edge studies in the following overlapping fields: population genomics, environmental adaptation, ecological genetics, quantitative genetics, systems genetics, genetic engineering and conservation genomics

In addition to a full scientific program, the symposium will feature a half-day interdisciplinary panel discussion and workshop on the ethics of genomic interventions for solving conservation challenges.

REGISTRATION AND ABSTRACT SUBMISSION IS NOW OPEN. For more information, visit https://goo.gl/2QrjF4

Travel awards are available for graduate students

Organizers: Zac Cheviron - University of Montana Lila Fishman 'V Unviersity of Montana Jeff Good 'V University of Montana Scott Mills 'V University of Montana Kristi Montooth 'V University of Nebraska Colin Meiklejohn 'V University of Nebraska Jay Storz 'V University of Nebraska

Zac Cheviron Assistant Professor Division of Biological Sciences Graduate Program in Organismal Biology and Ecology University of Montana Missoula MT 59812 ph. 406-243-4496 email. zac.cheviron@mso.umt.edu web. chevironlab.org

zac.cheviron@mso.umt.edu

NewZealand TDWG2018 Phylogenetics Aug25-Sep02

*Symposium on linking phylogeny and biodiversity data, TDWG2018 - Call for AbstractsWe are calling for abstract submissions to a symposium titled 'Linking biodiversity data through phylogenetic knowledge' at the Biodiversity Information Standards (TDWG) conference, August 25 - September 1, 2018, Dunedin, New Zealand. A description of the symposium is available here: https://tdwg.github.io/conferences/2018/sessions/S14 **We will be able to provide a limited amount of funding to offset expenses where needed and on a competitive basis.**The symposium aims to illuminate opportunities offered by integrating phylogenetic knowledge with biodiversity data, examine the methodological and computational challenges of doing so, and highlight approaches addressing these challenges. We especially encourage submissions that span the domains of evolutionary biology, bioinformatics (i.e. phyloinformatics) and biodiversity informatics to address the themes of this symposium. Symposium keynote speaker: Dr. Susan Perkins (American Museum of Natural History).To register your intent to submit an abstract, share demographic information, and/or to apply for funding, please go to this site and fill in the Google form: https://goo.gl/forms/bPhYCLSxakcEyBZe2 Even if you don't require funding, registering your intent to submit and sharing your demographic information will help us to foster a diverse group of speakers that provide a variety of perspectives on the symposium's subject.The deadline for abstract submission is Mar 12, 2018, but for the above reason we would appreciate hearing about your intent and receiving your application as early as possible. Please contact Dr. Guanyang Zhang <gyz151@gmail.com> with any questions.Thank you,Guanyang Zhang*, Emily Jane McTavish+, Gaurav Vaidya*, Hilmar Lapp^, Nico Cellinese** Florida Museum of Natural History, University of Florida+ University of California, Merced^ Duke University*

Guanyang Zhang <gyz151@gmail.com>

ParkCity Utah EvolutionMedicine Aug1-4

Abstract submission and Early Registration are now open for the 4th annual meeting of the International Society for Evolution, Medicine & Public Health Aug 1-4 in Park City Utah. Full information at https://-isemph.org/annualmeeting The International Society for Evolution, Medicine, & Public Health will offers its fourth annual conference in spectacular Park City, Utah, a mountain recreation destination near Salt Lake City. Health professionals, researchers, teachers and students from many scientific disciplines from around the world will gather to share their ideas, approaches and research findings at the intersection of evolutionary biology, medicine, and public health. A special wilderness medicine pre-meeting will be of interest to many. CME available. Society members get a substantial discount on registration fees.

Keynote speakers include:

Val Curtis, London School of Hygiene & Tropical Medicine Maria Gloria Dominguez-Bello, NYU School of Medicine Katie Hinde, Arizona State University Chris Kuzawa, Northwestern University Andrew Read, Penn State University Jacob Scott, Cleveland Clinic

Registration and abstract submission are open now for talks and posters. Abstracts must be submitted by March 15th, decisions will be announced March 31 and Early Registration closes April 30.

http://isemph.org Randolph Nesse <nesse@asu.edu>

PeurtoRico EvolAnthropology Nov1-4

CALL FOR SYMPOSIUM PROPOSALS

(due March 30, 2018 at www.pr-science.org) 15th Congress of the Latin American Association for Biological Anthropology (ALAB)

The ALAB is a corporation that brings together scholars interested in the fields of Physical Anthropology and Human Biology. Its members can be located in Latin American countries or elsewhere if their investigations relate to Latin America.

The ALAB congresses are held every two years since 1990, offering Latin American researchers and to those interested in anthropological studies on Latin America a periodic opportunity for the discussion of scientific experiences and issues linked to the development of the discipline in a local, regional and continental context.

The overall objective of the Congress is to bring together scholars in our field in a healthy environment for the contact, discussion of problems and new ideas, and the development of collaborative networks of researchers and students.

We will celebrate the fifteenth Congress of the ALAB in Mayaguez, Puerto Rico from November 1^stto 4^th, 2018. It will be the first time that the ALAB holds its Congress in the Caribbean. We expect a dynamic discussion of all the fields of action of biological anthropology, among them: * Nutrition and growth and child development * Nutrition, health and demographics of ancient peoples * The Peopling of the Americas * The settlement of Mesoamerica and the circum-Caribbean * Forensic anthropology and human identification * Mortuary rituals and treatment of corpses in ancient civilizations * Genetics of modern populations * Paleogenomics * Biocultural Anthropology * African ancestry in the Caribbean * Primatology * Resources and strategies for teaching biological anthropology * Bioarchaeology and cultural ecology * Reproductive health

Submit your symposium title and description to ALAB-2018 at www.pr-science.org In the submission form, please indicate why this particular symposium or panel discussion is timely and necessary and also how it is likely to be of interest to a broad range of researchers in the fields of biological anthropology. Symposium Overview: “ Each symposium will consist of one or two one-and-a-half hour sessions. Each session will consist of one invited speaker and 3 contributed speakers, or no invited speaker and 5 contributed speakers, but all symposiums will have at least one invited speaker. ” The local organizing committee (LOC) may suggest one additional invited speaker per symposium (Based on symposium title), at no cost to the symposium. “ The symposium organizers will be responsible for selecting at least one invited speaker for their symposium. ” The symposium organizers will select the contributed speakers from submitted abstracts. “ The final decision on the selection of symposia, invited and contributed talks will be made by the LOC. Invited Speakers: We ask you to bring 'invited speakers' of high quality capable of delivering an interesting talk of wide interest. Please indicate whether they have been approached and/or whether they have confirmed their participation and the likely topic for their talk. (e.g. Prof A.N. Other - confirmed or approached and likely to speak but not yet confirmed) Important Dates: Call for Symposia and Discussion Panels will close on Thursday March 15th 2018. Successful Symposium and Discussion Panel applications will be confirmed on April 1st 2018. The Online Abstract Submission will open on April 5th 2018. The LOC will make its decision on proposals received based on its standards of merit and wide interest. Symposium and discussion panel submissions from scientists in the Caribbean and Latin America are encouraged. If you have any questions, email us at cohemis@uprm.edu Subject Line: ALAB's 15th Congress, 2018 Symposium or Discussion Panel Submission Please Note: - Each successful symposium will be funded with $500 USD to help with the costs of inviting speakers to the meeting and waiver of the registration. If you have any queries about this please email the ALAB's 15th Congress secretary at cohemis@uprm.edu - Sponsored symposia and discussion panels are encouraged, however, please contact our Exhibition and Sponsorship Manager Yamarie Hernandez (cohemis@uprm.edu) before enquiring about sponsor prospectus and beginning sponsorship discussions.

Taras K Oleksyk <taras.oleksyk@upr.edu>

PlymouthU EvolAnimalBehaviour Apr4-6

Dear all,

This year's Easter ASAB conference will be held at University of Plymouth in beautiful Devon on the South West coast of England on the 4th-6th April 2018.

This three-day conference is aimed at postgraduates and post-docs studying animal behaviour (although open to everyone), with a relaxed and friendly environment to encourage first time conference goers to present their work.

Confirmed plenary speakers: -

* Dr Lynne Sneddon <http://www.liverpool.ac.uk/integrative-biology/staff/lynne- sneddon/>, Director of Bioveterinary Science, University of Liverpool. * Dr Audrey Dussutour < http://dussutou.free.fr/ >, Universite Paul Sabatier * Dr Damien Farine < http://collectivebehaviour.com/farine-bio/ >, Max Planck Institute for Ornithology (ASAB Christopher Barnard Award for Outstanding Contributions by a New Investigator)

As well as ample opportunity for poster and oral presentations, workshops will be offered on the first day of the conference:

Anti-CV workshop with Dr Carole Furieux and Svenja Tidau: - a refreshingly honest session about the trials and tribulations academics have experienced on their road to success.

ASAB grant writing workshop with Dr Nikolaus von Engelhardt: - focussing on applying for small grants, this workshop will involve input from grant reviewers themselves to help you write a successful proposal.

If that's not enough to entice you to join, Plymouth has a lot to offer. It's situated on the border of Devon and Cornwall, surrounded on one side by the sea and on the other by Dartmoor national park, perfect for exploring pre- or post-conference.

Best poster/talk prizes will be awarded at the conference.

Abstract submission is open until 16th February. To submit an abstract and register for the conference, follow this link: https://www.plymouth.ac.uk/whats-on/asab-easter-conference-2018 ASAB offer a grant for students to help cover the costs of attending. The deadline for this grant is 9th February: http://www.asab.org/conference-grants/ We hope to see you there!

Sarah Lane <sarah.lane@plymouth.ac.uk>

StAndrews MASAMB Mar19-20 DeadlineFeb8

*** Call for Abstracts and Participation - Deadline extension *** The 28th annual MASAMB workshop will be held on 19-20 March 2018 at University of St Andrews/ Scotland We have extended the deadline for registration and abstract submission to * February 8th *.

More details may be found at https://synergy.st-andrews.ac.uk/masamb/ Please forward this email to your fellow colleagues.

*** MASAMB *** 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, next generation sequencing, proteomic and metabolomic technologies. These immense data resources, and the underlying complexities of molecular and cell biology, provide exciting research opportunities for numerate scientists.

With a strictly limited number of participants from mathematics, statistics, computer science, bioinformatics, biology and related fields, MASAMB meetings provide an intimate setting for exchange of ideas in methodological and applied research. Research students and scientists newly entering the field of genomic research are particularly welcome.

*** Topics *** Next Generation Sequencing Population Genetics RNA Bioinformatics Phylogeny and Comparative Genomics Personalized medicine Biological networks

*** Important dates *** Registration opens: 15th December 2017 Abstract submission: 8th February 2018 Registration closes: 12th February 2018 Conference: 19th-20th March 2018

We wish you a happy new year 2018 and looking forward seeing you in St Andrews! MASAMB Organisers

Carolin Kosiol <ck202@st-andrews.ac.uk>

Toronto AGA WildQuantGen Mar23-25

Book your room at the Chelsea Hotel by Feb 21 to receive our great conference rate!

Book here: https://www.theaga.org/toronto-accomm.htm AGA symposia are small, friendly gatherings, and provide wonderful opportunities for researchers to engage with one another and share their science. This spring's meeting will take place March 23-25, at the beautiful Hart House on the University of Toronto campus. Invited talks and contributed posters are focused on quantitative genetics of fitness-related traits in an evolutionary context across diverse species.

We will open with a reception on Friday night, and our Key Distinguished Lecturer, Loeske Kruuk, will lead off a full day of talks on Saturday. A poster-session reception is planned for Saturday night. Finally, a half day of talks will be presented on Sunday.

Registration includes receptions, meals, and a complimentary 3-YEAR membership in the American Genetic Association, including subscription to Journal of Heredity.

For all details, visit https://www.theaga.org/program-genetic-arch.htm Best wishes,

Anne Bronikowski, 2017 AGA President John Stinchcombe, Local Host and Co-Organizer

Speakers:

Key Distinguished Lecture by Loeske Kruuk (Australian Natl U.) ˜ "Quantitative Genetics of Fitness in Wild Populations"

David Coltman, U. Alberta ˜ "Architecture of quantitative traits in bighorn sheep"

Jeff Conner, Mich State ˜ "Mechanisms of rapid adaptation"

Lynda Delph, Indiana U. ˜ "Sex-specific selection drives sexual dimorphism in correlated characters"

Ned Dochtermann, U. N Dakota ˜ "Is behavior fundamentally different from other types of traits: behavioral heritabilities and genetic correlations in crickets"

Kathleen Donohue, Duke U. ˜ "Regulating life-cycle phenology through developmental arrest: Seed dormancy and plant life cycles in seasonal environments"

Fred Janzen, Iowa State ˜ "Evolutionary quantitative genetics of sex determination in freshwater turtles"

Adam Jones, U. Idaho ˜ "Epistasis in the wild"

Emily Josephs, UCDavis & Mich State ˜ "Detecting polygenic adaptation in domesticated and wild plants"

Andrew McAdam, U. Guelph ˜ "Maternal effects in North American red squirrels"

Joel McGlothlin, Virgina Tech ˜ "Quantitative genetics of sexual dimorphism in brown anoles"

Mike Morrissey, U. St Andrews ˜ "Development and non-additive genetic variation"

Julia Saltz, Rice U. ˜ "Gene-environment correlation: implications for evolutionary quantitative genetics"

Jon Slate, U. Sheffied ˜ "Recent natural selection causes adaptive evolution of an avian polygenic trait"

John Stinchcombe, U. Toronto ˜ "Evolutionary genetics in wild and invasive plants"

Cynthia Weinig, U. Wyoming ˜ "Genetic underpinnings of plant-microbe interactions and their role in adaptation"

Jason Wolf, U. Bath ˜ "A genomic perspective on multivariate evolution"

Christina Zakas, New York U. ˜ "The genetic basis of evolutionary transitions in development using a polychaete model"

Anjanette Baker <theaga@theaga.org>

Toulouse EconomicsEvolution May24-25

Dear colleagues,

We are glad to announce that the 6th Toulouse Economics and Biology Workshop - Evolution, Cognition and Rationality will be held on May 24-25 2018. Please save the date.

We will circulate a preliminary program and registration information in a few weeks.

The speakers are:

Immanuel Bomze, University of Vienna - Operations Research Joanna J. Bryson, University of Bath & Princeton University - Computer Science Noam Brown, Carnegie Mellon University - Computer Science Iain Couzin, Max Planck Institute for Ornithology & University of Konstanz - Biology Audrey Dussutour, CNRS University Toulouse III - Biology Yuval Heller, Bar-Ilan University - Economics Cecilia Heyes, University of Oxford - Biology & Psychology Peter Gärdenfors, Lund University - Cognitive Science Alex Kacelnik, University of Oxford - Biology Marc Mézard, ENS Paris Sud University - Physics Erik Mohlin, Lund University - Economics Arthur Robson, Simon Fraser University - Economics Ariel Rubinstein, Tel Aviv University - Economics Aldo Rustichini, University of Minnesota - Economics

Besides the plenary sessions, there will be a poster session to which post-docs and Ph.D. students are most welcome to submit applications (abstract + CV + cover letter) to econbio_poster@iast.fr no later than March 15, 2018.

For any further information please contact us directly at econbio@iast.fr

We look forward to seeing you in May!

Organizers: Ingela Alger and Jörgen Weibull, Co-organizers: Lauriane Rat-Fischer and Slimane Dridi

Slimane Dridi <slimane.dridi@iast.fr>

UEdinburgh FisherQuantGenetics Oct9

Meeting to celebrate the centennial of R.A. Fisher's famous 1918 paper on the theory of quantitative trait inheritance: 100 years of quantitative genetics theory and its applications: celebrating the centenary of Fisher 1918

The meeting will take place on Tuesday October 9, 2018, at the Royal College of Surgeons, Edinburgh (https://www.rcsed.ac.uk/).

There will be 7 invited speakers (Nick Barton, Sharon Browning, Ed Buckler, Heather Cordell, Jarrod Hadfield, Richard Mott and Josephine Pemberton), plus Mike Goddard giving the Fisher Memorial Lecture. In addition, 4 early career speakers and up to 30 posters will be selected from submitted abstracts by the organising committee.

Registration will be through the website of the Royal Statistical Society (https://www.rss.org.uk/). Further details concerning registration will be announced approximately four months before the meeting.

B Charlesworth brian.charlesworth@ed.ac.uk

CHARLESWORTH Brian <Brian.Charlesworth@ed.ac.uk>

UMunster Evolution Oct4-6

Conference: 1st Münster Evolution Meeting (MEM) Date: October 4-6th, 2018 Location: University of Münster, Germany

Present and discuss evolutionary questions across all fields (Botany, Zoology, Microbiology, Medicine, Philosophy, ...) and levels (from molecules to societies)! The Münster Evolution Meeting (MEM) wants to provide a forum for all Evolutionary Biologists working across different fields. Besides having the opportunity to share and learn about excellent research in evolutionary biology MEM also aims at bringing together Evolutionary Biologists working in German-speaking countries in a smaller setting, to allow for intensive networking and discussion. Münster is a welcoming and vibrant university town, offering a perfect venue. It was the home of Prof. Dr. Bernhard Rensch, who contributed significantly to the “Modern Evolutionary Synthesis”.

Confirmed speakers: Tal Dagan, Kiel University Julia Fischer, German Primate Center Göttingen Susanne Foitzik, Johannes Gutenberg University Mainz Peter Hammerstein, Humboldt University Berlin Judith Korb, University of Freiburg Christian Kost, University of Osnabrück Axel Meyer, University of Konstanz Oliver Niehuis, University of Freiburg Katja Nowick, Freie Universität Berlin Susanne Renner, Ludwig-Maximilians-Universität München Thomas Schmitt, Julius-Maximilians-Universität Würzburg Hinrich Schulenburg, Kiel University Ralf Sommer, Max-Planck-Institute for Developmental Biology Tübingen Sandra Steiger, University of Ulm Wolfgang Stephan, Natural History Museum Berlin Diethard Tautz, Max-Planck-Institute for Evolutionary Biology, Plön

Organizers: Institute for Evolution and Biodiversity, University of Münster Münster Graduate School of Evolution, University of Münster

Chair: Prof. Dr. Jürgen Gadau

Registration and abstract submission is now open. Deadline for abstract submission is 1st May 2018. Regular registration ends 13th September 2018. Registration fee is 80 EUR.

All details: http://www.uni-muenster.de/Evolution/-MEM/main.shtml

We look forward to seeing you in Münster!

On behalf of the organizers, Vanessa Kloke mem2018@uni-muenster.de

“Evolution Meeting, Münster” <mem2018@uni-muenster.de>

UPotsdam BioMoveSymposium Sep26-28

Invitation to the 1st International BioMove Symposium

26th - 28th September 2018 Fraunhofer Conference Center Am Mühlenberg 12, 14476 Potsdam, Germany

Dear colleagues,

on behalf of the DFG Research Training Group BioMove, it is our great pleasure to invite you to the 1st BioMove Symposium on the interplay between movement and biodiversity. During four sessions we will tackle the question how individual movements shape biodiversity patterns, and vice versa.

Wed, 26th From individuality to biodiversity — — — — Keynote talk by Dries Bonte, Ghent University

Thu, 27th Tiny organisms travel long distances — — — — Keynote talk by Diego Fontaneto, CNR-ISE

Animal movements across scales — — — — Keynote talk by Wayne Getz, UC Berkeley

Fri, 28th Living in a landscape mosaic — — — — Keynote talk by Nina Farwig, Philips-University Marburg

The Symposium will be organized by the BioMove PhD students who are about to finish their projects by the end of this year and will present parts of their work.

With regards, BioMove Group

We are looking forward to your applications for talks and posters. Online abstract submission will be open from 3rd April until 11th May. Online registration for the symposium will be open from 15th June.

Please stay tuned for updates on the scientific program and social events: Homepage: https://biomove.org/-biomove-symposium-2018/ Twitter: @bio_move

If you have any further questions, feel free to contact us: Email: biomove2018@uni-potsdam.de

University of Potsdam Karl-Liebknecht-Str. 24-25, D-14476 Potsdam Germany

biomove2018@uni-potsdam.de

Magdalena Litwin <litwin@uni-potsdam.de>

UToronto Barrettfest Aug10-11

Dear Colleagues,

This year marks Professor Spencer Barrett’s 70th birthday and 40th year at the University of Toronto. We will celebrate this occasion and Spencer’s career so far with a symposium entitled ’Evolution of Plant Reproductive Systems: From Muddy Boots to Genomics’. The symposium, to be held at the University of Toronto August 10-11, will be an opportunity to explore the latest cutting edge research in this field. The list of confirmed speakers includes: Aneil Agrawal (U Toronto), Tia-Lynn Ashman (U Pittsburgh), Andrea Case (Kent State), Deborah Charlesworth (U Edinburgh), Joana Costa (U Lisbon), Lynda Delph (Indiana U), Chris

Eckert (Queens U), David Field (U Vienna), Jannice Friedman (U Syracuse), Sean Graham (UBC), Lawrence Harder (U Calgary), Kay Hodgins (Monash University), Brian Husband (U Guelph), Michael Lenhard (U Potsdam), John Pannell (U Lausanne), Daniel Schoen (U McGill), James Thomson (U Toronto), Stephen Wright (U Toronto). Many thanks to the University of Toronto's EEB department and the faculty of Arts & Science for co-sponsoring the event. Registration is now open. For details, registration and banquet tickets, please visit https://barrettfest.eeb.utoronto.ca/ Stephen I. Wright Professor and Canada Research Chair in Population Genomics Department of Ecology and Evolutionary Biology University of Toronto 25 WIllcocks St. Toronto ON M5S 3B2 Office: (416) 946-8508 http://labs.eeb.utoronto.ca/wright/Stephen_I._Wright/ stephen.wright@utoronto.ca

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WashingtonDC CrustaceanGenomics May22-25

Dear colleagues,

My co-organizer, Joanna Wolfe, and I would like to invite you to present your research in the session 'Molecular Insights: The Genomic Revolution in Crustacean Biology' at the upcoming International Crustacean Congress IX to be held May 22-25th 2018 in Washington DC. *The deadline forabstract submission is fast approaching: March 1st 2018*

This conference is hosted by the Smithsonian Institution and Renaissance Hotel. We hope this session will provide a platform to share and discuss studies incorporating crustacean genetics and/or genomics. We encourage submissions that cover any crustacean taxa and we are particularly interested in phylogenetics/omics, transcriptomics, gene expression studies, tree of life studies, and population genomics. Graduate Students, Postdoctoral Scholars and Professors (at all levels) are encouraged to participate!

If you are interested in participating please submit an abstract and list our session 'Molecular Insights: The Genomic Revolution in Crustacean Biology'

Abstract submission is found here: http://www.birenheide.com/ICC2018/abstracts.php We look forward to seeing you there!

Heather and Jo

Session details:

*Molecular Insights: The Genomic Revolution in Crustacean Biology *

Co-Coordinators: Heather Bracken-Grissom, Florida International University, hbracken@fiu.edu Joanna Wolfe, Massachusetts Institute of Technology, jowolfe@mit.edu The field of crustacean genetics has undergone an exciting revolution in recent years. The advancement of sequencing technologies and methods has transformed the way carcinologists ask questions and collect data, especially for non-model organisms that lack genomic references. For several groups within Crustacea, this 'genomic revolution' is still in its infancy. The potential to capitalize on recent technology is great, and findings from these studies will lead to unprecedented insights into the fields of evolutionary biology and molecular ecology.

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

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

We do not plan to publish a special issue.

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

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

– 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/ < http://heatherbracken.wix.com/brackengrissomlab > * heather.brackengrissom@fiu.edu <Valerie.Hall@fiu.edu> www.fiu.edu/˜marine Heather Bracken-Grissom <heather.bracken@gmail.com>

Yokohama SMBE Jul8-12 SatelliteRegionalMeetings

SMBE Satellite and Regional Meeting Call for Proposals

SMBE is now calling for proposals for workshops/satellite meetings. They are also calling for proposals for "interdisciplinary and regional actions". The proposed meeting or event should be held between Sep 1 2018 and Dec 31 2019. Funds will be awarded on a competitive basis to members of the molecular evolution research community, and the deadline for submission of proposals is April 1, 2018.

Satellite meeting/workshop proposals should be sent by email to the Chair of the SMBE Satellite Workshop Committee Joanna Masel (masel@u.arizona.edu). Interdisciplinary and Regional Actions proposals should be sent by email to the Chair of the SMBE Interdisciplinary Regional Actions Committee Maud Tenaillon (maud.tenaillon@inra.fr).

See http://www.smbe.org/smbe/MEETINGS/-SatelliteandRegionalMeetingGuidelines.aspx for more detailed information.

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

Yokohama SMBE Jul8-12 TravelDeadlineExt

Society for Molecular Biology & Evolution

SMBE Undergraduate Travel and Mentoring Awards - Deadline extended

The Society for Molecular Biology and Evolution offers travel awards for undergraduate students to attend their annual meeting and recent mentoring there, this year in Yokohama, Japan (http://smbe2018.jp). Eligibility includes Masters students under a 3+2 system. Eligibility is based on status at the time of application.

Awardees will receive 1500-2000 USD ($) toward travel and registration fees (the larger amount is for long-haul travel, the smaller for within Australasia). You will also be assigned a mentor at the meeting to advise you and to introduce you to potential collaborators, PhD supervisors, etc. You will also participate in the meeting's poster session with a poster you will prepare on your research.

In order to apply, you need to prepare the following: 1. an abstract describing your research (<250 words) 2. a short explanation of why you want to attend this meeting, including mention of whether you fall into a group traditionally underrepresented at SMBE, such as enrolling in university later in life or being the first in your family to attend university (<250 words) 3. a short letter of support from your academic supervisor, confirming that the research is your own (<250 words) 4. a scan or photo of your student ID to confirm eligibility

Applications can be made through the SMBE abstract submission system at http://smbe2018.jp/-cf_abstract.html, which has been extended to accept submissions until February 1. You can either submit all components there, or you can have your advisor email their support letter to Joanna Masel masel@email.arizona.edu. If you have already submitted your abstract but have not yet applied for the award, you can email in your award materials. The deadline for receiving award materials by email (conditional on having submitted an abstract) is February 8.

You can find more information on the travel awards at http://www.smbe.org/smbe/AWARDS/-AnnualMeetingTravelAwards/Undergraduate TravelandMentoringAward.aspx or send an email to Joanna Masel masel@email.arizona.edu.

Society for Molecular Biology & Evolution smbe@allenpress.com

Society for Molecular Biology & Evolution <smbe@allenpress.com>

YosemiteNatlPark Symbiosis May4-6

Dear Colleagues,

The Eigth annual Yosemite Symbiosis Workshop will take place on May 4th-6th, 2018 at the Sierra Nevada Research Institute, Yosemite National Park. This has become a great venue for a diversity of symbiosis researchers. We hope to continue to attract a diverse group in 2018!

Keynote speaker 2018: Dr. Tadashi Fukami from Stanford University!

Information about our meeting:

Why: Our continuing goal is to better integrate the broad groups of scientists that focus on symbiosis and microbiome research. Yosemite serves as an ideal site as it is both beautiful and secluded. This will be our 8th annual meeting and we have been consistently attracting scientists from all over the country and overseas.

Who: The meeting is small by design (~50 participants) and we seek to focus on scientists interested in the microbiome, cooperation, mutualism, and symbiosis. In the past we have covered a range of symbiosis topics from ecology and evolution to molecular mechanisms in different model and non-model systems. We would like to make room for a diverse group of people so we will initially accept up to 3 lab members per group (including the PI) on a first come first served basis.

When: The talks and formal meeting will be held May 5-6, 2018, though we make accommodation arrangements available for attendees to arrive on Friday the 4th to provide opportunities to enjoy the park. Since time at the conference is limited, we ask attendees to submit an abstract and a preference (talk versus poster). Priority will be given to those presenting.

Past attendees and talks can be found here: http://www.sachslab.com/symbiosis-2015.php Abstract and early bird registration are due on March 16th, 2018.

Where: SNRS has a set of cabins in Wawona and all within a short walk of the conference room. Costs: See details in the registration page. We will only be able to accept credit card payments this year.

Link to meeting information: http://www.sachslab.com/symbiosis-2015.php The registration form for the 2018 Symbiosis Workshop is active: https://snri.ucmerced.edu/form/symbiosis-workshop-2018-registration Payments should be made at: https://intelforms.ucmerced.edu/Form/Symbiosis Please direct any questions to the organizers:

Joel Sachs joels@ucr.edu

A. Carolin Frank cfrank3@ucmerced.edu

– *Joel L. Sachs* *Associate Professor & Vice Chair* Evolution Ecology & Organismal Biology University of California, Riverside

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

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

GradStudentPositions

AustinPeayStateU PlantPopulationGenetics

MS Graduate Research Assistantship, Plant Population Genetics (Deadline approaching!)

Highly motivated students wishing to earn an MS in Biology and interested in plant population genetics are invited to apply for a Graduate Research Assistantship in Dr. Carol Baskauf's lab at Austin Peay State University (APSU) in Clarksville, TN. The assistantship includes a tuition waiver and stipend for two years ($15,750 annually). The successful candidate will preferably begin lab/field work in the summer of 2018 before beginning graduate classes in the fall.

Generally, research in the Baskauf lab includes plant population genetics, ecology, and ecophysiology, with particular interest in rare species and comparative studies. Specifically, this NSF funded Graduate Research Assistantship involves genetic analysis of several rare and widespread congeners as part of a larger collaborative research project examining correlations between genetic diversity and phenotypic plasticity as well as potential adaptive and/or acclimatory responses to future environmental change by rare and widespread species.

An undergraduate degree in a biology-related field is required. Competitive applicants will have excellent written and oral communication skills, be able to work independently with attention to detail, and be able to work collaboratively and supervise undergraduates doing related research. Prospective students should send Dr. Carol Baskauf (baskaufc@apsu.edu) unofficial college transcripts and a single pdf file consisting of a brief letter of interest and background, a CV (including GPA, GRE, and, if applicable, TOEFL scores), and names and contact information for 3 academic or professional references. Review of applicants will begin immediately and continue until a suitable candidate is found. For full consideration, submit all materials prior to Feb. 1, 2018.

The successful applicant will enroll in the Masters program prior to APSU's March 15, 2018 application deadline in order to be eligible to complete coursework and a thesis leading to an M.S. degree in Biology. Information about the graduate program is at the Biology Department's web page (http://www.apsu.edu/grad-studies/-graduateprograms/biology.php). General questions can be directed to Graduate Admissions (1-800-859-4723, gradadmissions@apsu.edu). APSU is an equal opportunity employer, and underrepresented and minority groups are encouraged to apply.

BaskaufC@apsu.edu

BangorU ParallelAdaptationAndSpeciation

PhD position in Rapid Parallel Adaptation at Bangor University

Closing Date: 11th March 2018

Title: Parallel origins of contemporary heavy metal tolerance in sea campion

Supervisor: Dr. Alex Papadopulos (a.papadopulos@bangor.ac.uk, www.labadopulos.co.uk) Co-supervisors: Prof. Si Creer and Prof. Gary Carvalho

Project description: Climate change, urbanisation and exploitation of natural resources increasingly alter the environment, posing significant challenges for plants and animals. We have a poor understanding of how organisms will cope with such rapid and widespread disruption, particularly in terms of their evolutionary responses (e.g., adaptation). Key advances in determining the genetic and ecological characteristics that permit or facilitate adaptation to novel environments have come from a few iconic species in which the same adaptation has evolved multiple times. Repeated evolution of the same adaptive trait offers unique opportunities to investigate the replicability of evolution and ultimately inform us about the extent to which evolution might be predictable as our climate changes. This project will advance our understanding of the repeatability of rapid evolution by researching the ecological mechanisms underpinning multiple origins of adaptation to heavy metal contaminated soils in Silene uniflora (sea campion).

Sea campion is a predominantly coastal species which is native to the UK and Ireland. It has also colonised disused mines and adapted to the heavily contaminated soils which contain high concentrations of phytotoxic heavy metals. Remarkably, the heavy metal tolerant ecotype has evolved independently on at least three separate occasions in Wales, England and Ireland within the last 200 years. This exciting project will investigate the frequency and timing of this parallel evolution of heavy metal tolerance, the spatial scale over which adaptation takes place, the potential for local adaptation to drive reproductive isolation and speciation, and the possible role of adaptive introgression from related species. To do this, we will combine cutting-edge high-throughput DNA sequencing, with population genomics, phylogenetics and ecological experiments in both common garden and field settings. The project will provide unique insights into the adaptive process in plants responding to human-induced environmental change.

Funding: This is a fully funded PhD studentship to start October 2018 is available in the College of Natural Sciences at Bangor University, supported by its Great Heritage fund. The studentship will cover the full cost of UK/EU tuition fees, plus a maintenance stipend in line with RCUK rates (provisional 14,553 per annum for full time award holders) for 3 years as well as funding for the research. This project is one of three that is being advertised, and one PhD will be awarded to the best candidate determined after interview.

Apply: Applications are invited from candidates who have or are about to obtain a minimum of an Upper Second Class Honours degree, or an appropriate Master's degree in biological, environmental or related sciences. The closing date for applications is 11th March. Interviews will be held in Bangor approximately 4 weeks after the closing date. To apply candidates should email a Curriculum Vitae including names and addresses of two referees and a letter of motivation explaining why they want to apply for the project and detailing any relevant experience they have, to primary supervisor Alex Papadopulos (a.papadopulos@bangor.ac.uk).

Institution: Bangor University is a vibrant research-led institution, uniquely situated between the mountains of Snowdonia and the sea. The Molecular Ecology and Fisheries Genetics Laboratory (MEFGL) is a leading research division of the School of Biological Sciences (SBS), within the College of Natural Sciences at Bangor University. The MEFGL represents one of Europe's largest centres focusing on population, species and community diversity of aquatic animals, with additional activities on prokaryotic and eukaryotic groups, including plants, fungi and microbes throughout terrestrial and aerobiological biomes.

Rhif Elusen Gofrestredig 1141565 - Registered Charity No. 1141565

Alexander Papadopulos <a.papadopulos@bangor.ac.uk>

BotanicGardenMeise Belgium SpeciesDistModelling

Dear colleagues,

There is a vacancy for a PhD/Postdoc in Species Distribution Modelling at Botanic Garden Meise, Belgium, see http://www.plantentuinmeise.be/PUBLIC/-GENERAL/ABOUTUS/vacancies.php Please note that candidates should have graduated from a Dutch or Flemish university, or be fluent in the Dutch language. Deadline for submission of documents is Febr. 25th. For information about the job content, please contact Marc Sosef (marc.sosef@plantentuinmeise.be).

Best regards, Frederik

– Frederik Leliaert Botanic Garden Meise Nieuwelaan 38, 1860 Meise, Belgium www.botanicgarden.be | personal web page < http://frederikleliaert.wordpress.com/ >

Frederik Leliaert <frederik.leliaert@plantentuinmeise.be>

CharlesU Prague EvolutionaryImmunology

Dear colleagues,

The Evolutionary and Ecological Immunology (EEI) group at the Faculty of Science, Charles University, Prague, is currently advertising a four-year fully funded STARS PhD studentship position in avian neuroimmunology (deadline for applications 16th March 2018).

I would be very grateful if you could circulate the following advertisement at relevant fora or pass it to whom it may concern.

PhD project topic: *'Effect of peripheral immune response on neuroinflammation and learning in cognitively advanced birds'*

Neuro-immune interactions involved in neuroinflammation directly influence psychological processes including mood and cognition. Focusing on birds that represent superior models for research in cognition to rodents (passerines and parrots), this PhD project opens new possibilities for interdisciplinary research of neuroimmunology.

The objective of the PhD project is to describe at transcriptomic, proteomic, and behavioural levels the effects of inflammation on avian brain and its ability to resolve tasks indicative of learning capacities and mood. The successful candidate will generate and analyse brain transcriptomic data, verify differential gene expression of target genes using RT-qPCR and link these data to veterinary diagnostic records and behavioural data (collection of these may be part of the research project). Biodiversity-based approach will be adopted.

Requirements:

Candidates should have a strong interest in avian immunology, genetics and behavioural sciences. MSc degree in biology (immunology, zoology, genetics or related fields) and good English language skills required. For the formal requirement please check the STRAS web page (http://www.stars-natur.cz/).

Offers:

We offer a fully funded PhD position for four years *starting from 1st October 2018*. The PhD student will be part of a young and enthusiastic interdisciplinary team (http://web.natur.cuni.cz/zoologie/biodiversity/-eei/people). Despite close collaboration with several co-workers, the project allows independent intellectual input. We expect at least three articles being published in the course of the study in international peer-review journals. Active participation at international scientific conferences will be encouraged and supported.

Application:

Applications are submitted through the STARS application system (http://www.stars-natur.cz/application). Applications via postal service or e-mail will not be considered.

Links:

For further information see the EEI group web page (http://web.natur.cuni.cz/zoologie/-biodiversity/eei), STARS web page (http://www.stars-natur.cz/) and the web of the Faculty of Science, Charles University (https://www.natur.cuni.cz/-eng?set_language=en) or contact Dr. Michal Vinkler at michal.vinkler@natur.cuni.cz (no applications).

We look forward to receiving your on-line application until *16th March 2018. *

Kind regards,

Michal Vinkler

– RNDr. Michal Vinkler, PhD

Laboratory for Evolutionary and Ecological Immunology Division of Animal Evolutionary Biology Department of Zoology, Faculty of Science Charles University Vinicna 7, CZ 128 44 Praha 2 Czech Republic, EU e-mail: vinkler1@natur.cuni.cz tel: +420221951845 fax: +420221951841 http://web.natur.cuni.cz/zoologie/biodiversity/eei/ Michal Vinkler <vinkler1@natur.cuni.cz>

Dresden PDF PhD BedbugSpeciation

Job: Advanced microscopy and proteomics in ecological speciation of bedbugs

Our collaborative group of researchers from Brno, Prague, Bayreuth and Dresden is seeking to recruit a highly motivated researcher for an ambitious project examining how sperm metabolism and seminal fluid proteins contribute to reproductive isolation of diverging bedbug populations. The position is ideally suited for a PhD student for 3 yrs but postdoctoral applicants (for 2 yrs) can also be considered. Within the project, opportunities exist to apply artificial insemination, microsatellite-based paternity analysis, autofluorescence-based advanced microscopy and mass spectrometry to disentangle genetic from environmental effects on sperm function. The successful applicant will join an international laboratory at TU Dresden (Germany) (https://tudaz.net).

Successful candidates have previous experience, or strong interests, in at least one of the methods (proteomics, cell metabolism, confocal microscopy, paternity analysis) and one of the concepts (ecological speciation, phenotypic plasticity, sperm ecology). The position is paid at TVL E13 65%, amounting to at least 18-20 k Euros net annually for 3 yrs, or 25-27 k Euros for 2 yrs, depending on experience and family status etc.

Applications without photograph and without date of birth should contain a letter of motivation (1 page or less), a cv, your 3 favourite own publications (if you have any), a summary of previous research experience (1 page or less) and contact details of 2 references. Applicants are welcome to provide initials instead of first names. Inquiries can be made with Klaus Reinhardt (klaus.reinhardt@AT@tu-dresden.de). The application, all in one pdf should be sent to the Applied Zoology office (anja.jahn@AT@tu-dresden.de). The deadline for application is 22 March 2018.

Klaus Reinhardt Professor of Applied Zoology Faculty of Biology, TU Dresden Germany https://tudaz.net Klaus Reinhardt <klaus.reinhardt@tu-dresden.de>

EAWAG Switzerland DaphniaHostParasite

PhD position : Hostâparasite interactions in hybridizing Daphnia, from correlations to experiments

The PhD student will participate in a collaborative research project with PD Dr Piet Spaak (Eawag) and Prof. Justyna Wolinska (Leibniz-Institute of Freshwater Ecology and Inland Fisheries, IGB in Berlin, Germany), financed by the Swiss and German Science Foundations (SNF & DFG).

Eutrophication is a worldwide environmental problem accelerated by global warming, affecting the stability of aquatic ecosystems and having longâconsequences. We will investigate if and how eutrophication affects two interacting evolutionary processes: disease spread and interspecific hybridization. We will use water fleas (Daphnia), a well-established model in both host-parasite and hybridization research. This project is a combination of a field survey, a mesocosm experiment (where trophic conditions will be manipulated), the transcriptional profiling of Daphnia exposed to stressful eutrophic conditions, and the development and application of molecular markers to study parasite evolution in eutrophic environments. Overall, through the unique combination of expertise and methods, this project will improve our understanding of disease spread and biodiversity loss under different trophic conditions and, consequently, might provide tools for management of aquatic ecosystems.

Within the project this position focuses on interspecific hybridization. The main task will be participation in a large-scale field study and mesocosm experiment; data collection and processing. The student will screen the dynamics of natural and experimental Daphnia communities, using microsatellite and SNP markers. Also, the student will conduct a large laboratory experiment to assess Daphnia stress responses; here, RNA-Seq methods will be applied. The PhD student will take advantage of the draft D. galeata genome.

Although the student will be hosted primarily at Eawag, exchange stays are planned at IGB. Moreover, generous funds are available to cover attendance at national and international conferences. He/she will be enrolled at the

Swiss Federal Institute of Technology (ETH) in Zürich. The position will be for a period of four years, and should start as soon as possible (spring / early summer 2018).

The ideal candidate should have good molecular skills and a strong background in evolutionary biology, ecology or related fields. In addition, knowledge of statistics, bioinformatics and/or population genetics will be highly advantageous. Excellent communication and writing skills in English, good work ethic, and creative thinking are desired. A Master's Degree (or equivalent) in biology or a related subject is necessary for admission. The working language in the group is English.

Eawag offers a unique research and working environment (http://www.eawag.ch/en/aboutus/working/-researchenvironment/) 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. For more information about Eawag and our work conditions please consult www.eawag.ch and www.eawag.ch/en/aboutus/-working/employment . For further information please consult Piet Spaak (spaak@eawag.ch). The application should be submitted by 1 March 2018.

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 potential referees, and copies of certificates of academic qualifications 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/673277/0589/pub/1/-index.html Piet Spaak Eawag Aquatic Ecology Ãberlandstrasse 133 8600 Dübendorf Switzerland Phone: +41 58 765 —56 17

spaak@eawag.ch http://www.eawag.ch/abteilung/eco/-schwerpunkte/zooplankton-oekologie-und-evolution/ "Spaak, Piet" <Piet.Spaak@eawag.ch> "Spaak, Piet" <Piet.Spaak@eawag.ch>

Europe 15 ITN IGNITE CompGenomicsInverts deadlineFeb28

Dear all,

This is a reminder that the (strict) deadline for applying to the 15 PhD positions in the Innovative Training Network IGNITE (Comparative Genomics of Non-Model Invertebrates) is tomorrow February 28, 23:59 CET. This includes one PhD position in my group entitled "Using chromosome conformation capture to assemble genomes to perfection", i.e. applying contact genomics to generate completely assembled genomes (from telomeres to telomeres). Experience in computer science, bioinformatics, genomics and/or statistics would be highly desirable for this position.

Here is the link to the description of the project (which includes the sequencing and assembly of a chaetognath genome in order to better understand the evolution of these enigmatic metazoans): http://www.itn-ignite.eu/projects/11559_esr-project-5-using-chromosome-conformation-capture-to-assemble-genomes-to-perfection/ For details of the 15 PhD projects available, see: http://www.itn-ignite.eu/-projects/ Applicants should have a master degree or equivalent in a relevant field, but cannot already possess a doctoral degree. For the position in my group, the successful applicant will be registered in the PhD programme of the Université libre de Bruxelles. Candidates of all nationalities may apply, but must not have lived in Belgium for more than 12 months in the 3 years immediately prior to their appointment. The fellow will receive a competitive salary, including a mobility allowance, a family allowance (if applicable) and comprehensive social benefits.

Application website: http://portal.graduatecenter-lmu.de/ocgc/user/register Best regards, Jean-François

– Jean-François Flot Associate Professor Evolutionary Biology & Ecology - C.P. 160/12 Université Libre de Bruxelles Avenue F.D. Roosevelt 50 B-1050 Brussels - Belgium http://ebe.ulb.ac.be/ebe/Flot.html "jflot@ulb.ac.be" <jflot@ulb.ac.be>

GeorgiaSouthernU FishEvolutionaryBiomechanics

Dr. Emily Kane is looking for 1-2 Master's students to join the Department of Biology at Georgia Southern University. Students will contribute to an ongoing project < https://www.thekanelab.com/guppies > examining the evolution and heritability of performance integration in Trinidadian guppies. The specific project is flexible, but topics may include examining morphology, feeding kinematics, predator accuracy, swimming and escape kinematics, and respirometry. Our work with guppies is also being used to develop outreach and education initiatives in South Georgia. I am interested in students who are open to participating in and helping to develop these events. Creativity in research and outreach efforts is encouraged!

Funding will be in the form of teaching assistantships but other opportunities may become available. Interested students should insure they meet the minimum admission requirements < http://cogs.georgiasouthern.edu/-admission/master-of-science-biology/ >. Beyond this minimum, test scores or grades will not be used to evaluate potential students. Instead, I am interested in learning more about your motivation for pursuing a degree, what you would like to learn through this process, and how you might hope to apply your degree after graduation. Increasing representation and diversity of scientists is key to advancing scientific approaches and ideas. I am committed to the success of my students, and I welcome those from non-traditional or underrepresented backgrounds.

The priority deadline for Fall 2018 enrollment is March 1, 2018 but applications will be accepted through April 1, 2018.

Interested students should email me at ekane@georgiasouthern.edu with a statement of interest and CV.

Dr. Emily A. Kane Assistant Professor of Biology Georgia Southern University PO Box 8042-1 Statesboro, GA 30460 Office: (912) 478 - 0134 thekanelab.com < http://www.thekanelab.com > Twitter: @KaneLabGSU < https://twitter.com/-KaneLabGSU >

Emily Kane <ekane@georgiasouthern.edu>

GeorgiaSouthernU InsectEvolution

The Gibson lab in the Department of Biology at Georgia Southern University (GSU) is looking for a MS student in insect evolutionary genetics to begin Fall 2018. The research focus of the lab is on the genetic/genomic basis of traits in Hymenopteran insects, particularly metabolic and mitochondrial physiology. Current projects/systems in the lab include (1) speciation and evolutionary genetics in *Nasonia* parasitoid wasps (2) behavioral genetics in honey bees (*Apis mellifera*), and (3) studies investigating the invasive Argentine ant (*Linepithema humile*). Students are welcome to join existing projects, but are also encouraged to develop their own interests within the scope of the lab.

Student support will primarily be in the form of teaching assistantships, but partial support through research assistantships and summer supplementation are also available. In addition, there are competitive fellowships available through the Department and the College of Science and Mathematics. All students are expected to apply for external funding as well.

GSU is a 27,000-student comprehensive research university with three campuses in southeast Georgia (http:/-/www.georgiasouthern.edu/). The Department of Biology at the Statesboro campus has many resources available to students, including a new LEED certified research and teaching building, many possibilities for collaboration with our >40 faculty as well as outside the department, and facilities for insect rearing, high throughput sequencing preparation, and microscopy.

Prospective students should have (1) a BS degree in the life sciences, such as Biology, Entomology, Genetics, Ecology & Evolution, or a related field. (2) excellent communication skills, both oral and written, and (3) the ability to work both independently and with a team. Preferred, but not required, qualifications include (1) experience conducting laboratory research, particularly in molecular biology (2) analytical skills such as bioinformatics and/or statistics, and (3) demonstrated scientific communication skills such as scientific publications or presentations, or a thesis project.

Students should ensure they meet the academic requirements of the graduate program at Georgia Southern University (see links below). To apply, contact Dr. Josh Gibson at jgibson@georgiasouthern.edu with a single PDF file that includes (1) a statement of research interests and experience (2) a CV or resume (3) GRE scores if available and (4) names and contact information for 2 academic or professional references.

The application deadline is April 1, 2018.

Graduate Program

http://cogs.georgiasouthern.edu/admission/master-of-science-biology/ http://cosm.georgiasouthern.edu/-biology/graduate-program-2/ Department of Biology

http://cosm.georgiasouthern.edu/biology/ – Joshua D. Gibson, Ph.D. Assistant Professor Georgia Southern University Biology Department P.O. Box 8042-1 Statesboro, GA 30460 912-478-7826

Joshua Gibson <jgibson@georgiasouthern.edu>

HeidelbergU MammalianPhenotypicEvolution

EvoCELL Early Stage Researcher (PhD) position - Vertebrate Evolutionary Genomics

Host laboratory: The lab of Prof. Henrik Kaessmann: Center for Molecular Biology (ZMBH), Heidelberg University, Germany (http://www.zmbh.uni-heidelberg.de/-Kaessmann/). The Kaessmann lab seeks to unravel the molecular basis of phenotypic evolution in mammals and other vertebrates based on the analysis of extensive "omics" datasets generated in the lab as well as complementary data and experiments. A particular focus has been the evolution of gene expression/regulation across gene types, lineages, organs, cell types, developmental stages, chromosomes and sexes (see e.g. Brawand et al. Nature 2011, Necsulea et al. Nature 2014, Cortez et al. Nature 2014; selected publications are listed below).

General information: This PhD position (3 years, extension possible) is funded by the MSC Innovative Training Network "EvoCELL" (https://www.evocell-itn.eu). EvoCELL is a Marie Skłodowska-Curie Innovative Training Network aiming at studying the evolution of cell-types and tissues in a diverse array of vertebrates and invertebrates. To do so, the labs involved in the network will use the most recent single-cell and tissue genomic techniques, merging them with more traditional disciplines. EvoCELL's has an ambitious training program, also in the non-academic sector. Scientific outreach and communication of the project results to a wider public are a fundamental part of the project and all fellows will contribute to it. The network brings together 8 academic and 2 non-academic organisations from 6 European countries. The starting date is negotiable but will be no later than August 1, 2018.

The project: This project aims to trace the evolutionary and cellular origins of vertebrate nervous cell types and tissues, as well as the underlying genomic changes, based on the generation and analysis of extensive single-cell genomics datasets and complementary experiments (e.g., CRISPR/Cas) across representative vertebrates and outgroup species. The project is closely connected to the project of the Arendt partner lab; together, the labs' projects aim at reconstructing the neuron type complement of the common bilaterian ancestor.

The candidate: The ideal candidate has a strong interest (and potentially experience) in both wet lab (genomic/molecular) experiments and bioinformatics analyses. However, we will also consider candidates who prefer to emphasize either wet lab or bioinformatics work (the respective other aspect of the project may potentially be complemented by other lab members). The candidate should have a passion for evolutionary biology. EU fellowship eligibility criteria: at the time of recruitment, the candidate must not have resided or carried out her/his main activity (work, studies, etc.) in Germany for more than 12 months in the 3 years immediately prior to start of the project. Short stays such as holidays and/or compulsory national service are not taken into account. Candidates can be of any nationality, but are required to undertake transnational mobility. Candidates should ideally possess a Master's degree in a relevant academic field, or a degree that allows them to embark in a PhD. Candidates must be within the first four years of their research career. Applications from candidates who already possess a doctoral degree will not be considered.

Research environment and location: The PhD student will be supported by research technicians, wet lab scientist, and/or bioinformaticians in our interdisciplinary group. The language of our institute (ZMBH) is English and hosts scientists from around the world. It is located in Heidelberg, a picturesque cosmopolitan city that offers a very stimulating, diverse and collaborative research environment thanks also to neighboring cutting-edge institutions, in particular the European Molecular Biology Laboratory (EMBL) and German Cancer Research Center (DKFZ). As pointed out above, the project will be carried out in close collaboration with the Arendt partner lab as well as the other labs in the EvoCELL network. Interactions within the network are fostered through regular meetings, courses and visits to member labs.

Application: Please submit a CV, statement of research interest, references, and a list of publications or other research output to Henrik Kaessmann (h.kaessmann@zmbh.uni-heidelberg.de).

Selected publications: Marin, R., Cortez, D., Lamanna, F., Pradeepa, M.M., Leushkin, E., Julien, P., Liechti, A., Halbert, J., Brüning, T., Mossinger, K., Trefzer, T., Conrad, C., Kerver, H.N., Wade, J., Tschopp, P., Kaessmann, H. (2017) Convergent origination of a Drosophila-like dosage compensation mechanism in a reptile lineage. Genome Res. 27: 1974-1987.

Guschanski, K., Warnefors, M., and Kaessmann, H. (2017) The evolution of

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JGutenbergU Mainz BeeBehaviour

PhD position: Genomic basis of honeybee foraging and decision-making Application deadline: 1st April 2018

We invite applications for a 3-year DFG (German Research Foundation) funded PhD position (65% TVL E13) at the Johannes Gutenberg University of Mainz, Germany. We are looking for a highly motivated student to study the genomic basis of honeybee foraging behaviour. Honeybees exhibit sophisticated communication and decision-making processes. Their behaviour is highly flexible and is shaped by recent foraging experiences. However, the genomic and transcriptomic basis of decision-making in foraging bees is not well understood. The PhD project will investigates if and how the expression of behavioral genes in the brain affects foraging and decision-making. The successful applicant will perform behavioural experiments with free-flying bees, pharmacological treatments of bees, brain dissections and gene expression analysis using bioinformatic tools.

Students with a Masters degree in Biology and a strong background in behaviour and/or bioinformatics are particularly encouraged to apply. Good English skills and an ability to work as part of a team are important. Previous experience with honeybees, behavioral experiments, bioinformatics and a knowledge of German are helpful, but not a prequisite. The working language of our group is English. The Johannes Gutenberg-University Mainz is interested in increasing the number of women in science. Applications from women are therefore strongly encouraged. Similarly, qualified candidates with disabilities will be preferred. The successful applicant will join an international and interactive scientific environment with access to state-of-the-art, newly equipped laboratories. More information about our research interests and recent publications can be found here: http://www.bio.uni-mainz.de/zoo/evobio/index_ENG.php. The University of Mainz hosts many excellent scientific institutions (http://www.uni-mainz.de/eng/) and Mainz is a historic city located on the Rhine River with a large student population and a rich social and cultural life.

How to apply: applications should include (1) a 1-page cover letter describing your motivation, previous research activities and current research interests, (2) a CV and (3) the names and email addresses of 2 referees. Send all documents as a single pdf-file before 1st April 2018 to cgrueter@uni-mainz.de and foitzik@uni-mainz.de. Applications must be written in English. Skype-interviews for short-listed candidates will be scheduled for mid-April. The ideal start date is June 2018. Informal enquiries can be sent to: Dr. Christoph Gruter (cgrueter@uni-mainz.de) or Prof. Susanne Foitzik (foitzik@uni-mainz.de), Institute of Organismic and Molecular Evolution, University of Mainz, Germany

Dr. Christoph Gruter Institute of Organismic and Molecular Evolution University of Mainz Johannes von Muller Weg 6 Office 02-243 D-55099 Mainz Germany phone: +49 (0)6131-3927843 fax: +49 (0)6131-3927850 website: www.socialinsect-research.com "Grüter, Dr. Christoph" <cgrueter@uni-mainz.de>

LeibnizInst EvolutionRetroviruses

Advertisement of vacancies The Leibniz Institute for Zoo and Wildlife Research (Leibniz IZW) in Berlin is Germany's premier wildlife research institute. The Leibniz IZW focuses on the life histories and mechanisms of evolutionary adaptations of mammals and birds, their limits and their conservation in natural and anthropogenically influenced environments. The institute operates within the fields of evolutionary ecology, evolutionary genetics, wildlife diseases, reproduction biology and reproduction management.

For a new interdisciplinary research initiative , entitled "Genome invasion: understanding the evolutionary and functional roles of mutation and recombination at the earliest stages of retroviral endogenization" the Leibniz IZW offers a doctoral position (65%) in the department of wildlife diseases.

Job description:

Up to 11% of mammalian genomes are comprised of retroviral like sequences. The processes that generated this large fraction of the genome involved an invasion of germ lines by infectious retroviruses. The process of retroviral invasion is poorly understood as most entered the germ line millions of years ago. The research project will focus on characterizing relatives of the gibbon ape leukemia virus (GALV) and the koala retrovirus (KoRV) using hybridization capture and other high throughput sequencing based approaches on rodents and bats on both sides of the Wallace Line. The Wallace Line is a faunal barrier that separates Asia from a transitional zone between Asia and Australia, and GALV has crossed this line via unknown vector species. The GALV and KoRV clades both contain infectious exogenous retroviral variants but also contain endogenous retroviruses representing very recent or ongoing germ line invasions. Inter- and intra-retroviral recombination appears to be a frequent event for GALV and KoRV. The ultimate goal of this project is to determine the role that recombination plays in the earliest stages of the genomic invasion process of retroviruses. In addition to identifying new GALV and KoRV like retroviruses in novel species on both sides of the Wallace Line, retroviruses will be tested for the functional consequences of mutation and recombination of the gag and env genes in a heterologous retroviral expression system. Part of the project will be conducted in Australia where many of the sample collections for regional species are housed.

Prerequisites: - Completed university degree (Master of Science or Diploma) in molecular evolution, lab based evolutionary virology or related disciplines); - Strong background in molecular virology; - Experience generating and working with High Throughput Sequence data; - Experience with cell culture and the production of virus or viral vector particles; - Previous working experience in microorganism or genomics based bioinformatics would be an advantage; - Proficiency in English (oral and written). We offer state-of-the-art methodology and a stimulating research environment. For the successful candidate, organizational skills, high motivation and the willingness to work as part of a team within highly interdisciplinary projects are essential. The position will start May 1st, 2018 and is limited to three years. Working hours comprise 25,35 hours per week (65 %) with salary and benefits according to TVöD (Bund). The place of work is the Leibniz-IZW, Alfred-Kowalke-Str. 17, 10315 Berlin. As member of the Leibniz Association, the Leibniz-IZW is an equal opportunity employer, determined to increase the proportion of women in successful scientific careers, and particularly encourages women to apply. Preference will be given to disabled applicants with the same qualifications. For enquiries or further questions please contact Prof. Alex Greenwood (Leibniz IZW) Tel.: +49 (0)30 5158-233, email: assist3@izw-berlin.de. Please submit your application with a motivation letter, CV and copies of relevant degrees, list of publications and names and contact details of two referees before or latest February 16, 2018 to via IZW's online-job-market (button "Apply online").

We are looking forward to your application!

Stephanie Vollberg

Personalsachbearbeiterin Abteilung Verwaltung/Technische Dienste/Bibliothek

Leibniz-Institut für Zoo- und Wildtierforschung (IZW) im Forschungsverbund Berlin e.V. Alfred-Kowalke-Str. 17 10315 Berlin DEUTSCHLAND

Postfach 70 04 30, 10324 Berlin

Tel.: + 49 - 30 - 5168107 Fax.: + 49 - 30 - 5126104 http://www.izw-berlin.de :: Forschung für den Artenschutz ::

"Vollberg, Stephanie" <vollberg@izw-berlin.de>

MaxPlanck EvolBio ModelingAntibioticResistance

PhD position (3 years): Modeling the evolution of antibiotic resistance

The evolution of antibiotic resistance during treatment constitutes an instance of undesired evolutionary rescue. By evolving resistance, the pathogenic bacterial population rapidly adapts to the novel environmental conditions, escaping extinction and preventing patient recovery. Mathematical models can help to understand which circumstances hamper the emergence and spread of resistant strains, while successfully eliminating the sensitive bacteria. With this knowledge, we can hope to be able to tailor treatment strategies accordingly.

The precise PhD project will be determined together with the student. Potential topics concern, for example, the dynamics of resistance on plasmids, spatial drug heterogeneity, or the role of the immune system.

On the mathematical side, the analysis will be based on branching process theory, deterministic ODE systems, and stochastic computer simulations.

Applicants should have a degree in mathematics, physics, biology, or another related field. A prerequisite is a keen interest both in mathematical modeling and in biological systems. Good quantitative skills are essential. Experience in mathematical modeling and knowledge of a programming language (C, C++, Java, R, Python) is an advantage.

The group is part of the Department of Evolutionary Theory at the Max Planck Institute for Evolutionary Biology. The institute provides an international working environment with an excellent infrastructure. Departments span evolutionary genetics, experimental evolution, evolutionary ecology, and theoretical biology. With the close-by Universities of Lübeck and Kiel and the Kiel Evolution Center, the institute is embedded into a collaborative scientific community.

Interested students should send their application (motivation letter, CV, copies of certificates, contact details of two references) by email touecker@evolbio.mpg.de. Please use the code PhD2018 in the subject line.

The Max Planck Society is committed to employing more handicapped individuals and especially encourages them to apply. The Max Planck Society seeks to increase the number of women in those areas where they are underrepresented and therefore explicitly encourages women to apply.

Screening of applications will start on March 1, 2018. However, the position will remain open until filled by a qualified candidate.

Contact: Dr. Hildegard Uecker Department of Evolutionary Theory Max Planck Institute for Evolutionary Biology August-Thienemann-Strasse 2 24306 Plön Germany Email:uecker@evolbio.mpg.de Website:web.evolbio.mpg.de/~uecker

Hildegard Uecker <uecker@evolbio.mpg.de>

MaxPlanckInst Jena 10 HumanHistory

From: Ellen Richter <richter@shh.mpg.de> To: evoldir@evol Cc: Bcc: Subject: Graduate positions:MaxPlanckScience of Human History_Jena_update 2 Reply-To: Ellen Richter <richter@shh.mpg.de>

10 PhD positions at the Max Planck Institute for the Science of Human History, Jena, Germany.

The Archaeogenetics department at the Max Planck Institute for the Science of Human History in Jena, Germany, is offering up to 10 PhD positions beginning October 2018. The overarching research topic at the institute is the use of novel scientific approaches from high throughput sequencing of ancient DNA from human populations, their pathogens, and their beneficial microbes to explore research questions related to human history, migrations, gene-culture coevolution, microbiome evolution, and adaptation to infectious disease.

The institute hosts a multi-disciplinary research team and is looking for students from a variety of backgrounds including, but not restricted to, molecular biology, bioinformatics, microbiology, chemistry, biochemistry, mathematics, physics, computer science, anthropology and archaeology. Students holding a Master's degree (or equivalent) with a proven record of success in their discipline and a genuine interest in examining questions related to human history are encouraged to apply.

Deadline for applications is the 15th of March 2018.

Please submit your application in English, including the following:

§Cover letter, explaining research experience and reason for interest in this project

§CV

§Copies of degree certificates (Bachelor's and Master's diplomas or transcripts); if the candidate is enrolled in a Master's program and the degree is anticipated but not yet granted, please explain the circumstances in the cover letter

§Names and contact information (including email and phone) for 2-3 referees. Note these individuals will be automatically contacted to provide a reference letter.

Please apply online at

https://s-lotus.gwdg.de/mpg/mjws/perso/shh_d007.nsf/application The students will be part of the newly founded International Max Planck Research School (IMPRS) for Human history. The Max Planck Institute is not itself part of a university, but is affiliated to the Friedrich Schiller University, in Jena Germany. Doctoral degrees will be granted by the affiliated university.

Doctoral candidates enrol in a 3-year fully-funded graduate program that provides excellent research conditions. Graduate courses and all other degree requirements necessitate proficiency in English.

The Max Planck Society is committed to employing individuals with disabilities and especially encourages them to apply. The Max Planck Society seeks to increase the number of women in areas where they are underrepresented and therefore explicitly encourages women to apply. Information regarding the Max Planck Institute for the Science of Human History can be found at www.shh.mpg.de . For queries, please contact: Ms. Johanna Allner allner@shh.mpg.de

Projects offered in 2018

Please find below a list of topics we offer for this year's recruitment. All projects are highly integrative and require collaboration between different research groups. Applicants should choose up to three topics of interest. If you are invited to Jena for a recruitment event/interview it is possible to change your preferences after talking to the supervisors.

Topic 1: Historical Human Population Genetics Main supervisor: Dr. Stephan Schiffels

Co-supervisors: Dr. Wolfgang Haak, Prof. Johannes Krause

Description: Human history leaves its traces in genomes, via changes in population size and structure. By analysing the genomes of living and ancient populations, we can therefore directly learn about historical events, such as migrations. In recent years, this approach has led to many new insights, mainly in prehistoric time periods. In this project, we want to develop advanced analytical methodology and analyse new data to investigate events in more recent, historical, time periods, as has been done for example in the case of the Anglo-Saxon migrations into England (Schiffels et al. 2016). Applicants for this topic should have a Master's degree in some field of the Sciences, technical/analytical skills (including programming experience), and an interest in human history.

Topic 2: Pleistocene Human Population Genetics

Main supervisor: < http://www.shh.mpg.de/2890/johanneskrause > Prof. Johannes Krause, < http://www.shh.mpg.de/ > Dr. Wolfgang Haak

Co-supervisor(s): < http://www.shh.mpg.de/ > Dr. Stephan Schiffels, Dr. Choongwon Jeong

Description: Recent years have seen the emergence of the first genome

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MaxPlanckInst UKiel EvolutionaryBiology

The International Max Planck Research School for Evolutionary Biology is offering up to 10 PhD positions and fellowships.

The graduate school is dedicated to highest level of research and training in all areas of contemporary Evolutionary Biology. It is a joint initiative of the Max Planck Institute for Evolutionary Biology, the University of Kiel and the Helmholtz Center for Ocean Research Kiel (GEOMAR). The school offers an internationally competitive research environment with state of the art facilities. The participating groups are working on a broad variety of scientific topics including molecular, behavioral, theoretical and organismal approaches.

The graduate program starts with a rotation period of three months followed by a PhD project of three years including seminars, courses and workshops. The language of the graduate school is English. Financial support is provided throughout the program.

To obtain further information about our PhD program and application details (only online application possible), please visit our website at http://www.evolbio.mpg.de/imprs . Well-motivated and highly-qualified students from all countries are welcome to apply. A Master of Science degree or a Diploma as well as a strong interest in Evolutionary Biology and flexibility in the research project are prerequisites for entering the program. We are looking forward to your online application for a PhD project in the beautiful landscape of Northern Germany.

The deadline for applications is March 25, 2018.

The selection week will be held from June 25- 29 and

the program itself starts on September 17, 2018.

Contact: Dr. Kerstin Mehnert,

August-Thienemann-Str. 2, 24306 Plon, Germany

email: imprs@evolbio.mpg.de phone: +49(0)4522 763 233

Kerstin Mehnert <mehnert@evolbio.mpg.de>

MichiganStateU DemographyGenetics

A research assistantship for a PhD student is available at the Department of Entomology at Michigan State University beginning in May or June 2018. Research will focus on testing the roles of demography and genetics in the establishment and impact of biological control agents in the field. The project will involve lab rearing of a moth classical biological control agent, and experimental releases and monitoring of agent and target populations in the field in southern Michigan over multiple years.

Candidates should possess an M.S. in entomology, ecology, evolution or related field and have valid driver's license. The ideal candidates have experience working with insects and/or weeds and interest in understanding ecological and evolutionary mechanisms underlying demography and genetics of populations.

Applicants should send a CV, cover letter, unofficial transcripts, contact information for three references and a sample of scientific writing (e.g. thesis, published or in preparation manuscripts) to Dr. Marianna Szucs (szucsmar@msu.edu). The position comes with a generous stipend, tuition waiver and health benefits. Applicants will have the opportunity to graduate with a dual degree of Ecology, Evolutionary Biology, and Behavior and Entomology. Screening of applications will begin immediately and the position will be filled as soon as a qualified applicant is identified.

"Szucs, Marianna" <szucsmar@msu.edu>

MurrayU Kentucky EvolutionCommunication

Graduate position (M.S.) in evolution of animal communication at Murray State University (KY)

Note: Funding opportunities have recently become available (see below). To be considered for a TAship and/or the biodiversity stipend starting in the fall semester 2018, application should be submitted by 2/21/18.

The Beckers' Lab at Murray State University accepts a Masters student who is interested in the evolution of animal communication starting in the fall of 2018. Our lab uses Orthopterans (i.e., katydids, and crickets) as model organisms to address questions pertaining the evolution of animal behavior. More specifically, we study the effects of the environment (i.e., phenotypic plasticity) on mating songs. In our main study species, Neoconephalus triops, day length induces two substantially different mating songs. These differences in the songs are comparable to species differences within the genus. In a collaboration with two other labs (Missouri and West Virginia), we study the genetic underpinnings of this behavioral plasticity and how the involved genes relate to speciation.

A second line of research focuses on the evolutionary arms race between katydid hosts and their eavesdropping parasites in the local population of N. triops. The flies use the katydid mating songs to find their hosts and deposit deadly larvae on them. Thus, sexual selection and natural selection act in opposing directions on male singing behavior. The evolutionary ramifications of this deadly parasitism on male singing and mate acquisition behavior are the focus of future studies.

The Masters students could work on either of these projects or on other projects related to animal communication in katydids and crickets.

I seek driven, enthusiastic, and focused students to join our lab at Murray State University. Successful applicants have a B.S. in biology, ecology, or related discipline and are interested in studying animal behavior and evolution. If you are interested in this opportunity and/or have any questions, please email Dr. Beckers at obeckers@murraystate.edu. For your application, make sure to address in an attached document your research interests, how they relate to the Beckers' lab research, and your GPA.

Funding for tuition and a summer stipend are available for the N. triops project through a grant. In addition, a TAship and/or a biodiversity stipend ($5000 per semester) are available on a competitive basis. Review of applications starts immediately. Deadline for applications is February 21, 2018 to be considered for a TAship or the biodiversity stipend for the fall semester of 2018. Once you indicated interest in the position, an interview will be set up shortly after.

Please find more information on Dr. Beckers' research here:

https://www.murraystate.edu/academics/CollegesDepartments/CollegeOfScie nceEngineeringandTechnology/CollegeOfSciencePrograms/biologyDept/facult y/oliver-beckers/index.aspx

Information on the Department of Biological Sciences at MSU:

https://www.murraystate.edu/academics/CollegesDepartments/CollegeOfScie nceEngineeringandTechnology/CollegeOfSciencePrograms/biologyDept/facult y/

Oliver Beckers <obeckers@murraystate.edu>

NorthernArizonaU TreeEvolution

Graduate Research Assistantships in Tree Genomics & Evolution @ NAU

The School of Forestry at Northern Arizona University (NAU) is seeking 2 highly motivated Master of Science students to join the newly formed lab of Genetics, Genomics and Evolution of Tree Species. Both positions include a stipend, tuition waiver, and health benefits for 2 years.

Position 1: Students will use genomic tools to identify genes underlying resistance to the devastating disease white-pine blister rust in Sugar Pine. This position involves only data analyses.

Position 2: Students will use genomic tools to identify patterns of hybridization, introgression and local adaptation between two varieties of Douglas fir. This position involves data analyses, molecular lab work, and greenhouse work.

Minimum qualifications:

- Bachelor degree in Genetics, Forest Sciences, Biology, Plant Sciences, Evolutionary Biology, Bioinformatics or related fields of study.

- Have taken at least one undergraduate course in Genetics.

- Ability to program in R, Perl or Phyton (familiarity with Linux is a plus)

- Willingness to work with big data sets in a computer cluster.

- Availability to start by July 1^st, 2018 .

- No greenhouse or molecular lab experience is required.

How to apply:

Please send a 1-page statement of interest, CV, unofficial copy of transcripts, GRE scores, and TOEFL scores (international students), and the names and contact information of 3 references by March 5^th, 2018. If found to be a good match for the position, you will be encouraged to apply to the graduate program at NAU. Please note that NAU has the following admission requirements: GPA equal or higher than 3.0 and TOEFL = 213 (computer-based) or 80 (internet-based).

Contact Information:

Dr. De La Torre, Amanda.de-la-torre@nau.edu

https://nau.edu/CEFNS/Forestry/Faculty-and-Staff/-Directory/De-La-Torre/ Institution:

Northern Arizona University is a 29,000 student-institution with its main campus in Flagstaff, a four-season community of about 70,000 at the base of the majestic San Francisco Peaks. Flagstaff has all-year easy access to the Arizona snowbowl ski resort and is located at 1-hour drive from the Gran Canyon.

Useful links:

School of Forestry- http://nau.edu/forestry Amanda Rosa Maria De la Torre Cuba <Amanda.de-la-Torre@nau.edu>

QueenMaryULondon EvolutionSpiralCleavage

A PhD studentship is available for a project on the evolution of axis specification modes in spiral cleaving animals. The project will focus on the annelid species Owenia fusiformis, which occupies a key phylogenetic position as the sister lineage to all remaining annelids, and it has recently proven very informative for the study of animal development and evolution (Martin-Duran et al. 2017 Nat Ecol Evol; Martin-Duran et al. 2018 Nature). The project will characterise cellular dynamics during spiral cleavage with high-resolution live microscopy, and investigate the evolution of the genomic and molecular mechanisms involved in the establishment of bilateral symmetry in spiralians.

We are looking for a highly self-motivated and enthusiastic candidate with a strong interest in evolutionary developmental biology, some research experience in molecular biology, and an aptitude with computers. The project will involve both experimental and computational approaches, as well as molecular biology and microscopy techniques. The successful applicant will also have the opportunity to present their work at national and international conferences, and to collaborate with other research groups at an international and interdisciplinary level. The successful candidate will need to be able to work independently, as well as part of a team. While training will be available, the student will also be expected to develop proficiency in molecular techniques (e.g. gene cloning, in situ hybridization, immunohistochemistry, epigenomic approaches), live microscopy, and computational analyses of next-generation sequencing datasets.

Our group is one of several in Evolutionary Genetics and Organismal Biology within Queen Mary's School of Biological and Chemical Sciences. The School benefits from state-of-the-art equipment and expertise in molecular biology, next-generation sequencing technologies, genomics and bioinformatics. Queen Mary is a Russell Group University, a college of the University of London and located in London's vibrant East End (10 min bicycle ride to Tower Bridge; 10 min walking to Victoria Park; 30 min walking to Shoreditch nightlife).

The studentship is open to UK and EU nationals. It will cover tuition fees and provide an annual tax-free maintenance allowance for 3 years at Research Councils UK rates (16,553 in 2017/18). Applications are invited from candidates with, or expecting to be awarded, a degree (UK 1st or 2:1 or equivalent qualification) in a relevant area (e.g. biology, biochemistry, biomedicine). Although not essential, ideally applicants will have a Master's degree, or appropriate relevant work experience. Experience in molecular biology, microscopy, and/or bioinformatics are desirable. Students outside the UK are required to provide evidence of their proficiency in English language skills.

Applications should include a statement of purpose (motivation letter), a CV, transcripts, and two referee details.

Informal enquiries are encouraged and can be made by email to Dr. Jose M. (Chema) Martin-Duran (chema.martin@qmul.ac.uk). For more information about Dr. Martin's research profile, please see https://scholar.google.no/citations?user=aLUuC-oAAAAJ&hl=en chema.martin@qmul.ac.uk

StockholmNHM Palaeogenomics

PhD Student Position on Palaeogenomics of Prehistoric Climate Change

Swedish Museum of Natural History & Stockholm University

PROJECT DESCRIPTION

This PhD project will investigate how species are affected by climate change. To do this, we will use a palaeogenomic approach to analyse ancient DNA from prehistoric bones and teeth sampled across several well-known severe and rapid changes in climate that took place during the last ice age. The analyses will comprise several animal species in Eurasia. The specific aims of the project are to i) assess the degree to which past warm periods led to demographic bottlenecks, ii) examine to what extent climate-induced range contractions led to losses of unique genetic variation, and iii) use a comparative genomic approach to investigate whether species adapted genetically in response to rapid climate fluctuations.

For this project, good knowledge in population genetics, bioinformatics as well as experience of laborative DNA analysis are important qualifications. The PhD student will join the ancient DNA research group at the Swedish Museum of Natural History (for further details, see www.palaeogenetics.com/adna).

ENVIRONMENT The PhD student will be employed by Stockholm University (SU), but will be based at the Department of Bioinformatics and Genetics at the Swedish Museum of Natural History (SMNH). The museum is located in Stockholm, which by many is regarded as one of the most beautiful capitals in the world and is home to a vibrant scientific community with several leading research institutes as well as the National Genomics Infrastructure at the Science for Life Laboratory. The SMNH has a strong mission in natural history research, and its research division has more than 170 employees. The main supervisor for the PhD project will be Prof. Love Dalen at the SMNH. The project is funded by the Bolin Centre for Climate Research and the Department of Zoology at SU, and will be co-supervised by Prof. Anders Gotherstrom at SU.

QUALIFICATIONS In order to meet the general entry requirements, the applicant must have completed a second-cycle degree, completed courses equivalent to at least 240 higher education credits, of which 60 credits must be in the second cycle, or have otherwise acquired equivalent knowledge in Sweden or elsewhere. In order to meet the specific entry requirements, the general syllabus for doctoral studies in the field of Systematics and Evolution stipulates that applicants must have completed a research degree (e.g. Master's), or have passed at least 120 hp (2 years) of biological studies, including an approved independent project of at least 30 hp at advanced level ("examensarbete") within systematics and evolution, ecology, population genetics, bioinformatics or a similar subject. Applicants who have in principle acquired the corresponding competence in Sweden, or abroad, are also qualified. The qualification requirements should preferrably be met by the deadline for applications.

CONTACT For questions about the position and further information about the project, contact Prof. Love Dalen, Email: love.dalen@nrm.se

HOW TO APPLY Applications should be done using Stockholm University's online application system. Please follow the link below to obtain further information about how to write your application and how to access the online application system: https://www.su.se/english/about/working-at-su/phd?rmpage=3Djob&rmjob=3D4861&rmlang=UK Closing date: 22 March 2018 Reference number: SU FV-0556-18

"Love.Dalen@nrm.se" <Love.Dalen@nrm.se>

StockholmU PlantSystematics

PhD position in Plant Systematics at Stockholm University

Closing date: 23 February 2018.

We have an opening for a highly motivated postgraduate fellow to work on the research project “Genome evolution in parasitic plants” in the group of Dr. Gitte Petersen at Stockholm University.

The complete ad with information on how to apply is available on the Stockholm University webpage: https://www.su.se/english/about/working-at-su/-phd?rmpage=job&rmjob=4621&rmlang=UK Project description The Department of Ecology, Environment and Plant Sciences invites applications for a four-year PhD position part of the project Genome evolution in parasitic plants. Several groups of angiosperms are parasites, which makes them more or less dependent on a host for nutrient supply. This project aims at understanding the evolution and consequences of host-parasite interactions at the genomic level. The current PhD project will primarily focus on evolution of organelle genomes in parasitic plants. Special emphasis will be given to Mistletoes and related genera, in which substantial and unexpected alterations of the mitochondrial genome are already documented. Comparative studies of completely assembled organelle genomes will be supplemented with targeted sequencing and analysis of selected genes.

Qualification requirements In order to meet—the general entry requirements, the applicant must have completed a second-cycle degree, completed courses equivalent to at least 240 higher education credits, of which 60 credits must be in the second cycle, or have otherwise acquired equivalent knowledge in Sweden or elsewhere. In order to meet—the specific entry requirements, the general syllabus for doctoral studies in the field of Plant Systematics stipulates that applicants must have completed at least 60 higher education credits in the second cycle, of which 15 credits must be from a course in Plant Systematics, and 30 credits from a project in Plant Systematics. Applicants may also have otherwise acquired equivalent knowledge in Sweden or elsewhere. The qualification requirements must be met by the deadline for applications.

Selection The criteria used in the selection for admittance to research training in Plant Systematics are knowledge of theory and applications in the research field, ability to communicate orally and in writing, knowledge of English, creativity, initiative, independence and collaboration ability. Hands-on experience with Next Generation Sequencing and bioinformatics tools will be considered special merits, as well as good knowledge of phylogenetics. Admission Regulations for Doctoral Studies at Stockholm University are available at:—www.su.se/rules . Terms of employment Only a person who will be or has already been admitted to a third-cycle programme may be appointed to a doctoral studentship. The primary assessment criteria in appointing a doctoral student should be the capacity to benefit from the training. The term of the initial contract may not exceed one year. The employment may be extended for a maximum of two years at a time. However, the total period of employment may not exceed the equivalent of four years of full-time study. Doctoral students should primarily devote themselves to their own education, but may engage in teaching, research, and administration corresponding to a maximum of 20 % of a full-time position. Please note that admission decisions cannot be appealed. Stockholm University strives to be a workplace free from discrimination and with equal opportunities for all.

Contact For more information, please contact the Head of Department, Professor Ove Eriksson, telephone: +46 8 16 12 04, ove.eriksson@su.se or Dr. Gitte Petersen, gittep@snm.ku.dk.

Application Apply for—the—PhD student position at Stockholm University’s recruitment system by clicking the “Apply” button. It is the responsibility of the applicant to ensure that the application is complete in accordance with the instructions in the job advertisement, and that it is submitted before the deadline.

Gitte Petersen <gittep@snm.ku.dk>

StockholmU SexualSelection

PhD position in Ethology

at the Department of Zoology, Stockholm University, Sweden

Deadline for application: March 2, 2018.

A PhD position focused on sexual selection is available in John Fitzpatrick’s research group in the Department of Zoology at Stockholm University. The aim of this project is to examine how trade-offs between sexual ornaments, weapons and ejaculates influence animal sexual evolution. To successfully reproduce and leave offspring to future generations animals must be able to find a mate and produce fertilized eggs. However, animals have limited amounts of energy they can devote to reproduction. Therefore, animals must balance how they invest their sexual resources before and after mating. Yet, we know surprisingly little about these potential trade-offs. This project will use a multidisciplinary approach to rigorously test the hypothesis that trade-offs exist between sexual behaviours and traits that are important in securing a mate and fertilizing eggs. To do this, this project focuses on the wrestling halfbeak, Dermogenys pusilla, a small freshwater fish where males invest simultaneously in sexual weapons, ornaments, and ejaculates. This project will combine breeding designs, genomic approaches, artificial selection and experimental manipulations to determine if and how trade-offs among sexual traits impact male fertility.

The work will be mostly lab oriented. However, as the lab is currently establishing field sites in Singapore and Indonesia, there is the possibility for a field component in the project as well. The lab work will take advantage of the new tropical freshwater fish labs in the Department of Zoology, with room for over 6,000 aquaria and several experimental rooms. The Department of Zoology is already home to state-of- the-art facilities to assess behaviour and sexually selected traits (e.g. unique 2D and 3D behavioural tracking software, computer-assisted sperm analysis software (similar to what is used in human fertility clinics), high-speed cameras, spectrophotometers for colour analyses). The successful candidate will join a rapidly growing sexual selection group in the Department and will be provided with excellent opportunities for personal and professional development towards a successful academic career.

Qualification requirements

We are looking in particular for candidates with a strong interest in evolutionary biology and sexual selection, with excellent analytical ability and experience with quantitative analyses of behaviour and other traits of interest. Experience in working with aquatic animals in the lab is especially meriting. Applicants who have in principle acquired the corresponding competence in Sweden or in another country are also qualified. Therefore, overseas applications are encouraged.

Applications written in English are preferred.

For more information on the position (Ref. SU FV-4326-17) and to apply follow this link: https://www.su.se/english/about/working-at-su/-phd?rmpage=job&rmjob=4812&rmlang=UK Contact Questions? Please contact Dr John Fitzpatrick, john.fitzpatrick@zoology.su.se

For more information about research in the Fitzpatrick lab see: http://www.zoologi.su.se/en/about/-staff/person.php?suuid=jfrit John Fitzpatrick <john.fitzpatrick@zoologi.su.se>

StockholmU YeastExperimentalEvolution

PhD in Experimental Evolution with Yeast, Stockholm University Application closes 1 March 2018 Starting date: as soon as possible but latest 1 August 2018 Selected candidates will use experimental evolution with the budding yeast Saccharomyces to study evolutionary processes. Potential topics include but are not limited to 1) adaptation to changing environments, 2) the genetic architecture of fitness and 3) hybrid speciation.

I am looking for a highly motivated candidate with a strong interest in evolutionary and conservation biology, ideally with experience in experimental evolution and quantitative/molecular/population genetics. Prior training in Saccharomyces yeast cultivation, statistics and programming (e.g. R, Python) is a plus. Applicants should be able to think quantitatively, be well-organized, good communicators, and happy to work in our growing team as well as independently. The applicant is expected to be fluent in English.

Training will be provided in experimental evolution, forward and reverse molecular genetics, statistics, bioinformatics, yeast cultivation, and microbiology. The work will mostly be lab-based but may include some fieldwork with natural yeasts. There is flexibility within the project for the student to develop their own interests. The graduate program covers four years of full-time study. The position can be combined with teaching (maximum 20%), which prolongs the employment with the corresponding time. The successful candidate will receive salary and full social benefits according to local agreements. The position is funded by the Swedish Research Council (VR).

All applications must be sent through this platform: https://www.su.se/english/about/working-at-su/instructions-applicants. The application should include 1) a letter describing yourself, your research interests, and your motivation to apply for this position, 2) a CV with a list of degrees, other completed courses, and work experience, 3) an authorized copy of your master degree and course grades, 4) degree projects/theses/publications; 5) the names and email addresses of at least two referees. The application should be written in English.

Contact: For more information, please contact Rike Stelkens: rike.stelkens@zoologi.su.se, +46 8 16 42 23.

Environment: The campus is located four metro stops from the centre of Stockholm, one of the most beautiful and dynamic European capitals. The campus is home to a vibrant scientific community, and we are well-connected to the Science for Life Laboratory (a leading genomics core facility that we routinely use) and the Swedish Museum of Natural History. Sweden is a free and open society, and one of the world's most innovative and research-intensive nations. People here enjoy a respected system of democracy and individual rights, freedom of speech, a free press, the right to scrutinize those in power, and access to beautiful nature. Most Swedes speak English.

Relevant references: 1. Stelkens RB, D Greig, Fungal evolution: On the origin of yeast species, NATURE Microbiology 2016, 1 (1): 15017, doi: 10.1038/nmicrobiol2015.17; 2. Stelkens RB, M Brockhurst, G Hurst, D Greig, Hybridization facilitates evolutionary rescue, Evolutionary Applications, 2014, 7(10): 1209-1217; 3. Stelkens RB, M Brockhurst, G Hurst, E Miller, D Greig, The effect of hybrid transgression on environmental tolerance in experimental yeast crosses. Journal of Evolutionary Biology, 2014, 27(11): 2507-2519;

rike.stelkens@zoologi.su.se

UBasel Switzerland HostParasiteEvolution

University of Basel, Switzerland *Department of Environmental Sciences, Zoology* ** *PhD-position in **host-pathogen interactions* is available in the group of Dieter Ebert at Basel University, Basel, Switzerland.

I am looking for a highly motivated candidate with interests in evolutionary genetics/genomics and host-parasite interactions. The PhD project is concerned with the coevolution of parasites and its host Daphnia. The aim of the project is to gain insights into the (co-)evolutionary and genetic interactions of parasites and its Daphnia host using field-based, experimental and population genetic/genomic approaches. The position is supported by the Swiss National Science Foundation and the University of Basel. The Ebert research group covers the entire range from epidemiological and ecological aspects of host-symbiont interactions, to studies on the population genetics and genomics of hosts and symbionts.

Starting date for the PhD isnegotiable (any time from April 2018 onwards). The working language in the group is English. Speaking German is helpful in every day life in Basel, but is not a requirement. A Master degree (or equivalent) in biology or related subject is necessary for admission. PhD program takes about 3.5 years.

Please send your application by E-mail (all material in one PDF please) to Dieter Ebert. Applications should include a motivation letter, a CV, a list of publications and a statement about research interests. Please give names and email addresses of two persons who are willing to write a letter of recommendation. Application deadline is 1. March 2018.

Further information and address for application: Prof. Dr. Dieter Ebert, University of Basel, Department of Environmental Sciences, Zoology, Basel, Switzerland, Email: dieter.ebert@unibas.ch <mailto:dieter.ebert@unibas.ch>Tel. +41-(0)61-207 03 60.

Web:http://evolution.unibas.ch/ebert/ Dieter Ebert <dieter.ebert@unibas.ch>

UBern 2 EvolutionOfCooperation

Two 3-year PhD positions: Animal Physiology and Behavioural Ecology

In the context of a research project financed by the Austrian Science Fund (FWF), the private research and animal conservation entity Waldrappteam (www.waldrapp.eu) is offering two PhD positions to investigate the costs and benefits of formation flight in birds using the northern bald ibis as a study species.

One PhD project will focus on energy consumption during migration flight, with the main question "Why do birds fly in formation?" While we believe to know the answer to this question (formation flight allows them to save energy), the specific challenge will be to provide direct empirical evidence for that assertion by quantifying how much energy the birds can save. This requires a candidate with a firm background in animal physiology.

The focus of the second PhD project is on social dynamics of formation flight, with the question "How do the birds in a formation co-ordinate and cooperate?" Concerning this question, there are many tentative suggestions but few empirical data at hand. In this context, we are seeking a candidate with an interest in behavioural ecology and/or flight mechanics and aerodynamics of birds.

Data for both PhD projects will be collected using high-resolution GPS devices and heart rate loggers fitted to free-flying birds. In addition, we plan to conduct respirometry measurements with birds in the lab. Achieving this will be technically demanding and requires a readiness for tinkering around with sensors and electronic devices and spending a lot of time handling and analysing large data sets (programming experience in Python, Matlab, or any comparable environment will be a plus).

The research project is aligned with an ongoing European LIFE+ reintroduction scheme by Waldrappteam and partners, which aims to establish a self-sustaining migratory northern bald ibis population in Europe. More information about this project can be found here: www.waldrapp.eu. The research project will mainly take advantage of the annual human-led migrations with human-imprinted juvenile birds. The research project will be managed by Waldrappteam in Mutters, Tyrol, though the PhD candidates will be based in Vienna, affiliated either with the University of Vienna or the Veterinary University of Vienna (to be decided based on interest and academic supervision).

The research project includes several months of field work in summer and autumn, during which the researchers will stay with the birds at field camps in Austria, Germany or Italy or follow the birds during the autumn migratory journey throughout these countries. German language skills are not required but a willingness to learn basic German will facilitate living in Austria and positively affect social life. Payment will be according to the salary scheme of the FWF (yearly gross pay of approx. 37.000 Euro, for three years).

Please send your application letter together with a motivation statement, your CV and contact details of one or two reference persons (reference letters are not required for the initial application) to: bvoelkl@waldrapp.eu. We encourage applications of people with unusual career tracks. Applicants from non-EU countries will have to ensure that they are eligible to work in Austria (for the time being, the UK still counts as part of the EU). Please indicate your preferred and earliest possible start date in the application letter.

Application deadline: March 18th 2018; Project start: May 2018. For informal enquiries please contact Dr. Bernhard Voelkl at: bvoelkl@waldrapp.eu.

"bernhard.voelkl@vetsuisse.unibe.ch"
<bernhard.voelkl@vetsuisse.unibe.ch>

UBielefeld AvianMalariaTolerance

Short-term and long-term consequences of avian malaria-like infection

A PhD position in behavioural ecology is available at the Faculty of Biology at Bielefeld University, in the Department of Animal Behaviour (with Dr. Nayden Chakarov, see http://www.uni- bielefeld.de/biologie/animalbehaviour). The position runs for three years from early 2018 to 2021 and is funded by the German Research Foundation (DFG). The PhD student will be part of the buzzard research team (together with the group of Prof. Dr. Oliver Krüger) and of a large PhD cohort, which is supported by a DFG-funded collaborative research centre NC3 (full details at www.uni-bielefeld.de/biologie/crc212).

The aim of the PhD project is to explore physiological causes and consequences of a very common blood parasite infection in a common buzzard population (Leucocytozoon in Buteo buteo). The student will conduct medication experiments in the field, produce transcriptomic data and analyse it in combination with fitness correlates. The long-term fitness consequences for buzzards will be monitored using lifelong wing-tags, and survival and recruitment data will be collected. So far, over 2500 individual buzzards have already been fitted with lifelong wing tags and the resulting data set will be used.

Main responsibilities

- Research tasks (90%) - Conducting field work on a buzzard population, including chick-ringing and treatment from late March to early July each year;

RNA extraction and library preparation; Transcriptomic and statistical analyses; Writing scientific publications

- Organisational tasks in the research group and collaborative efforts (10%)

Applicant's profile

We seek a bright and highly motivated student with a university degree in a relevant discipline with specialization in either behavioural ecology, ornithology, population ecology and/or bioinformatics, and a strong eagerness to delve into the other; interest to develop scientific capabilities and questions; experience with field work, preferably in birds of prey; experience with molecular lab work; interest in behavioural and life history, immunological and parasitological questions; coding experience, preferably with Unix command-line, omics-techniques, and R; ability to work both independently and as part of a team; excellent oral and written communication skills in English. The following qualifications would additionally be of advantage: papers in peer-reviewed international journals; experience in tree-climbing with rope techniques; experience with large-scale research projects.

Remuneration

Salary will be paid according to Remuneration level 13 (65%) of the Wage Agreement for Public Service in the Federal States (TV-L).

Bielefeld University is particularly committed to the career development of its employees. It offers attractive internal and external training and further training programmes. Employees have the opportunity to use a variety of health, counselling, and prevention programmes. Bielefeld University places great importance on a work-family balance for all its employees.

Application procedure

To apply, please provide: (i) a letter of motivation including a statement of your research interests and skills and experience relevant to the position, as well as specific ideas and plans related the project outline; (ii) a CV including publication list; (iii) names and contact details of two referees willing to write confidential letters of recommendation. All materials should be emailed as a single PDF file to: nayden.chakarov@uni-bielefeld.de. The application deadline is March 5th 2018 and interviews will take place shortly thereafter. After the decision, the position should start as soon as possible. For further information on the project and the department, please contact Nayden Chakarov nayden.chakarov@uni-bielefeld.de with any informal inquiries.

Bielefeld is a city of 325,000 inhabitants with all expected amenities and easy access to the Teutoburger Wald for hiking and other outdoor pursuits. It offers a high standard of living and is well connected to most major European cities. Bielefeld University has received a number of awards for its achievements in the provision of equal opportunity and has been recognized as a family friendly university. The University welcomes applications from women. This is particularly true with regard both to academic and technical posts as well as positions in Information Technology and Trades and Craft. Applications are handled according to the provisions of the state equal opportunity statutes.

Applications from suitably qualified handicapped and severely handicapped persons are explicitly encouraged.

Nayden Chakarov <nayden.chakarov@uni-bielefeld.de>

UBritishColumbia InvasionGenetics

I am looking for an MSc student to join my research team at The University of British Columbia (Okanagan Campus) to take part in an invasion genetics study to support on-going ecosystem restoration efforts in Haida Gwaii, an archipelago off the west coast of British Columbia, Canada. This opportunity recently emerged and I am hoping to find a highly motivated graduate student to join the project in May or September 2018. The project offers opportunities for both laboratory and field-based research, and direct collaboration with researchers and managers from government and participating universities. Individuals with a population genetics background, bioinformatics experience and strong analytical skills are especially encouraged to apply.

Visit the Ecological and Conservation Genomics laboratory website (http://people.ok.ubc.ca/mirussel/) for more information on our current research directions. Additional information about our Biology graduate program at UBC can be found at the following website: http://biol.ok.ubc.ca/graduate/biology.html . To apply, send me via e-mail (michael.russello@ubc.ca) a CV, unofficial transcripts, and contact information for at least two references.

Dr. Michael Russello Professor The University of British Columbia Okanagan Campus Department of Biology 3247 University Way, FIP346 Kelowna, BC Canada V1V 1V7 michael.russello@ubc.ca

michael.russello@ubc.ca

UCanterburyNZ EucalyptusPopGenomicsTaxonomy

A fully-funded PhD scholarship is available for a project on the population genomics and taxonomy of Eucalyptus at University of Canterbury, New Zealand.

The New Zealand Dryland Forests Initiative (nzdfi.org.nz) aims to create plantations of high-value Eucalyptus species in dry environments on the east coast of the South Island. For this purpose, Australian seed collections of five Eucalyptus species were planted in New Zealand to determine if these species produce desirable growth and wood qualities (e.g. low growth stress, high natural durability) in the New Zealand environment. The proposed project aims to use genomic tools to understand how genomic and environmental variation interact to influence commercially important traits of selected Eucalyptus species in the NZDFI common garden experiments to: (1) Inform future genomic selection in breeding programs, (2) Resolve the taxonomic delimitation of two morphologically similar species (E. argophloia and E. bosistoana), and (3) Inform the conservation management of E. argophloia (Vulnerable) and E. bosistoana (Near Threatened) in Australia.

We are looking for a highly motivated PhD student with field and lab research experience in population genetics/genomics or molecular systematics, preferably in plants, and an interest in building strong multidisciplinary relationships. Good written and spoken communication skills are essential. Candidates must have a valid driver's licence and be willing to undertake field work.

The successful applicant will be supervised by a multidisciplinary team of researchers in the Schools of Forestry (Drs Apiolaza and Altaner) and Biological Sciences (Drs Pelser and Steeves) of University of Canterbury (Christchurch, New Zealand). The research team is committed to Kindness in Science (kindnessinscience.wordpress.com); we aim to capture diverse perspectives and foster a science environment where early career researchers flourish and better science outcomes are achieved.

The scholarship contributes to living expenses (NZ$ 22,000 p.a.) and all university fees (NZ$ ~8,200) for a maximum of 3.5 years.

The position remains open until filled. Starting date is open for discussion, but an early start is preferred.

Inquiries and applications (cover letter, CV) are to be addressed to pieter.pelser@canterbury.ac.nz

Tammy Steeves <tammy.steeves@canterbury.ac.nz>

UCork MRes EvolutionOfCognition

MRes Studentship 18 months "Trade-offs in sexual selection and cognition" Why do individuals vary in their cognitive abilities? EVOECOCOG, an ERC funded project, takes the disciplines of cognition and evolutionary biology into a natural setting to answer this question. It aims to do this by investigating a variety of proximate causes and population-level consequences of individual cognitive variation using a great tit Parus major population.

This MRes position will explore potential trade-offs between traits involved in pre-copulatory and post-copulatory sexual selection and their relationships with mating success and cognitive ability. The student will perform laboratory analyses of sperm sampled from male great tits in the breeding season to measure sperm quality and viability, and then relate this to mating success by performing paternity analysis using a newly purchased state-of-the-art DNA sequencer. These measures will be compared to measures of signal quality and cognitive ability to detect potential trade-offs among these traits.

The chosen study system, the great tit Parus major, is one of the most widely used in Europe, and consists of 12 subpopulations across deciduous and conifer woodland fragments in Co. Cork, Ireland. A recent state of the art aviary is also available for experimental study at the School of BEES.

This advert is for an 18 month MRes studentship. The successful student will be based in the UCC Ornithology lab at the School of BEES http://ornithology.ucc.ie. They will join a research team led by Prof. John L. Quinn, consisting of 8 early career biologists working on this project (see http://ornithology.ucc.ie/-current-projects/evolutionary-ecology-of-cognition/), a Research Support Officer, and a range of other students and postdocs working on a variety of different projects in behavioural and applied ecology. The studentships will be cosupervised by Prof. J. Quinn and Dr Michael Reichert.

Candidates should possess a 2.1 BSc (Hons) degree or higher in a relevant discipline (e.g. Ecology, Zoology, Evolution, Physiology, Psychology). Applicants must be self-motivated with good numerical, communication, organisational, experimental design, and writing skills. Students with experience working under difficult conditions in the field or with an MSc are likely to have a strong advantage. A full, clean driving license will be important early in the MRes, and experience working with birds in captivity or in the wild would also be advantageous. A willingness to spend long periods of time in the field in spring, and to travel and work across different research sites is important. This position covers EU fee rates ('Ã5,750 p.a.; non-EU members may apply but would need to cover extra international rate fees themselves), plus a tax-free stipend of approx. 'Ã16,000 p.a.

Please direct informal inquiries to Prof. John L. Quinn at j.quinn@ucc.ie

Application: To apply please send by email to Prof. John Quinn, j.quinn@ucc.ie a CV, details of 2 referees, and an accompanying 1 page letter. The letter should outline of your relevant experience, explaining why you want the studentship.

Dates: Application deadline is 28 February 2018. Interviews will be held in person or by Skype within 1 weeks. Start dates are 1 April 2018 or sooner!

University College Cork is one of Ireland'Âs largest and most successful universities and the studentships will be based at the School of BEES. Currently there are 28 faculty, ca. 20 postdocs and 35 PhD students across Zoology, Ecology, Plant Sciences and Geology. Cork is situated on the south coast of Ireland, 2.5 hours from Dublin, is served by an international airport, has a population of about 200,000, and is on the doorstep of some of the most beautiful coastline in Europe.

John Quinn (Professor in Zoology & Head of Discipline), School of Biological, Earth and Environmental Science (BEES), UCC, North Mall, Cork, Ireland. T23 N73K Tel (work): 00353-21-4904546 ; Tel (mobile): 00353-(0)852266122 Personal http://ornithology.ucc.ieSchool https://www.ucc.ie/en/bees/UCC http://www.ucc.ie/-en/ "Reichert, Michael" <michaelreichert@ucc.ie>

UEdinburgh ComputationalPhylogeny

MASSIVELY PARALLEL PHYLOGENY RECONSTRUCTION FOR THE AGE OF DNA BIG DATA

Supervisors:

Dr Daniel Barker, University of Edinburgh, UK, Daniel.Barker@ed.ac.uk and Professor Thomas Meagher, University of St Andrews, UK

Note:

This opportunity is only open to UK nationals (or EU students who have been resident in the UK for 3+ years immediately prior to the programme start date) due to restrictions imposed by the funding body.

Project Description:

How are species related? This question, of fundamental importance across life sciences, can in principle be addressed using DNA sequence data. Implicit in these data is the pattern of relationships of the species the DNA came from, known as their phylogeny, usually represented as a tree. However, algorithms and software to reconstruct phylogenetic trees for very large input are lagging behind the recent explosion in availability of DNA sequence data.

The goal of this project is to create parallel algorithms and open-source software for reconstructing large phylogenies by heuristic searches suited to very large data.

The project will use theoretical and computational approaches. These will include use and characterisation of nature-inspired advanced heuristics (e.g. Strobl and Barker 2016), programming and use of massively parallel computer systems, optimisation of algorithms and implementations, and cross-site, distributed machine learning techniques.

Research training will be provided through various means, including meetings with the supervisors and with Dr Martyn Winn (STFC Scientific Computing Department), attendance at short courses and conferences, and attendance at local and regional seminars and discussion groups.

It is anticipated the successful candidate would gain valuable skills and insight for subsequent employment in computational science or life sciences, in academia or industry.

Literature Reference:

Strobl MAR, Barker D (2016) On simulated annealing phase transitions in phylogeny reconstruction. Molecular Phylogenetics and Evolution, 101, 46-55. http://dx.doi.org/10.1016/j.ympev.2016.05.001 Further Information:

Before applying, potential applicants are encouraged to contact Daniel Barker informally. https://www.ed.ac.uk/biology/people/profile/dbarker Application:

Deadline 14 March 2018.

Please follow the instructions on how to apply at http://www.ed.ac.uk/biology/prospective-students/postgraduate/pgr/how-to-apply – Dr Daniel Barker Institute of Evolutionary Biology University of Edinburgh Charlotte Auerbach Road The Kings Buildings Edinburgh EH9 3FL United Kingdom

The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

"Daniel.Barker@ed.ac.uk" <Daniel.Barker@ed.ac.uk>

UEdinburgh TreeImprovement

We invite candidates to apply for a PhD position based at the University of Edinburgh, UK and Forest Research, UK

Title: Monitoring and managing genetic diversity in Sitka spruce

Supervised by Professor Richard Ennos (University of Edinburgh - rennos@ed.ac.uk) and Dr. Joan Cottrell (Forest Research - joan.cottrell@forestry.gsi.gov.uk)

Genetic diversity is a key component of the resilience of tree populations to threats such as climate change, and novel pests and diseases. Reduction in genetic diversity leaves tree populations vulnerable to rapid climate change, and novel pest and pathogen epidemics (Ennos, 2015). Despite its importance, we currently have no quantitative estimates from genetic markers of genetic diversity in our most important commercial conifer, Sitka spruce (Picea sitchensis Bong. Carr). This is true both for the unimproved population introduced from North West America and naturalised throughout Britain in the twentieth century, and for the genetically improved populations which increasingly dominate Britain's productive forestry. These have been produced either via open pollinated seed orchards containing selected parents, or through vegetative propagation of offspring from a limited number of half and full sib families (Lee & Watt, 2012). The primary objective of this PhD project is to determine the extent to which genetic diversity has been reduced during this process of domestication of Sitka spruce and to identify the stages in the process that are particularly vulnerable to loss of diversity.

The genetic tools required for this study, a set of highly polymorphic microsatellite loci, have already been developed by Forest Research (A'Hara & Cottrell, 2004). They will be used to follow changes in genetic diversity associated with the introduction of Sitka spruce from North West America, the selection of genetically improved parents, the production of seeds in open pollinated seed orchards, and the vegetative multiplication of a limited number of superior genotypes produced by controlled crosses. The involvement of both the Conifer Breeding Co-operative and the Forestry Commission in the initiation of this project means that there will be opportunities for the student to gain at first hand an understanding of the practice of commercial tree breeding, and to have ready access to the samples required to conduct the study.

The student will receive training in the application of molecular markers to investigate a range of applied questions e.g. how population genetic theory can be used to understand mating patterns within artificial seed orchard populations. Apart from documenting the effects that the current tree improvement programme has had on Sitka spruce genetic diversity, the student will also be encouraged to explore how novel tree improvement strategies may be used in the future not only to ensure that genetic diversity is maintained, but also to ensure that improved planting stock remains well adapted to a rapidly changing climate and a biotic environment with increased numbers of introduced pathogens.

The student will benefit from complementary expertise present at the Northern Research Station of the Forestry Commission, and the Institute of Evolutionary Biology in the University of Edinburgh. By gaining experience in these two very different applied and academic research settings, the student will be in an ideal position to appreciate how fundamental evolutionary principles can be applied to tackle real world problems. The results of the study are keenly awaited by the forestry industry, and are likely to influence future forestry practice.

A'Hara SW, Cottrell JE. 2004. A set of microsatellite markers for use in Sitka spruce (Picea sitchensis) developed from Picea glauca ESTs. Molecular Ecology Notes, 4, 659-663.

Ennos RA 2015. Resilience of forests to pathogens: an evolutionary ecology perspective. Forestry, 88, 41-52.

Lee S, Watt G. 2012. Choosing Sitka spruce planting stock. Forestry Commission Practice Note 18. Forestry Commission, Edinburgh.

To apply please follow this link

https://www.ed.ac.uk/biology/prospective-students/postgraduate/pgr/how-to-apply Closing date for applications 1st March How to apply | The University of Edinburgh < https://www.ed.ac.uk/biology/prospective-students/postgraduate/pgr/how-to-apply > www.ed.ac.uk A successful Graduate School application depends on a series of required steps. Our main deadlines for applicants wishing to start a PhD in October 2018 are as follows:

ENNOS Richard <rennos@ed.ac.uk>

UExeter EvolutionBacterialResistance

We are looking for a highly motivated student to apply for a PhD studentship “Combining a novel phenotypic virulence screen with genomic approaches to uncover bacterial acquisition of multi-drug resistance and virulence in aquatic environments” with Dr. Michiel Vos at the University of Exeter in collaboration with Prof. Will Gaze (University of Exeter), Prof. Ed Feil (University of Bath) and Dr. Jonathan Porter (Environment Agency).

The project will combine a novel bioassay with state-of-the art genomics methods to characterise the evolutionary and ecological drivers of antibiotic resistant pathogens in freshwater environments. Specifically, we will use state-of-the-art genetic and genomic methods to determine co-carriage of resistance and virulence genes on plasmids carried by environmental bacteria, a potentially highly significant, but virtually unexplored topic.

The student will be encouraged to participate in the wide range of professional development opportunities available at the University of Exeter and will be embedded within a multi-disciplinary research group with NERC, MRC and BBSRC PhD students situated within the Medical School laboratory based in the Environment and Sustainability Institute at the Exeter Cornwall Campus.

Eligibility: you should be a citizen of the UK or other EU country and have been residing in the UK for the last 3 years (apart from temporary or occasional absences). Application deadline: 15th February.

For a full project description, information on the wider doctoral training program and ongoing science in our labs in Cornwall, please refer to:

https://coastalpathogens.wordpress.com/ For information on the NERC FRESH Centre for Doctoral Training program, see:

http://www.gw4fresh.co.uk/ Informal inquiries are welcomed and can be directed to Michiel Vos m.vos[AT]exeter.ac.uk.

Michiel Vos European Centre for Environment and Human Health University of Exeter ESI Building, Penryn Campus TR10 9FE, Penryn, Cornwall, United Kingdom m.vos@exeter.ac.uk tel: 0044(0)1326259464 http://www.ecehh.org/people/dr-michiel-vos/ https://coastalpathogens.wordpress.com/ “Vos, Michiel” <M.Vos@exeter.ac.uk>

UExeter SquirrelInvestmentDecisions

Dear colleagues,

We are advertising a fully funded SWDTP BBSRC/ESRC PhD position in the Centre for Research in Animal Behaviour, Psychology, University of Exeter.

Project Title: Executive control and investment decisions: an ecological perspective on planning for the future, Psychology MPhil/PhD (Funded) Ref: 3027

About the award: This studentship is offered as part of a call between SWBio DTP (BBSRC) and SWDTP (ESRC) for a competition-funded studentship to commence in September 2018.

Location: Streatham campus, University of Exeter

Academic Supervisors: Dr Lisa A. Leaver (University of Exeter) Prof. Sarah Smith (University of Bristol) Dr Tim W. Fawcett (University of Exeter)

Project Description: An individual’s ability to inhibit a pre-potent response or “executive control”, often conceptualised as self-control, is an important aspect of cognitive flexibility and has been used as an assay of cognitive performance in a number of studies. Psychological studies of executive control often involve abstract tests in the laboratory to measure specific inhibition-of-response times across individuals. Executive control has been identified as an important factor in gambling and drug addiction, but the importance of executive control in less extreme behaviours has been largely overlooked. One such behaviour that is crucial for wellbeing and ensuring future security is investment behaviour, which necessarily entails planning for the future. Investment in the future can take many forms across species, and requires some degree of executive control because an individual needs to inhibit current use of an asset to store it away for a future which is, inevitably, uncertain. Grey squirrels are an ideal model species for studying the link between executive control and investment because they are natural and prolific investors. Grey squirrels are well known to cache food widely for later use, a risk-averse behavioural strategy that involves storing nuts during times of plenty in order to provide a reliable source of food when resources are scarce. Squirrels not only decide whether to cache a food item, eat it, or reject it, but caching itself involves a series of predation and pilferage risk trade-offs, which reliably co-vary with food value. As such, investment decisions and effort directly reflect future discounting and ought to be linked to executive control. This PhD project will provide a unique opportunity to engage in cross-disciplinary research that incorporates ecological relevance and economic decision making. The project will investigate the role of executive control in investment decisions by wild grey squirrels. The student will begin by reviewing economic models of saving (standard and behavioural) and identify how these models might apply to squirrels. The student will then construct a mathematical model of adaptive investment behaviour based on executive control and future discounting, to generate predictions that can be tested in both squirrels and people. He/she will test the model by collecting experimental data on squirrels and use panel data on humans for a comparative study. By devising field experiments to verify abstract laboratory tests of executive control, he/she will generate reliable measures of executive control in squirrels and measure their investment outcomes, a real-life measure of delaying gratification.

For more information on how to apply please see: http://www.exeter.ac.uk/studying/funding/award/-?id=3D3027 The closing date for applications is midnight on Thursday 22nd February 2018. Interviews will be held at the University of Bristol on the 22nd and 23rd of March.

Dr. Lisa Leaver Psychology, Washington Singer 101 University of Exeter http://-psychology.exeter.ac.uk/staff/index.php?web_id=-3Dlisa_leaver "T.W.Fawcett@exeter.ac.uk" <T.W.Fawcett@exeter.ac.uk>

UGlasgow ResistanceEvolution

PhD Studentship: Worms, sheep and environment: integrating ecological perspectives into anthelmintic resistance management.

Where? University of Glasgow and Moredun Research Institute Supervisory Team: Barbara Mable, Roz Laing (Institute of Biodiversity, Animal Health & Comparative Medicine, University of Glasgow), David Bartley (Moredun Research Institute, Edinburgh) Funding Source: Natural Environment Research Council Industrial CASE PhD studentship

Project Details: The purpose of this multidisciplinary studentship is to integrate fundamental and applied perspectives on a research problem with direct societal relevance but which also informs key questions in evolutionary ecology and parasitology. The development of resistance to chemical control measures is a key concern in human and veterinary medicine and in agricultural production systems. To increase the efficiency and effectiveness of chemical control measures in the face of resistance, adaptive management approaches have been proposed that customise intervention strategies to the biology and ecology of the particular target pathogens and their hosts. However, these would ideally consider the specific mechanisms of the control agent, genetics of resistance, rates of migration between susceptible and resistant populations, and the strength of selection imposed by the control agents, while taking into account other types of environmental variation, such as the type of pasture that hosts feed on, the community of hosts that share pastures, and how isolated hosts are from new infections. This requires integration of ecology, evolution, genetics/genomics, parasitology, veterinary science, quantitative analyses of "big data", and mathematical modelling, which has not often been achieved.

The overall aim of this studentship is to take a multidisciplinary approach to investigate the nature and consequences of anthelmintic resistance in an important parasite of sheep, the nematode Haemonchus contortus. The project will focus on resistance to ivermectin, which is one of the key anthelmintics for controlling livestock parasites. The student will benefit from support and resources provided by a large UK-wide consortium investigating anthelmintic resistance (https://-

bugconsortium.wordpress.com). The project will involve four main elements but there will be flexibility for the student to take the project in different directions: 1) using previously developed crosses between resistant and susceptible parasites to test the genetic basis of resistance; 2) examining 'real life' fitness (e.g. ability to establish infection, competition, mating success) and the influence of mating preferences, by genotyping the adults and progeny resulting from mixed infections; 3) testing the segregation of resistance markers in previously established lines of a free-living nematode model system (Caenorhabditis remanei) that was selected for ivermectin resistance to test whether there is a common basis of resistance and similar phenotypic consequences; and 4) using deep sequencing approaches to genotype individuals from agricultural environments that differ in resistance management practices to test predictions about expected rates of resistance evolution.

The student will spend at least 3 months per year with the Industrial CASE partner (Moredun Scientific), to receive specific training in the requirements of the animal health industry involved in the development and registration of veterinary medicines. The company has a remit to promote animal health and welfare through research and education, with a particular focus on therapeutics and vaccines.

Funding Details - Research Councils UK standard stipend (pounds 14,764 pa + full fees). This is one of three NERC CASE studentships to start October 2018 in the Institute of Biodiversity, Animal Health & Comparative Medicine at Glasgow.

Duration - 4 years Who is eligible? The candidate must have been ordinarily resident in the UK throughout the 3-year period preceding the date of application for an award, not wholly or mainly for the purposes of full time education. A 2:1 (B) or equivalent is required at undergraduate level.

Students who have not met this but have taken a masters-level course could be considered.

How to apply - Full CV + contact details of at least 2 referees. Cover letter indicating motives and qualifications for undertaking the project Who to send applications to - Please initially send a CV and cover letter to Barbara Mable (Barbara.mable@glasgow.ac.uk). Eligible applicants will be asked to submit a formal application to the University.

Deadline: Applications will be reviewed until the position is filled.

Selected Publications by the Supervisory Team: Kenyon, F., Hutchings, F., Morgan-Davies, C., van Dijk, J., & Bartley, D.J. (2017). Worm Control in Livestock: Bringing Science to the Field.

Trends in Parasitology.33(9): 669-677. DOI:

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UGreifswald EnvironmentalAdaptation

PhD position in responses to changing environments in bats: Ecological drivers and genetic consequences of range expansion in lesser horseshoe bats Application deadline: 13.02.2018. Starting date: 01.04.2018. Duration: 3 years. Salary: German salary scale (TV-L 13, 65%). Project leaders: Sébastien Puechmaille & Gerald Kerth, Zoological Institute & Museum, University of Greifswald

Background: The European vertebrate fauna is highly dynamic due to both historical climatic variation and anthropogenic pressures. The ability of a species to track climatic changes by range shift is expected to be a major determinant of extinction risk (Science 313: 789). For some species, such as the Palearctic bat species Rhinolophus hipposideros, regressions and advances are quite well documented and represent unique opportunities to study how and why range limits move. Such dynamic range boundaries can be observed at the Northern edge of the current distribution of R. hipposideros, regions in which models of climate change predict a northward progression of this species during the next decades (Global Change Biol. 16: 561). Based on a large existing dataset (20,000 genotyped samples) and newly gathered data we will investigate colonisation and colony formation via dispersal in the focal species, study trade-offs / associations between dispersal and life history traits, and elucidate factors influencing dispersal, paying special attention to social and environmental factors.

Goals of the projects: Interconnected wild colonies at the Northern edge of the species'Â range will be surveyed in Germany and combined with data already obtained from France (via associated partner E. Petit). Droppings will be collected from all colonies and genotyped using available microsatellite loci (protocol already optimized; Mol. Ecol. Res. in press), allowing for individual identification and pedigree reconstruction. Non-invasive genotyping over consecutive years in the colony networks will be used to estimate demographic parameters (i.e. population size, population growth, vital [births, deaths] and dispersal [emigrations, immigrations] rates). Temperature and humidity will be monitored throughout the year within and outside the colonies, and habitat characteristics around the colonies will be mapped (Corine Land Cover). The project will focus on associations between realised dispersal and reproductive rate as well as on the influence of population density, social and environmental factors on dispersal and colony formation. Specifically, we will test the following hypotheses: (1) Dispersal (threshold trait) and dispersal distance are heritable traits; (2) individuals from newly formed colonies consistently exhibit higher dispersal rates and invest more into reproduction (due to less intense intraspecific competition in new colonies); (3) dispersal distance is influenced by habitat quality and availability. The obtained results will be used to parametrize a hybrid correlative/mechanistic model to predict range expansion in the species. This study will be carried out in collaboration with local conservation agencies and Dr. E. Petit, INRA (Rennes, France).

Required skills: - The candidate should have (*or at least be willing to develop*) skills in population dynamics and population genetics, landscape ecology, management/treatment of geo-referenced databases (GIS) - Good writing skills in English - Basic knowledge of German is a plus - Knowledge of statistics - Good knowledge of programming in R (important) - Experience with fieldwork (preferentially with bats) will be an advantage but is not mandatory, - Driving license and willingness to use own car for field-work - Good organizational skills and ability to work in a team (incl. with NGOs)

Applications (application form [=Appendix 3], CV, degree certificates, motivation letter, two recommendation letters [=Appendix 4]) should be sent to: s.puechmaille@gmail.com Forms (Appendix 3 & 4) can be found here: https://biologie.uni-greifswald.de/forschung/dfg-graduiertenkollegs/-research-training-group-2010/job-offers/forms/
The official job offer and the legal requirement for the recruitment is available in German on the internet: https://www.uni-greifswald.de/-universitaet/information/stellenausschreibungen/-oeffentliche-stellenausschreibungen/wissenschaftliches-personal/graduiertenkolleg-rtg-2010-zoologisches-institut-und-museum-18wi06/ Sébastien Puechmaille <s.puechmaille@gmail.com>

UGroningen PhenotypicPlasticity

The Groningen Institute for Evolutionary Life Sciences (GELIFES) offers an NWO-funded PhD position for a project on the role of phenotypic plasticity in speciation, using African cichlid fish as a model system.

Phenotypic plasticity is a key determinant of organismal performance, allowing rapid adjustment to environmental variation. In this project, we aim to investigate plasticity's role in species divergence. On the one hand, plasticity may promote evolutionary differentiation by facilitating range expansion. On the other hand, plastic responses will weaken selection for genetic change, hampering adaptive evolution.

We study the role of visual plasticity in the evolution of cichlid fish species diversity. Variation in colour vision, among individuals, populations and species, is determined by both genetic factors and phenotypic plasticity. Since visually mediated behaviours influence both mating behaviour and ecological performance in cichlids, plasticity in colour vision could be important in divergent evolution. The PhD student will conduct experiments and analyses addressing the consequences of visual plasticity for both 1) macro-evolutionary processes and 2) individual behaviour and fitness. Approaches include behavioural experiments, molecular analysis of visual pigments (sequencing, qPCR, HPLC) and phylogenetic comparative analyses.

For more information and online application, please visit https://www.rug.nl/about-us/work-with-us/job-opportunities/overview? details

"Rampal S. Etienne" <r.s.etienne@rug.nl>

UInnsbruck EvolutionaryGenomicsDEADLINE FEB 16TH

PhD position: Evolutionary genomics of a Daphnia waterflea species complex - DEADLINE_FEBRUARY_16th_2018!!!

We are looking for a PhD candidate interested in studying the genomic consequences of human-facilitated gene flow in a Daphnia species complex. The position is part of the INTERREG SEEWANDEL research initiative, which includes seven institutions in Switzerland, Germany, and Austria and seeks to investigate the effects of environmental change on biodiversity and resilience in Lake Constance and other large peri-Alpine lakes.

The position is funded for 48 months and to be filled at the earliest possible date. The successful candidate will be based at the Molecular Ecology Group at the Institute of Ecology of the University of Innsbruck which is highly interdisciplinary and internationally very well connected: https://www.uibk.ac.at/ecology/forschung/-molecular_ecology.html.en Lake-eutrophication during the last century has facilitated secondary contact between ecologically important Daphnia species in peri-Alpine lakes. The extent of secondary contact depends on the degree of trophic change. The successful candidate will use recent population samples and Daphnia resting eggs from sediment cores to quantify and characterize gene flow between species and study the consequences of the secondary contact on species integrity and functional traits. The project comprises sedimentological work (collecting sediment cores), molecular lab work (DNA extractions and library preparation), and extensive bioinformatics analyses as well as some experimental work with Daphnia. The study will focus on three large peri-Alpine lakes with different trophic histories - Lake Constance, Lake Walen, and Lake Zurich - and will include close collaborations with the members of the SEEWANDEL initiative. Part of the experimental work will be conducted at Eawag (Switzerland).

Candidates should be highly motivated and have a strong interest in evolutionary biology, ecology, and population genetics. The planned work will require a high degree of independence and the ability to work in a team. Experience in (i) molecular lab and field work, (ii) analysis of whole-genome re-sequencing data, (iii) and basic programming skills (e.g. R, Python, bash) will be an advantage. The project includes several collaborators and international groups in Switzerland, Germany, and the UK, and therefore good English skills are essential.

Salary The annual gross salary is EURO 28,994 for a 48-months employment. The contract includes health insurance and 5 weeks of holidays per year. Furthermore, the university has numerous attractive offers: https://www.uibk.ac.at/universitaet/-zusatzleistungen/index.html.en ***How to apply*** Please send a single pdf file including a letter of motivation, curriculum vitae, a complete list of publications and contact details of two references to Markus.Moest@uibk.ac.at. Applications must be written in English and submitted until 16 February 2018. The University of Innsbruck is striving to increase the percentage of female employees and therefore invites qualified women to apply. In the case of equivalent qualifications, women will be given preference. An offer of employment is contingent on a satisfactory pre-employment background check.

The research institution and its environment Detailed information about the Molecular Ecology group can be found here: http://www.uibk.ac.at/ecology/-forschung/molecular_ecology.html.en. The University of Innsbruck has a long-standing and internationally renowned tradition in life sciences and offers a vibrant research atmosphere. It has 27,000 students and 4,000 staff members. Innsbruck is situated in the Alps, very close to Switzerland, Germany, and Italy. Excellent train connections and airports in Innsbruck and close by in Munich and Salzburg ensure good connections and easy travelling. The scenery and possibilities for outdoor recreation are fantastic.

Any questions? For more information on the position, the project, the group, or the University, please do not hesitate to contact Markus Möst or Birgit Schlick-Steiner directly.

MÃST Markus, PhD University of Innsbruck Institute of Ecology Research Group: Molecular Ecology Technikerstrasse 25 (Room 517) A-6020 Innsbruck Tel: +43 (0)512 507-51771 Fax: +43 (0)512 507-51799 E-mail: markus.moest@uibk.ac.at

SCHLICK-STEINER Birgit Dr., Univ.-Prof. University of Innsbruck Institute of Ecology Deputy Head of the Institute Head of the Research Group: Molecular Ecology Technikerstrasse 25 (Room 516) A-6020 Innsbruck T +43 (0)512 507-51750 F +43 (0)512 507-51799 E-mail: Birgit.Schlick-Steiner@uibk.ac.at

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ULeicester ForensicsOfFood

Project Title: Protecting the Food Chain by Rapid On-Site Nanopore DNA Sequencing

University of registration: University of Leicester

Project supervisors: Prof Mark Jobling, Dr Jon Wetton, Dr Celia May 'V Department of Genetics & Genome Biology

Industrial partner: Cranswick plc

Project outline:

Adulteration of the food chain with products derived from undeclared species greatly affects consumer confidence, can pose health risks and may involve the illegal exploitation of protected species. High-profile cases such as the 2013 horsemeat scandal increased pressure to improve the reliability and speed of species identification. Unfortunately, current methods for checking the species of origin of raw meats require out-sourced laboratory testing using expensive equipment, which can take up to a week. Similar delays occur when testing for pathogenic microbes, by which time food from potentially contaminated production lines may have already reached retailers and consumers. Species identification is also key in combatting the multi-billion dollar illegal wildlife trade which often involves substitution of species on a massive scale, particularly in commercial fisheries worldwide, and the sale of bushmeat - wild animals caught in developing countries that are butchered and sold in markets.

We seek a highly-motivated student with an interest in genetics, genomics or forensic genetics, whose research project will develop rapid, on-site DNA analysis methods using the Oxford Nanopore Technologies (ONT) MinION portable third-generation sequencing device. The focus will be on mitochondrial barcode genes that show characteristic sequence differences between species; a similar approach can identify bacteria from their 16S rRNA sequences. ONT sample and sequencing preparation devices currently in development, including the VolTRAX microfluidics platform and hand-held disposable DNA library preparation systems will be trialled for utility upon release.

The student will gain an appreciation of the technology needed to ensure food-chain integrity and will be trained in existing approaches to species identification. During the course of the project the student will spend three months working with our industrial partner Cranswick plc exploring how such tests can be integrated into the commercial environment.

Supervision, training and academic environment:

You will be part of the Midlands Integrative Biosciences Training Partnership (MIBTP), a BBSRC-funded Doctoral Training Partnership between the Universities of Warwick, Birmingham and Leicester. As an iCASE student, you must fulfil the MIBTP entry requirements and will join the MIBTP cohort for the taught modules and masterclasses during the first term. You can then start your PhD project in Jan 2019 but must complete a 3-month miniproject (at Warwick or Birmingham) before the end of their first year. You will remain as an integral part of the MIBTP cohort and take part in the core networking activities and transferable skills training.

You will be supervised by an experienced team and form part of a dynamic and productive research group studying human and animal genetic diversity, with projects in population genetics, forensics, recombination and mutation biology, and human disease genetics.

Closing date for applications: 11th February 2018

Interview dates: February 2018 TBC

Prof Mark A. Jobling, MCSFS, FHEA Professor of Genetics Department of Genetics & Genome Biology Room G5, Adrian Building University of Leicester University Road Leicester LE1 7RH UK

tel.: +44 (0)116 252 3427 mob.: +44 (0)7955 882334 fax: +44 (0)116 252 3378 email: maj4@le.ac.uk web: http://www2.le.ac.uk/departments/genetics/people/jobling

"Jobling, Mark A. (Prof.)" <maj4@leicester.ac.uk>

ULethbridge PopGeneticsDuckweeds

An NSERC-funded MSc position is available in the Department of Biological Sciences at the University of Lethbridge (Alberta, Canada). The focus of the project is on the biodiversity and population genetic structure of small, floating, aquatic plants in the genus *Lemna *(duckweeds). The project will involve a combination of lab and field work, with an emphasis on the former, and will primarily involve techniques from molecular ecology. The research will be co-supervised by Drs. Robert Laird and Theresa Burg. To apply, please send your CV along with a cover letter indicating your research experience and interests to Robert Laird (robert.laird AT uleth.ca) by March 15, 2018 (institutional application deadline: May 1, 2018; position start date: September 1, 2018).

Robert Laird <robert.laird@uleth.ca>

UNewcastle Metabarcoding Deadline31stMarch

Fully-funded PhD opportunity

Developing DNA-metabarcoding technologies for the nationwide surveillance of pest and beneficial insects Supervision team: Dr Darren Evans (darren.evans@ncl.ac.uk) & Dr James Kitson (Newcastle), Dr Larissa Collins (Larissa.Collins@fera.co.uk) & Prof Neil Boonham (Fera), Dr Ramiro Morales-Hojas (ramiro.morales-hojas@rothamsted.ac.uk, Rothamsted Research), Dr Dave Lunt (University of Hull)

Summary: This project will integrate advances in DNA-metabarcoding with ecological network analysis for the rapid nationwide surveillance and future forecasting of insect pests and beneficials. It will develop and evaluate Next-Generation Sequencing tools for network construction using historic Rothamsted Insect Survey suction-trap samples and the Fera yellow water-pan trap network (YWT).

Aims and objectives: The aim of the project is to understand and quantify the spatial and temporal dynamics of insect pest-predator interactions within agro-ecosystems using Next Generation Sequencing (NGS) technology applied to current and historic samples collected from biomonitoring networks. The specific objectives are: (1) to establish the ecological interactions of target insect pests using DNA-metabarcoding and examine how these vary in space and time; (2) to identify agricultural landscapes with higher ecosystem service provision by examining both target and non-target insect 'by-catch'; (3) to determine how the structure and 'robustness' of these networks vary; and (4) develop models that integrate species-interactions to predict how network structures will change over the next century. For full Project Specification, go to: http://www.ncl.ac.uk/iafri/learning/-opportunities/project3/ Location of training and research: The student will primarily be based in the School of Natural and Environmental Sciences at Newcastle University (under the primary supervision of Dr. Evans, co-supervised by Dr. Kitson) but will be expected to spend short periods of time (4 weeks per year) at Rothamsted Research to process RIS samples and gain training in taxonomic identification and DNA-extraction methods (co-supervised by Dr. Morales-Hojas). He/she will spend between 3-4 months per year at Fera receiving training in laboratory automation and Next Generation Sequencing protocols for DNA-metabarcoding YWT, RIS and other target-insect samples (co-supervised by Dr. Collins and Prof. Boonham). Bioinformatics and ecological network analysis training will be given at Newcastle University, but in close collaboration with supervisors at Rothamsted and the University of Hull (Dr. Lunt).

Person specification: The ideal candidate should have a BSc in Biology or related subject (first/upper second class degree, essential) and an MSc in Ecology/Molecular Ecology/Bioinformatics or related subject (desirable). Experience in Next Generation Sequencing technology/bioinformatics would be beneficial.

Eligibility: This award is available to UK/EU and International candidates. If English is not your first language, you must have IELTS 6.5 with at least 5.5 in each component.

Value of award: 100% tuition fees at UK/EU rate plus an annual stipend of 14,553 (subject to Research Council UK increase for 2018/19 entry). Successful non-EU international students will be required to make up the difference between the UK/EU fees and international fees.

Application procedure: Applicants are strongly advised to discuss the project informally with members of the supervisory team before applying. Please go to http://www.ncl.ac.uk/postgraduate/funding/-sources/allstudents/nes003.html for information regarding formal application procedures. In addition, applicants should also send a covering letter and CV to Mr Steven Hall (e-mail to steven.hall@newcastle.ac.uk). Please note this is project is competitively funded - only six out of the ten IAFRI projects currently advertised will be funded based on the strength of the applicants.

Closing date is midnight on Saturday 31 March 2018 (BST). Interviews will take place during April/May 2018.

Dr. Darren M. Evans FRES Reader in Ecology and Conservation School of Natural and Environmental Sciences Office 5.71 Ridley Building 2 Newcastle University Newcastle upon Tyne NE1 7RU United Kingdom

kirsten.wolff@newcastle.ac.uk

UppsalaU GenomicsPlasticity

We are looking for a highly motivated PhD student to join Dr. Arild HusbyÂs lab group at Uppsala University (http://www.ieg.uu.se/evolutionary-biology/husby-lab/) to study genetic basis of plasticity in wing development in waterstriders in collaboration with Prof. Abderahman Khila at IGFL, Lyon (http://igfl.ens-lyon.fr/equipes/a.-khila-developmental-genomics-and-evolution).

Phenotypic plasticity is one of the main mechanisms by which plants and animals adapt to changing environmental conditions and thus of major evolutionary interest. This project will combine fieldwork, lab experiments and genomic work (crosses, RNA seq, RNAi) to study how temperature and photoperiod influence plasticity in wing development in different species of waterstriders. Waterstriders are a well known group of insects displaying wing polymorphism both between species as well as within species in response to the environment (e.g. Järvinen & Vepsäläinen1976. Hereditas, 84, 61-68) and are also model species in evolutionary biological studies (Rowe et al. 1994. TREE, 9, 289-293). Several species of waterstriders will be collected in early summer 2018 and nymphs raised in the lab under different photoperiod and temperature regimes followed by RNA seq analyses to identify differentially expressed genes between apterous (wingless) and macropterous/brachypterous morphs. Functional work will be done using established RNAi protocols developed for waterstriders (Khila et al. 2012 Science 336, 585-589).

The overall goal is to identify the genetic variants responsible for wing development and their interaction with temperature and photoperiod but there are several lines to examine depending on the candidate interests and qualifications.

We are looking for candidates with a strong interest in evolutionary developmental biology and evolutionary genetics, with excellent analytical ability and experience in the analyses of life history traits. Experience in working with aquatic animals in the lab is meriting.

The venue for the position, the Evolutionary Biology Centre, is situated in central Uppsala (http://-www.ieg.uu.se). The working atmosphere is highly international with a regular recruitment of PhD students and post-docs from abroad. The Centre constitutes an exciting arena for multidisciplinary research in evolutionary biology in a broad sense, housing some 300 scientists and graduate students, and with research programs in, for example, ecology, genetics, genomics and developmental biology. Our graduate school offers a creative and stimulating environment and offers a rich variety of seminars, journal clubs, courses and possibilities to interact with other scholars and students. Local platforms for next-generation sequencing (http://www.scilifelab.uu.se) and high-performance computational analyses are very useful. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant college town with beautiful surroundings conveniently situated 40 minutes by train from Stockholm. The graduate program covers four years of full-time, fully paid study. The position can be combined with teaching (maximum 20%), which prolongs the employment with the corresponding time.

Informal inquiries are welcomed and can be directed to Arild Husby (arild.husby[AT]ebc.uu.se).

Applications will only be accepted when submitted through the Uppsala University web portal no later than 28th February using this web address: https://www.uu.se/en/about-uu/join-us/-details/?positionId=190120 Arild Husby Department of Evolutionary Biology Norbyvägen 18D, Uppsala University, SE-75236 Uppsala, Sweden

labpage: http://www.ieg.uu.se/evolutionary-biology/-research/husby-lab Office phone: 018-471 4120 E-mail: arild.husby@ebc.uu.se Room:1041, 1st floor EBC

Arild Husby <arild.husby@ebc.uu.se>

UPrague ArabidopsisAdaptation

PhD-position Ecophysiology of adaption to alpine environments in Arabidopsis arenosa

The position is available as of 1st April 2018

The PhD project is embedded in the three-years' FWF-project “Disentangling evolutionary adaptation from transient acclimation to alpine environments in Arabidopsis arenosa” and will be conducted under the supervision of Profs. Gilbert NEUNER, Ilse KRANNER, Peter SCHÃNSWETTER and Dr. Filip KOLÃÃ (University of Prague; genomics, RNAseq) in close collaboration with Drs. Erwann ARC (metabolomics) and Karl HÃLBER (University of Vienna; ecology). The PhD project focuses on the eco-physiology of photosynthesis and stress physiology of lowland populations and independently evolved alpine populations of Arabidopsis arenosa from different mountain ranges. It will also offer the possibility to integrate the results in a wider framework of genomic, transcriptomic & metabolomic investigations carried out under related projects that focus on the same species. We are looking for a highly motivated and enthusiastic young scientist to join our international research team. The gross salary is 37,680 per year.

The successful candidate will be tasked with - planning and conducting field work in alpine sites together with other team members; - assessment of functional (ecophysiological) and structural leaf traits (lab work in Innsbruck and approximately two months of field work per year); - statistical data analyses; - dissemination of the results through publications in scientific journals and presentations at international conferences.

Applicants must - hold a MSc degree in plant sciences or a related field; - have an excellent knowledge of plant physiology; previous experience with physiological ecology, functional ecology or alpine ecology are desirable; - be able to conduct fieldwork in remote areas; - be proficient in English, both written and orally; - have excellent social skills; - be able to work in a team as well as independently; - provide the following documentation (all in one file): - Cover letter stating the motivation - Curriculum vitae including copies of all university degrees received - Letter of recommendation by the supervisor of the Master thesis

Please send your application and enquiries for further information to A.Univ.-Prof. Mag. Dr. Gilbert NEUNER (Gilbert.neuner@uibk.ac.at).

"Neuner, Gilbert" <Gilbert.Neuner@uibk.ac.at>

USunshineCoast PhD Evolution biomechanics

PhD Position in Musculo-skeletal modelling in lizards, University of the Sunshine Coast, Australia.

The Clemente Lab at the University of the Sunshine Coast, Australia is seeking outstanding applicants for fully-funded PhD scholarships.

Our research focuses on the relationship between form, function and ecology of living and extinct animals. One fundamental goal in evolutionary biology is to understand how size can constrain the evolution of morphological traits and limit the ability to exploit ecological niches. Size influences all biological functions from cellular respiration, up to how fast an animals can run or climb. Yet to completely understand the influence of size on performance, we require information on the integration of multiple systems, including the nervous, muscular and skeletal systems.

The PhD project will contribute to research that investigates the neuromuscular and biomechanical mechanisms associated with changes in body size using varanid lizards as a model. We have collected an extensive morphological dataset for this group including the muscle architecture of varanid lizards ranging from the smallest (7.6 g Varanus brevicauda) to the largest extant species (40 kg Varanus komodoensis), as well as their maximum speeds. We will use musculoskeletal models of varanid lizards in OpenSim to predict higher level biological parameters (e.g. running speed) in both living and extinct species. We will be able to scale our model up or down, exploring size, or change its shape (e.g. limb length). This will allow us to understand what the limitations to size are, in biological systems, and at what size certain structures no longer work. This research will have direct implications for understanding evolution as a process of optimisation.

Essential qualities for candidates include: - strong computational and analytical skills in biomechanics

- experience using biomechanical assessment tools (e.g. high speed video, force plates)

Preferred qualities for candidates include: - interpersonal skills to work effectively with patients, research subjects, team members, and project collaborators. - excellent critical thinking skills, ability to work independently - research experience and practical knowledge of research principles is required whether through previous internship, work experience, or coursework.

- interest or previous experience in musculo-skeletal modelling, e.g. SIMM/ OpenSim.

- interest in evolutionary theory

The Clemente Laboratory (https://www.usc.edu.au/-explore/structure/faculty-of-science-health-education-and-engineering/staff/dr-christofer-clemente) is part of the Animal Ecology Lab within the University of Sunshine Coast. We are located on the Sunshine Coast, approximately an hour north of Brisbane Queensland on the Sippy Downs campus.

Course fees and a living stipend (currently $26,300 AUD per annum, tax free) will be included as part of the scholarship.

The opportunity is open to both Australian/New Zealand nationals and international candidates, however exceptional international candidates will be considered (with top-up scholarships available to cover international tuition fees).

For queries or if you are interested in applying please contact Christofer Clemente, PhD, School of Science and Engineering, cclement@usc.edu.au with your CV.

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

"cclement@usc.edu.au" <cclement@usc.edu.au>

USussex PlantGenomeEvolution

PhD Studentship Subject area: Plant genome evolution and epigenetics University of Sussex

Project title: Evolutionary and epigenetic interactions between transposable elements and their plant hosts

A Ph.D. studentship (42 months) is available from September 2018 under the supervision of Dr. Alexandros Bousios, in the Evolution, Behaviour and Environment Group, School of Life Sciences.

Deadline: 31 March 2018

The Bousios lab is looking for a PhD student to study the impact of transposable elements (TEs) in the function and evolution of plant genomes. TEs represent the most abundant component of eukaryotic genomes, and especially in plants they can occupy up to 80-90% of their genomic content. TE activity can be deleterious for the host, because it can cause chromosomes to break or because new copies can insert within genes and disrupt their function. As a result, hosts have developed epigenetic defence mechanisms to suppress TE activity, although given the abundance of TEs, these mechanisms are not always successful.

By focusing on maize but also other fully-sequenced plant genomes, and mostly using in silico approaches, the candidate will attempt to shed light on the very first steps of TE silencing, i.e. how epigenetic defences recognize the mRNA of active TEs. We hypothesize that specific regions of complex structure on the TE may play a crucial role in this process, and, hence, are the foci of an ongoing evolutionary battle between TEs and hosts. In addition, the candidate will study the extent to which TEs positively influence gene function after they become obsolete, by 'lending' some of their cis-acting sequences to the host regulatory system. This process, known as TE exaptation or co-option, is poorly understood in plants.

For an overview of our research, please visit http://www.sussex.ac.uk/lifesci/bousioslab/ Please submit a formal application using our online application system at http://www.sussex.ac.uk/study/phd/apply, including a CV, degree transcripts and certificates, statement of interest and names of two academic referees. On the application system use Programme of Study - PhD Biology.

Please make sure you include the project title and Supervisor's name with your statement of interest on the application form.

This funded position is open to Home / EU applicants and covers fees and a stipend at RCUK rates. The funding/duration of the studentship will not be affected when UK leaves the European Union in 2019. Ideal candidates will have a solid background in bioinformatics or computational biology, while a good understanding of epigenetics, genome evolution or transposable element biology is desirable. Eligible applicants will have recently received an MSc and/or a First or high 2:1 BSc in a relevant subject. Candidates for whom English is not their first language will require an IELTS score of 6.5 overall, with not less than 6.0 in any section.

Contact Anna Izykowska for application enquiries (a.izykowska@sussex.ac.uk) Contact Alexandros Bousios (ab35@sussex.ac.uk) for enquiries about the project.

– Alexandros Bousios, PhD Royal Society University Research Fellow

University of Sussex | UK

alexandros.bousios@gmail.com | email http://www.sussex.ac.uk/lifesci/bousioslab/ | www http://infspire.org/ | www alexandros bousios | Skype

Alexandros Bousios <alexandros.bousios@gmail.com>

UVienna PDF PhD EvolutionGenomics

Title: UVienna.EvolutionGenomics

Dear Colleagues:

Applications are invited for one Ph.D. and one postdoc position in the group of Qi Zhou in the Department of Molecular Evolution and Development at University of Vienna, Austria. Both are supported by the European Research Council (ERC) grant, and planned for two years for postdoc, and three years for Ph.D. with possible renewal. The successful applicants will use bioinformatic and experimental methods to study the evolution of Drosophila sex chromosomes. Most model species' sex chromosomes, e.g., those of human and D. melanogaster bear few traces of their evolution, because they are too ancient and have become too repetitive in sequence for investigation. A fundamental question concerns evolution biologist is what are the causes and consequences of Y chromosome degeneration? We will be using Drosophila species with recently born sex chromosome ('neo-sex') systems to address: How does the Y chromosome become epigenetically inert? How does this universal evolution process drive the adaptation of small RNA defence systems? And how does such a male-specific arms race between parasitic transposable elements and small RNAs fuel the changes of the female genome? The candidates are expected to be independent and highly motivated. Essential qualifications include demonstrated experience either in Drosophila genetics experiments (transgenics, CRISPR/Cas9 mutagenesis, in situ hybridisation) or bioinformatic studies (RNA-seq, ChIP-seq and corresponding data analyses).

Successful applicants will receive very competitive salary and benefits (https://www.fwf.ac.at/en/research-funding/personnel-costs/), and enjoy the diverse and vibrant research environment of the Department and the University. The group members have frequent interactions with other neighbour labs of Drosophila neurobiology (Prof. Thomas Hummel) and developmental biology (Prof. Ulrich Technau), and have a chance to develop other collaborative research projects. The university is located in the city centre of Vienna, which houses numerous world's leading research institutes including Gregor Mendel Institute, Institute of Molecular Biotechnology and Institute of Science and Technology etc. The city now has gathered many great scientists in evolutionary biology (http://www.univie.ac.at/evolvienna/?page_id=6), RNA biology (http://www.mfpl.ac.at/rna-biology/) and there is an encouraging plan to move the biology departments of the University near other institutes of Vienna Biocenter to form a new research cluster. Vienna has been voted as the world's most livable city for the eighth time, and is famous for its history and culture, and now also a modern and international lifestyle. Interested candidates please send her/his CV and contact information of three referees to Dr. Qi Zhou (qi.zhou@univie.ac.at). We will start reviewing the application immediately until the position is filled.

Qi Zhou

https://scholar.google.at/citations?user=-XwJHKgkAAAAJ&hl=en Qi Zhou <muntjaczhou@gmail.com>

UWageningen 2 SymbiontDrivenParasitoidResistance

Two PhD positions: The role of symbiont-driven resistance to parasitoids in greenhouse biocontrol success Application deadline: 26 March 2018

Are you interesting in working on the fore-front of biological control in a multidisciplinary project? Do you enjoy combining field work in greenhouses with experiments in the laboratory?

If so, we have two PhD candidate positions available in the NWO funded project: "Aphids out of control? The role of symbiont-driven resistance to parasitoids in greenhouse biocontrol success".

Aphids are major crop pests, both in greenhouses and in the field. They are now still predominantly controlled using pesticides, which is not environmentally friendly, nor sustainable. A very effective alternative is biocontrol through the use of parasitoids that prevent early-stage aphid population expansion. Unfortunately, endosymbiotic bacteria associated with aphids can confer resistance against parasitoid attacks leading to biocontrol failure. Current knowledge is scarce on endosymbiont variation. Moreover, research about the functionality and the specificity of aphid-endosymbiont associations, and the role that the symbiont community plays in resistance is mostly lacking.

In this project, two PhD students will work closely together to provide this essential information through, (i) monitoring and establishing the extent of aphid-endosymbiont associations, aphid resistance, and parasitoid virulence, (ii) unravelling the aphid-symbiont interactions and mechanisms of defence, (iii) determining the aphid-parasitoid interactions and variation in virulence, in order to (iv) deliver advice on biocontrol resource development and biocontrol application strategies.

Our ideal candidates: Are highly motivated and enjoy working in a team with the PhD candidate, a technician and the supervisors; Have a strong background in entomology, evolutionary biology and/or molecular ecology. Some experience with bioinformatics will be a bonus; Like to do field work in greenhouses (and preferably have some experience) and are good in communicating (with growers); Are proficient in the English language; Have a driver'Âs license, because the field work involves a driving between greenhouses, fields, and the laboratory.

We offer a full-time position (38 hours), initially for 1 year after which a go/no go decision will be taken on extension with another three years. Gross salary per month 'Ã 2.222,- in the first year rising to 'Ã 2.840,- per month in the fourth year, for a fulltime appointment. The candidates will be based at both the Laboratory of Genetics and the Laboratory of Entomology of Wageningen University & Research in Wageningen, the Netherlands. The Laboratory of Genetics is part of Wageningen University and works closely together with other groups of Wageningen University. The group investigates causes and consequences of natural genetic variation within species. Because genetic variation plays an essential role in ecological and evolutionary processes, we ask ecologically and evolutionary motivated research questions. We use a wide array of organisms, ranging from bacteria, fungi, plants and insects. The Laboratory of Entomology aims at an interdisciplinary approach from cellular to community level to unravel biological phenomena underlying the functioning of insect sex determination, plant-insect communities, insect vectored diseases, insect neurobiology and insects as food and feed.

More information on the research project and selection procedure: Dr. Bart Pannebakker (bart.pannebakker@wur.nl) or Prof. Bas Zwaan (bas.zwaan@wur.nl).

For this position you can only apply on line: https://www.wur.nl/en/Jobs/Vacancies/Show/2-PhD-positions-The-role-of-symbiont-driven-resistance-to-parasitoids-in-greenhouse-biocontrol-success.htm Don't email directly to the people mentioned above but use the website to apply.

"Pannebakker, Bart" <bart.pannebakker@wur.nl>

UWyoming PlantMicrobeAdaptation

Graduate Research Associate in Plant-Microbe Interactions: The Weinig lab at the University of Wyoming is seeking a graduate student to collaborate on research studying 1) the effects of host plant genetic pathways on microbial distributions and 2) the consequences of microbes to host plant performance, including local adaptation of plants to native microbes.

This GRA is part of a cluster hire of 4 faculty, 10 postdoctoral research associates, and 10 graduate students supported by a new 5-year, $20 million NSF EPSCoR RII Track-1 grant. In this project we will study microbial life and its consequences; additional details can be found at http://www.uwyo.edu/epscor/microbial-ecology . Cynthia Weinig <cweinig@uwyo.edu>

WageningenU ViralManipulationOfInsects

Wageningen University, Laboratory of Virology

PhD position: Viral manipulation of the insect brain

We are searching for a motivated PhD candidate to execute the research project 'Insane in the brain: How a virus manipulates a caterpillar's brain function and behaviour to enhance transmission'. The project focuses on parasitic manipulation of host behaviour, which is a common strategy exploited by parasites to increase transmission. Although exquisite examples of such behavioural alterations are known, the underlying mechanisms are poorly understood. Baculoviruses, which are viruses specifically infecting insects, provide a unique system to study these mechanisms. Baculoviruses alter the behaviour of caterpillars, causing increased locomotion (hyperactivity) and migration to the top of plants (tree-top disease), where the caterpillars liquefy and virus particles are released. Earlier studies have demonstrated that the baculovirus protein tyrosine phosphatase (PTP) is involved in inducing hyperactivity. The project aims to identify the pathway(s) activated by the baculovirus ptp gene that eventually lead(s) to hyperactive host behaviour. Since locomotion is primarily controlled by the central nervous system, we will focus on the brain of the infected caterpillars. The PhD candidate will combine a proteomic and transcriptomic approach with detailed morphological studies on viral invasion of the host brain and on infection of specific neurons. Identified genes, proteins, pathways and neural networks will be further studied in-depth for their role in host behavioural manipulation. The proposed research will reveal the mechanism of an appealing case of parasitic manipulation of host behaviour and contribute to our understanding of insect behaviour in general.

For this position you can only apply online, before February 19, 2018.

See this link for more details: https://www.wur.nl/en/Jobs/Vacancies/Show/PhD-position-Viral-manipulation-of-the-insect-brain.htm For more information about this position, please contact dr. Vera Ros, assistant professor, by e-mail vera.ros@wur.nl or telephone +31(0)317-484461.

Dr. ir. Vera I.D. Ros Assistant Professor

Laboratory of Virology | Plant Sciences Group | Wageningen University | Droevendaalsesteeg 1 | 6708 PB Wageningen, The Netherlands | +31-317-484461 | vera.ros@wur.nl | www.vir.wur.nl "Ros, Vera" <vera.ros@wur.nl>

WesternU 3 VirusEvolutionBioinformatics

The Virus Evolution and Bioinformatics lab of Dr. Art Poon at Western University (Canada) is seeking applications to fill 3 PhD graduate student positions. All positions are fully funded for up to 5 years by two newly awarded grants.

Research areas

Evolution of HIV-1 within hosts.

Despite the availability of highly effective drug treatments, HIV-1 establishes a life-long chronic infection for which we have yet to develop a cure. When HIV-1 infects a cell, it integrates itself into the host genome and, in some cases, enters a dormant state where it becomes invisible to the immune system. This creates a long-lived reservoir of "latently" infected cells that is the main barrier to a cure. We are developing new phylogenetic methods to reconstruct how this rapidly-evolving virus spreads through the body and to identify potential targets to eradicate the virus reservoir.

Detecting transmission outbreaks.

For infectious diseases, a genetic cluster is a subset of infections that have barely accumulated any genetic differences since their recent descent from a common ancestor. Clustering has become a popular method for rapidly screening clinical databases for potential transmission outbreaks. Based on recent work, we now know that clustering methods can be badly confounded by when the infections were sampled from the population. We are developing and validating a new approach inspired by speciation models to detect lineage-specific shifts in branching rates, and working with global partners to develop open-source monitoring systems to support public health efforts in real time while protecting individual privacy.

Training environment

The Poon lab is an entirely "dry" research computing and open-source software development group (http://github.com/PoonLab). The lab is housed in a newly renovated space in the Department of Pathology, and equipped with custom-built Linux workstations, a small high-performance computing cluster and an espresso machine. My lab mostly runs on Python, R and LaTeX – my objective is to enable all my trainees develop a working knowledge of all three languages.

Western University is one of Canada's top research-intensive universities, and home to the Western HIV Investigators Group (WHIG), a highly collaborative team of 8 principal investigators with diverse and complementary research programs, including evolution and pathogenesis (Dr. Eric Arts), natural resistance and host microbiomes (Dr. Jessica Prodger), and bioinformatics and phylogenetics (Dr. Poon). The adjacent London Regional Genomics Centre provides state-of-the-art next- generation sequencing services on Illumina MiSeq and NextSeq systems.

Known as "Forest City", the city of London, Ontario, features river valleys, abundant parks, tree-lined streets, bicycle paths, frequent city festivals, an international airport and a reasonable cost of living.

Qualifications

* An undergraduate (bachelor's) and/or master's (MSc) degree in biology, microbiology, bioinformatics, mathematics, statistics, computer science, or a related field.

* An avid, demonstrable interest in evolutionary biology and infectious disease research.

* Previous training or experience in *any* programming or scripting language from course work, workshops, or online/self-directed learning. Applicants without prior programming experience may be considered if they have a strong background in quantitative methods (e.g., statistics, linear algebra, probability, discrete math).

* Proficiency in communicating and writing in the English language.

* An ability to work effectively in a collaborative environment.

All applicants must also meet the admission requirements of the university (http://grad.uwo.ca/prospective_students/applying/index.html) as well as the specific department (I hold appointments at the

Departments of Pathology, Microbiology, and Applied Mathematics).

If you're interested and meet these qualifications, please contact me with a cover letter, CV, and contact information for at least two references at <apoon42@uwo.ca>.

Best, - Art.

— Art FY Poon MSc PhD

Assistant Professor Department of Pathology & Laboratory Medicine Western University

CIHR New Investigator MSFHR Career Investigator

github.com/ArtPoon

"apoon42@uwo.ca" <apoon42@uwo.ca>

Jobs

BenGurionU EvolutionHostParasite

We are looking to support excellent candidates in applications for prestigious postdoctoral fellowships at Ben-Gurion University of the Negev, Israel to study the evolutionary ecology of host-parasite interactions. This research project aims to identify conditions favoring increased parasite evolvability (the ability of parasite populations to produce novel variation) using evolutionary experiments with wild rodents and their bacteria. This study lies at the interface of evolution, ecology, microbiology, immunology, and molecular genetics.

The successful candidates will be part of a collaborative project between University of Michigan (Dr. Luis Zaman), Ben-Gurion University of the Negev (Dr. Hadas Hawlena), the University of Texas at Austin (Dr. Jeffrey Barrick), Michigan State University (Prof. Richard Lenski), and the Hebrew University of Jerusalem (Prof. Shimon Harrus).

A background in evolutionary biology, community ecology, or disease ecology is desired, and skills in molecular biology, bioinformatics, and microbiology are advantageous.

Interested candidates are encouraged to send an application to Dr. Hawlena: hadasaw@bgu.ac.il as soon as possible (the first deadline is on March 4, 2018)

Hawlena Hadas <hadashaw@bgu.ac.il>

BroadInstitute MalariaGenomics

This position is a unique opportunity to join the malaria genomics group at the Broad Institute and Harvard T.H. Chan School of Public Health. We apply genomic and transcriptomic investigations to malaria parasites, mosquito vectors, and human hosts to understand the biology of malaria and develop tools and approaches informed by population genetics and evolution for its control. Specific interests of the group include drug/insecticide resistance mechanisms, antigenic diversity and its impact on vaccine efficacy, and transmission biology.

We are looking for a talented PhD-level computational biologist to join our team at the Broad. The successful candidate will develop and manage genomic and transcriptomic projects, actively and effectively manage relationships with collaborators around the world, assemble high-impact publications, assist in grant applications, and become an active and engaged citizen of the wider community of bacterial, fungal, and viral genomicists that make up the Broad's Infectious Disease and Microbiome Program. This position offers an opportunity for growth of an independent research program through development of new projects and acquisition of independent funding, and may be attractive to candidates who will soon be completing a postdoctoral fellowship.

The candidate will maintain a portfolio of projects that include highly collaborative efforts as well as independently conceived studies. She/he will interact closely with molecular parasitologists and computational biologists in the Neafsey Lab at the Harvard T.H. Chan School of Public Health (https://sites.sph.harvard.edu/neafsey-lab/), as well as with the Associate Director of Malaria and Viral Genomics at the Broad and other malaria investigators at Harvard.

CHARACTERISTIC DUTIES

*Perform analysis on large-scale genomic and transcriptomic datasets

*Collaborate and clearly communicate with both computational biologists and molecular parasitologists to develop innovative and impactful collaborative projects

*Design and lead independent projects

*Give presentations on research to internal Broad/Harvard audiences as well as at international conferences, explaining ideas clearly and compellingly to both specialized and non-specialized audience

*Provide advice and mentoring to trainees

*Contribute to the generation and curation of analysis pipelines and databases

*Liaise with information technology groups within the Broad to manage data storage and computational analysis cluster resources

QUALIFICATIONS

*Ph.D. in computational biology, genetics, computer science, statistics, math, molecular biology, or related field, or equivalent practical experience.

*Expertise in Illumina sequencing data analysis tools and general knowledge of statistical methods for genomic and transcriptomic data analysis.

*Demonstrated ability to clearly communicate scientific ideas and results in oral presentations.

*A publication record reflecting high productivity and the ability to write clearly.

*Interest in infectious diseases and global health

*Familiarity with population genetic and molecular evolutionary analysis methods, including tests of natural selection and phylogenetics

*Fluency in Unix, standard bioinformatics tools (Python, R, or equivalent), and a programming language (C/C++, Java)

*Excellent communication, organization, and time management skills

*Creative, organized, motivated, team player

Please apply via the Broad Institute Careers website (position 5564):

https://broadinstitute.wd1.myworkdayjobs.com/en-US/broad_institute/job/Cambridge-MA/Computational-Biologist–Malaria_5564-1 *EOE / Minorities / Females / Protected Veterans / Disabilities*

neafsey@broadinstitute.org

ColoradoCollege PlantEvolution

The Department of Organismal Biology and Ecology at Colorado College announces a one-year, non-tenure track Assistant Professor position in Plant Biology and Ecology to begin in August 2018. A review of completed applicant files will begin immediately and continue until the position is filled.

Responsibilities for this Plant Biology & Ecology position entail teaching six courses, including introductory botany/plant biology, field-based ecology, either an upper-level or non-majors course in the candidate's area of specialty, and directing student research. The ability to integrate subfields of botany, ecology, and evolutionary biology and a familiarity with Rocky Mountain or Southwestern ecosystems are highly desirable. Apply electronically to: https://employment.coloradocollege.edu/postings/3192 Colorado College is a private, undergraduate, selective liberal arts institution enrolling approximately 2000 students. The college uses the Block Plan calendar in which students take one class at a time, allowing for significant field experiences. The Organismal Biology and Ecology (OBE) Department at Colorado College studies the structure and function of organisms in an ecological and evolutionary context. OBE research foci include botany, animal and plant ecology, comparative physiology, conservation biology, and molecular ecology. The department strives to perform cutting-edge research and include students in these opportunities.

PhD (or near completion) and teaching experience required. Applications will include the following: 1) a description of relevant professional background, 2) statements of teaching philosophy and research interests, 3) curriculum vitae with email address, 4) unofficial copies of undergraduate and graduate transcripts, and 5) three letters of recommendation. Information about Colorado College and OBE can be found at our web site: https://www.coloradocollege.edu/academics/dept/obe/ . Colorado College welcomes members of all groups and reaffirms its commitment not to discriminate on the basis of race, color, age, religion, sex, sexual orientation, gender identity, gender expression, national origin, or disability in its educational programs, activities, and employment practices. The College is committed to increasing the diversity of the college community. Candidates who can contribute to that goal are particularly encouraged to apply.

Shane Heschel <sheschel@coloradocollege.edu>

CRI Paris ResFellow SystemsBiol

Dear colleagues,

Center for Research and Interdisciplinarity (CRI) in Paris is opening group leader positions to join our Collaboratory, research.cri-paris.org, which may be of particular interest for you.

The detailed call can be found at cri-paris.org/fellows (deadline: April 15th).

We particularly call for candidates with interest in:

- Open synthetic and systems biology - from foundational understanding of living systems to open biotech and open health and pharma solutions.

- Open Artificial Intelligence - Understanding and shaping current digital transition in context of learning, health and/or human-machine paradigms

Other candidacies, focusing on other focal points of the CRI: Open health - from data-rich research to development of frugal software and hardware solutions, Open learning - from understanding learning process to new learning paradigms, Open phronesis - tackling contemporary ethical challenges at interfaces of Life, Digital and Learning Sciences, will be considered as well.

We seek candidates at different career stages, from postdoctoral young investigators to tenured scientists, who will join our current cohort of Fellows (more about them and their projects https://research.cri-paris.org/-our-fellows/).

We are looking for scientists seeking a home to expand their research focus or jump start a new research program within the premise of CRI research priorities either as Core fellows (5 years) or Long-term fellows (1-3 years). In addition, Core fellows are expected to contribute as pillars and mentors of the CRI Research community, and are required to hold a permanent position in France. Additionally, we draw your attention to the year-long open call for short-term fellows (3-6 months).

Anyone capable of carrying an autonomous research project, from young PhD graduates to established researchers (including sabbaticals) is eligible to apply to become a CRI Research Fellow. We expect a gradual recruitment build-up to reach a 60-70 strong cohort within our dedicated building at the historical heart of Paris (the Marais) that will open its doors during the summer 2018. This 6500m2 building will include state-of-the-art wet lab space, makerspace, pedagogic facilities and studio apartments for students and young researchers. Fellows are eligible for research support funding, as well as support for a small team of PhD students/postdocs. We strongly encourage applications from researchers with independent funding, including grants, sabbatical allowances, and temporary detachment from permanent positions. A limited number of salary stipends are available.

Please share the information around you or nominate people by sending me an email (with title: [nomination]...) with contact details and a short paragraph why you think she/he would fit for the call.

The 2nd Fellows calls are now open (deadline: April 15th) can be accessed at cri-paris.org/fellows and will be renewed bi-anualy.

Do not hesitate to contact us for any further information, questions.

Sincerely,

Dule

Dusan Misevic Assistant Director for Research

Centre de Recherches Interdisciplinaires (CRI) INSERM, Paris Descartes University

research.cri-paris.org contact.research@cri-paris.org

Dusan Misevic <dule@alife.org>

DebrecenU BreedingSystems

Research Assistant Position University of Debrecen, Hungary ELVONAL (cutting edge) - Breeding system evolution in shorebirds

The Hungarian government recently opened up a new funding stream to support cutting edge research across all scientific fields (Nature 551: 425), and our team was one of the 12 winners. This will be a 5-year project focusing on testing key hypotheses of breeding system evolution through the use of genomic, immunological, and demographic approaches. The project focuses on shorebirds (i.e., plovers, sandpipers, and allies) that exhibit an unusual diversity of mating systems and parental care (see references).

This job offers an opportunity for an ambitious research assictant who wants to combine fieldwork with coordinating practical aspects of field research across numerous field sites. The main tasks of the Research Assistant are to carry out field studies in Madagascar, Cape Verde, Mexio, Russia or China, possibly in other countries, and coordinate practical aspect of the field projects that include securing permits, ensuring standardized data collection, availablity of research tools and equioment. We seek candidates with experience in behavioural ecology and field biology preferable with birds. Excellent communication skills and database handling are essential.

This is a full-time position and the salary will be above the normal Hungarian level (up to 1200 EUR, depending on experience). Note that the cost of living in Hungary is substantially less than in the US or in Western Europe. This position is available for 3 years (subject to probation period) with the possibility of extension for the duration of the ELVONAL project (5 years). See further specifications below.

Application deadline is 28 February 2018. The application should include a (1) max two pages cover letter, (2) CV with list of publications, and (3) the name and contact details of three referees preferably from research, academia or conservation. The applications should be emailed to Ms Emese Kapczar kapczar.emese@science.unideb.hu Interviews will be in early March and the position is available from 1 April 2018. Applications from women and minority candidates are especially welcome.

Debrecen is the second largest city in Hungary and has a lively university community. The University of Debrecen < https://en.wikipedia.org/wiki/University_of_Debrecen > was established in 1538, and it is one of the prestigious universities in Central Europe The university has over 4000 students - many are from abroad. The Dept. of Evolutionary Zoology and Human Biology < http://zoology.unideb.hu/home/ > is one of the leading departments in natural sciences Debrecen Airport has connections with some of the main European airports. Debrecen's surrounding has impressive wildlife and landscape that include Hortobagy National Park < https://en.wikipedia.org/wiki/Hortob%C3%A1gy_National_Park >, a UNESCO-recognised protected area. See details at https://en.wikipedia.org/wiki/University_of_Debrecen http://zoology.unideb.hu/home/ https://en.wikipedia.org/wiki/Hortob%C3%A1gy_National_Park For further information please contact Ms Emese Kapczar kapczar.emese@science.unideb.hu

Selected publications Bulla, M. et al. 2016. Defying the 24 1 day: Unexpected diversity in socially synchronized rhythms of shorebirds. Nature 540: 109-1013.

Eberhart-Phillips, L. J. et al. 2017. Adult sex ratio bias in snowy plovers is driven by sex-specific early survival: implications for mating systems and population growth. Proceedings of The National Academy of Sciences of the United States of America 114: E5474-E5481.

Liker, A., R. P. Freckleton & T. Szekely. 2013. The evolution of sex roles in birds is related to adult sex ratio. Nature Communications 4: 1587.

Rosa, M. E. et al. 2017. The effects of adult sex ratio and density on parental care in Lethrus apterus (Coleoptera, Geotrupidae). Animal Behaviour 132: 181-188.

Vincze, O. et al. 2016. Parental cooperation in a changing climate: fluctuating environments predict shifts in care division. Global Ecology and Biogeography 26: 347-358.

Further specifications of the position Employer: University of Debrecen, Dept of Evolutionary Zoology & Human Biology, University of Debrecen, H-4032, Egyetem ter 1, Hungary

Job description: * The Research Assistant will carry out research in shorebird populations included in the ELVONAL project eg Madagascar, China, Russia or South Africa in regards to mating system and parental care * coordinate practical aspects of research associated with the ELVONAL

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DebrecenU ResAssist AvianBreedingSystems

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Further specifications of the position Employer: University of Debrecen, Dept of Evolutionary Zoology & Human Biology, University of Debrecen, H-4032, Egyetem ter 1, Hungary

Job description: * The Research Assistant will carry out research in shorebird populations included in the ELVONAL project eg Madagascar, China, Russia or South Africa in regards to mating system and parental care * coordinate practical aspects of research associated with the ELVONAL project: preparations of fieldwork, data collection, field notes, reports, permits, and field equipment and coordinate research with external collaborators

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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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France ReefEvolution

I would like to diffuse on the EvolDir list the following position. It is being made available in France on the subject of “Evolutionary complexity of microbiomes on coral reefs”.

Link: https://www.ephe.fr/actualites/recrutement-des-enseignants-chercheurs-2018 Profile: The successful candidate will join the USR 3278, a research group recognised nationally and internationally for its work on coral reefs.

The research project will integrate the microscopic components (bacteria, protists, algae, ...) of the coral reef ecosystem, which have become increasingly central to the assessment of resilience and adaptation capacities of coral reefs to the impacts of climate change.

’Meta-barcoding’ approaches, based on high throughput sequencing techniques, have created new perspectives to increase our understanding of biodiversity and its potential role in adaptation processes. While recent advances in genomic developments have revealed new complexities within the microbiome, the physiological consequences and deep physio-genomic impacts of the microbiome have yet to be fully examined.

In addition to the descriptive genomic aspect of this project, the candidate will document the evolution of the microbiome through evolutionary scenarios as well as the processes which have underpinned the patterns of genetic diversity through time. It is essential that the successful candidate has demonstrated expertise in both genetics and in population genetics. These innovative approaches will not only allow for an in-depth analysis of the impacts of past climate change events, a process which is essential to better understand and manage the coral reefs of today, but will also lead to new developments in the field of conservation genetics.

Many thanks Regards John

John Edward <edwards.jrb64@gmail.com>

Frankfurt BiodiversityBioinformatics

Job offer ref. #12-18001 The Senckenberg Gesellschaft für Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. LOEWE Centre for Translational Biodiversity Genomics (LOEWE-TBG) is a joint venture of the Senckenberg Gesellschaft für Naturforschung (SGN), Goethe-University Frankfurt, Justus-Liebig-University Giessen and Fraunhofer Institute for Molecular Biology and Applied Ecology IME aiming to intensify biodiversity genomics in basic and applied research. We will establish a new and taxonomically broad genome collection to study genomic and functional diversity across the tree of life and make genomic resources accessible for societal-demand driven applied research.

The Senckenberg Gesellschaft für Naturforschung and the LOEWE-TBG invite applications for a

Bioinformatician for high-throughput genome assembly and annotation (100%)

Your tasks: - Developing, maintaining and running high-throughput pipelines for the assembly and annotation of de novo genomes from diverse eukaryotes - Organising and documenting the work-flow from receiving the raw data over issuing the assembled genomes to the client users to archiving in public databases - Communication with user groups, service providers and external database managers

Your profile: - PhD in Bioinformatics or related subjects - Experience with de novo genome assembly of non-model organisms - Developing large scale, high-throughput procedures for de novo genome assembly and annotation - Experience and solid understanding of comparative genomics or evolutionary biology research in non-model organisms - Familiarity in leading a service orientated unit and excellent communication skills

What is awaiting you? - An interesting task in a dynamic team of researchers in an internationally research institution - The opportunity to gain experience in the above-mentioned research field - The occasion to build a network with scientists in interdisciplinary fields - The prospect to assume a management role for the bioinformatics unit - Flexible working hours - annual special payment - company pension scheme - Senckenberg ID card for free entry in museums in Frankfurt - 30 days holidays

Salary and benefits are according to a full time public service position in Germany (TV-H E13). The contract should start on May 1st, 2018 and will initially be limited for two years. The Senckenberg Gesellschaft für Naturforschung support 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 is in Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung.

Please send your application, mentioning the reference of this job offer (ref. #12-18001) before April 1st, 2018 by e-mail (attachment in a single pdf document) and including a cover letter detailing research interests and experience, a detailed CV and a copy of your certification to:

Senckenberg Gesellschaft für Naturforschung Senckenberganlage 25 60325 Frankfurt am Main E-Mail: recruiting@senckenberg.de

recruiting <recruiting@senckenberg.de>

GeorgeWashingtonU ResearchScientist NGSCore

Research Scientist, NGS Core

Job Posting at https://www.gwu.jobs/postings/49245 Application Review Begins February 20^th, 2018

The Computational Biology Institute in the Milken Institute School of Public Health at The George Washington University is seeking a highly-motivated candidate for a position as a Research Scientist with the Next-Gen Sequencing (NGS) Core. A successful applicant will be ready and willing to assist with the startup for a brand-new facility and to guide the facility toward strong operations. The Core already possesses some of the most cutting-edge equipment necessary, with the goal of processing thousands of samples per year. The applicant should be prepared to lead the facility further still with regards to building up the resources of the Core and to hire new staff members.

Responsibilities Include:

- Lead the collaboratively efforts with faculty, staff, students, and collaborators - Lead the design of comprehensive project objectives - Manage the evaluation of data analytics and formulate informatics solutions; - Manage collaborative relationship relationships of key stakeholders to build a robust research infrastructure; - Develop and implement bioinformatics analyses, applications, and workflows; - Integrate statistical analyses to project design and data interpretations; - Manage NGS data analysis and delivery, pipeline development and automation; - Provide customer support for NGS data analysis results; - Manage the sale and marketing of the NGS Core; - Performs other related duties as assigned. The omission of specific duties does not preclude the supervisor from assigning duties that are logically related to the position.

Minimum Qualifications:

Qualified candidates will hold a master's degree/PhD and at least 5 years of experience in a related discipline, to include at least 2 years of research and/or college level teaching in a field basic to the work to be performed. Degree must be conferred by the start date of the position.

Preferred Qualifications:

- Master's degree in life sciences or related field required, Ph.D. preferred

- Two or more years of related genomics experience required

- Essential knowledge of key biological processes and NGS technology desired

- Concrete bioinformatics skills in analysis of data from various omic platforms

- Experience in NGS data generation and analysis

- Experience with the Illumina sequencing platform, especially MySeq and NextSeq

- Two years of documented hands-on (wet lab) experience with NGS assay development, validation, troubleshooting, and reviewing of run QC data.

- In-depth knowledge of different NGS platforms and technologies (experience with long reads sequencing is a plus).

- Familiar with different NGS software platforms, bioinformatics pipelines and NGS data processing and interpretation solutions.

- Technical expertise with other molecular technologies, including but not limited to: PCR, quantitative real-time PCR, digital PCR, NanoString, etc. is also highly desired.

- Strong organizational and interpersonal skills, must display excellent leadership and people skills, and demonstrate ability to work collaboratively with others in a highly matrixed environment.

Professor Keith A. Crandall, PhD Director, Computational Biology Institute Director of Informatics, CTSI-CN Milken Institute School of Public Health The George Washington University 800 22nd Street, NW - Suite 7000D Washington, DC 20052-0066 USA (o): 571-553-0107 (m): 202-769-8411 Twitter / LinkedIn

"Professor Keith A. Crandall" <kcrandall@gwu.edu>

GeorgeWashingtonU SoftwareEngineer

Research Associate, Software Development (Software Engineer)

https://www.gwu.jobs/postings/49354 Job Description Summary:

The Computational Biology Institute (CBI) at George Washington University is seeking a Research Associate in Software Development to contribute to ongoing research projects and developing diverse tools for analyzing omic data. The successful candidate will have a background in computer science and informatics, and will have programming experience in Python, C/C++, JAVA, and/or R. This position will report to the Director of CBI (Keith Crandall, kcrandall@gwu.edu). The software development is part of an NIH funded collaborative effort in informatics at the Clinical and Translational Science Institute Children's National (CTSI-CN, https://www.ctsicn.org/).

Responsibilities include: - Manage the development of new software modules - Lead communication efforts with members of the Institute to understanding existing needs and forecast the future requirements of software development - Develop educational modules, tutorials, and workshops for training purposes - Develop and manage databases and interface for DNA sequence analysis, and develop and implement tools for omics analysis within a comprehensive pipeline framework

Minimum Qualifications:

Qualified candidates will hold a Master's degree and 1 year of experience in a related discipline. Degree must be conferred by the start date of the position.

Preferred Qualifications:

A Bachelor's in computer science or a related field is required, or an equivalent combination of education, training and experience. Master's in computer science, data science or related field is preferred, with two years experience. The successful candidate will have experience in multiple programming languages with some applications to bioinformatic analyses. Experience with clinical health data is also a plus. Application review will begin March 1, 2018.

Keith A. Crandall, PhD Director, Computational Biology Institute Professor, Department of Biological Sciences The George Washington University 45085 University Drive Innovation Hall, Suite 305 Ashburn, VA 20147 (o): 571-553-0107 (m): 202-769-8411 Twitter / LinkedIn

"Professor Keith A. Crandall" <kcrandall@gwu.edu>

GhentU EvolutionLandPlants

??? Apply until 27/02/2018 23:59 CET ??? Discipline: Integrative Botany: Evolution of Landplants ??? 100% Assistant professor tenure track ??? Faculty of Sciences ??? Reference number: 201711/WE/ZAP/002

ABOUT GHENT UNIVERSITY

Ghent University is one of the most important education and research institutions in the Low Countries. On a daily basis, over 9,000 staff members and 41,000 students implement its motto "Dare to Think". Ghent University's mission statement is characterised by qualitative education, internationally renowned research and a pluralistic social responsibility.

ASSIGNMENT

This position in the rank of assistant professor, funded by the Special Research Fund, is a tenure track appointment for a period of 5 years with a focus on research and with a teaching load limited to no more than 8 ECTS credits per semester on average over a period of 3 years. For the further development of the academic career, please see ???Appointment information??? below.

During the recent decades, research on plant diversity has evolved from descriptive taxonomy to modern integrative phylogeny. Morphological, molecular and ecological knowledge is used as an instrument to answer questions about the origin and evolution of characteristics and their consequences at different levels. As a BOF TT in the requested domain, you will set up new integrative research lines to answer questions regarding evolution and diversity of land plants (Embryophyta). Integrated research questions bridge macro (phylogeny, diversification) and micro evolution (evolution of populations, phylogeography) to gain insight into plant speciation, development and evolution of features and functions, and the underlying mechanisms and processes.

Academic education

You give high-quality lectures and tutorials at both undergraduate and graduate level, in the discipline of Botany (systematics, anatomy, phylogeny, evolution). The teaching and lecturing will be evaluated on actuality, connection with the educational program and interaction with the students.

Academic Research

You engage in research at an internationally competitive level in the discipline of integrative botany: evolution of Landplants. You seek funding to realize projects and to hire PhD student, and you act as their supervisor.

Academic service

You take part in the internal and external service activities of the department of Biology. During your career you are willing to engage in your share of administrative duties or leadership positions.

PROFILE Experience

- You have already conducted excellent academic research in the given discipline, which is clearly reflected in outstanding publications in national and international peer-reviewed books and/or journals;

- You are didactically skilled to teach university students to develop academic competences;

- You have proven knowledge of and interest in diversity and evolution of Landplants

- Recommended are:

- Experience in supervising research and/or coaching Ph.D. students;

- International mobility, among other things thanks to research stays at institutions external to the one where you acquired your highest academic degree;

- Positively evaluated experience in provided or organised academic lecturing;

- Professionalisation of education.

Skills / Attitude

- You are quality-oriented;

- You take initiative;

- You have strong interpersonal skills, making you a team player and an efficient communicator to colleagues, employees, students and other stakeholders.

Admission requirements

- You hold a thesis-based doctorate or a diploma or certificate that is recognised as equivalent (article V.20 Codex Higher Education).

Upon evaluation of a foreign (non-EU) diploma, a certificate of equivalence may still have to be requested at NARIC. If this is the case, we advise you to initiate this recognition procedure as soon as possible. You are required to have the recognition no later than on the date of your appointment.

- You have at least two years of postdoctoral experience October 1, 2018. This term of two years is determined by the date written on the above-mentioned required diploma.

APPOINTMENT INFORMATION

- We offer you a temporary appointment as an assistant professor in a tenure track system for a term of five years with a focus on research. If positively evaluated by the University Board, the term of office will be transferred into a permanent appointment as an associate professor. At that moment the time devoted to research, education and academic services may be altered.

- Should you already be a member of the professorial staff or hold an equal post at another university or research institution, you can immediately be appointed as an assistant professor, without prejudice to the possibility of a temporary appointment offered in article V.28 of the Codex of Higher Education.

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ImperialC London 3mnths AvianFieldAssist

I am urgently looking to recruit a field assistant for the breeding season, this position is paid. Duties include the collection of field data on a wild blue tit population in Silwood Park. You will work in a team of students and technical assistants, collecting data on blue tits breeding in nest boxes. Duties involve nest box monitoring, catching of adults and young birds, ringing, data entry and management. There is the option to also contribute to ongoing research projects. We can offer accommodation on-site. Starting date would be late March but no later than 1st April for approximately 3 months depending on season.

Required skills: passerine handling and ringing skills (license a big plus), team work, field work experience, independence and able to work in a team. Must be conscientious with data.

Must be allowed to work in UK.

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

https://www.imperial.ac.uk/visit/campuses/silwood-park/research/

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

Julia_Schroeder <julia.schroeder@gmail.com>

JamesCookU 2 PlantEvolution

The Australian Tropical Herbarium (ATH) in tropical north Queensland, Australia seeks to fill two research positions. The ATH is located on the Cairns campus of James Cook University (www.jcu.edu.au).

The Research Fellow/Senior Research Fellow is an ongoing appointment (Academic level B/C AU$89,859 - $125,429); the Postdoctoral Fellow is a three year appointment (Academic Level A AU$64,020 - $85,546). The two positions will be appointed together. We seek outstanding plant scientists with complementary capabilities to build an internationally significant research team in plant and environmental biosecurity, with scope to also contribute to research in the fields of ethnobotany and biology of crop wild relatives. Particularly relevant skill sets include genetics, systematics, ecology, bioinformatics and niche modelling. Evolutionary biologists are especially encouraged to apply.

These vacancies are now open and interested persons can access further details and apply online via Jobs@JCU (under 'Â¥Current Vacancies'Â search for position numbers 16248 - Postdoctoral Research Fellow and 16249 - Research Fellow / Senior Research Fellow). Applications will close on 1 March 2018.

Cairns is a small vibrant city nestled between two World Heritage sites'Xthe Wet Tropics World Heritage Area and the Great Barrier Reef Marine Park. There are multiple nearby opportunities for field research, including the Daintree Rainforest Observatory field station. For more information on the Australian Tropical Herbarium, see our most recent annual report at https://issuu.com/thepagestudio/docs/ath_tpkss_2016_final, or visit www.ath.org.au and www.facebook/tropicalherbarium.

Please direct inquiries to enquiry@ath.org.au

“Crayn, Darren” <darren.crayn@jcu.edu.au>

LondonCrick AncientDNAscientist

Senior Laboratory Research Scientist

Reports to: Group Leader Pontus Skoglund

This is a full-time, permanent position on Crick Terms and Conditions of Employment.

Summary A long-term position as a Senior Laboratory Research Scientist (SLRS) has been created to ensure efficient operation of the molecular ancient DNA activities at the Ancient Genomics Lab of the Francis Crick Institute, led by Dr. Pontus Skoglund. The post holder will lead the management and operation of the specialized ancient DNA clean room facility; sample processing, ancient DNA extraction, library preparation and sequencing. Additional roles include training other scientists in established workflows, purchasing, safety and general organization, and interaction with other scientists and technicians at the Crick. Additional opportunities include methodological research projects and sampling travels. Applications are welcome from candidates with a strong background in ancient DNA analysis, excellent organizational skills and an interest in molecular biology techniques and instrumentation. The position is open to candidates of varying experience levels and this will be reflected in salary grade. Two-way scientific interactions will occur between the post holder and other members of the ancient genomics lab, as well as scientific collaborative partners within the Crick Institute, including Science Technology Platforms (STPs), post-doctoral researchers, students, and group leaders.

Project summary The Senior Laboratory Research Scientist will provide comprehensive support for ancient DNA sequencing projects at the ancient genomics laboratory. The successful applicant will be centrally involved in implementation of ancient DNA sequencing workflows, including sample preparation, instrument operation, and laboratory organisation.

Key responsibilities These include but are not limited to: —Clean lab management. Maintenance and day-to-day operation of the specialized ancient DNA clean room space, instruments, and supplies (post-PCR and sequencing facilities are separately managed). —Ancient sample handling and cataloging. Databasing, handling, shipping and organization of samples. Sampling visits with partner groups and institutions. —Training of other scientists in laboratory workflows. —Ancient DNA extraction. Bone and tooth powder extraction from skeletal material, genomic library preparation and targeted capture of genomic DNA. —Automation. Implementation of ancient DNA workflows on an Agilent Bravo Workstation in collaboration with the Advanced Sequencing core facility. —Genome sequencing. Organize and enable sequencing by liaising with the Advanced Sequencing Technology Platform core facility at the Crick. —Implementation of new workflows. Improving laboratory techniques by in-house optimization and innovation, and implementing new advances and best practices. —Scientific interaction and publication. Participation in scientific meetings within the group and wider community. Contribute to scientific publications and presentations.

Key experience and competencies The post holder should embody and demonstrate our core Crick values: bold, imaginative, open, dynamic and collegial, in addition to the following:

Essential qualifications, experience and competencies: —BSc or MSc in Biochemistry, Biology or a related field, or PhD in a field incorporating ancient DNA techniques, or equivalent qualification/experience —Experience with ancient DNA extraction from skeletal material —Experience with ancient DNA library preparation and high-throughput sequencing —Experience with managing ancient skeletal material —Strong skills in organizing and recording experiments —Experience with training other scientists in molecular biology workflows —Strong collaborative ability and teamwork experience —Experience with in-solution DNA enrichment —Experience with installation and management of new instruments

Desirable qualifications, experience and competencies: —Experience with automated liquid handling instruments —Experience with laboratory management —Experience with ancient DNA method development and optimisation —Experience with a wide set of DNA techniques outside of ancient DNA —Experience with museum or field sampling —Experience and track-record of ancient genomic research —Experience with bioinformatics processing of ancient genomic sequence data

Beneficial: —Experience with ancient protein analysis —Experience with other ancient biomolecules —Experience with the use of databases

The post holder may be trained in specific techniques by Postdoctoral fellows and will receive support by the advanced sequencing STP. Lab web page: www.skoglundlab.org Informal enquiries relating to this role can be addressed to Pontus Skoglund: pontus.skoglund@crick.ac.uk

Apply at https://jobs.crick.ac.uk pontus.skoglund@gmail.com

MaxPlanck Jena Bioinformatics

Senior Bioinformatician position (E14 100%) Max Planck Institute for the Science of Human History, Jena, Germany

The Archaeogenetics department at the Max Planck Institute for the Science of Human History in Jena, Germany, is offering a position for a senior bioinformatician (E14 100%) beginning in summer 2018.

The overarching research topic at the institute is the use of novel scientific approaches from high throughput sequencing of ancient DNA from human populations and their pathogens to explore research questions related to human history, gene-culture coevolution, and adaptation to infectious disease. The main foci are the relationship between humans and pathogens through time, population migrations and dynamics on a historical time-scale, and microbial evolution.

The senior bioinformatician position will focus on the core business of data management, establishment and maintenance of state-of-the-art analytical pipelines, guaranteeing high quality outputs. The candidate is required to manage and run the core facilities of high throughput sequence data analysis, but will also be given ample opportunity to develop new analytical methods and pipelines for the analysis of large ancient DNA genomic and metagenomic datasets. The position will be at the heart of a large range of multidisciplinary projects dealing with the (pre)history of ancient human populations, and the evolution of microbial and pathogen communities, working closely with the researchers leading these projects. The ability to work in a large international team is therefore essential, while a passion or interest for human history and evolution is also desirable. Since this role also includes co-supervision of postgraduate students in bioinformatics and biostatistics tasks, experience in this area is welcome.

Applicants should have completed a Master's degree or equivalent in biostatistics, bioinformatics, computer science or relevant neighboring discipline, worked with large high-throughput sequencing or SNP datasets, and have experience with maintaining bioinformatics analysis pipelines in a server and/or cluster environment. Prerequisites also include evidence of strong oral and written communication skills and the ability to complete tasks in a timely and structured fashion. Experience in working in a scientific environment (e.g. completed PhD) is of advantage.

The position is appointed for three years with the possibility of extension and conversion into a permanent position.

For detailed information on the institute please visit our website: http://www.shh.mpg.de/en The Max Planck Institute for the Science of Human History promotes women and encourages especially women to apply. Handicapped candidates will be given

priority in case of the same professional qualification.

Your application:

Please submit your application consisting of a letter of intent, a CV, relevant certificates and references, as a single pdf file and in English, by upload via the following link:

https://s-lotus.gwdg.de/mpg/mjws/perso/-shh_p003.nsf/application Deadline for application: April 30th, 2018

For detailed information on the position please contact

Prof. Johannes Krause, E-mail: krause@shh.mpg.de

Ellen Richter <richter@shh.mpg.de>

Miami FieldTechs Taxonomists

The Heffernan Lab at the Nicholas School at Duke University seeks 3-4 technical research assistants to conduct urban field sampling in the Miami, FL this spring (~March-June). Duties will primarily include conducting surveys of vegetation, insects, and birds in residential yards and local parks.

Desired qualifications include any of the following: experience with field work in urban environments; ability to identify plant, insects, and/or birds of south Florida.

For more info and to apply: https://academicjobsonline.org/ajo/jobs/10749 Anika Bratt, PhD Postdoctoral researcher – Heffernan Lab Nicholas School of the Environment Duke University, Durham NC

anika.bratt@duke.edu anikabratt@gmail.com

website: https://anikarbratt.wordpress.com/ Anika Bratt <anikabratt@gmail.com>

MichiganStateU Bioinformatician

Bioinformatician at Michigan State University

Several faculty in the Department of Integrative Biology at Michigan State University (Mariah Meek, Ingo Braasch, Gideon Bradburd, Julia Ganz) are looking to collectively hire a highly motivated bioinformatician/computational scientist with a biology background for a full-time position. Typical research projects will use RNA-sequencing, RAD-sequencing, whole genome sequencing and assembly, and targeted capture sequencing to address questions in ecology, evolution, comparative genomics, and developmental biology. We are looking for an enthusiastic and organized individual to join our team, who is skilled at working for multiple people and on different projects. The position will be based in East Lansing, MI on the MSU campus and comes with a competitive benefits package.

Primary duties will include: 1. Curating sequence data (10%) 2. Analyzing sequence data (65%) 3. Producing tables and figures and writing data analysis methods and results (10%) 4. Mentoring students on bioinformatics methods (10%) 5. Reading scientific literature to stay up to date on newest analysis methods (5%)

Required Qualifications: The job requires knowledge equivalent to that which normally would be acquired by completing a four-year college degree in bioinformatics or related field and up to six months of related and progressively more responsible or expansive bioinformatics experience; or an equivalent combination of education and experience. The candidate should be well-versed in unix/linux, as well as at least one other programming language (e.g. R, python, perl). Applicants should have extensive experience analyzing large 'Â¥'Vomic'Â datasets.

Desired Qualifications: A Master'Âs or PhD degree in bioinformatics or related field. Experience in at least some of the following key areas: 1. Analyzing complex RNA-seq experimental data sets for differential gene expression 2. Analyzing RAD-seq datasets'Xaligning to reference and creating de novo assemblies, SNP discovery, genotyping, etc. 3. Genome assembly and annotation 4. Genome comparisons 5. Phylogenomics 6. Epigenomics

Required applicant materials: 1) Brief cover letter describing research and data analysis experience and career goals 2) CV 3) Names and email addresses for 3 references

How to apply Interested candidates should apply through the MSU Applicant Page at careers.msu.edu (job ID 480028). If you have questions, email Dr. Mariah Meek (mhmeek@msu.edu), with “Bioinformatics position” in the subject line. DO NOT EMAIL APPLICATION MATERIAL TO DR. MEEK.

Review of application material will begin on March 14, 2018. Position is open until filled.

“Braasch, Ingo” <braasch@msu.edu>

NationalSunYat-senU

Faculty position at Department of Biological Sciences in

National Sun Yat-sen University

The Department of Biological Sciences in National Sun Yat-sen University in Taiwan is seeking candidates for non-tenure track faculty position at the assistant professor (or higher level) in the area of Biology.

1. Position: At least one assistant professor (or higher level) in the area of Biology.

2. Required qualifications:

a. Hold a Ph.D degree.

b. At least 2 year postdoc. experience.

c. Publish at least 2 SCI journal papers.

d. Non-Taiwan national and can contribute to teach undergraduate and graduate courses in biology using English language.

3. Applicants should send (1) CV, (2) Certificate of Ph.D degree and postdoc., (3) Publication list (Please assign one paper as the primary publication), (4) Publication copies (2013-2018), (5) Teaching and research plan, (6) Three letters of recommendation

4. Please email the PDF file to kzlee@mail.nsysu.edu.tw before March 9th, 2018

5. Please also mail the hard copy item (1) ˜ (5) to

Prof. Chiang, Yu-Chung.

Chairman

Department of Biological Sciences

National Sun Yat-Sen University

#70, Lien Hai Rd., Kaohsiung, TAIWAN

6. Contact information

Kun-Ze Lee, Ph.D

National Sun Yat-sen University

Dept. Biological Sciences

Phone: +886-7-5252000 ext: 3615

Email: kzlee@mail.nsysu.edu.tw

Department website: http://biology.nsysu.edu.tw/-bin/home.php?Lang=en Shu-Ping Huang <sphuang0711@gmail.com>

NorthernArizonaU Flagstaff ViralEvolution

Position: Research Specialist - Viral Genomics and Evolution

The Pathogen and Microbiome Institute (PMI) at Northern Arizona University seeks a Research Technician to perform basic and applied research focused on viral genomics and evolution. The top candidates for this position should be highly motivated and have experience with viral and cell culture, molecular genetic analyses, including RNA/DNA isolation, PCR/qPCR, gel electrophoresis, next-generation sequencing, and the ability to work with viruses under biosafety level 2 (BSL2) conditions. There is a possibility of future work in the PMI BSL3 laboratory that would involve handling viral pathogens such as Rift Valley fever virus, Oropouche virus and Western equine encephalitis virus. Extra emphasis will be given to candidates with command line scripting experience, though this is not a requirement.

Primary duties will include:

- Maintaining cell cultures
- Passaging viruses
- Molecular cloning
- PCR/qPCR assay development and validation
- Library preparation for next generation sequencing, including Illumina, PacBio and Oxford Nanopore platforms
- Working under BSL2 conditions, with the possibility of future work under BSL3 conditions.
- Working both independently and in a team-based environment
- Laboratory management and maintenance of shared reagent stocks
- Working safely with potentially hazardous materials, such as laboratory chemicals and disease-causing organisms

Opportunities will also be available for command line scripting and data analysis.

Northern Arizona University is located in Flagstaff, AZ, a beautiful mountain town with a surprisingly vibrant restaurant scene. Located a little over an hour from the Grand Canyon and ˜45 min from Sedona, Flagstaff is a hiker's paradise. In fact, the city of Flagstaff operates more than 50 miles of unpaved trails and there are, on average, 266 sunny days per year with which to enjoy them. At 7000 ft in elevation, Flagstaff experiences all four seasons, but the summers are mild and, in the winter, you can be on the slopes within 30 min!

For additional information and to apply:

https://hr.peoplesoft.nau.edu/psp/ph92prta/-EMPLOYEE/HRMS/c/HRS_HRAM.HRS _APP_SCHJOB.GBL?Page=HRS_APP_JBPST&Action=U&FOCUS=Applicant&SiteId=1&JobOpeningId'3610&PostingSeq=1

Jason Thomas Ladner <Jason.Ladner@nau.edu>

Norway GenomicsBioinformatics

A position as a researcher is available in the department Breeding and Genetics with a workplace at Ãs. Research in genetics and breeding in Nofima has laid the foundation for the development of modern breeding programs for important breeding species such as salmon, rainbow trout, tilapia, carp and tropical prawns.

The Department of Breeding and Genetics in Nofima has an overall goal of contributing to R & D for efficient and sustainable breeding programs for farmed species. The department currently has 12 researchers with very good results in the form of viticulture publishing and facilitation for commercial use of research results.

The main areas for research are breeding programs for aquaculture species, quantitative genetics and genomics, genetic diversity in wild fish populations and ethical, legal and social aspects of aquaculture genetic resources.

We are currently seeking one researcher with high level of expertise and experience before research and bioinformatics. The positions require one doctorate, preferably before this subject area. We want one senior researcher with strong publications history and research and development experience before breeding species. However, we also encourage young talented junior graduates with doctorate and relevant experience before genomics and bioinformatics to apply.

Interested applicants are encouraged to visit the following website for more information: https://-www.jobbnorge.no/ledige-stillinger/stilling/148373/-forskar-akva kultur-genomikk-og-bioinformatikk

Forskar - Akvakultur genomikk og bioinformatikk (148373) | Nofima AS www.jobbnorge.no Stillingstittel: Forskar - Akvakultur genomikk og bioinformatikk (148373), Arbeidsgiver: Nofima AS, Soknadsfrist: 11. mars 2018

Hooman Moghadam <Hooman.Moghadam@Nofima.no>

QueensU EvolutionaryEcol

Tenure-track position in Evolutionary Ecology

The Department of Biology at Queen's University invites applications for a Tenure-track faculty position at the rank of Assistant Professor with specialization in Evolutionary Ecology, with a preferred starting date of July 1, 2018.

We seek a broadly-trained evolutionary biologist with research interests in both fundamental and applied questions related to the evolutionary consequences and management of rapidly changing environments. This position could include aspects of plant or animal biology related to climate change, pollution, resistance to pesticides/herbicides/antibiotics, biological invasion, vector-borne diseases, habitat degradation and fragmentation, and restoration ecology. Priority will be given to candidates who envision studying contemporary evolution utilizing the diverse land-holdings and facilities at the Queen's University Biological Station (QUBS). QUBS includes more than 3400 ha of diverse aquatic and terrestrial habitat, located 60 km north of Kingston (https://-qubs.ca/). Situated on the Frontenac Arch, QUBS lands provide access to diverse terrestrial and aquatic habitats with a range of human disturbance. The station offers laboratory and teaching spaces as well as accommodation. Queen's is a research-intensive university, with an integrated Biology Department that encompasses observational, experimental and theoretical approaches to gain a fundamental understanding of biological systems and processes. Strong collaborative linkages exist with other departments and faculties at Queen's, and with other national and international institutions.

Candidates must have a PhD or equivalent degree completed at the start date of the appointment. The main criteria for selection are academic and teaching excellence. The successful candidate will provide evidence of high-quality scholarly output that demonstrates potential for independent research leading to peer assessed publications and the securing of external research funding, as well as strong potential for outstanding teaching contributions at both the undergraduate and graduate levels, and an ongoing commitment to academic and pedagogical excellence in support of the department's programs. Candidates must provide evidence of an ability to work collaboratively in an interdisciplinary and student-centred environment. The successful candidate will be required to make substantive contributions through service to the department, the Faculty, the University, and/or the broader community. Salary will be commensurate with qualifications and experience. This position is subject to final budgetary approval by the University.

The University invites applications from all qualified individuals. Queen's is committed to employment equity and diversity in the workplace and welcomes applications from women, visible minorities, Aboriginal peoples, persons with disabilities, and LGBTQ persons. All qualified candidates are encouraged to apply; however, in accordance with Canadian immigration requirements, Canadian citizens and permanent residents of Canada will be given priority.

To comply with federal laws, the University is obliged to gather statistical information as to how many applicants for each job vacancy are Canadian citizens / permanent residents of Canada. Applicants need not identify their country of origin or citizenship; however, all applications must include one of the following statements: "I am a Canadian citizen / permanent resident of Canada"; OR, "I am not a Canadian citizen / permanent resident of Canada". Applications that do not include this information will be deemed incomplete.

A complete application consists of:

- a cover letter (including one of the two statements regarding Canadian citizenship / permanent resident status specified in the previous paragraph);

- a current Curriculum Vitae (including a list of publications);

- a statement of research interests, and how the QUBS would be used to fulfil your interests and research goals;

- a statement of teaching interests and experience (including teaching outlines and evaluations if available);

- a diversity statement describing your past and planned commitment to promoting diversity, inclusion, and equity in your research programs and outreach activities;

- Three letters of reference to be sent directly to Brian Cumming, Professor and Head, Department of Biology, c/o Anne Dumont (ad142@queensu.ca)

The deadline for applications is February 18, 2018. Applicants are encouraged to send all documents in their application packages electronically as PDFs to Anne Dumont at ad142@queensu.ca, although hard copy applications may be submitted to:

Brian Cumming

Professor and Head

The Department of Biology

Room 3102, BioSciences Complex

116 Barrie St.

Queen's University

Kingston, Ontario

CANADA K7L 3J9

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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

RutgersU TeachingEvolution

Position Information: Recruitment/Posting Title Teaching Instructor

Department FASN - Biological Sciences

Salary Open

Posting Summary The Department of Biological Sciences, Rutgers University-Newark (RU-N) seeks to hire a full-time, non-tenure track member at the rank of Teaching Instructor. The candidate is expected to have a Ph.D. degree in Biology and should be able to demonstrate excellence at lecture and laboratory course instruction and development. The successful applicant will be expected to develop at least one introductory biology major course, teach a more advanced lecture/lab course, and participate in additional undergraduate teaching.

Qualifications Minimum Education and Experience Ph.D. in Biology

Posting Details Posting Number 18FA0056

Posting Open Date 02/12/2018 Posting Close Date 03/05/2018

Special Instructions to Applicants Please provide the following; 1. Cover letter; 2. Curriculum Vitae; 3. Two letters of recommendation; 4. Statement of Teaching Philosophy; 5. Research Statement; 6. Example(s) of course syllabi

Quick Link to Posting http://jobs.rutgers.edu/postings/60104 Campus Rutgers University-Newark

Home Location Campus Rutgers University-Newark

Affirmative Action/Equal Employment Opportunity Statement It is university policy to provide equal employment opportunity to all its employees and applicants for employment regardless of their race, creed, color, national origin, age, ancestry, nationality, marital or domestic partnership or civil union status, sex, pregnancy, gender identity or expression, disability status, liability for military service, protected veteran status, affectional or sexual orientation, atypical cellular or blood trait, genetic information (including the refusal to submit to genetic testing), or any other category protected by law. As an institution, we value diversity of background and opinion, and prohibit discrimination or harassment on the basis of any legally protected class in the areas of hiring, recruitment, promotion, transfer, demotion, training, compensation, pay, fringe benefits, layoff, termination or any other terms and conditions of employment. For additional information please see the Non-Discrimination Statement at the following web address: http://uhr.rutgers.edu/non-discrimination-statement Jessica Ware <jware42@newark.rutgers.edu>

Smithsonian GenomicsTechnician

A permanent, full-time, federal positions (on US citizens may apply).

We are particularly looking for someone well-versed in genomics knowledge and techniques including library making, running a miSeq sequencer, and analyzing genomics data.

Full job description at: https://www.usajobs.gov/-GetJob/ViewDetails/490597500 Summary This position will provide technical support for molecular genetics research and collections in the Laboratories of Analytical Biology (L.A.B.), National Museum of Natural History (NMNH), Smithsonian Institution, Washington, DC (primary duty station is at the Natural History Museum in DC but some work may take place at the Museum Support Center, Suitland, MD).

Responsibilities

* Assists LAB-associated with molecular genetic research projects, following laboratory protocols. * Works with individual researchers on multiple projects with a wide diversity of non-human and non-microbial biological genetic material. * Generates publishable data using molecular genetic laboratory techniques and equipment. * Analyzes and publishes genetic data. * Tracks samples and experimental results using appropriate software in order to clearly communicate results to researchers.

“Driskell, Amy” <DRISKELLA@si.edu>

StMarysC Maryland EvolutionaryNeurology

Evolutionary Neurobiologists are encouraged to apply. Visiting Assistant Professor of Biology (Neurobiologist)

The Department of Biology and the Neurosciences Program at St. Mary’s College of Maryland jointly invite applications for a one-year *visiting assistant professor position* beginning August 2018. Teaching responsibilities include: Principles of Biology, Neurobiology, Introduction to Neurosciences, and Seminar in the Neurosciences. We especially encourage applicants with research interests in cellular and/or molecular neuroscience. Ph.D. required; postdoctoral training and/or teaching experience preferred. Employment will be contingent upon successful completion of a criminal background check.

Non-sectarian since its founding, St. Mary’s College of Maryland, a public Carnegie Baccalaureate, Arts and Sciences institution located in St. Mary’s City, 70 miles southeast of Washington, D.C., has been designated as Maryland’s public honors college. With selective admissions policies, academically talented students, and a rigorous curriculum, we offer a small college experience similar to that found at exceptional private colleges. The quality of life is enhanced by the recreational opportunities of the Chesapeake region and by our proximity to Washington, D.C. and Baltimore. The SMCM Biology Department maintains estuarine/marine aquatic facilities that would be available for faculty and student research.

St. Mary’s College (www.smcm.edu) embodies diversity and inclusion in its mission. We create an environment that recognizes the value of individual and group differences and we encourage inquiries from applicants who will contribute to our cultural and ethnic diversity. Application materials should include a cover letter, curriculum vitae (including e-mail address), statement of teaching philosophy, statement of research interests, evidence of teaching effectiveness (if available), and three letters of recommendation. Applicants should indicate in their cover letter how their teaching at the College will contribute to a culture of inclusion and campus diversity. Applications are being accepted online at: apply.interfolio.com/48566. Questions may be directed to 240-895-4362.

Review of applications will begin immediately and continue until the position is filled. St. Mary's College of Maryland is an affirmative action/equal opportunity employer.

Visit our website: *www.smcm.edu/hr* Employment will be contingent upon successful completion of a criminal background check.

St. Mary's College of Maryland is an affirmative action/equal opportunity employer.

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Kevin J Emerson, PhD Assistant Professor of Biology Biology Department St. Mary's College of Maryland 18952 E. Fisher Rd St. Mary's City, MD 20686-3001 kjemerson@smcm.edu http://faculty.smcm.edu/kjemerson Office: 240 - 895 - 2123, Shaefer Hall 231

"Emerson, Kevin" <kjemerson@smcm.edu>

StMarysC Maryland VisitingProf

Evolutionary Biologists using molecular approaches are encouraged to apply. Visiting Assistant Professor of Biology (Molecular Geneticist)

The Department of Biology at St. Mary's College of Maryland invites applications for a two-year visiting assistant professor position in the field of molecular genetics beginning August 2018. Teaching responsibilities include participating in the biology core courses Genetics and Principles of Biology, a non-majors biology course, and an upper division elective in their specialty. We especially encourage applicants who can take advantage of our estuarine/marine aquatic laboratory facilities. Ph.D. required; postdoctoral training and/or teaching experience preferred. Employment will be contingent upon successful completion of a criminal background check.

Non-sectarian since its founding, St. Mary's College of Maryland, a public Carnegie Baccalaureate, Arts and Sciences institution located in St. Mary's City, 70 miles southeast of Washington, D.C., has been designated as Maryland's public honors college. With selective admissions policies, academically talented students, and a rigorous curriculum, we offer a small college experience similar to that found at exceptional private colleges. The quality of life is enhanced by the recreational opportunities of the Chesapeake region and by our proximity to Washington, D.C. and Baltimore.

St. Mary's College (www.smcm.edu) embodies diversity and inclusion in its mission. We create an environment that recognizes the value of individual and group differences and we encourage inquiries from applicants who will contribute to our cultural and ethnic diversity. Application materials should include a cover letter, curriculum vitae (including e-mail address), statement of teaching philosophy, statement of research interests, evidence of teaching effectiveness (if available), and three letters of recommendation. Applicants should indicate in their cover letter how their teaching at the College will contribute to a culture of inclusion and campus diversity. Applications are being accepted online at: *apply.interfolio.com/48608 < http://apply.interfolio.com/-48608 >*. Questions may be directed to 240-895-4362.

Review of applications will begin February 9, 2018 and continue until the position is filled. St. Mary's College of Maryland is an affirmative action/equal opportunity employer.

Visit our website: www.smcm.edu*/hr* Employment will be contingent upon successful completion of a criminal background check.

St. Mary's College of Maryland is an affirmative action/equal opportunity employer.

–

Kevin J Emerson, PhD Assistant Professor of Biology Biology Department St. Mary's College of Maryland 18952 E. Fisher Rd St. Mary's City, MD 20686-3001 kjemerson@smcm.edu http://faculty.smcm.edu/kjemerson Office: 240 - 895 - 2123, Shaefer Hall 231

"kjemerson@smcm.edu" <kjemerson@smcm.edu>

SwanseaU 2 EvolutionaryBiol

Lecturer (Research) Swansea University - College of Science Location: Swansea Salary: 33,518 to 38,833 Hours: Full Time Contract Type: Permanent Placed on: 8th February 2018 Closes: 11th March 2018 Job Ref: AC02551 Salary Lecturer (Research) (2 posts)

33,518 to 38,833 per annum together with USS pension benefits

The normal expectation is that the successful applicant will be appointed to the minimum of the scale with annual increments on 1 October each year (subject to completing six months service).

The Athena SWAN Charter recognises work undertaken by institutions to advance gender equality. The College of Science is an Athena SWAN bronze award holder and is committed to addressing unequal gender representation across academia and professional and support functions.

The University is committed to supporting and promoting equality and diversity in all of its practices and activities. We aim to establish an inclusive environment and particularly welcome applications from diverse backgrounds.

Introduction

To deliver its sustainable top 30 ambition, Swansea University needs a workforce with the skills necessary to ensure that it can deliver excellence in research, teaching, learning, and the wider student experience, and be a powerhouse for the regional economy and internationally.

The College is seeking to appoint up to 2 Lecturers in Bioscience and would welcome applications from early career academics with a developing portfolio of research, particularly with expertise in ecological research aligned to the current departmental strengths. This person should have the potential to play a significant role in the future development of the Department. It is expected at least one position will be targeted at a candidate with a marine biology background.

Background

For more information about the Department of Biosciences, see our website www.swansea.ac.uk/biosci The College of Science is a cutting-edge research and teaching environment with state-of-the-art facilities across six departments encompassing Biosciences, Chemistry Computer Science, Geography, Mathematics and Physics.

The department has benefited from external funding totalling more than 6 million in the last year, allowing a suite of research officer appointments and further enhancement of excellent aquatic laboratory- and seagoing facilities, and has also built a unique new lab to visualize and analyse animal movement and behaviours as well as a laboratory to conduct molecular research. Recent departmental research highlights include; climate change impacts in marine environments, the molecular and biochemical intricacies of microbial communities, elucidating the behavioural ecology of animal movement and describing the ecosystem structure and the impacts of invasion.

To apply

Applicants are asked to provide a completed online application providing evidence against the essential criteria in the recruitment documentation. Applicants should also attach to the application 2 separate documents:

1. A Curriculum Vitae; 2. A statement detailing your aspirations to enhance teaching and the student experience.

Informal enquiries contact details and Further Information

For informal enquiries please contact the Head of College, Professor Matt Jones matt.jones@swansea.ac.uk or directly to the Head of Department, Professor Daniel Eastwood d.c.eastwood@swansea.ac.uk

This post will close at midnight 11 March 2018.

Applicants will find full job details together with the online application link: www.swansea.ac.uk/personnel/jobs/-details.php?nPostingIda08&nPostingTargetId012&id=QHUFK026203F The University is committed to supporting and promoting equality and diversity in all of its practices and activities. We aim to establish an inclusive environment and particularly welcome applications from diverse backgrounds.

Christopher B. Cunningham, Ph.D. Lecturer | Darlithydd 102B Margam Building | 102B Adeilad Margam Department of Biosciences | Adran Biowyddorau Swansea University | Prifysgol Abertawe Singleton Park Campus | Campws Parc Singleton SA2 8PP Swansea, Wales, UK | Abertawe, Cymru, UK O: +44.01792.513247

"Cunningham C.B." <c.b.cunningham@swansea.ac.uk>

TexasAMU PlantSystematics

Assistant Professor of Plant Systematics/Phylogenetics, Texas A&M University

The Department of Ecosystem Science and Management at Texas A&M University invites application for a full-time tenure-track faculty position at the rank of Assistant Professor in Plant Systematics/Phylogenetics. Applicants whose research integrates field and collection-based studies with state-of-the-art molecular approaches to address fundamental questions in systematics, evolution, or biogeography of vascular plants are encouraged to apply. Specific research areas of emphasis may include, but are not limited to: phylogenetics and genomics applied to organismal evolution; community phylogenetics, including research that complements existing ESSM Departmental strength in savanna ecosystems; systematics applied to conservation and management of plant communities and ecosystems.

Essential Duties: The position is approximately 50% research, 35% teaching and 15% service and herbarium administration. The new faculty member will establish a competitively funded research program in Plant Systematics/Phylogenetics. Teaching responsibilities may include undergraduate classes in Agrostology and Rangeland Plant Taxonomy, along with a graduate course in the candidate's area of expertise. The successful candidate is also expected to hold the position of Director of the S.M. Tracy Herbarium, which currently houses approximately 345,000 specimens including one of the largest collections of grasses in the region, and has ample representation from most vascular plant families. Applicants interested in continuing efforts to diversify and modernize the collection resources are encouraged to apply.

Required: - PhD in Plant Systematics or close equivalent by the time of hire with a researchemphasis as described above. - Evidence of potential to secure extramural funding and a demonstrated ability topublish research results in refereed journals. - The appointee will also show evidence of ability or potential to effectively teach and mentor undergraduate and graduate students.

Desired: - Demonstrated interest and ability to teach Agrostology and Rangeland Plant Taxonomy. - Postdoctoral or similar experience. - A successful record of extramural funding for research. - Experience working with herbarium collections. - Experience and interest in collaborations addressing contemporary research questionsin savannas. - Familiarity with the land grant mission.

A competitive remuneration package with excellent benefits will be offered commensurate with the appointee's capabilities, qualifications, and experience.

Resources: Texas A&M University (TAMU) is a public, land-grant institution with access to excellent resources including Genomics and High Performance Computing facilities, core laboratories, field stations, as well as opportunities to interact and collaborate with a broad range of TAMU System researchers throughout the state of Texas. The Department of Ecosystem Science and Management (ESSM) is an interdisciplinary faculty committed to creating and synthesizing new knowledge on how ecosystems and their components persist, function, assemble, process nutrients and water, evolve, and respond to environmental change. ESSM relies on science- based problem solving to guide departmental education, research, and extension programs. http://essm.tamu.edu/ Application Process: For full consideration, applications should be submitted by February 15, 2018. The position will remain open until finalists have been selected. Applicants should submit a cover letter addressing each of the required/desired qualifications (up to 3 pages), a curriculum vitae, unofficial transcripts, names and contact information for three references, and statements on Teaching and Research relative to the position (up to 2 pages each). Individuals should apply at: https://tamus.wd1.myworkdayjobs.com/-AgriLife_Research_External/job/College-Station-TAMU/Assistant-Professor_R-000843-1 For inquiries please contact Dr. Carol Loopstra, c-loopstra@tamu.edu . The Texas A&M System is an Equal Opportunity/Affirmative Action/Veterans/ Disability Employer committed to diversity. The college is especially interested in qualified candidates who can contribute, through their research, teaching, and/or service, to the diversity and excellence of the academic community. Women, minorities, individuals with disabilities, and veterans are encouraged to appl

ccasola@tamu.edu

TrinityU Texas DistinguishedProfessorBiology

The Biology Department of Trinity University invites applications for the Brackenridge Distinguished Professorship in Biology. We seek a candidate with an established record of scholarship and teaching commensurate with an endowed professorship. The successful candidate is expected to be a leading scholar in any area of the biological sciences who will continue to pursue a substantive research agenda and mentor undergraduate researchers. In addition to research, the successful candidate will teach introductory and upper division undergraduate courses and will demonstrate a commitment to innovation in course development. The candidate will also have the opportunity to provide programmatic vision and leadership in one of the following interdisciplinary areas: environmental studies, global health, or neuroscience. Selection of candidates will involve consideration of their ability to complement and extend the expertise of the department in research and teaching, and to engage with outreach and service initiatives with the greater community. In addition, we seek candidates who can broaden participation among members of underrepresented groups.

Trinity University is a top-ranked, small, private liberal arts and sciences university that values high quality teaching and supports high impact undergraduate research. The Department of Biology is located in Trinity's state-of-the-art Center for Sciences and Innovation, consists of 13 highly collaborative faculty. The department serves majors in Biology, Neuroscience, Biochemistry and Molecular Biology, and Environmental Studies. Trinity is located in San Antonio, a large, vibrant, cosmopolitan city located in south central Texas. The city's cost of living is relatively low for a major metropolitan area. More information on the city of San Antonio can be found at http://visitsanantonio.com/ . Application Deadline: Applications should be submitted as soon as possible. The search will remain open until the position has been filled. Applications submitted on or before April 6th, 2018, will be given full consideration.

How to apply: Applicants should electronically submit a cover letter, curriculum vitae, statement of teaching philosophy, research plan, and names and contact information of three references to the contact listed below.

Contact: Prof. Jonathan King Biology@trinity.edu Department of Biology One Trinity Place San Antonio, Texas 78212 –

Michele A. Johnson, Ph.D.

Associate Professor Trinity University Department of Biology One Trinity Place San Antonio, TX 78212 michele.johnson@trinity.edu office phone: 210-999-8918 lab phone: 210-999-8914 twitter: @LizardMichele

Michele Johnson <mjohnso9@trinity.edu>

TrinityU Texas VisitingProfessor

Trinity University Department of Biology invites applications for a full-time, Visiting Assistant Professor to begin in August 2018. Candidates must possess a Ph.D. Responsibilities include teaching in the Biology major curricular sequence and departmental service.

Applicants with the ability to teach introductory and advanced undergraduate lecture and lab courses on topics such as Ecology and/or Evolution will be highly competitive.

Trinity University is a top-ranked, small, private liberal arts and sciences university that values high quality undergraduate teaching and supports high impact undergraduate research. The Department of Biology is located in Trinity's state-of-the-art Center for Sciences and Innovation, has 13 highly collaborative faculty and serves majors in Biology, Neuroscience, Biochemistry and Molecular Biology, and Environmental Studies. Trinity is located in San Antonio, a large, vibrant, cosmopolitan city located in south central Texas. San Antonio's cost of living is relatively low for a major metropolitan area. More information on the city of San Antonio can be found at http://visitsanantonio.com/ . Application Deadline: Review of applications will begin April 6th, 2018 and continue to position is filled.

How to apply: Applicants should electronically submit a cover letter, curriculum vitae, statement of teaching philosophy and contact information for three references to the contact listed below.

Contact: Prof. Jonathan King Biology@trinity.edu Chair of Search Committee Department of Biology One Trinity Place San Antonio, Texas 78212 –

Michele A. Johnson, Ph.D.

Associate Professor Trinity University Department of Biology One Trinity Place San Antonio, TX 78212 michele.johnson@trinity.edu office phone: 210-999-8918 lab phone: 210-999-8914 twitter: @LizardMichele

Michele Johnson <mjohnso9@trinity.edu>

UAmsterdam EvolCommunicationMoths DeadlineExt

The application deadline of the job announcement below has been extended to 4 March.

WHERE: University of Amsterdam, Institute of Biodiversity and Ecosystem Dynamics (IBED), Department Evolutionary and Population Biology

WHAT: Assistant professor evolutionary chemical ecology

We are looking for a dynamic researcher (F/M) with a specific interest in the evolution of sexual communication in moths. We are especially interested in candidates who can combine behavioral analyses with genetic and molecular analyses, and are keen to develop both fundamental and applied research lines. The candidate will contribute to teaching courses at BSc and MSc level for Biology, Psychobiology and Future Planet Study students.

Requirements

* PhD in the field of evolutionary chemical ecology and entomology, preferably experience with research in Lepidoptera; * experience with molecular biological techniques, preferably also with genetic analyses; * experience with electrophysiological techniques, such as EAGs, wind tunnel bioassays, pheromone extractions and analyses; * interest to combine laboratory and field studies with genetic and chemical analyses * skills in experimental design and statistical analysis; * proficiency in scientific writing and communication; * some teaching and outreach experience; * international experience as a PhD candidate and/or postdoctoral researcher.

For more information: http://www.uva.nl/en/content/vacancies/2018/01/18-046-assistant-professor-in-evolutionary-chemical-ecology-tenure-track.html Astrid T. Groot Professor Population and Evolutionary Biology Institute for Biodiversity and Ecosystem Dynamics (IBED) University of Amsterdam Science Park 904 1098 XH Amsterdam +31 20 525 5400 a.t.groot@uva.nl http://www.uva.nl/profiel/g/r/a.t.groot/a.t.groot.html Astrid Groot <a.t.groot@uva.nl>

UAmsterdam EvolutionMothCommunication

WHERE: University of Amsterdam, Institute of Biodiversity and Ecosystem Dynamics (IBED), Department Evolutionary and Population Biology

WHAT: Assistant professor evolutionary chemical ecology

We are looking for a dynamic researcher (F/M) with a specific interest in the evolution of sexual communication in moths. We are especially interested in candidates who can combine behavioral analyses with genetic and molecular analyses, and are keen to develop both fundamental and applied research lines. The candidate will contribute to teaching courses at BSc and MSc level for Biology, Psychobiology and Future Planet Study students.

Requirements

* PhD in the field of evolutionary chemical ecology and entomology, preferably experience with research in Lepidoptera; * experience with molecular biological techniques, preferably also with genetic analyses; * experience with electrophysiological techniques, such as EAGs, wind tunnel bioassays, pheromone extractions and analyses; * interest to combine laboratory and field studies with genetic and chemical analyses * skills in experimental design and statistical analysis; * proficiency in scientific writing and communication; * some teaching and outreach experience; * international experience as a PhD candidate and/or postdoctoral researcher.

For more information: http://www.uva.nl/en/content/vacancies/2018/01/18-046-assistant-professor-in-evolutionary-chemical-ecology-tenure-track.html – Astrid T. Groot Professor Population and Evolutionary Biology Institute for Biodiversity and Ecosystem Dynamics (IBED) University of Amsterdam Science Park 904 1098 XH Amsterdam +31 20 525 5400 a.t.groot@uva.nl http://www.uva.nl/profiel/g/r/a.t.groot/a.t.groot.html Astrid Groot <a.t.groot@uva.nl>

UCaliforniaSantaBarbara Temporary TeachingEvolution

The Department of Ecology, Evolution and Marine Biology (EEMB; www.eemb.ucsb.edu) at the University of California, Santa Barbara invites applications for a Temporary Academic Coordinator position, at the rank of Academic Coordinator I.

The Academic Coordinator assists in administering course activities in the Introductory Biology Program consisting of a laboratory course and one or two lecture courses each quarter. These courses have enrollments of approximately 800-1100 students each quarter.

The Academic Coordinator will provide logistical assistance to the operation of both lecture and lab courses. This includes scheduling of lectures, exams and laboratories, production of syllabi, maintaining the course web sites, and honors sections. Additionally, the Coordinator will work collaboratively with the Program Manager in scoring of lecture and laboratory exams, and distribution of teaching materials to faculty. The Coordinator will be included in lab planning, assisting with weekly training sessions, the preparation and maintenance of supporting documentation of all quarterly lab expenditures, manage inventory of all equipment and lab consumables, and coordinate repair and maintenance service for all lab equipment.

The Coordinator will work closely with and report to, the Academic Coordinator II but must be capable of all duties with a minimum amount of supervision.

Candidates should be able to demonstrate the ability to integrate material from different parts of the Introductory Biology course(s) and understand how they relate to one another by providing evidence of previously managing an instructional program in the biological sciences. Candidates with prior experience coordinating and managing large (several hundred students) Lecture / Laboratory courses in biology are preferred.

The department is especially interested in candidates who can contribute to the diversity and excellence of the academic community through research, teaching and service.

This position requires a Bachelor's degree. This position will start as soon as possible and will be for an initial period of one year with the possibility of an additional year. Electronic applications (including a cover letter, CV and contact info only of 3 references) should be submitted to: https://recruit.ap.ucsb.edu/apply/JPF01190 . For Full consideration, please apply by 02/16/18. Thereafter, position will be open until filled.

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

Alice Trang Nguyen (alice.nguyen@lifesci.ucsb.edu)

alice.nguyen@lifesci.ucsb.edu

UCentralFlorida Bioinformatics

The University of Central Florida (UCF) recently established several interdisciplinary clusters to strengthen its academic and research missions. The Genomics and Bioinformatics Cluster (GBC) (http://www.ucf.edu/-research/genomics) is one of these clusters, and it was established with a goal to develop a nationally and internationally recognized program in the broad area of genomics and computation. As part of the GBC, we are currently seeking to hire a tenure-earning Assistant Professor in the area of Bioinformatics and Computational Biology. Candidates must have a strong research publication record and demonstrated independent research, with either existing research funding, or strong potential to initiate and obtain funding for their research program. The GBC emphasizes interdisciplinary research in genomics that covers at least two disciplines among biology, biomedical sciences, and computer science. In particular, the GBC is looking to expand research programs in genomics that are enabled by next-generation sequencing technologies and that address one or more areas among molecular evolution, biodiversity, microbiome research (environmental and plant/animal health), biological model systems, infectious diseases, translational applications for cancer, computational biology, systems biology, machine learning and data mining. Strong candidates in other areas of genomics will also be considered.

The GBC members will be expected to strengthen their individual tenure homes as well as the cluster. The list of host departments includes Burnett School of Biomedical Sciences (College of Medicine), Biology (College of Sciences), and Computer Science (College of Engineering and Computer Science). A candidate can be hosted in one of the three departments listed above. A candidate may also be jointly appointed among these as appropriate to qualifications and interest. All GBC faculty members (and their students) will be housed jointly to facilitate collaboration.

For more details, please see https://www.jobswithucf.com/postings/52262 Eric Hoffman Associate Professor and Undergraduate Program Coordinator UCF Department of Biology

"Eric.Hoffman@ucf.edu" <Eric.Hoffman@ucf.edu>

ULeuven CichlidSpeciation

Research Scientist in Evolutionary Genomics: Cichlid-Speciation

The Royal Belgian Institute of Natural Sciences

Evolutionary and Behavioural Genomics of Cichlid Speciation

Context :

Since Darwins' "The Origin of Species" there has been a continued interest to gain insight in the speciation process. Initially, theories on speciation were mostly narrative and focussed on the geographic modes of speciation, while more recent work investigated the importance of sexual selection or whether speciation rates can be triggered by environmental changes. All these questions have been addressed in the cichlid fishes from the Great African lakes that are often cited as the ultimate animal models to investigate adaptive radiation and speciation.

To date, recently developed techniques that allow exploring genomic evolutionary issues in cichlids have for the most part been used to link genes with the observed phenotypic changes that are so characteristic in the African cichlid species flocks. In contrast, we propose to make use of the opportunities offered by the availability of these novel techniques to investigate the genetic basis of the speciation process itself. Therefore, our two main objectives are to characterize the genomic differentiation that drives the speciation process, and to verify whether/and to what extent the same genomic changes are involved in to maintain the ???????integrity' of the gene pools of the resulting sister species.

GENBAS: a BRAIN.be project: 'Genetic Basis of Speciation' http://genbas.be/ Tasks :

- Assistance of the GENBAS team [RBINS (Brussels), RMCA (Tervuren), University of Leuven and University of Liege) in NGS data analyses (genotyping-by-sequencing and RNAseq data)

- Applying phylogenomic, phylogeographic and population genomic data analysis to resolve species boundaries and connectivity questions

- Identification of divergent genomic regions within and between populations/species

- Linking adaptive genomic regions with gene expression data, potentially linked to speciation/mate choice/sexual selection genes

Profile :

- Diploma: Master in Bioinformatics, Biology or Bioengineering with a strong interest in evolutionary genomics (phylogenomics or population genomics)

- Technical skills: Experience with NGS data analysis (raw data, VCF genotypes), excellent knowledge of R, familiar with scripting in Python/Perl ....

- General skills: eager to learn, team player, good knowledge of English

We offer :

- A fixed-term contract of 12 months with the possibility of extension (but application to National Research Fund mandatory)

- Salary according the standard scale for an assistant (SW1);

- Free public transport;

- A dynamic and interesting working environment

- Starting date: March 2018

How to apply?

E-mail your motivation letter, 2 references and CV before 15/02/2018

to : Erik Verheyen via: erik.verheyen@naturalsciences.be

Gregory Maes, Ph.D.

University of Leuven (KU Leuven)

Laboratory for Cytogenetics and Genome Research

Centre for Human Genetics | Genomics Core

O&N I Herestraat 49 - box 602

UZ Leuven

B-3000 Leuven

Belgium

Phone: +32 (0)16 37 25 22

E-mail: gregory.maes@kuleuven.be

Logo_GC

Gregory Maes <gregory.maes@kuleuven.be>

UMichigan MuseumRegistrar

The University of Michigan is seeking applicants for a full-time museums registrar position working with the collections of the University of Michigan Museum of Zoology and Herbarium.

The position is posted until February 13. The link to the posting and the job description can be found here:

http://careers.umich.edu/job_detail/152910/-museum_registrar_intermediate "cwthomp@umich.edu" <cwthomp@umich.edu>

UMichigan MuseumRegistrar ExtendedDeadline

The deadline for applications for the full-time museums registrar position working with the collections of the University of Michigan Museum of Zoology and Herbarium has been extended until 11 March.

The link to the posting and the job description can be found here:

http://careers.umich.edu/job_detail/152910/-museum_registrar_intermediate "Thompson, Cody" <cwthomp@umich.edu>

UNewHampshire InsectCollectionManager

Job Title: Collection Manager, University of New Hampshire Insect Collection, University of New Hampshire, Durham, NH

*UNHC background: *The College of Life Science and Agriculture maintains the University of New Hampshire Insect Collection, which contains over 700,000 specimens of insects and other arthropods. The collection is a preserved, documented, and curated assemblage that is important to a wide array of research and teaching activities. The presence and growth of the collection at UNH is important to the University, New Hampshire and New England because it is a readily available local resource of identified voucher specimens for the region, as well as being used in research at the national and international levels.

The University of New Hampshire Insect Collection is seeking to hire a Collection Manager in our Department of Biological Sciences. The start date for the position is July 1, 2018. Application deadline is March 9, 2018.

The Collection Manager is responsible for the maintenance and organization of the collection. This involves oversight and documentation of all collection-related procedures, including filing, labeling, and preparation of specimens. It also requires strong management skills in the leadership of a team of entomology collection staff. The Collection Manager is expected to maintain working knowledge modern techniques in systematic biology, database management, entomological collections maintenance, and fieldwork.

The Collection Manager in conjunction with the curators will develop collection improvement grants. The Collection Manager reports to the Curator, works closely with students, and supervises all technical entomology collection staff and volunteers. The Collection Manager will have the opportunity to conduct research to a limited extent, and will be expected to teach one undergraduate course each year.

Minimum qualifications include a Master's or PhD in Biology (with an emphasis in Entomology and experience with Hymenoptera is desirable), four years of experience in curatorial or closely related work required (or an equivalent combination of education and experience), and prior supervisory experience.

*About **UNH and COLSA*: The University of New Hampshire, located in Durham, is a Research Land, Sea and Space Grant University that has been recognized both nationally and internationally for research excellence and a commitment to sustainability. The College of Life Sciences and Agriculture is newly reorganized into four interacting academic units and includes the state's Agricultural Experiment Station.

The University of New Hampshire is an Equal Opportunity/Equal Access/Affirmative Action institution. Application by members of all underrepresented groups is encouraged.

Application Process: Information, including detailed position descriptions and complete application information is available at https://jobs.usnh.edu/postings/26098. All applicants will be required to apply online at http://jobs.usnh.edu. The online application will ask for a letter of application, current vitae and names, addresses, email and phone number of three professional references. The candidate will be notified before any references are contacted. Review of applications will begin on March 9, 2018 and will continue until the position is filled. The University actively seeks excellence through diversity among its administrators, faculty, staff and students and prohibits discrimination on the basis of race, color, religion, sex, age, national origin, sexual orientation, gender identity or expression, disability, veteran status, or marital status.

Sandra Rehan, Assistant Professor Department of Biological Sciences University of New Hampshire Durham, NH, USA 03824 (603) 862-5310 www.rehanlab.com sandra.rehan@gmail.com

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UNorthCarolina Charlotte TeachingBioinformatics

The Department of Bioinformatics and Genomics at the University of North Carolina at Charlotte (http://bioinformatics.uncc.edu/) is seeking candidates for a full-time, 9-month non-tenure-track Teaching Assistant Professor position. The appointment will be for three years, and is eligible for renewal. A Ph.D. in Bioinformatics, Computational Biology, Computer Science (CS) or a related field is required.

Anticipated start is Fall 2018. Applications must be made electronically at https://jobs.uncc.edu (Position No. 001076) and must include vita, teaching statement with evidence of teaching excellence, and complete contact information for three references.

As an EOE/AA employer and an ADVANCE Institution that strives to create an academic climate in which the dignity of all individuals is respected and maintained, the University of North Carolina at Charlotte encourages applications from all underrepresented groups.

rebekah.rogers@gmail.com

UNottingham EvolutionaryGenomics

Dear Colleagues

The School of Life Sciences at the University of Nottingham is advertising for an Associate Professor in Evolutionary Genomics. Please see: http://www.jobs.ac.uk/job/BHI813/associate-professor-of-evolutionary-genomics/ Best wishes Andrew MacColl

Official text follows:

Associate Professor of Evolutionary Genomics University of Nottingham - Life Sciences Location: Nottingham Salary: 50,618 to 60,410 per annum Hours: Full Time Contract Type: Permanent Placed on: 29th January 2018 Closes: 11th March 2018 Job Ref: MED464417 Location: University Park Salary: 50,618 to 60,410 per annum, depending on skills and experience. Salary progression beyond this scale is subject to performance.

As part of its ambitious Research Strategy the University is making a significant investment in its research capacity and capability through six multi-million pound cross-disciplinary Beacons of Excellence (Beacons). Beacons will represent a critical mass, undertaking a coherent and integrated portfolio of research, doctoral training and knowledge exchange activities in a well-defined research area, carrying out discovery and challenge-led research and related activities, with an objective to be demonstrably amongst the best in the world. This position will be funded by the Future Food Beacon which has a mission to deliver world class research to help address the challenge of providing sufficient quantities of nutritious and palatable food to a growing world population within a changing environment“.

At the University of Nottingham, our researchers have expertise across the food chain - from soil to molecule to meal to deliver sustainable solutions to the global food challenges; such as hidden hunger, less diverse diets, naturally low nutrients in our staple crops and an increasing reliance on over-processed foods mean that more than a quarter of the world population are not getting the goodness they need from the food they eat.

In the face of climate change we must develop new, resilient crops with increased yields to feed the additional two billion people expected by 2050.

The Beacon is to proactively engage with the research ecosystem within and across Faculties, in particular Research Centres and Institutes. The Beacon will have clearly identified objectives against which they will be required to deliver in order to release funding to enable ongoing delivery. The role holder will advance the discipline of Evolutionary Genomics through research, knowledge transfer and teaching. The role holder will also provide academic leadership to colleagues, research staff and students.

Candidates should hold a Degree and a PhD or equivalent in plant evolutionary genomics, genetics, or a closely related field, have a strong publication record and International scientific reputation evidenced through a track record of high quality publications and demonstrated success in obtaining sources of funding, Please identify 4 papers you consider your best.

This permanent role is available immediately, the first 5 years will focus on performing high quality research within the Beacon. To recognise this focus the first 5 years of the role will be 80% original research within the Beacon, 20% contribution to other activities in the School of Life Sciences.

The School of Life Sciences holds an Athena Silver SWAN Award, in recognition of our commitment to supporting and advancing women's careers in the life sciences (STEMM). You can read more about this initiative at http://www.nottingham.ac.uk/life-sciences/documents/athena-swan-silver-award.pdf Informal enquiries may be addressed to Professor David Salt (David.Salt@nottingham.ac.uk) or Professor Victoria Chapman (victoria.chapman@nottingham.ac.uk). Please note that applications sent directly to this email address will not be accepted.

Further details: http://www.jobs.ac.uk/job/BHI813/-associate-professor-of-evolutionary-genomics/ The University of Nottingham is an equal opportunities employer and welcomes applications from all sections of the community.

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

UofGuelph ComputationalBiolBioinformatics

Dear colleagues,

We are currently searching for a tenure-track Assistant Professor in the areas of Computational Biology/Bioinformatics/Genomics to join the Department of Integrative Biology at the University of Guelph (https:/-/www.uoguelph.ca/ib/).

Further details about the position and application process can be found here: http://www.uoguelph.ca/-facultyjobs/postings/ad17-80.shtml Applications will be considered beginning on Feb. 19, 2018.

The University of Guelph is a research-intensive institution, with major strengths in the Biological, Environmental and Agricultural Sciences, and ranks among the top agri-food universities in the world. The position is part of a cluster hire to support a University-wide research program to increase exponentially our ability to leverage big data for the benefit of food production and biodiversity at three scales of research and innovation: global, landscape, and microscale (https://-arrellfoodinstitute.ca/food-from-thought/).

Thank you for your consideration,

John Fryxell (Chair of the search committee) Sarah Adamowicz Nick Bernier Moira Ferguson Andreas Heyland Hafiz Maherali

Sarah Adamowicz <sadamowi@uoguelph.ca>

UOregon LabManager

The Singh lab at the University of Oregon invites applications for a lab manager. Current work in the Singh lab is aimed is at determining the individual and joint contributions of genetic and environmental factors to recombination rate variation and to assess the impact of that variation for adaptation and genome evolution. A competitive applicant would be someone who is self-motivated and has excellent organizational and communication skills. The lab manager will be required to oversee both the animal care and molecular aspects of the lab on a daily basis and to participate in a variety of new and ongoing research.

For more information and to apply, visit http://careers.uoregon.edu/cw/en-us/job/521845/research-assistant-or-associate-lab-manager < http://careers.uoregon.edu/cw/en-us/job/521721/postdoctoral-research-scholar >

Nadia Singh <nsingh@uoregon.edu>

UPretoria PlantTaxonomySystematics

LECTURER / SENIOR LECTURER / ASSOCIATE PROFESSOR: PLANT TAXONOMY / SYSTEMATICS AND HERBARIUM CURATOR (ONE POST)

Faculty of Natural and Agricultural Sciences, Department of Plant and Soil Sciences, University of Pretoria

LINK: http://upnet.up.ac.za/psp/career/EMPLOYEE/HRMS/c/HRS_HRAM.HRS_APP_SCHJOB.GBL?Page=HRS_APP_SCHJOB&Action=U&FOCUS=Applicant&SiteId=1 In pursuit of the ideals of excellence and diversity, the University of Pretoria wishes to invite applications for the following vacancy.

The University of Pretoria's commitment to quality makes us one of the top research Universities in the country and gives us a competitive advantage in international science and technology development.

RESPONSIBILITIES: The incumbent will be responsible for: - Undergraduate and honours level teaching (e.g. second year contributions to BOT 251 Flora and Vegetation of South Africa; BOT 366 Plant Diversity; BSc honours (4th year) level courses on systematics and taxonomy);

- The curation of the Schweickerdt Herbarium (PRU; 110,000 plant specimens), financial management and management of associated support staff;

- Supervising postgraduate students;

- Acquiring research funding;

- Conducting and leading research in plant evolution, systematics, taxonomy and biogeography/floristics that build upon and complement departmental and institutional strengths in plant systematics and biodiversity;

- Initiating community engagement projects, and engaging in professional development activities.

MINIMUM REQUIREMENTS: - A PhD degree in Plant Taxonomy/Systematics;

- Expertise and experience in herbarium curation; - Good knowledge of the African and Southern African flora, and expertise in at least one large/important African plant group/family; - A track record of publications in the relevant field in ISI accredited journals; - Experience in most of the following: 'Traditional' taxonomy (including nomenclature), molecular systematics, phylogenetics, phytogeography/biogeography, plant anatomy, cytology and morphology; - Driver's license.

REQUIRED COMPETENCIES (SKILLS, KNOWLEDGE AND BEHAVIOURAL ATTRIBUTES):

- Sufficient knowledge of the required subjects to lecture and present practicals in plant evolution, taxonomy, identification, diversity, and biogeography to undergraduate and honours classes; - Documented proof of own research outputs in plant evolution, taxonomy, systematics, biogeography or a related field; - Ability to seek out funding opportunities and successfully apply for local and international funding; - Must be able to plan and participate in field trips and undertake field work in southern Africa; - Appropriate language and communication skills, both written and verbal.

Applicants are requested to apply online at www.up.ac.za, and follow the link: Careers@UP.

CLOSING DATE: 20 February 2018

ENQUIRIES: Ms Rene Fryer, Tel: (012) 420 3770, or Prof Nigel Barker, Tel: (012) 420 2593

Gary Stafford <garyistafford@gmail.com>

URhodeIsland WildlifeGenetics

Research Associate I (Posting Number SF00569) position at the University of Rhode Island Perform independent research work at the Wildlife Genetics & Ecology Laboratory at the University of Rhode Island. Conduct conservation genetic analyses on non-invasively collected samples from lagomorphs.

Organize, coordinate, and supervise support staff, including volunteers and students, engaged on the projects.

This position is limited to 02/16/2019 with extension contingent on funding. Visit the URI jobs website at:

http://jobs.uri.edu/postings/3163 to apply and view complete details.

This is an open until filled search. First consideration will be given to applications received by March 3, 2018. Second consideration may be given to applications received by March 23, 2018. Applications received subsequent to second consideration date (March 23, 2018) may not be given full consideration. The University of Rhode Island is an AA/EEOD employer and values diversity.

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T.J. McGreevy Jr., Ph.D. Research Assistant Professor Director, Wildlife Genetics & Ecology Laboratory Department of Natural Resources Science Room 113 Coastal Institute in Kingston 1 Greenhouse Road University of Rhode Island Kingston, RI 02881 tjmcg@.uri.edu office: (401) 874-4040 cell: (401) 481-6151 lab: (401) 874-5812

Thomas McGreevy Jr <tjmcg@uri.edu>

UTulsa EvolutionaryGenomics

ASSISTANT PROFESSOR ? TENURE TRACK EVOLUTIONARY GENOMICS, DEPT. OF BIOLOGICAL SCIENCE COLLEGE OF ENGINEERING AND NATURAL SCIENCES

The Department of Biological Science at The University of Tulsa invites applications for a tenure-track Assistant Professor position in Evolutionary Genomics beginning the fall of 2018. Applicants are expected to have demonstrated interests and expertise integrating the genomics, transcriptomics, proteomics, and/or venomics of non-model vertebrate organisms.

We are particularly interested in creative and interactive individuals whose research integrates field or collection-based studies with next-generation molecular approaches to address fundamental questions relating to the evolution of novel phenotypes, rapid adaptation, and gene-expression driven differentiation.

Applicants must have a Ph.D., post-doctoral experience, and a substantial record of research excellence. The successful applicant will be expected to establish a vigorous extramurally funded research program involving both undergraduate and graduate students. Teaching responsibilities will include appropriate upper-level/graduate courses in genomics and bioinformatics, in addition to courses in his or her area of expertise. Applications are especially welcomed from candidates that can contribute to the teaching of Tropical Ecology.

The Faculty of Biological Science is in the College of Engineering and Natural Sciences of The University of Tulsa (www.utulsa.edu) and offers BS, MS and PhD degrees. https://engineering.utulsa.edu/academics/-biological-science/ At present, there are 13 full-time faculty members, 22 MS/PhD students, and approximately 135 undergraduate Biology majors. The department houses a complete genomics core facility including an Illumina MiSeq, Covaris sonicator, ABI capillary sequencer, StepOnePlus real-time PCR system, Agilent Bioanalyzer, and both Nanodrop and Qubit fluorometric quantifiers.

APPLICATION INFORMATION: The review of applications will begin March 2, 2018 and continue until the position is filled.

The University of Tulsa seeks to recruit and retain talented students, faculty and staff from diverse backgrounds. The University of Tulsa is an affirmative action/equal opportunity employer and encourages qualified candidates across all group demographics to apply. The University does not discriminate on the basis of personal status or group characteristic including, but not limited to race, color, religion, national or ethnic origin, age, sex, disability, veteran status, sexual orientation, gender identity or expression, genetic information, ancestry, or marital status.

Interested parties should submit a cover letter, current curriculum vitae, statements of research and teaching interests (max. two pages each), and names and complete contact information for three references.

Application information should be submitted electronically to Evolutionary Genomics Search Committee Chair, Dr. Harrington Wells at: harrington-wells@utulsa.edu

The University of Tulsa is an Equal Opportunity Employer Disabled/ Veteran.

Ronald Bonett <ron-bonett@utulsa.edu>

UVienna TheoreticalEvolutionaryBiology

Open to new ideas, since 1365. As a research university with high international visibility and a wide range of degree programmes, the University of Vienna is committed to basic research open to application and research-led teaching, as well as to career development of young researchers and to the dialogue with economy and society. That way, the University of Vienna contributes to the education of future generations and to the society'Âs ability to innovate.

At the Faculty of Life Sciences of the University of Vienna, the position of a:

University Professor of Theoretical Evolutionary Biology

is to be filled. (full time, permanent position; in case of a first time appointment to a professorship, the appointment may be initially limited 'V with an extension option)

The advertised professorship shall cover the advancement and application of theoretical approaches 'V including conceptual, mathematical, and statistical analysis 'V to different levels of organismal complexity. The candidate should have a background both in biology and a theoretical or computational discipline, with an emphasis on interdisciplinary and integrative research. Preference is given to approaches to understand biological systems from the molecular to the inter-organismal level, encompassing developmental to evolutionary time scales. To foster and complement cooperation among the research groups, the candidate's research should link to animal development, behavior or morphology, in an evolutionary context. The candidate should be enthusiastic to teach a theoretical discipline (e.g. mathematics, statistics, systems theory) and its application to evolutionary and organismal biology.

For further details, see:

http://personalwesen.univie.ac.at/en/jobs-recruiting/-professorships/detail-page/news/theoretical-evolutionary-biology/ nick.barton@ist.ac.at

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WesternU Canada EvolutionaryNeurobiology

WesternU_Canada.InvertebrateNeurobiology

The Faculty of Science at Western University invites applications for a Tier 2 Canada Research Chair (CRC) in Invertebrate Neurobiology at the rank of Assistant Professor (Probationary Tenure-track), or Associate Professor (Probationary Tenure-track or Tenured). The successful candidate will have a research program that investigates invertebrate neurophysiology from an evolutionary, genetic, biochemical, or purely physiological perspective. Rank and salary will be commensurate with educational qualifications and experience. The starting date will be July 1, 2018 or as negotiated. The successful candidate will be expected to apply for a Tier 2 Canada Research Chair in the first available competition after their appointment.

Candidates should submit a curriculum vitae, two-page research plan, one page teaching and mentoring statement including a description of experiences and contact details of at least three referees to:

Professor Mark Bernards, Chair, Department of Biology, Faculty of Science Western University London, Ontario N6A 5B7, Canada Email: hrbio@uwo.ca

For more information and details, please see: https:/-/www.uwo.ca/facultyrelations/careers/Science-Tier2-CRC-Biology_Invert_Neurobiology_2018.pdf

Amanda Moehring <amoehrin@uwo.ca>

Other

BotanyConferences UndergradTravelAwards

Subject:— Undergraduate Travel Awards:— Enhancing Diversity at the Botanical Society of America Conferences

PLANTS Grants Preparing Leaders and Nurturing Tomorrow's Scientists Undergraduate Travel Awards:— Enhancing Diversity at the Botanical Society of America Conferences The PLANTS program (Preparing Leaders and Nurturing Tomorrow's Scientists: Increasing the diversity of plant scientists) will fund up to 12 talented and diverse undergraduates to attend the BOTANY 2018 meeting on July 21-25, 2018 in Rochester, Minnesota. Topics range across all aspects of botany including ecology, conservation, biodiversity, plant genomics, evolution, plant systematics, ethnobotany, and botanical education. There are also a number of social functions, specifically targeted at students for networking and fun. The meetings are a great way for undergraduates to understand the breadth of botanical research and education, to meet undergraduate and graduate students with similar interests, and to network with professionals in their area of interest. Students will receive mentoring from graduate students, postdocs and faculty/professionals, and participate in networking events including the Diversity Luncheon and career-oriented activities.— The program covers the normal costs of travel, registration, food and lodging at the meeting. Participants are required to attend the entire meeting, including several scientific talks per day with a mentor, as well as certain professional development and networking activities.—— An overview of the scientific conference is available at: botanyconference.org APPLICATIONS: Applications are due by MARCH 15, 2018 and include completion of the online form (including a statement of interest, letter of recommendation, and unofficial transcripts). Applications are welcome from undergraduates from the US including Puerto Rico (we are unable to accept applications from international students) who have interest in plant sciences; the admissions goal is to increase the diversity of students interested in the plant sciences. The application form is located online at http://botany.org/Awards/F_PLANTS.php . Funding is provided by the National Science Foundation and Botanical Society of America,

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

DEADLINE: extended to March 15, 2018

– Heather Cacanindin Interim Executive Director Botanical Society of America | Society for the Study of Evolution | Society for Economic Botany www.botany.org www.amjbot.org http://www.bioone.org/loi/apps www.plantingscience.org www.evolutionsociety.org www.econbot.org 314-577-9554

Heather Cacanindin <hcacanindin@botany.org>

FundingForEvolBotany SymposiaWorkshops

Funding available!

The deadline to apply for funds to run a New Phytologist Symposium is approaching. More information, including application forms, is available here: https://www.newphytologist.org/news/view/145 The deadline for Symposium proposals is 28 February 2018.

Workshop proposals are welcomed throughout the year.

With best wishes, and apologies for cross-posting, Mike

Dr Mike Whitfield Development Coordinator, New Phytologist

New Phytologist Central Office, Bailrigg House, Lancaster University, Lancaster, LA1 4YE, UK Tel: + 44 1524 592839; Fax: + 44 1524 594696 newphytologist.org < http://www.newphytologist.org/ > Twitter: @NewPhyt < https://twitter.com/newphyt > Facebook: fb.com/NewPhytologist < https://www.facebook.com/NewPhytologist >

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Funding available! < https://www.newphytologist.org/news/view/145 > Apply for Symposium funding now. Deadline 28 February.

New Phytologist Symposia in 2018 < https://newphytologist.org/symposia > Plant sciences for the future | The biology of wood: from cell to trees

“Whitfield, Mike” <m.whitfield@lancaster.ac.uk>

Life SpecialIssue Phyloinformatics

The open access journal “Life - Origins and Evolution of Life” (http://www.mdpi.com/journal/life) is pleased to invite submissions to a new special issue, “Open Science Phyloinformatics: Resources, Methods, and Analyses.” (< http://www.mdpi.com/journal/life/special_issues/phyloinformatics >)

This special issue, with a target submission deadline of 28 February 2018, will be guest edited by William H Piel and Rutger Vos.

The purpose of this special issue is to publish results from phylogenetic and phylogenomic analyses. Since phylogenetics is becoming increasingly complex and data-intensive, we are particularly interested in papers that demonstrate good standards for open access science, sharing, and data integration (e.g. sharing digital results through on-line repositories, sharing data pipeline scripts, sharing sets of pHMMs for ortholog selection, etc.).

In addition to publishing “Tree of Life” and phylogenetic findings, we also welcome papers that describe digital data resources, new computational methods, and big data analysis methods in phyloinformatics.

Dr. William H Piel Dr. Rutger Vos Guest Editors

“William H. Piel” <william.piel@yale-nus.edu.sg>
“William H. Piel” <william.piel@yale-nus.edu.sg>

LongMicrosatellites

Hello all- I’m trying to gather some information regarding very long ’microsatellite’ repeats. I’ve been working on a plant pathogenic fungus that has some mono repeats of almost 800 repeats, dinucleotides of ˜300 repeats and trinucleotide of over 900 repeats. I can’t seem to find much information regarding any other organism that has such long repeats or, from an evolutionary perspective, do they mean anything? Any insight would be appreciated-Thanks.

Greg

gdouhan@ucanr.edu

Manipal India SummerIntern EvolBiol

SUMMER RESEARCH INTERNSHIPS: (SRI2018)

Start Date: Monday 04ˆth June, 2018

End Date: Saturday 14ˆth July, 2018

Venue: Manipal Centre for Natural Sciences, Manipal

Academy of Higher Education, Dr. TMA Pai Planetarium building, Madhav Nagar, Manipal 576 104, Karnataka, India

Applications are invited from outstanding students for the Summer Research Internship (SRI2018) Program at the Manipal Centre for Natural Sciences (MCNS), Manipal Academy of Higher Education, Manipal, Karnataka. MCNS carries out fundamental research in the natural sciences.

The SRI Program is an annual event which runs for 6 weeks over the summer.

Opportunities for SRI2018 are available in the following research areas:

- Paleontology and Stratigraphy
- Evolutionary Biology
- Computational Biology

Selections are highly competitive and only a limited number of supported internships are available.

Support for internships includes:

- A consolidated stipend of Rs. 15,000/-
- Free shared, on-campus hostel accommodation

Who can apply:

Highly motivated students currently enrolled or completed M. Sc./ M. Tech./ fourth year integrated M. Sc./ M. Tech. programs and highly motivated third or fourth year B. Sc./ B. Tech. students may apply.

How to apply:

- Application form is available from https://manipal.edu/mu/academics/centers-of-excellence/mcns-manipal/mcn s-manipal-news/mcns-manipal-events-list/summer-research-internships-201 8.html.

- Filled Application form in a single PDF file must be sent by email to sri@manipal.edu on or before 29^th April 2018.

- Two letters of recommendation (to be sent to the above e-mail address) from referees, who have taught you or are familiar with your academic work.

- List of selected candidates will be uploaded to this website by 5^th May, 2018.

Contact: Dr. Ranajit Das

The Coordinator Summer Research Internship Program (SRI2018) Manipal Centre for Natural Sciences Dr. T.M.A. Pai Planetarium Building Manipal University, Manipal - 567 104, Karnataka

Email: sri@manipal.edu Telephone: +91 820 2923571

Mobile: +918582802871

"Ranajit Das [MAHE-MCNS]" <ranajit.das@manipal.edu>

Phyloseminar MichaelLandis Mar14

Next on http://phyloseminar.org/ :

Phylogenetic models of pulsed evolution Michael Landis (Yale) Wednesday, March 14, 2018, 1:00 PM EDT

One of the most apparent features of life is its diversity of forms. Biologists are especially driven to learn what evolutionary processes generated which components of life's variation. Central to this puzzle is whether or not phenotypic change tends to accumulate by slow but steady increments or by rare but sudden pulses. Although many phylogenetic models and methods are known for describing incremental change, such as Brownian motion and the Ornstein-Uhlenbeck process, models of pulsed change have received less study, making it difficult to measure the prevalence of competing evolutionary modes. My talk provides an overview of evidence, theory, and methods that have advanced our understanding of evolutionary pulses of trait change. I share some of my contributions on the exploration of this topic, including recent findings that phylogenetic models of pulsed evolution explain a major component of vertebrate body size evolution. I conclude with some remarks regarding the potential for models of pulsed evolution to aid in the study of macroevolution.

Frederick "Erick" Matsen, Associate Member Fred Hutchinson Cancer Research Center http://matsen.fredhutch.org/ ematsen@gmail.com

PlantTaxonomists BotanySoc LeadershipAward

Link: https://cms.botany.org/home/awards/special-funds-and-awards/botany-advocacy-leadership-grant.html "The Public Policy Committee is accepting applications for the Botany Advocacy Leadership Award for 2018. Please review the award details at THIS LINK. The award is only given to either BSA or ASPT members and is open to any level of botanical scientist or activist. Applications are due March 30th to our Awards Officer, Andrew Pais (alpais@ncsu.edu).

The American Society of Plant Taxonomists (ASPT) and the Botanical Society of America (BSA) are pleased to invite applications for the annual Botanical Advocacy Leadership Award. This award organized by the Environmental and Public Policy Committees of ASPT and BSA aims to support local efforts that contribute to shaping public policy on issues relevant to plant sciences.

Examples of such efforts include: * Founding or expanding a native plant society or enhancing its activities. * Hosting a lecture series on plant conservation issues. * Leading campaigns or holding events that spread awareness of plant-related public policy issues (e.g., conservation of native species, control of invasive species, land use management). * Organizing local plant conservation events, such as removal of invasive species, planting a native garden, or restoration of native communities. * Traveling to meet with local or state representatives to lobby for legislation or other initiatives that benefit plant conservation, plant science research and education, or collections.

The recipient of this award will receive $1000 to be used in the proposed project. They will be recognized at the annual Botany meeting during the awards ceremony. To apply, please send a one-page letter describing the proposed local efforts and their anticipated impact along with a basic one-page budget to show how the funds will be used. All active members of ASPT and BSA are eligible to apply. Applications are due March 30th, 2018 and should be sent as a single .pdf ("YourName_BALAapp.pdf") to Andrew Pais (alpais@ncsu.edu) with the subject line "2018 BALA application". The selected applicant will be notified by April 15th, 2018.

Awardees will be required to submit a brief summary of their activities with an image to the Plant Science Bulletin (PSB) by January 15th of the following year. This synopsis will appear in the March/April issue of the PSB and is intended to highlight the impact of the recipient's efforts in shaping public policy and awareness of plant-related issues. Inquiries about the award may be directed to the chairs of the EPPC for both societies: ASPT/BSA EPPC Awards Chair - Andrew Pais (alpais@ncsu.edu), BSA-Krissa Skogen (kskogen@chicagobotanic.org) and Kal Tuominen (ktuominen@jcu.edu), or ASPT-Ingrid Jordon-Thaden (ingrid.jordonthaden@wisc.edu)."

Morgan Gostel <gostelm@gmail.com>

PortlandStateU REU PlantGenomics

NSF Research Experience for Undergraduates (REU) in Plant Ecology and Genomics (second posting 'V updated)

We have funding for two enthusiastic students interested in enhancing their research skills and experience in plant ecology, genomics, and bioinformatics in the Cruzan lab at Portland State University in Portland, Oregon.

Successful applicants will become part of a research team working on dispersal and gene flow in upland prairie plants in Oregon and Washington under pressure from climate change. Dispersal is critical for colonization, gene flow, and range expansion 'V it is one of the most important but least understood aspects of the ecology of plants. Our research utilizes genomic techniques to detect the effects of dispersal over different spatial scales. This is an integrative research program that includes field work, wet lab preparation of genomic DNA for next-generation sequencing, bioinformatics processing of sequence data, and analysis of patterns of gene flow using GIS and landscape genetic methods. Students will be exposed to a wide range of methods and are expected to develop an independent research project within the scope of the larger research program. More information on our research is posted on our lab web site: https://cruzanlab.weebly.com/ . Students will be fully supported for 10 to 12 weeks during the summer of 2018. Funding is provided from an REU supplement to our National Science Foundation Macrosystems Biology grant. Housing will be provided on campus along with a daily allowance for food and a $500 weekly stipend. The start of the REU is negotiable with optimal start dates between May 1 and June 17.

To apply please email us an updated copy of your CV (including GPA) and a short (one page) statement of your research interests and experience, as well as goals for your education and career. Applicants should arrange to have one or two faculty members provide a letter of recommendation (email is fine). Students with experience in computer programming and/or bioinformatics are encouraged to apply. Application deadline is 20 February 2018. Feel free to email us with questions.

Pam Thompson, Postdoctoral Research Associate: thompson@pdx.edu

Mitch Cruzan, Principle Investigator: cruzan@pdx.edu

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

Smithsonian Panama Intern LizardAdaptation

Internship opportunity: Evolutionary responses to climate change in tropical lizards

Application deadline: March 15th, 2018

Recent studies have argued that tropical organisms are particularly vulnerable to climate change because they are adapted to the thermally stable tropics. In other words, they are "thermal specialists" incapable of dealing with even small changes in temperature. For animals like lizards that have limited dispersal ability, evolutionary adaptation may be their primary means to avoid extinction. But can lizards evolve fast enough to keep pace with global warming? Is there sufficient phenotypic variation in tropical lizard populations for selection to act upon? If so, what is the genomic basis of this variation?

We are conducting a large-scale transplant experiment aimed at measuring evolutionary change in real time, testing hypotheses about thermal adaptation and the evolutionary capacity of tropical animals in the face of rapid, catastrophic warming. We are looking for one or more interns to join us at the Smithsonian Tropical Research Institute (STRI) as we sample lizards from a series of experimental islands in the Panama Canal. The internship will run from September through November, 2018, and is open to undergraduate or graduate students (or recent grads looking for additional field experience). Prior experience with hand-catching lizards is preferred, but not necessary, as is prior experience in the tropics (preferred but not necessary). We particularly encourage members of underrepresented groups (women, minorities, first-generation college students, etc.) to apply.

The intern will be integrated into an international team of evolutionary biologists and ecologists working on this project. The intern will be trained in a number of field and laboratory techniques. These include (but are not limited to) field capture and processing of live Anolis lizards, measuring morphological traits, respirometry, estimation of thermal tolerance and field body temperatures, habitat monitoring using a drone, tissue sampling and DNA preservation, and visual elastomer marking techniques for mark-recapture studies. In general, the intern will be exposed to a vibrant scientific atmosphere of dedicated, passionate researchers working in one of the most complex and pristine tropical environments on the planet.

The intern will apply through the STRIs internship program: http://www.stri.si.edu/english/education_fellowships/internships/research_experience_tropics.php

The deadline for applications is March 15^th. The internship stipend is $1000/month which comfortably covers room and board in Panama. There is no allowance specifically for travel. This program is competitive, will applications being evaluated by a committee of Smithsonian staff scientists. As such, there is no guarantee that any individual application will be approved. However, project PI Mike Logan (Biodiversity Genomics Postdoctoral Fellow at STRI; www.evolutioninthetropics.com) will work with individual applicants to improve their essay and increase their chances at getting accepted. Please email Mike (mike.logan1983@gmail.com) for more information and to see if you're interests match the goals of the project. Please attach your CV to the first email.

Michael Logan <mike.logan1983@gmail.com>

Software NewRelease BAli-Phy3 0

BAli-Phy version 3.0 is now available (http://www.bali-phy.org).

BAli-Phy is a Bayesian MCMC program for estimating— alignments and phylogenies simultaneously from unaligned sequence data.— Version 3.0 should be faster than version 2.3 and allows specifying priors.

The main new features in version 2.3 are: (http://www.bali-phy.org/releases/3/) - Up to 300% faster and 300% less memory. - Allow specifying priors and values for all model parameters. - Ancestral sequences with indels in sampled alignments. - 2D and 3D tree MDS convergence plots. - 'bali-phy help <topic>' for models, functions, distributions, and commands.

You can download binaries for Linux, Mac, and Windows here: - http://www.bali-phy.org/download.php

Mac users can also install using homebrew.

You can read the updated manual here: - http://www.bali-phy.org/README.xhtml

An example of the output for ITS data: - http://bali-phy.org/Examples/ITS/ITS1-TN-DP3-2/ If you have any trouble using bali-phy, please post your questions to bali-phy-users@googlegroups.com I should be able to respond fairly quickly.

-BenRI

Ben Redelings http://www.ben-redelings.org Benjamin Redelings <benjamin.redelings@duke.edu>

THHuxley Award Nominations

The SSE Education Committee is pleased to announce the T. H. Huxley award, named in honor of Darwin's very public supporter, which recognizes and promotes the development of high quality evolution education resources. If you have an interesting project or educational activity to share, consider applying for this award. Information on previous awards is available here: http://bit.ly/2kP2pPM. Graduate students and postdoctoral fellows are encouraged to apply. This award provides funding for an SSE member to present evolution education resources at the National Association of Biology Teachers (http://nabt.org/) annual conference. This year's NABT conference will be held Nov. 8-11, 2018 in San Diego, CA. The deadline for applying for the Huxley award is March 23, 2018. Apply here: https://goo.gl/forms/vm9DDTabepV2PuCu2 . "Gibson, Phil" <jpgibson@ou.edu>

UCincinnati REU SensoryEvolution

Dear Colleagues:

I am writing to let you know about a summer research opportunity for undergraduate students in the Department of Biological Sciences at the University of Cincinnati - the National Science Foundation-sponsored Research Experiences for Undergraduates (REU) Site in Sensory Ecology. Our program is focused on research at the intersection of neurobiology, behavior, ecology and evolution, and is directed at understanding how animals sense and respond to their environment at functional and evolutionary levels. Sophomore and junior Biology major students will be chosen to join active lab groups for the summer and conduct cutting edge research over a broad spectrum of topics in sensory ecology, including:

- Genomics and development of sensory systems - Neural mechanisms of sensory system function - Sensory perception and behavioral influences of the physical environment - Neuroethology - Animal communication - Behavioral ecology of animal movement and dispersal

An educational program will develop student research and professional skills and prepare them for graduate school or careers.

- 10 weeks in summer (May 29- Aug 3, 2018) - Students will receive a summer stipend plus dorm and meal expenses - Students will work in labs, interact w/ faculty mentors, post-docs and grad students

- Weekly group seminars and meetings for students (e.g., career development, responsible research conduct, panel discussions) - Social events for students (e.g., trips to Cincinnati Zoo, Reds baseball) - Concluding student research 'mini-symposium' presentation session

Student applicants will be selected based on multiple criteria. Applications for the REU program will be screened by a committee to select individuals whose interests are well-matched with faculty in the program. Emphasis will be placed on faculty recommendations and student statements, along with academic performance and other indicators of future research success. Note: Implementation of the REU program is contingent on National Science Foundation funding.

The application deadline is March 15, 2018. Students can apply online at:http://www.artsci.uc.edu/departments/biology/undergrad/REU.html We hope you will encourage your students to visit our website and consider applying.

Thank you.

Stephanie Rollmann, PhD (stephanie.rollmann@uc.edu) and John Layne, PhD (john.layne@uc.edu)

"Layne, John (laynejn)" <laynejn@UCMAIL.UC.EDU>

UGeorgia REU PlantAdaptation

Jill Anderson at the University of Georgia is searching for an enthusiastic undergraduate with a strong interest in evolutionary ecology for field research in an NSF REU position (National Science Foundation, Research Experience for Undergraduates) from June-August 2018. We study the ecological and evolutionary consequences of climate change for natural plant populations. We focus on research on Drummond's rockcress (Boechera stricta in the plant family Brassicaceae), a mustard plant native to the Rocky Mountains. Our studies take place around the Rocky Mountain Biological Lab (http://www.rmbl.org/), which is located in Gothic, Colorado near the wildflower capital of Colorado (Crested Butte). We quantify plant fitness and traits to ask whether climate change could disrupt long-standing patterns of local adaptation, and to test whether phenotypic plasticity will enable populations to persist in the short-term. We perform large-scale reciprocal transplant experiments to examine patterns of adaptive evolution and natural selection in contemporary landscapes. Since fall 2013, we have planted >150,000 seeds and seedlings into five experimental gardens ranging in elevation from 2500 m to 3340 m (8202 feet to 11000 feet). Our summer research involves intensive monitoring of these experimental plants to record data on germination success, survival, growth, reproductive success, as well as life history and morphological traits. We conduct most of our work in the field, with a small proportion of indoor lab work.

The successful candidate will assist with ongoing fieldwork. In addition, there are many opportunities for students to develop independent projects associated with our overall objectives, including studies on: 1) population divergence in ecologically-relevant traits, especially drought, UV tolerance, and herbivore resistance; 2) phenotypic plasticity at multiple spatial scales; 3) population density and species composition of the herbivore community that attacks Drummond's rockcress; 4) flower color polymorphism; and 5) the importance of maternal effects in biological responses to climate change.

We are offering a stipend of $500/week for a full time REU student (40 hours/week) for 10 weeks. The exact start and end dates are flexible. We will cover room and board at the Rocky Mountain Biological Laboratory and reimburse travel expenses up to $500. Fieldwork will involve hiking to experimental gardens through rough terrain (1-3 miles one-way daily).

The University of Georgia is committed to maintaining a fair and respectful envi ronment for living, work, and study. To that end, all qualified applicants from individuals with a strong interest in evolutionary biology will receive conside ration for employment without regard to race, color, religion, sex, national ori gin, sexual orientation, gender identity, disability status, or age. The applic ation consists of a cover letter listing your qualifications, a CV/ resume and contact information for two references, all of which can be emailed to Dr. Jill Anderson at: jta24@uga.edu

Applications are due by March 16^th, 2018.

Feel free to contact Dr. Anderson if you have any questions about the position. Additional information about our work can be found at: http://andersonlab.genetics.uga.edu/Home.html Jill T Anderson <jta24@uga.edu>

ULausanne SIBVirtualSeminar JeromeGoudet February28

Dear all,

We are pleased to announce the next speaker at the SIB Virtual Computational Biology Seminar Series:

Jerôme Goudet, Population Genetics and Genomics, University of Lausanne & SIB Wednesday 28 February 2018 at 16:00 - Genopode Auditorium A - UNIL campus "Of men and owls: insights into past demography using computer simulations"

The seminar will also be broadcast live for those unable to attend it physically (https://collab.switch.ch/sib-cbss/). For more information about these seminars as well as the upcoming speakers list and previous screencasts, please visit the SIB virtual seminar series webpage: http://www.sib.swiss/training/virtual-seminars-series Important: If you want to remain informed about our upcoming seminars, please subscribe to the dedicated mailing list: http://lists.isb-sib.ch/mailman/listinfo/sib-virtual-seminars Looking forward to seeing you all there.

Best regards, Diana Marek

"Diana.Marek@sib.swiss" <Diana.Marek@sib.swiss>

UNewSouthWales Volunteer ZebrafishEvol

Scientific Internship/Apprenticeship in Evolutionary Biology at UNSW, Australia

Our lab (www.i-deel.org) is offering one scientific internship/apprenticeship (or volunteer position) for 6 months to help conduct behavioural and physiological experiments on zebrafish. We are located at the Evolution & Ecology Research Centre (E&ERC) within the School of Biological, Earth and Environmental Sciences (BEES) at the University of New South Wales (UNSW), Sydney, Australia. The intern will be engaged in a variety of scientific work (e.g, running zebrafish behavioural and metabolic experiments, helping in fish breeding and database management as well as molecular work such as DNA extraction, sequencing, PCR and qPCR). We expect that the apprentice will learn essential skills as well as gain experience necessary for conducting their own projects. As such, an ideal candidate would be someone who plans to undertake a PhD in the future, within the fields of Evolutionary Biology, Ecology and Behavioural Sciences (i.e. someone with BSc or MSc). We will provide an allowance to cover accommodation and food (˜up to AU$2000 per month). Importantly, the intern needs to be an Australian or New Zealand resident. Please read our webpage to see what kind of research we conduct (www.i-deel.org). If you are passionate about our science and would like to join our team, please contact Shinichi Nakagawa (s.nakagawa@unsw.edu.au) or Daniel Noble (daniel.noble@unsw.edu.au) with your CV and a one-page letter of motivation.

Shinichi Nakagawa

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

UTexas ElPaso REU DesertBiodiversity

REU Opportunity Summer 2018: "Research Experience for Undergraduates in Chihuahuan Desert Biodiversity" - DEADLINE FEB 26, 2018

The University of Texas at El Paso (UTEP) Department of Biological Sciences invites applicants for the NSF sponsored Research Experience for Undergraduates (REU) in Chihuahuan Desert Biodiversity. This is a 10 week summer program. The goal of this program is to provide undergraduate students with experience in hypothesis-driven collaborative research utilizing field based and/or laboratory methods and fully engage students in projects associated with the ecology and evolution influencing Chihuahuan Desert biodiversity.

The program provides:

* High quality research experience in ecology and evolutionary biology in the field and/or lab * Research opportunities at the Indio Mountains Research Station (IMRS), a 40,000 acre facility controlled by UTEP * One-on-one and group mentoring from active research faculty in multidisciplinary fields * Training in bioethics and other relevant professional skills

The program includes:

* $5500 stipend for 10 weeks

* Housing in shared apartments and field station

* Travel reimbursement of up to $600

For more information on the program, research projects or to apply please visit: http://science.utep.edu/cdb-reu/ Enquiries: CDB-REU@utep.edu

"mlmoody@utep.edu" <mlmoody@utep.edu>

UZurich FieldAssist BirdsLapland

Expenses paid field assistant position to study avian diversity in Swedish Lapland.

For the upcoming field season (15 June- 30 July 2018), we are looking for a highly motivated, expenses paid field volunteer to join our project (main responsible Dr. Michael Griesser, University of Zurich) investigating bird diversity in boreal forests. The study site is located near Arvidsjaur, Swedish Lapland.

Our current project investigates the influence of habitat quality on the diversity and breeding success of different bird species. The work of the field volunteers will be to help with bird census work, habitat census work, and data management in managed and pristine boreal habitats. The work can be physically strenuous at times.

Qualifications:

(1) BSc/MSc in Biology, Ecology, Evolution or similar qualification (2) Ability to recognize the common birds of Lapland by ear and sight (3) Previous experience with bird census work (4) Ability to work in small teams and a sociable personality (5) Driving licence and ability to drive manual transmission (6) Fluent in English or German

We will cover the accommodation, travel expenses to and from 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 sent to Paul Haverkamp (paul.haverkamp@ieu.uzh.ch), preferably in a single PDF.

Applications received by 16 March 2018 will be given full consideration.

paul.haverkamp@ieu.uzh.ch

PostDocs

ArizonaStateU EvolMedicineEducation

Postdoctoral Research Associate in Evolution & Medicine: Evolution education and curriculum development in evolutionary medicine

This postdoc will work with education researchers, other postdocs and staff to develop education resources for the field of evolutionary medicine, including http://evmeded.org and http://evmedreview.com. The position will be about half developing resources and half research on education strategies for evolutionary medicine. The ASU Center for Evolution and Medicine is a world leader in this area. http://evmed.asu.edu Full information about the position is at https://evmed.asu.edu/research/postdoctoral-research-associate-evolution-medicine Salary: $48,000

Reference #12284

Full-time

The Center for Evolution & Medicine (CEM) and the Biology Education Research Lab at Arizona State University (ASU) invite applications for a Postdoctoral Research Associate to pursue projects related to evolution education research and the development and testing of evidence-based evolutionary medicine curriculum materials. The position offers opportunities for both education research, and practical development and implementation of new kinds of online resources for the field.

Candidates must have a Ph.D. in anthropology, biology or other natural science or science education field that provides an extensive background in evolutionary biology. Crosstraining and experience in education is desirable. Candidates with experience in the following are preferred: developing and accessing education resources. The successful candidates will have a commitment to science education, must have outstanding writing and organizational skills, demonstrated capacity for independence and innovation, and the ability to work as part of a team. Applicants cannot have had more than five years of previous postdoctoral experience, nor have been employed previously as an assistant professor, associate professor or professor on the tenure track. Nominees who are non- US citizens are encouraged to apply, and will need to be eligible for a J-1 Scholar visa status for the duration of the Fellowship. CEM does not support H1B visa status. A background check is required for employment.

Postdocs will receive a salary of $48,000 and will have access to funding of up to $6,500 per annum to support their research, of which $1500 may be allocated for moving expenses. The initial closing date for receipt of complete applications is April 1, 2018; applications will be reviewed weekly thereafter until the search is closed. The earliest anticipated start date is July 2018, the latest is January 2019. This is a full-time (1.0 FTE) benefits-eligible, fiscal year (July 1 - June 30) appointment. Renewal is possible on an annual basis contingent on satisfactory performance, availability of resources, and the needs of the program. A background check is required for employment. For additional information and policies regarding postdoctoral scholars at ASU, please see http://provost.asu.edu/postdoc .

To apply, please email a single pdf document to evmed-search@asu.edu that contains:

a letter of application that states your interest in and qualifications for the position a curriculum vitae copies of up to three representative research publications names of three references

Please use 11 point Times font with 1 inch margins and 1.5 line spacing for all items except the CV. The postdoctoral research associate will join a vibrant community of educators and researchers at ASU committed to evidence-based teaching. The Center for Evolution and Medicine, led by Dr. Randolph Nesse, is a universitywide presidential initiative whose mission is to establish evolutionary biology as an essential basic science for medicine. As a worldwide hub for evolutionary medicine, the Center for Evolution and Medicine is committed to developing evidence-based teaching resources, curricula, and degree programs for evolutionary medicine. The Biology Education Research Lab is led by Dr. Sara Brownell and is a team of biology education researchers who are committed to improving the way we teach undergraduate biology, including evolution education. For additional information on the Center for Evolution & Medicine, visit https://evmed.asu.edu. For additional information on the Biology Education Research Lab, visit http://sebbers.wixsite.com/biology-ed-lab . For additional information on the position, please contact Jennifer Vazquez, Assistant Director, at

Jennifer.Vazquez@asu.edu

Arizona State University is a new model for American higher education, an unprecedented combination of academic excellence, entrepreneurial energy

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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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Bamfield PostdoctoralFellowship

Postdoctoral Fellowship Opportunity at the Bamfield Marine Sciences Centre on Vancouver Island, Canada.

The Bamfield Marine Sciences Centre (BMSC) is pleased to announce a new Postdoctoral Fellowship (PDF) opportunity. Preference will be given to supervisors who nominate outstanding candidates with demonstrated research accomplishments and excellent communication skills. The successful candidate is expected to conduct original research consistent with the mandate of the BMSC to support high calibre research and provide unparalleled access to the natural and cultural sites where the major scientific questions and challenges of the 21st century persist in the marine sciences, biodiversity, ecology, evolution, comparative physiology, archaeology/anthropology, indigenous studies and the development of research-informed teaching. The PDF will be expected to work full-time at the BMSC, foster interactions within the BMSC, organize a working group retreat and facilitate directed studies in undergraduate student research. BMSC is a shared campus of five Western Canadian Universities (Universities of Victoria, Calgary, Alberta, British Columbia, and Simon Fraser University), but nominations of candidates will be accepted from any supervisors with research programs being conducted at the BMSC.

Application deadline: March 2, 2018

Start date: as early as April 1, 2018.

Salary: $48,000 annually

Research stipend: $5,000 annually to cover station related expenses (e.g., boat time)

The nomination package should include: the Curriculum Vitae of the nominee; free-form proposal describing the research (2 pages), a one-page letter from the supervisor describing the professional development program to be offered to the nominee and the potential contributions of the nominee to training and learning; two letters of recommendation for the nominee.

Application packages should be emailed as a single PDF to the BMSC Research Coordinator [research@bamfieldmsc.com >

Once the nomination package is reviewed and the proposed PDF is approved, an 18-month term position will be offered. Funding permitting, renewal of the fellowship may be approved following an evaluation of progress after the first term.

The BMSC is a world-class teaching and research facility located in traditional territories of the Huu-ay-aht First Nation, on the outer west coast of Vancouver Island, Canada. Our campus is situated on 65 hectares in Barkley Sound with access to a remarkable diversity of marine, terrestrial, freshwater and cultural sites of the North East Pacific basin. Located in the heart of Canada's Pacific Rim National Park, the town of Bamfield has a small but exceptionally vibrant community that shares a history of trust and collaboration with the Huu-ay-aht First Nation. The town is also the northern terminus of an iconic Canadian Trail, the West Coast Trail. The stunning surroundings of the rain forest, deserted beaches, uninhabited islands, rugged coastline, and world class diving inspire creativity and discovery.

See www.bamfieldmsc.com -> http://egw.bamfieldmsc.com/index.php?menuactionÃ¾lamimail.uidisplay.displayBody&uid31&mailb
SU5CT1gvU2VudA%3D%3D#] for more details.

Tao Eastham <teastham@bamfieldmsc.com>

Brest LabexMER MarineEvolution

The 2018 edition of the LabexMER *post-doctoral program* is open: < http://www.labexmer.eu/en/international/postdoctoral-fellowships >

In the context of this program, population geneticists and other evolutionary biologists are invited to propose a project relevant to the research axis "Evolution of marine habitats and adaptation of populations" (axis 6 of the LabexMER): < https://www.labexmer.eu/en/research/axis6/ >

LabexMER 'A changing ocean' is a cluster of Excellence ('Labex') funded by the French 'Investment for the future' program, supported by the French Ministry of Research and Education. It gathers a diversity of laboratories in Western France to tackle fundamental issues related to our understanding of ocean functioning in the context of climate change. The LabexMER is organized around 8 research axes. More information on LabexMER website < http://www.labexmer.eu >

The post-doctoral program is co-sponsored by the LabexMER, Ifremer, the University of Brest and the Brittany Regional council, and aims to provide an opportunity to young creative scientists to develop their own research project in one of the LabexMER laboratories (France).

Fellows are appointed for two years. Funding includes salary and support for travel or small equipment and supplies. Minimum of four fellowships will be awarded in 2018.

Deadline for applications: *April 15th, 2018* *Apply now*: < http://www.labexmer.eu/fr/international/bourses-post-doctorales/AAP-bourses-post-doctorales >

All the best,

Gregory Charrier

Gregory Charrier <gregory.charrier@univ-brest.fr>

CanadianMuseumNature EvolArcticSpecies

The Centre for Arctic Knowledge and Exploration Postdoctoral Fellowship

Call for Applications

The Canadian Museum of Nature is Canada's national natural-history and natural-sciences museum with a long, respected history of collection development and research related to biological, palaeobiological and mineral diversity in Canada.

The museum has over 100 years of experience in applying its scientific expertise to Arctic exploration and is using that strong base of knowledge to transform people's understanding of the Arctic and its importance to Canada in a global context.

Fellowship Description

The museum is seeking applicants for The Centre for Arctic Knowledge and Exploration Postdoctoral Fellowship who wish to conduct research that addresses issues related to Arctic biological, palaeobiological, or mineral diversity.

Applicants must propose research in one of the disciplines of study at the Canadian Museum of Nature: botany, mineralogy, palaeobiology, or zoology. Proposed research is expected to be collections-based, and may involve field work. The candidate will work closely with one or more museum researchers in their area of expertise.

Applicants should contact the museum's science experts to identify a potential advisor and determine the feasibility of the proposed research being conducted at the Canadian Museum of Nature.

The two-year award is for a recent doctoral graduate.

Facilities

The successful candidate will be based at the Canadian Museum of Nature's research and collections facility, in Gatineau, Quebec.

There, they will have the opportunity to use the collections and laboratory facilities, which include a wide range of light-microscope equipment, an electron microscope, a molecular biology laboratory, a photographic studio and a library. These facilities at our Natural Heritage Campus are designed to support projects in taxonomy, systematics, evolution and ecology.

For mineralogical research, an electron microprobe facility at the Advanced Research Complex at the University of Ottawa is available, through a partnership between the museum and the university.

Public Engagement

The candidate will be expected to make their research accessible to the public through such means as oral presentations, the use of popular social media, and media interviews.

Program Development

As part of this position, the candidate will be an active member of The Centre for Arctic Knowledge and Exploration. The candidate will be expected to contribute to the goals of the centre and may be asked to engage content developers, designers and other team members on Arctic issues that are appropriate to nature-literacy programming for the general public.

Compensation

This unique opportunity will provide a valuable research experience that will be compensated at a rate of $45 000 per year, renewable for one year, with up to $5000 per year available to support the research program.

Fellowship Start Date

April 2, 2018 (negotiable)

Candidate Requirements

- Completion of all doctoral requirements, in a field related to the proposed research, prior to start date and no earlier than January 1, 2013

- Experience conducting research and publishing research in peer-reviewed journals

Candidate Assets

- Canadian citizen or permanent resident

- Demonstrated ability to communicate science to the public

- Experience working with museum specimens

- Ability to communicate in both official languages.

How to Apply

Applications must include the following:

- A description of the research question(s), methodology, relevance of the work to the broader discipline and to Canada, and a basic budget (maximum 2000 words)

- An explanation of why the research should be conducted at the Canadian Museum of Nature, and of how museum collections and laboratories will be utilized (maximum 300 words)

- Identification of a research-and-collections staff member at the museum who has agreed to serve as principal advisor and host

- A curriculum vitae

- Contact information for three references.

Application Deadline

February 15, 2018

Contact Us to Apply

Jeff Saarela, Ph.D. Director, The Centre for Arctic Knowledge and Exploration Canadian Museum of Nature P.O. Box 3443, Station D Ottawa, ON K1P 6P4 jsaarela@mus-nature.ca

The Canadian Museum of Nature supports employment equity.

https://nature.ca/en/about-us/careers-volunteering/careers/centre-arcti c-knowledge-exploration-postdoctoral-fellowship

- Achevement de toutes les exigences de doctorat, dans un domaine lie Ã la recherche proposee, avant la date de debut et pas plus t0t que le 1ˆer janvier 2013

- Experience de la realisation de recherches et de l'edition dans des revues Ã comite de lecture.

Actifs des candidats

- Citoyen canadien ou resident permanent

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CharlesU EvolutionaryImmunology

Dear colleagues,

The Evolutionary and Ecological Immunology (EEI) group at the Faculty of Science, Charles University, Prague, is currently advertising a 2.5-year PostDoc position in avian neuroimmunology with deadline for applications 1st March 2018.

I would be grateful if you could circulate the following advertisement at relevant fora or pass it to whom it may concern.

Impact of neuroinflammation on brain development and learning in cognitively advanced birds *Available from May 2018 to December 2020 (the starting date is flexible) ** **Application deadline: 1st March 2018*

Neuro-immune interactions involved in neuroinflammation directly influence psychological processes including mood and cognition. Inflammation plays an important role in aetiology of depression, a mood disorder that affects 350 million people worldwide. Since ~40% of patients do not respond to current therapy, novel research approaches are needed to allow deeper insight into evolutionarily conserved interactions between immunity and brain function.

*The objective *of this PostDoc project is to link local inflammation in birds with neuroinflammation and provide evidence for its effect on brain development and function. Methods such as immunocytochemistry, isotropic fractionation, tissue-specific RNA-seq, RT-qPCR and proteomic analysis of cerebrospinal fluid through gel-free quantitative LC-MS/MS will be used and biodiversity-based approach adopted. Focusing on birds that represent superior models for research in cognition to rodents (passerines and parrots), this PostDoc project opens new possibilities for interdisciplinary research of neuroimmunology.

This project solves 3 main scientific questions: 1)——— What is the effect of inflammation in periphery on immunological activity in avian brain? Inflammation in periphery triggers cytokine signalling that acts systemically to affect distant organs. Inflammation may be propagated across the blood-brain barrier to induce neuroinflammation in which microglia are activated in brain. Task 1 (T1): To describe the gene expression changes (transcriptomic and proteomic) in brain regions that respond to acute/chronic inflammation in periphery in selected species. T2: To show the patterns of inflammation-induced microglia activation in distinct brain regions.

2)——— How the neuroinflammation influences neurogenesis and neuronal activity in birds? Activated microglia alter synthesis of monoamine neuromodulators, which disturbs neurocircuits involved in decision-making, mood-regulation and memory. Long-term failure to regulate neuroinflammation may significantly affect brain function including neurogenesis. T3: To explore brain neurogenesis and neuronal activity changes induced by experimentally induced neuroinflammation (adult/early-life).

3)——— Does neuroinflammation alter avian learning or mood? Inflammation-induced changes in brain may alter behaviour. In birds, behaviour indicating cognitive abilities and mood can be measured. The early-life inflammation may increase probability of developing mood disorders later in life. T4: To investigate the effect of inflammation in early life/adulthood on cognition and mood.

Requirements: We seek for a researcher with experience in neurobiology, histology, immunology and/or zoology - PhD degree in one of these or related fields, good English language skills and (at least basic) statistical skills required.

Offers: We offer a Research Fellow position at the Department of Zoology, Faculty of Science, Charles University based in Prague, Czech Republic, EU. This is a full time, ~ two and half (~2.5) year fixed term contract *starting from April-June 2018 (flexible), ending on 31.12. 2020 (fixed)*. *Salary: **37,000 CZK per month** (444,000 CZK ~ euro 17,500 per annum; * above local average salary, fully sufficient to cover living costs in Prague) plus moving in allowance of *72,000 CZK* (~ euro 2850 - will be spread over the 1st year salary). The research fellow will be part of a young and enthusiastic interdisciplinary team (http://web.natur.cuni.cz/zoologie/biodiversity/eei/-people) and where she/he will be co-supervised by Dr. Michal Vinkler (http://web.natur.cuni.cz/zoologie/-biodiversity/eei/people/#post-73) and Dr. Pavel NÃ(https://web.natur.cuni.cz/zoologie/biodiversity/-index.php?page=nemec). Despite close collaboration with several co-workers, the project allows independent intellectual input. We expect at least three articles being published in international peer-review journals in the course of the

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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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ConcordiaU Montreal FisheriesInducedEvolution

Postdoc, ConcordiaU_Montreal.genomic consequences of fish harvesting

Concordia University in Montreal, Canada is currently accepting applications for a postdoctoral fellowship valued at $47,500 per year (plus benefits) for each of two years that will examine the gene to ecosystem consequences of fisheries-induced evolution on sustainable fisheries. Supervisors: Dr. Dylan Fraser, Dr. Pedro Peres-Neto.

We are seeking a highly motivated postdoctoral fellow to advance knowledge of the genomic consequences of fisheries-induced evolution for fish and fisheries. This is an unprecedented opportunity to conduct experimentally-replicated depletion of natural populations of a socio-economically important fish (brook trout) in closed ecosystems where the species is invasive and the target of removal efforts, in exceptionally pristine places (Rocky mountain alpine lakes). The position will be based at Concordia University (Montreal, Canada) and the research offers an outstanding opportunity for training in applied genomics and fisheries science and is affiliated with an NSERC Strategic Project between three universities (Concordia University, UQAM, Calgary), Parks Canada, Alberta Environment and Sustainable Resource Development and Fisheries & Oceans Canada.

Academic qualifications required: A PhD in population, evolutionary and/or conservation genomics. Applicants should be team-oriented and autonomous, and have a strong publication record and demonstrable quantitative skills (e.g. R stats, bioinformatics); experience with GWAS is an asset.

Eligibility requirements:

-Applicants must not currently hold a postdoctoral appointment at Concordia

-Priority will be given to postdoctoral fellows who have obtained their PhD from another university although in exceptional cases Concordia graduates may be considered

-Applicants must adhere to the postdoctoral fellow eligibility criteria outlined in Concordia University's Postdoctoral Policy

Timeline and Application Process: Application deadline: open until the position is filled but no later than April 1, 2018 Fellowship start date: no later than July 1, 2018 Submission process:

Â§All documents must be submitted to Cynthia Raso at (Horizon.Postdocs@concordia.ca)

Â§Please include the reference number with your application Application checklist:

Â§One to three (1-3) page research statement demonstrating fit with the program described above

Â§Current curriculum vitae demonstrating research excellence and a capacity for leadership in the domain (maximum 5 pages).

Â§Two letters of reference from academic supervisors or current employers to be sent via e-mail directly to: Cynthia Raso at (Horizon.Postdocs@concordia.ca) Concordia University is a vibrant research and teaching environment, with state-of-the-art research facilities and many research centers. Concordia is located in Montreal, Canada, a diverse and creative city, often ranked as offering one of the best quality of living experiences in North America. More information on the supervisors' research programs can be found at the following links. Interested candidates are also encouraged to contact Dr. Dylan Fraser (dylan.fraser@concordia.ca) if they have any questions about the postdoctoral research: Dr. Dylan Fraser: www.dylanfraser.com Dr. Pedro Peres-Neto: https://communityandquantitativeecology.weebly.com/ Dylan John Fraser <dylan.fraser@concordia.ca>

CSIRO EnvironmentalGenomics

Future Science Postdoctoral Fellowships in Environmental Genomics

- Are you an up-and-coming scientist with a flair for innovation? - An outstanding opportunity to launch your research career. - Join CSIRO's Environomics Future Science Platform (FSP) and be part of the next scientific revolution.

The Environomics Future Science Platform (Environomics FSP) is pleased to announce the opening of its first round of Future Science Fellowships focused on the development of environmental genomic technologies.

We are seeking to recruit outstanding and inventive early career scientists who will develop the environmental genomics technologies of the future.

Two categories of Future Science Fellowship are offered: 1. Fellowships embedded within existing Environomics Future Science Platform projects (3 fellowships); 2. Open-call fellowships where you can propose a line of research that you would like to pursue and that meets the brief of "re- defining the limits of what genomics can do for environmental science and management" (1-2 fellowships).

Postdoctoral Fellows in Environomics are appointed for three years at various CSIRO locations within Australia. You will be mentored by a CSIRO Research Scientist or Engineer and participate collaboratively within the Environomics FSP research program. We strongly encourage collaboration with university, government, and industry partners. The fellowships include research costs.

Further information on these fellowships and how to apply can be found on the following links: - FSP Postdoctoral Fellowship in Molecular Systematics and Taxonomy (ref 55763) Mobile DNA Sequencing: Genome-power in your pocket https://career10.successfactors.com/sfcareer/jobreqcareer?jobIdU763&company=CSIRO&username - FSP Postdoctoral Fellowship in Ecology and Evolution (ref. 54642) Using insects as molecular biosensors of biodiversity and ecological interactions https://career10.successfactors.com/sfcareer/jobreqcareer?jobIdT642&company=CSIRO&username - FSP Postdoctoral Fellowship in Future Environmental DNA (ref. 54801) eCells: developing novel ways to non-invasively estimate animal abundance through genomics https://career10.successfactors.com/sfcareer/jobreqcareer?jobIdT801&company=CSIRO&username - FSP Postdoctoral Fellowship in Environmental Genomics, (ref. 54643) Open call CSIRO Future Science Postdoctoral Fellowships in Environomics https://career10.successfactors.com/sfcareer/jobreqcareer?jobIdT643&company=CSIRO&username - Rapid epigenetic age-estimators for vertebrates (coming soon)

Information about these positions and working for the FSP Environmental Genomics program is available here: https://research.csiro.au/environomics/work-with-us/ The Environomics Future Science Platform is developing the next-generation technology to investigate and manage genetic resources hidden within Australia's vast biodiversity. Find out more here: https://research.csiro.au/environomics/ . Further enquiries can be directed to: EnvironomicsFutureSciencePlatform@csiro.au

The Commonwealth Scientific and Industrial Research Organisation (CSIRO) We imagine. We collaborate. We innovate. At CSIRO, we do the extraordinary every day. We innovate for tomorrow and help improve today for our customers, all Australians and the world. We do this by using science and technology to solve real issues. Diversity is the compass that navigates our innovation. We provide an inclusive workplace that respects, values and actively pursues the benefits of a diverse workforce.

We work flexibly at CSIRO, offering a range of options for how, when and where you work.

Applications close: 11:59pm AEDT, 18 March 2018.

Apply here: https://jobs.csiro.au/go/Postdoctoral-research-fellows/990000/

"Noni.Lauder@csiro.au" <Noni.Lauder@csiro.au>

DebrecenU AvianBreedingSystems

Scientific Coordinator/ Post-doc Position University of Debrecen, Hungary ELVONAL (cutting edge) - Breeding system evolution in shorebirds

The Hungarian government recently opened up a new funding stream to support cutting edge research across all scientific fields (Nature 551: 425), and our team was one of the 12 winners. This will be a 5-year project focusing on testing key hypotheses of breeding system evolution through the use of genomic, immunological, and demographic approaches. The project focuses on shorebirds (i.e., plovers, sandpipers, and allies) that exhibit an unusual diversity of mating systems and parental care (see references).

This job offers an opportunity for an experienced postdoc who wants to combine fieldwork with cutting-edge evolutionary and behavioural science. The main tasks of the Scientific Coordinator are to carry out and supervise field studies in Madagascar, Cape Verde, Mexico, Russia, and/or China, possibly in other countries. We seek candidates with experience in behavioural ecology and field biology (preferable with birds), and skills in one of the following fields: behavioural analyses, demography, immunology, epidemiology or comparative genomics. Publications in top peer-reviewed journals, excellent communication skills, and database handling are essential.

This is a full-time position and the salary will be above the normal Hungarian level (up to 2000 EUR, depending on experience). Note that the cost of living in Hungary is substantially less than in the US or Western Europe. The position is initially for 3 years (subject to probation period) with the possibility of extension until the lifetime of the ELVONAL project (5 years). See further specifications below.

Application deadline is 28 February 2018. The application should include a (1) max two pages cover letter, (2) CV with list of publications, and (3) the name and contact details of four referee preferably from research, academia or conservation. The applications should be emailed to Ms. Emese Kapczar (kapczar.emese@science.unideb.hu). Interviews will be in early March and the position is available from 1 April 2018. Applications from women and minority candidates are especially welcome.

Debrecen is the second largest city in Hungary and has a lively university community. The University of Debrecen < https://en.wikipedia.org/wiki/University_of_Debrecen > was established in 1538, and it is one of the prestigious universities in Central Europe The university has over 4000 students - many are from abroad. The Dept. of Evolutionary Zoology and Human Biology < http://zoology.unideb.hu/home/ > is one of the leading departments in natural sciences Debrecen Airport has connections with some of the main European airports. Debrecen$B!G(Bs surrounding has impressive wildlife and landscape that include Hortobagy National Park < https://en.wikipedia.org/wiki/Hortob%C3%A1gy_National_Park >, a UNESCO-recognised protected area. See details at https://en.wikipedia.org/wiki/University_of_Debrecen For further information please contact Ms Emese Kapczar kapczar.emese@science.unideb.hu

Selected publications Bulla, M. et al. 2016. Defying the 24$B!>(Bh 1 day: Unexpected diversity in socially synchronized rhythms of shorebirds. Nature 540: 109-1013.

Eberhart-Phillips, L. J. et al. 2017. Adult sex ratio bias in snowy plovers is driven by sex-specific early survival: implications for mating systems and population growth. Proceedings of The National Academy of Sciences of the United States of America 114: E5474-E5481.

Liker, A., R. P. Freckleton & T. Szekely. 2013. The evolution of sex roles in birds is related to adult sex ratio. Nature Communications 4: 1587.

Rosa, M. E. et al. 2017. The effects of adult sex ratio and density on parental care in Lethrus apterus (Coleoptera, Geotrupidae). Animal Behaviour 132: 181-188.

Vincze, O. et al. 2016. Parental cooperation in a changing climate: fluctuating environments predict shifts in care division. Global Ecology and Biogeography 26: 347-358.

Further specifications of the position Employer: University of Debrecen, Dept. of Evolutionary Zoology & Human Biology, University of Debrecen, H-4032, Egyetem ter 1, Hungary

Job description: * The scientific coordinator/post-doc will carry out research in shorebird populations included in the ELVONAL project (e.g., Madagascar, China, Russia, and South Africa) in regards to mating system and parental care * coordinate research associated with the ELVONAL project: supervise PhD students and research assistants, and coordinate research with external collaborators * coordinate sampling, behavioural recording, data analyses, and

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DebrecenU BreedingSystem

Scientific Coordinator/ Post-doc Position University of Debrecen, Hungary ELVONAL (cutting edge) - Breeding system evolution in shorebirds

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This job offers an opportunity for an experienced post-doc who wants to combine fieldwork with cutting-edge evolutionary and behavioural science. The main tasks of the Scientific Coordinator are to carry out and supervise field studies in Madagascar, Cape Verde, Mexico, Russia, and/or China, possibly in other countries. We seek candidates with experience in behavioural ecology and field biology (preferable with birds), and skills in one of the following fields: behavioural analyses, demography, immunology, epidemiology or comparative genomics. Publications in top peer-reviewed journals, excellent communication skills, and database handling are essential.

This is a full-time position and the salary will be above the normal Hungarian level (up to 2000 EUR, depending on experience). Note that the cost of living in Hungary is substantially less than in the US or Western Europe. The position is initially for 3 years (subject to probation period) with the possibility of extension until the lifetime of the ELVONAL project (5 years). See further specifications below.

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Selected publications Bulla, M. et al. 2016. Defying the 24 1 day: Unexpected diversity in socially synchronized rhythms of shorebirds. Nature 540: 109-1013.

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Dresden PDF PhD BedbugSpeciation

Job: Advanced microscopy and proteomics in ecological speciation of bedbugs

Our collaborative group of researchers from Brno, Prague, Bayreuth and Dresden is seeking to recruit a highly motivated researcher for an ambitious project examining how sperm metabolism and seminal fluid proteins contribute to reproductive isolation of diverging bedbug populations. The position is ideally suited for a PhD student for 3 yrs but postdoctoral applicants (for 2 yrs) can also be considered. Within the project, opportunities exist to apply artificial insemination, microsatellite-based paternity analysis, autofluorescence-based advanced microscopy and mass spectrometry to disentangle genetic from environmental effects on sperm function. The successful applicant will join an international laboratory at TU Dresden (Germany) (https://tudaz.net).

Successful candidates have previous experience, or strong interests, in at least one of the methods (proteomics, cell metabolism, confocal microscopy, paternity analysis) and one of the concepts (ecological speciation, phenotypic plasticity, sperm ecology). The position is paid at TVL E13 65%, amounting to at least 18-20 k Euros net annually for 3 yrs, or 25-27 k Euros for 2 yrs, depending on experience and family status etc.

Applications without photograph and without date of birth should contain a letter of motivation (1 page or less), a cv, your 3 favourite own publications (if you have any), a summary of previous research experience (1 page or less) and contact details of 2 references. Applicants are welcome to provide initials instead of first names. Inquiries can be made with Klaus Reinhardt (klaus.reinhardt@AT@tu-dresden.de). The application, all in one pdf should be sent to the Applied Zoology office (anja.jahn@AT@tu-dresden.de). The deadline for application is 22 March 2018.

Klaus Reinhardt Professor of Applied Zoology Faculty of Biology, TU Dresden Germany https://tudaz.net Klaus Reinhardt <klaus.reinhardt@tu-dresden.de>

Eilat Israel EvolutionSuctionFeeding

Postdoctoral position in Fish Functional Morphology/Feeding kinematics at the Red Sea, Eilat, Israel and UNC Chapel Hill

Qualifications:The position, funded in part by the US-Israel Bi-national Science Foundation, represents a joint position in the labs of Roi Holzman (http://iui-eilat.ac.il/People/AcademicStaffProfile.aspx?sid6) and Christopher Martin (http://labs.bio.unc.edu/martin/). The candidate will be positioned at least 9 months per year in the lab of Roi Holzman in Eilat, Israel (http://iui-eilat.ac.il/), and may spend up to 3 months at UNC.

The research will center on the evolution of suction feeding. The researcher will use in situ high-speed video cameras to capture feeding events by reef fishes in the Red Sea. They will then compare the kinematics of these natural capture events to kinematics predicted as optimized according to a hydrodynamic simulation (the SIFF model, Holzman et al 2012 JEB). Ultimately, these analyses will test the hypothesis that a complex performance landscape for suction-feeding may drive kinematic diversification within the Red Sea community.

For the successful candidate, there will be a relatively high degree of flexibility in terms of specific research questions and methods as long as they are within the overall framework of our grant. We aim to do fundamental research on fish ecology and diversity in order to better predict the evolution of phenotypic diversity in coral reef fishes.

The appointment is for one year, with possible extensions for two more years. Annual support will amount to 102,000NIS (~$30,000 at current exchange rate). Traveling expanses to UNC will be covered by the grant. Applicants from under-represented and diverse backgrounds are especially encouraged to apply. We broadly define diversity to include race, gender identity, national origin, ethnicity, religion, social class, age, sexual orientation, political background, and physical ability.

The work place is at the Inter-University Institute for marine sciences in Eilat, Israel (http://iui-eilat.ac.il/). Research activities at the IUI span the whole spectrum of marine sciences, including ecology, chemical, physical and biological oceanography, ichthyology, Invertebrate and vertebrate biology, neurobiology, molecular biology and marine biogeochemistry. IUI is located on the shores of the Gulf of Aqaba, Red sea, next to a natural and flourishing coral reef. IUI is the home of seven resident faculty groups, with ~40 students and ~40 technical and administrative staff. Many of the students and staff in IUI are international, and virtually all the academic activity in IUI (seminars, lectures, discussion groups) is done in English.

UNC Chapel Hill supports a vibrant community of evolutionary biologists interested in speciation, adaptive radiation, and functional morphology, both within the department and the greater Triangle area through the Physical Biology of Organisms (PBO) group. The postdoc will be integrated into departmental activities and will receive mentoring in professional skills. The quality of life in this area is consistently rated among the highest in the nation.

Basic qualifications:

Strong background in fish functional morphology, biomechanics, or evolutionary ecology. Applicants should have a PhD in a relevant field of biology, ecology, or environmental science and a strong interest in fish evolutionary ecology, functional morphology/ecology, biomechanics, and adaptive radiations. Statistical programming experience is also required. This position involves extensive underwater fieldwork using high-speed video cameras to film reef fishes in the Red Sea at Eilat, hence ability to work in the sea is needed.

Preferred qualifications:

Advanced statistical programming skills in R and background in fish functional morphology, particularly kinematics or PIV. Additional experience with morphometrics, Matlab or python, and marine fieldwork is also a plus. SCUBA certification is desired.

Applications must be submitted by 15th March 2018 by e-mail to Roi Holzman (holzman@post.tau.ac.il).

Applications should include an application letter describing your interests and their relevance to this position, a CV, and the names and contact information for three references. The starting date should optimally be around Sept 2018, but is very flexible. The position is for 12 months with the possibility of renewal dependent on performance. For further information, please contact Roi Holzman (holzman@post.tau.ac.il) or Christopher Martin (chmartin@unc.edu).

Roi Holzman <holzman@post.tau.ac.il>

GeorgeWashingtonU Bioinformatics

Postdoctoral Scientist

Job Posting at https://www.gwu.jobs/postings/49199 Application Review Begins February 20^th, 2018

The Computational Biology Institute in George Washington University's Milken Institute School of Public Health is seeking a highly motivated Postdoctoral Scientist (PDS). The work performed by the PDS will contribute to our diverse research program devoted to the investigation of: i) the role of microbial infection and host immunity in the etiology of respiratory and gastrointestinal disorders and ii) the impact of microbiomes in natural and artificial ecosystems.

The PDS will focus on Omic-based research (metagenomics, metatranscriptomics and transcriptomics) on two main topics: i) the impact of microbial diversity and function on human heath (host-microbe interactions), and ii) the ecological role of microbes in soil-plant ecosystems (microbe-environment interactions).

These studies are part of ongoing collaborations between national (Children's National Hospital, Washington DC) and international institutions (University of Vigo, Spain and Universidad Andres Bello, Chile) and the Computational Biology institute, George Washington University.

The selected candidate will be based on the Computational Biology Institute in Washington DC. For further information about the Computational Biology Institute at George Washington University, please seehttp://cbi.gwu.edu. All applications for consideration must be submitted online but for questions relating to this opportunity, please contact Dr. Perez-Losada, Computational Biology Institute, Milken Institute School of Public Health, The George Washington University, at mlosada@gwu.edu.

Responsibilities Include:

- Design and carry out analysis of high-throughput sequencing data (16S rRNA, DNAseq and RNAseq) - Engage in research projects on the basis of the analysis of sequencing data - Collaborate with other lab members in the development of strategies for high-throughput sequencing data analyses - Prepare research papers and presentations to disseminate research results through academic journals and conferences - Work with other lab members on projects as assigned - Performs other related duties as assigned. The omission of specific duties does not preclude the supervisor from assigning duties that are logically related to the position.

Preferred Qualifications:

- Applicants must possess a PHD in a relevant discipline (Computational Biology, Bioinformatics, Microbiology and Microbial Ecology), with experience in Genomic and Systems Biology analyses and an understanding of the key issues and relevant tools in the field.

- A good understanding of multivariate statistics is essential.

- A strong quantitative background and good programming skills (R, Python/Perl), Big data managing and integration are all required

- Experience with DNA and RNA extraction and sequencing is useful but not essential.

Professor Keith A. Crandall, PhD Director, Computational Biology Institute Director of Informatics, CTSI-CN Milken Institute School of Public Health The George Washington University 800 22nd Street, NW - Suite 7000D Washington, DC 20052-0066 USA (o): 571-553-0107 (m): 202-769-8411 Twitter / LinkedIn

"Professor Keith A. Crandall" <kcrandall@gwu.edu>

HarvardMedSchool MicrobialEvolGenetics

Summary

The Department of Biomedical Informatics (DBMI) at Harvard Medical School and the Farhat-Lab is looking for a Postdoctoral Fellow in infectious disease genomics.

Mycobacterium tuberculosis displays a remarkable range of variability in antibiotic resistance phenotype. Elucidating the biological mechanisms for these differences is a fundamental question in the study of infectious diseases in general and in Mycobacterium tuberculosis specifically as it allows for the more accurate prediction of phenotype from genotype, and improved clinical and diagnostic interpretation of molecular diagnostics. Specifically here the project will focus on the detection of gene-gene/mutation-mutation interaction effects using whole genome sequencing data from clinical isolates of M.tb.

Responsibilities

The Postdoctoral Fellow will be responsible for developing and applying computational methodologies to identify novel infectious disease genomic markers and to assess their diagnostic and surveillance potential.

Basic Requirements

We are an interdisciplinary lab. Candidates may have a PhD degree in Network science, evolutionary biology, bioinformatics, computational biology, biostatistics, or a related field. The candidate interested in this position must be highly motivated and demonstrate initiative in assigned tasks and have experience working with large multivariate data sets, and have thought of or is highly interested in studying variable interactions in such datasets.

Additional Requirements

Experience in programming R, Python, and/or Perl and statistical analysis or at least an interest in learning these skills will be necessary. The candidate and PI can work together to delineate the fellows training needs and develop a program to fulfill this utilizing the department and university's wide range of resources.

Terms

The position is available on 3/15/2018 and can be renewed annually.

How to apply

Email applications including curriculum vitae, summary statement of personal objective and research interests, PDFs of the best two papers, and the names and email addresses of three references to mrfarhat@partners.org

Harvard Medical School is an Equal Opportunity/Affirmative Action Employer.

Women and minorities are especially encouraged to apply.

For additional information:

http://farhat-lab.hms.harvard.edu/ Maha Farhat, MD, MSc Assistant Professor Department of Biomedical Informatics, Harvard Medical School Assistant Physician

Pulmonary and Critical Care, Massachusetts General Hospital

"Farhat, Maha Reda" <Maha_Farhat@hms.harvard.edu>

Hobart Tasmania KinMarkRecapture

Advertised Job Title: CSIRO Postdoctoral fellow 'V Close-kin Mark Recapture Methods Reference Number: 56089 Classification: CSOF4 Salary Range: AU $83K to AU $91K plus up to 15.4% superannuation Location: Hobart Tenure: Specified Term of 3 years Relocation assistance: Will be provided to the successful candidate if required. Applications are open to: All Candidates

Functional Area: Research Scientist / Engineer 'V Postdoctoral Fellow Reports to the: Team Leader, Pelagic Predator Ecology and Dynamics

Role Overview: Postdoctoral Fellows at CSIRO provide opportunities to scientists and engineers, who have completed their doctorate and have less than three years relevant postdoctoral work experience. These fellowships will help launch their careers, provide experience that will enhance their career prospects, and facilitate the recruitment and development of potential leaders for CSIRO.

Postdoctoral Fellows are appointed for up to three years and will work closely with a leading Research Scientist or Engineer in their respective field. They carry out innovative, impactful research of strategic importance to CSIRO with the possibility of novel and important scientific outcomes. They present the findings in appropriate publications and at conferences.

This role requires a statistician to work on population modelling and genetics aspects of Close-kin Mark Recapture. The primary role will be to develop and extend a suite of statistical methods for identifying genetically related pairs of individuals in large samples, to estimate the abundance and other demographics of wild marine populations. The main goal is to find parent-offspring, half-sibling pairs and more distant kin. A central component of the research is to develop statistical techniques to take advantage of the latest genetic sequencing technologies, and to investigate their potential through applications to species with different life-histories. Data are available from existing and planned projects on sharks, tunas, and other fish species. A second task will be to explore development of new approaches to inferring population structure in large, highly fecund marine populations through the combination of close-kin and conventional population genetics data. For both tasks, we expect the incumbent to work with population geneticists to refine the genetic techniques to facilitate large-scale, cost-effective implementation for monitoring commercially harvested species and species “at risk” from a conservation perspective.

The successful candidate will be part of an internationally recognised research group in population dynamics, assessment and applied resource and conservation management.

Duties and Key Result Areas:

Under the direction of the Project Leader, evaluate a range of genetic techniques and their utility for a range of close-kin mark-recapture applications. - Develop and apply close-kin methods for new species based on next generation sequencing techniques and genome complexity reduction. - Develop and trial genetic and statistical techniques to detect a range of close-kin relationships, using low-cost approaches to coarse-level genome assembly. - Explore the integration of close-kin and population genetics approaches for estimating structure and connectivity in marine populations. - Communicate effectively and respectfully with all staff, clients and suppliers in the interests of good business practice, collaboration and enhancement of CSIRO’Âs reputation. - Work collaboratively with colleagues within your team, the business unit and across CSIRO, to reach objectives. - Adhere to the spirit and practice of CSIRO’Âs Values, Health, Safety and Environment plans and policies, Diversity initiatives and Zero Harm goals. - Other duties as directed.

CSIRO’Âs postdoctoral training program is developed between the Postdoctoral Fellow and a CSIRO scientist. The program will focus on enhancing the Fellows’Â capabilities to the level expected of an independent researcher and will include on-the-job and course-based development encompassing: - Discipline-specific techniques and protocols - Professional growth - Project management - Communication and influencing skills - Working and collaborating with others http://www.csiro.au/en/Careers/Student-and-graduate-programs/Postdoctoral-fellowships Selection Criteria: Under CSIRO policy only those who meet all essential criteria can be appointed

Pre-Requisites: - Education/Qualifications: A doctorate (or will shortly satisfy the requirements of a PhD) in statistics, population modelling or quantitative population genetics and evidence of original work in this field.

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INRA ValdeLoire QuantPopulationGenetics

We are looking for a highly motivated, creative and enthusiastic young scientist to join our team “/prediction and management of genome and population diversity in forest trees/” within the BioForA research Unit at INRA Val de Loire (Orléans, France). Our ideal starting date is June 2018, but there is some flexibility.

Context and project description

Genome-wide evaluation (GWE) is a disruptive breeding methodology for many species. One of the key advantages is the accuracy with which the Mendelian sampling term can be assessed, with the consequence being that extra genetic gain can be produced without further increase in inbreeding. Last two decades have seen GWE research focused on factors affecting accuracy (estimation methods, data integration and design of training populations among others). Comparatively little has been done on the impacts that this extra accuracy might have on the genetic diversity at the whole genome scale. GWE can accelerate the sequence of selection cycles, with consequently faster accumulation of inbreeding / time. This happens whenever phenotypic evaluation determines the length of the breeding cycle and both genotyping and mating are available at much earlier stages, which is the case of many perennials like forest trees. Therefore, GWE presents some contrasting prospects for tree breeding, with earlier precision but faster drift, in a global context of climatic change that requires a rationalization in the use of available forest genetic resources over the long term.

Some solutions exists since the advent of pedigree-based evaluation, like optimum contribution selection and mate allocation, which use average coancestry constraints. However, information of inbreeding or diversity variation across genomic regions is neglected when constructing such constraints. Indeed, genomic regions might be affected differentially by boosted selection pressures, like those of GWE, and this be reflected into variation in drift and loss of diversity across markers.

The successful candidate will contribute to perfect a prototype under development in our team for selection and mate allocation that accounts for the across genome diversity in prospective offspring. The tool will be devised to improve coherently genetic gain and diversity management in the context of GWE, by setting specific weights depending on the genomic regions of interest. This tool will be assessed via computer simulations with in-house tools and through a proof-of-concept in black poplar, for which mating is a key element in the breeding. Real data and tools are already available. Work will be done in collaboration with a PhD student of our team, who has already developed the first GWE models in poplar and has monitored the first impacts of their use on genome-wide diversity. The goal of the postdoc is to produce a methodological paper, accompanied by the release of a tool, and to contribute to a case study paper.

Research environment

Our team has long research experience in genetics, genomics and biometry, as well as in conducting breeding programs for several of the main commercial tree species in France, including the model species of the project, black poplar. The successful candidate will interact with a multidisciplinary team of geneticist and physiologists, and will find readily local support on key issues like bio-informatics, if revisiting genomic data is eventually required, or high performance computing where the host has all required resources, locally and remotely.

The postdoc is funded by H2020 GenTree (http://www.gentree-h2020.eu/), and there will be opportunities to interact on the subject with the consortium scientific community.

We believe our team will make a great scientific environment for a young scientist. Moreover, Orléans is attractively situated by the beautiful Loire River, offering rich culinary, cultural, and outdoor possibilities.

Required qualifications & skills

We are looking for candidates with a Ph.D in quantitative, population genetics or statistical genomics, with experience in genetic analysis and programming (C, FORTRAN, R). Experience in developing and/or using simulation tools in quantitative/population genetics is a definite plus.

The candidate will be encouraged to contribute to the scope and reach of the project by own ideas and approaches. An eventual extension of the grant will be highly conditioned to the holder's input, to the level of fulfillment and holder's involvements. We expect from the successful candidate to be independent, creative, and with strong collaborative skills.

Terms & salary

12 months contract. Salary could vary depending on experience. For the equivalent to a permanent researcher with 5 years postdoctoral experience: 3,700 euro before taxes.

Application instructions

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IowaStateU AvianComparativeImmunology

Beginning as soon as April 2018, a postdoctoral position is available to study tolerance of infection in the lab of Dr. James Adelman at Iowa State University. This project will use comparative, molecular, and experimental techniques to uncover patterns, mechanisms, and consequences of tolerance in an ecologically relevant host pathogen system: house finches infected with Mycoplasma gallisepticum. The postdoc will be responsible for overseeing field and laboratory objectives of this project, while generating additional, related experiments that augment the project's goals. The postdoc will also help mentor graduate and undergraduate students in the lab to enhance their abilities in independent research.

Minimum requirements include a PhD in biology, ecology, or a related field, with some experience in immunological and molecular techniques, experience working with birds or other small vertebrates, excellent written and oral communication skills, a strong publication record, and the ability to work both independently and with diverse research teams. Ideal applicants will have an interest in travel, as this project involves fieldwork in diverse locations and collaboration with colleagues at Virginia Tech. Experience with RNA expression, disease ecology, and successful mentoring of undergraduates is also desirable.

To apply, please submit a cover letter outlining your interest in the position, research experience, and career goals; a curriculum vitae; reprints of up to two published papers; and contact information for three references. All materials should be sent to Dr. James Adelman at adelmanj@iastate.edu.—

Review of applications will begin March 15, 2018, with an anticipated start date before June 1, 2018. Salary for postdocs at Iowa State begins at $46,000 per year, with benefits, and increases depending on prior postdoctoral experience. Funding is available for three years, dependent on favorable annual performance evaluations. Iowa State University is an Equal Opportunity/Affirmative Action employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability, or protected Veteran status and will not be discriminated against.

"Adelman, James S [NREM]" <adelmanj@iastate.edu>

IST Austria SnapdragonPopulationGenetics

A postdoctoral position is available, for field research into the population genetics of Antirrhinum (snapdragon). The project focusses on a hybrid zone in the Pyrenees, between subspecies that differ in flower colour: plants in the hybrid population have been genotyped for major genes that determine flower pattern, and for large numbers of SNPs that allow the pedigree to be determined over multiple generations. The aim is to find why the subspecies remain distinct, and how they diverged from each other, and more generally, to use this long-term study to understand the interplay between selection and population structure in nature.

This is a joint project between Nick Barton, at the Institute of Science and Technology, Austria (http://ist.ac.at/research/research-groups/barton-group/) , David Field, at the University of Vienna (http://molecology.univie.ac.at/about-us/david-field/), and Enrico Coen, at the John Innes Institute in Norwich (http://rico-coen.jic.ac.uk). The postdoc would be based at IST; she/he would be involved in fieldwork and analysis of genetic data.

The Institute of Science and Technology is a new multidisciplinary research institute, located in the Wienerwald, just outside Vienna (www.ist.ac.at < http://www.ist-austria.ac.at/ >). There are close links with other population genetics groups in the Vienna area (www.univie.ac.at/evolvienna/).

The position will be available for two years in the first instance, but with the possibility of extension; the salary scale starts at Â51K p.a. Applicants should have a Ph.D. in a relevant area, with good quantitative skills, and an interest in evolutionary biology. For further details, please contact nick.barton@ist.ac.at. Applications should be sent by February 23rd, and should include a CV, a statement of research interests, and names of referees.

Nick Barton

IST Austria Am Campus 1 Klosterneuburg 3400 'phone: (43)2243 9000 3001 www.ist-austria.ac.at nick.barton@ist.ac.at

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JamesCookU QuantGenomics

The link to apply is

https://www.jcu.edu.au/careers-at-jcu/vacancies/-research-jobs 16277: Research Fellow- (Quantitativegeneticist/ genomicist) - James Cook University

Position closes Monday 26/02/2018 </p>

Position Overview:

The Research Fellow will guide and conduct research activities within a collaborative CRC DNA project, Breeding for resistance to juvenile pearl oyster mortality syndrome (JOMS). The incumbent will primarily determine correlative factors associated with the occurrence of JOMS and gather the essential genetic knowledge required to instigate a selective breeding program within a functional pearling farm via commercial partners.

The Research Fellowwill conduct research activities within the research team under the primary supervision of the project leader. The incumbent will also complete project specific administration functions, report writing and the co-supervision of postgraduate students.

Principal Accountabilities:

1. Contribute to the design and conduct of experiments, including acquisition and modelling of phenotypic / environmental data to understand tolerance to JOMS in pearl oysters.

2. Undertake quantitative genetic analyses to estimate phenotypic genetic parameters (eg., heritability, breeding values and trait correlations)

3. Undertake quantitative genetic and QTL localisation analyses to identify any genes of major effect and trait architecture.

4. Undertake bio-statistical analyses to estimate correlative relationships between JOMS resistance; and nutritional, physiological, bacterial and environmental

factors.

5. Use Genotype by Sequencing (GBS) methodology, incorporating computational and statistical approaches, to determine relatedness and diversity of pearl oysters to inform a selective breeding program.

6. Co-supervise honours and higher degree research students.

7. Communicate quality research in high ranking international scientific journals and provide conceptual support to projects.

8. Utilize appropriate and current techniques/protocols in experimental laboratorymanagement to ensure integrity, security and replicability of experimentalprocedures.

Contact Phone (07) 4781 6532

Contact Name KyallZenger

Contact Email kyall.zenger@jcu.edu.au

Kristin Nunn

Research Project Officer College of Science and Engineering James Cook University, Townsville QLD 4811 AUSTRALIA Ph: (07) 47816318

Mob: 0401 579 414

Email:kristin.nunn@jcu.edu.au

"Nunn, Kristin" <kristin.nunn@jcu.edu.au>

MasseyU ComputationalGenomics

Postdoc in Computational Genomics Massey University, New Zealand

I am looking for a motivated postdoctoral fellow to explore the evolution of genome structure in filamentous fungi. My group is interested in interactions between genome structure and gene expression, epigenetic modification and 3D conformation. A key focus of this postdoc will be on how interactions like these change over evolutionary time. This research program will build on a growing set of genomic data for the genus Epichloe, an increasingly important model system for studying the genome evolution of haploid and polyploid fungi.

The postdoc will be expected to help develop her/his own research program, with an emphasis on addressing novel hypotheses rather than data description. This analytical position requires solid quantitative and computational skills, with the ability to develop and apply new bioinformatic applications to genome analysis. At a minimum, some confidence in bioinformatics and a programming language is required. Training in fungal biology or genomics can be provided as needed, and candidates from non-standard research backgrounds with a clear fit to the position are encouraged to apply.

Funding is guaranteed for two years and three months, but may be extendable. Salaries are extremely competitive, starting at NZ$69,000, considerably higher than comparable salaries in the US and Europe. Items considered benefits in some other countries, such as healthcare coverage, are a standard right in New Zealand.

My research group aims to achieve work-life balance within a productive scientific environment. The team is firmly embedded in the international scientific community, with extensive collaborative links to Australia, Asia, Europe and the United States. Ongoing training is a key focus for postdocs. As a computational biology group, I offer a supportive environment for computationally-inclined postdocs to work towards independence. The successful candidate will not be a lone bioinformaticist isolated in a bench biology group.

My group is highly international, and applicants from all countries and backgrounds are actively encouraged to apply. Members of underrepresented groups are welcome, as are postdocs with families.

The position will be based in my computational biology research group at Massey University in the city of Palmerston North, New Zealand. This offers a rare opportunity to experience New Zealand's unique natural and cultural environment, while still undertaking world leading research. Palmerston North, a university town with a large international community, offers a full range of social and cultural amenities. The city is located between mountains and the sea, and presents regular opportunities for hiking, skiing, surfing and adventure sports. It also has a good café scene for those of a more cosmopolitan bent.

For further information, please visit my group's website (http://massey.genomicus.com) and the website of our funder, the Bio-Protection Research Centre (http://-bioprotection.org.nz). Please contact me directly if you have any further questions (m.p.cox@massey.ac.nz).

To apply for this position, upload the following documents at the official Massey University job website: http://massey-careers.massey.ac.nz/10118/-postdoctoral-fellow-in-computational-genomics 1. A brief statement of research interests and experience, focusing on short to mid-term career goals. 2. A curriculum vitae, including qualifications and scientific publications. 3. The names and contact details of three referees willing to provide a confidential letter of recommendation upon request.

APPLICATION DEADLINE: Saturday 24 February 2018

Prof Murray Cox Statistics and Bioinformatics Group Institute of Fundamental Sciences Massey University Palmerston North New Zealand

http://massey.genomicus.com m.p.cox@massey.ac.nz

murray.p.cox@gmail.com

Montpellier Classification eDNA

Postdoc position on alignment-free taxonomic classification of environmental DNA

The Methods and Algorithms for Bioinformatics (MAB) team at the computer science department of the University of Montpellier, France (the LIRMM) is looking for talented individuals to fill an 18-months postdoctoral position. The successful candidate will work on a novel approach for the identification of the species behind the DNA found in an environmental sample. The originality of the approach lies in the application within evolutionary analyses of ideas from string algorithmics that avoid the computationally-intensive task of sequence alignment. A detailed description of the research project can be found here: https://sites.google.com/site/fabiopardi/postdocs . The applicant should have a background in bioinformatics with an emphasis on algorithmic and software developments for biological sequence analysis and computational genomics. Previous research experience in one of the following topics in bioinformatics will be considered as an advantage: metagenomics, alignment-free sequence analysis, molecular evolution, computational phylogenetics. Regardless of her/his background, the applicant's past research should show a strong motivation towards solving biologically-relevant problems in a rigorous way, using state-of-the-art techniques and/or developing novel methodologies. Good programming skills, as well as an ability for autonomous work, are essential.

Interested applicants should send a CV, and a brief description of research accomplishments and goals to F. Pardi (pardi@lirmm.fr) and E. Rivals (rivals@lirmm.fr). Applicants should have been awarded a Ph.D. within the last 4 years or should be graduating imminently. Successful candidates are required to start by 1 October 2018 at the latest. The salary for the position is about 2,200 euros net per month plus benefits.

A one-thousand-year-old city, Montpellier is a thriving research community with a multitude of research centers in life sciences. It is the fastest growing city in France where approximately one third of the population are students, and a great location for outdoor activities. The LIRMM is one of the most visible computer science laboratories in France.

Fabio Pardi <pardi@lirmm.fr>

Montpellier EvolutionSexPygmyMice

A two-year post-doctoral position is open at Institut des Sciences de l'ÂEvolution, Université de Montpellier, France, to study evolutionary genomics of natural sex-reversal in a mouse species.

In natural populations of the African Pygmy mouse (Mus minutoides), two types of X chromosomes co-exist, one of which (named X*) is feminizing. This induces a drastic change in the modes of transmission of sex chromosomes, which in this system can thus be either strictly female (X*), or bisexual (X and Y). We study in the lab differences of life-history traits associated with the different sexual types (XX, X*X and X*Y females, XY males), in order to understand how this new mode of transmission contributes to the evolution of sex-linked phenotypic differences and of potential antagonism over their control.

The post-doc will study the genomic aspects of this question, by analyzing various available datasets:

-Participate in the /de novo/ assembly and annotation of the X and X* chromosomes.

-Analyse differential gene expression between sexual types from RNA-seq data.

-Analyse population genomics data.

The post-doc will work in Montpellier at Institut des Sciences de l'ÂEvolution (with Frédéric Veyrunes and Pierre Boursot), in close collaboration with The Earlham Institute, Norwich, UK (David Thybert) and the Institut de Génétique Humaine, Montpellier (Francis Poulat).

The candidate should have strong proven skills in bioinformatics for genomic data analyses (genome and transcriptome sequences). A background in biology (molecular or evolutionary biology) would be a plus.

The candidate should preferably have defended his/her PhD no longer than 4 years before the start of the post-doc, and should preferably not have worked in Montpellier during the last two years.

Salary will be according to the rules of Université de Montpellier, up to 2200 Euros/month net, depending on experience.

Starting date: from May 2018 to October 2018 at the latest.

Deadline for application: March 12, 2018. The call may be prolonged beyond this date in case it is not fruitful.

Send a CV, a motivation letter and the coordinates of at least two references to frederic.veyrunes@umontpellier.fr and pierre.boursot@umontpellier.fr

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Dr. Pierre BOURSOT Institut des Sciences de l'Evolution (UM-CNRS UMR5554, IRD UMR226) Universite Montpellier Case Courrier 063 Place Eugene Bataillon 34095 Montpellier cedex 5 FRANCE tel: +33 (0)4 67 14 46 86 Email: pierre.boursot@umontpellier.fr

Pierre Boursot <pierre.boursot@umontpellier.fr>

Munich PlantSexDetermination

Postdoc position to work on floral-development genes and plant sex determination at the Ludwig-Maximilians University in Munich and in Gif-sur-Yvette

We are seeking to recruit a scientist at the post-doctoral level ('Wissenschaftlicher Mitarbeiter'; salary TV-L 13 = DFG postdoc E 13 Level 3) to work on sex determination in the economically important Cucurbitaceae family, specifically on the assembly of a genome of a dioecious species in the Cucumis/Citrullus clade. The project centers on bioinformatics and involves collaboration between the labs of Abdel Bendahmane (Institut of Plant Sciences Paris-Saclay) and Susanne Renner (University of Munich). The postdoc will spend time in both labs, with Munich being the main location. The data will come from third-generation sequencing platforms uses single-molecule sequencing, namely Oxford Nanopore Technology (MinION) and Pacific Biosciences (PacBio). The position will start when the data are ready for analysis. The assembly will focus on three gene families known to be involved in floral sex determination; functional characterization of X- and Y-linked sex genes will be carried out in the Bendahmane lab.

The position starts in the late spring of 2018 and is for initially two years, with the possibility of a one-year extension. Candidates must have a doctoral degree in the area of plant genomics and experience in bioinformatics. Knowledge of German or French is not required, but obviously helpful for enjoying life in Munich and Paris.

Candidates should submit their CV, including a list of publications and a statement of research interests, along with the contact information of two referees to Professor Susanne Renner (renner@lmu.de). Deadline: 28 February 2018 or when position is filled.

Recent and ongoing work in the Bendahmane lab: http://www.versailles.inra.fr/urgv/analysis-cropFunctionalGen.htm Work in the Renner lab: https://scholar.google.de/citations?user=-uzOGmTgAAAAJ&hl=en Susanne Renner <renner@lmu.de>

NortheasternU GenomicsComputationalBiology

We are still accepting applications for the postdoc position advertised below until Feb 28, 2018. We are looking for someone enthusiastic about the research and encourage applicants with a diverse range of skills and backgrounds to apply.

A postdoctoral position is available with K. E. Lotterhos at Northeastern University and Sam Yeaman at the University of Calgary. The successful candidate will be part of an NSF-funded project to develop and evaluate multivariate methods for analyzing genomic data, including machine learning methods.

Qualifications Applicants will be expected to develop and lead projects. Candidates are required to have a Ph.D and knowledge of one or more programming languages (command line, R, python, etc). Candidates should demonstrate a strong track record of publication; have strong organizational, written, and oral communication skills; and be able to work both independently and as part of a collaborative team.

Additional Information The appointment is for 24 months. Start date is flexible.

The Lotterhos Lab is based at the beautiful in Nahant campus north of Boston (NUMSC). The NUMSC has a strong research presence in evolution and ecology research, and there are many opportunities for interaction and collaboration both there and in the greater Boston area.The successful candidate will also have opportunities to travel to Calgary for extended periods of time for collaboration, and to manage a diverse team of collaborators. We welcome applications from candidates with diverse backgrounds.

To apply, please prepare a CV, cover letter, references, and one peer-reviewed publication and upload them at this site: https://neu.peopleadmin.com/postings/49443 Please contact Dr. Lotterhos with any questions at k.lotterhos@neu.edu

K. E Lotterhos Assistant Professor Department of Marine and Environmental Sciences Northeastern University Marine Science Center, Room 113 430 Nahant Rd Nahant, MA 01908 Phone: 781.581.7370 ext 304

Katie Lotterhos <k.lotterhos@northeastern.edu>

NotreDame LifeHistoryEvolution

A postdoctoral position is available to study developmental and social origins of individual health and fitness in the Archie Lab at the University of Notre Dame (http://sites.nd.edu/archielab/). The position is for 1 year with the option to extend for up to 3 years. The postdoc will have access to extensive longitudinal data from the well-studied Amboseli baboon population (http://amboselibaboons.nd.edu/), a leading primate model in evolution, ecology, and for understanding social-behavioral predictors of health and aging. The Amboseli baboon population has been the subject of long-term, individual-based study on baboon ecology, social behavior, health, and demography since 1971. Prior publications especially relevant to this project include Tung & Archie et al. (2016) in Nature Communications, Archie et al (2014) in Proceedings of the Royal Society, and Lea et al. (2018) in Evolution, Medicine, and Public Health.

Several projects are available, including: (i) testing evolutionary hypotheses to explain developmental origins of health and disease, such as predictive adaptive response and developmental constraints models; (ii) testing health selection and social causation hypotheses to understand the causal links between early adversity, social context, adult health, and aging; and (iii) testing critical periods and windows of sensitivity in explaining developmental origins of health and disease. Strong, experienced applicants are also encouraged to develop their own research questions. The Amboseli baboon data set is exceptionally rich and amenable to a wide range of projects, either on the baboons themselves or in a comparative context with other species, including humans.

Qualifications

Candidates must have a PhD in biology or a relevant social science (or plan to graduate in the summer or fall of 2018). The ideal candidate will have outstanding skills in data analysis, writing, and oral communication. Candidates with experience in one or more of the following areas are especially encouraged to apply: population-based database analysis, population biology, biodemography, life history evolution, social behavioral research, demographic modeling, mixed modeling, longitudinal data analysis, path analysis, causal inference, and/or epidemiology. Familiarity or experience with long-lived social vertebrates, including humans, may be helpful, but is not essential.

Application Instructions

To apply for the position please send an email to Elizabeth Archie (earchie@nd.edu), including a cover letter, CV, and contact information for three references. The anticipated start date is in summer or fall 2018. Applicants should submit their materials by March 30, 2018 to ensure full consideration.

The Archie lab offers a congenial research environment that fosters strong interdisciplinary training and collaborative exchange. Collaborators on this project include Susan Alberts (https://sites.duke.edu/albertslab/-), Fan Li (http://www2.stat.duke.edu/~fl35/), and Ran Blekhman (http://blekhmanlab.org/), all of whom are available for advice and interaction.

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

OmahaZoo SequencingData

Summary:

Omaha's Henry Doorly Zoo & Aquarium Department of Conservation Genetics based in Omaha, Nebraska, is seeking one post-doctoral researcher with interest/expertise in the generation and analysis of next-generation sequencing data of lemurs, tortoises, and other taxa from Madagascar.

Duties and Responsibilities (include but not limited to):

The successful applicant will be proficient in the construction genomic libraries and in solution hybridization methodologies for high throughput sequencing as well as all relevant analysis of large datasets, and manage next-generation sequence workflows.

The researchers will be responsible for development, implementation, and support of software applications related to variant detection and interpretation from high-throughput experiments involving multiple species of lemurs, tortoises, and taxa from Madagascar.

Assembly of whole genomes is in-progress, but will likely require additional analysis pertinent to specific research projects. Interested candidates should be highly motivated, organized, independent, and have extensive experience with molecular genomics and bioinformatics, and be able to efficiently write and revise manuscripts. Data on a variety from a variety of species has already been generated, thus candidates will be able to quickly start analysis and manuscript preparation.

Travel to Madagascar to support the field programs of Omaha Zoo and the Madagascar Biodiversity Partnership to Madagascar is required for a single three-week interval once a year.

WORKSKILLS: Strong people skills, detailed oriented, willingness to learn and contribute, follow directions, meets deadlines

Basic Qualifications:

The applicant should hold a PhD in bioinformatics, computer science, molecular genomics or related field and have more than one year of experience in high-throughput genome sequence analysis. Applicant should be experienced at software related to next generation sequencing data and be able to manipulate genomic data for phylogenetics and phylogeography. Our group's focus is large-scale sequencing for phylogenetics, phylogeography and evolutionary studies of lemurs (specifically the genera Daubentonia Lepilemur, Microcebus, Propithecus, and Varecia) and tortoises (genera Astrochelys and Pyxis) from Madagascar. Thus, previous experience in genome assemblies, annotation and analysis of a variety of next generation sequencing (NGS) pipelines is preferable. The ideal candidate will be independent, highly motivated, productive, and able to work effectively in a team with members from a variety of diverse backgrounds, and have outstanding written and verbal communication skills. The successful applicant must be interested in interdisciplinary science and field research and have a solid publication record that illustrates ability to conduct novel, independent research.

Preferred Qualifications

Candidate should have 3+ years of experience in molecular biology, genetics, or bioinformatics. The position requires proficiency in programming (perl or python) and bash scripting using Linux operating systems. Applicants are also expected to be familiar with bioinformatics tools, should be able to implement complex computational pipelines, incorporate genomics databases and have extensive and creditable laboratory experience with constructing genomic libraries. The applicant will need to work closely with two full time technicians to manage NGS lab work, as well as with a full time bioinformatician. While in Omaha the researchers will work with a variety of Malagasy graduate students, and is expected to assist with the progression of a variety of projects, and assist with completion of their degrees and peer-reviewed manuscripts. Based on all these above duties requires a candidate with excellent interpersonal skills, and the ability to train and teach both national and international audiences is necessary. Candidates must also be able to jump between a variety of projects, based on needs of the research group.

Time Frame

These positions will be part of an on-going team of rotating postdoc fellows. This position is expected to begin in mid-2018. Initial appointment will be for two years, with possibility to extend to three years.

Application

Please submit your CV with the contact information for 3 professional references, a letter describing your interests and goals, and copies of a few publications. Please apply at: http://www.omahazoo.com/careers/ Learn more at: https://madagascarpartnership.org/

From: Genetics Department Sent: Thursday, December 7, 2017 2:34:51 PM To: Golding@McMaster.CA Subject: EvolDir -for announcement section

Omaha's Henry Doorly Zoo & Aquarium Department of Conservation Genetics (OHDZA-CG) based in Omaha, Nebraska, is seeking a postdoctoral researcher with interest/expertise in the generation and analysis of

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Salford UK eDNA metabarcoding

Dear all,

We are looking for an enthusiastic, motivated, skilful postdoc, to join us in the final phases of the project SeaDNA. The candidate will be primarily responsible for preparing metabarcoding libraries, analyse data, and contribute to several manuscripts.

The post is for 15 months and will be based in S. Mariani's group at Salford (www.marianilab.org) and will be part of a NERC-funded team that includes Bristol, Imperial College, BAS and the MBA.

We seek someone ready to start in March/April - details here:

https://atsv7.wcn.co.uk/search_engine/jobs.cgi?owner=3D5036328&ownertype=3Dfair&jcode=-1697922&vt_template=919&adminview=1
"S.Mariani@salford.ac.uk" <S.Mariani@salford.ac.uk>

SarsCentre Norway ComparativeGenomics

Research Fellow Position (post-doctoral grade) in Comparative genomics and single-cell transcriptomics of animals

http://www.sars.no/jobs/2018-1711_researchfellow_ERC_Hejnol.php A 2-year Research fellow position (code 1109) is available at the Sars International Centre for Marine Molecular Biology, in the research group headed by Andreas Hejnol. The position is within the project "Comparative genomics and single-cell transcriptomics", and is available from August 2018. The position is funded in the framework of the ERC Consolidator Grant "EVOMESODERM - The evolution of mesoderm and its differentiation into cell types and organ systems" (http://cordis.europa.eu/project/rcn/197107_en.html) awarded to Dr. Andreas Hejnol.

About the project/work tasks: The project will be conducted at the Sars International Centre for Marine Molecular Biology (Bergen, Norway) in the group "Comparative Developmental Biology of Animals" of Dr. Andreas Hejnol. The Hejnol group studies a broad range of mainly marine invertebrates using genomic, embryological, and advanced microscopic and molecular methods. The successful candidate will analyze de-novo sequenced genomes of marine invertebrates and analyse single-cell sequencing data from a comparative and developmental perspective. The project is also in close relationship with project within two MSC Innovative Training Networks EvoCELL (https://www.evocell-itn.eu) and IGNITE (http://www.itn-ignite.eu).

Qualifications and personal qualities:

- The applicant must hold a PhD or equivalent degree or must have submitted his/her doctoral thesis for assessment prior to the application deadline. It is a condition of employment that the PhD has been awarded - Strong motivation to perform research at an internationally competitive level - Experience in a programming language (C/C++/Perl, Python) and proficiency in shell scripting in a Unix environment is required - Previous experience in genome analyses and a good background in evolutionary biology and developmental biology is of advantage - Ability to work both independently and in close collaboration with others in a structured manner - Proficiency in both written and oral English

We can offer:

- A good and professionally challenging working environment - Good career perspectives through intersectoral networking through the affiliation with two Innovative Training Networks comprising more than 20 research labs in Europe and four innovative companies - Salary at pay grade 57 upon appointment (Code 1109), currently NOK 490.900 gross p.a. Further promotions are made according to length of service in the position - Enrolment in the Norwegian Public Service Pension Fund - A position in an inclusive workplace (IA enterprise) - Good welfare benefits

Your application in English must include:

- A cover letter that includes a brief account of the applicant's research interests and motivation for applying for the position - CV - List of publications - The names and contact information for two reference persons. One of these must be the applicant's main PhD supervisor - Transcripts and diplomas and an official confirmation that the doctoral thesis has been submitted - Relevant certificates/references The application and appendices with certified translations into English must be uploaded at Jobbnorge. Please go to "Apply for this job" - see here. Please note that applications will be assessed only with the information available in JobbNorge when the deadline expires. It is the applicant's responsibility to ensure that all relevant attachments are submitted by the deadline.

Application deadline: February 28, 2018

General information: Detailed information about the position and project can be obtained from Group Leader Andreas Hejnol, email andreas.hejnol@uib.no.

The state labour force shall reflect the diversity of Norwegian society to the greatest extent possible. Age and gender balance among employees is therefore a goal. It is also a goal to recruit people with immigrant backgrounds. People with immigrant backgrounds and people with disabilities are encouraged to apply for the position.

We encourage women to apply. If multiple applicants have approximately equivalent qualifications, the rules pertaining to moderate gender quotas shall apply.

The University of Bergen applies the principle of public access to information when recruiting staff for academic positions.

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Slovenia 2 BearPopulations

University of Ljubljana, Biotechnical Faculty, Department for Forestry, Wildlife Ecology Research Group

Post-doc Position in Ecology & Wildlife Management

Reference: Position 1 ’ Adaptive behaviour of brown bears in contrasting landscapes of Europe

Application deadline: 20.3.2018, or until the position is filled

A full-time post-doc position is available at the Department for Forestry, Wildlife Ecology Research group. We encourage applications from highly-motivated post docs with strong background in research work.

Starting date: as soon as possible, but no later than June 1st 2018

Duration: until July 2019, with possible extension.

Location: VeÃÂna pot 83, Ljubljana (Slovenia).

KEY WORDS: anthropogenic disturbances, human impacts, brown bear, *Ursus arctos*, GIS, landscape, resource selection, movement, activity, habitat selection, adaptive behaviour, Europe, Dinaric Mountains, Slovenia, Sweden

JOB DESCRIPTION:

We invite applications from highly motivated candidates with a passion for and experience in research related to animal behaviour ’ adaptive responses to anthropogenic disturbances. The position is a part of an (inter)national project “Development of a multi Â’method approach to study wildlife behaviour: investigating human Â’bear conflicts in contrasting landscapes of Europe” (

http://www.bf.uni-lj.si/index.php?eID=dumpFile&t=f&f!155&tokená3870a35b32898fd5309aa8cfe66202a8e41ddd).

Specifically, the applicant will explore the responses in the spatial ecology (circa-diurnal activity, resource selection) of brown bears (*Ursus arctos*) to different intensities of anthropogenic disturbances in the landscape by performing a large-scale comparative study of GPS collared brown bears from various populations in Europe (e.g. Slovenia, Sweden; see also http://bearproject.info/), where bears live in landscapes with contrasting intensities of anthropogenic disturbances. The main aims are to better understand: (1.) adaptive behaviour of brown bears as a response to increasing human disturbances (2.) the spatial use of brown bears across yearly, seasonal and circadian cycles and the effects of anthropogenic structures, and (3) the role of social interactions in spatial ecology of brown bears and its variation among individual life-stages (age classes, sex, female bears with cubs) and different landscapes. The main collaborators of the applicant will be the leader (prof. dr. Klemen Jerina) , the supervisor dr. Mariano RodrÃÂ’guez Recio (https://www.researchgate.net/profile/Mariano_Rodriguez_Recio) and other members of the Wildlife research group at the Forestry department in Ljubljana and of research groups collaborating in both projects (prof. dr. Jon Swenson https://www.researchgate.net/profile/Jon_Swenson, prof. dr. Andreas Zedrosser https://www.researchgate.net/profile/Andreas_Zedrosser from Scandinavian Brown bear Research project: http://bearproject.info/)

We seek a highly motivated and creative post-doc with good communication skills in English (oral and written), a strong capacity for work, and ability to think independently. The successful candidate is expected to publish results in scientific journals and present them at scientific meetings and conferences as well as to more general public.

REQUIREMENTS:

Successful applicants will:

§hold a Ph.D. degree (or equivalent) in forestry, biology, ecology or another relevant discipline;

§have a solid background in animal ecology and spatial ecology;

§have experience with statistical analyses (multivariate modelling, GLMM, etc.) and particularly spatial statistical analyses (habitat selection, landscape permeability, simulation of animal movement);

§have experience with handling large datasets and good knowledge of geographic information systems and tools (preferably ArcGis);

§have relevant working experience from collaborating on similar research projects;

§can work independently as a researcher and has previous experience with publishing results in scientific papers (peer-reviewed scientific journals);

§very good English skills.

SALARY:

Full-time contract.

Yearly gross salary:

24.396-29.275 /year (depending on job performance; post-doc position, salary class 40), and reimbursements for living costs (up to cca 10 % increase of nett salary), for more details, please see the Public Sector

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SmithCollege 2 GenomicsTeachingResearch

The Department of Biological Sciences at Smith College invites applications for two full-time postdoctoral fellowship positions in genomics, to begin in July 2018. More information is below and here: http://apply.interfolio.com/48740

Postdoctoral fellows will be expected to teach two courses each year in the areas of genetics and molecular biology, bioinformatics, and/or a seminar in the area of specialization of the candidate. Research will focus on genomic approaches to studying microscopic eukaryotes or animal parasites, and postdocs will be encouraged to work with and mentor undergraduates.

One postdoctoral fellow will work in the laboratory of Laura Katz (microbial eukaryotes) while the other will work in the laboratory of Steven Williams (human and other animal parasites), both in the Department of Biological Sciences. Ph.D. in Biology or relevant field is expected by time of appointment.

*****

Research in the Katz lab aims to elucidate principles of the evolution in eukaryotes through analyses of microbial groups, and to assess how these principles apply (or fail to apply) to other organisms. Currently the Katz lab focuses on three interrelated areas: (1) characterizing evolutionary relationships among eukaryotes using single-cell 'omics' and phylogenomics; (2) Exploring the evolution of germline vs somatic genomes; and (3) describing the phylogeography and biodiversity of protists in local environments (bogs, fens, coastal habitats). Information about the Katz lab can be found at http://www.science.smith.edu/departments/Biology/lkatz/Research.htm Research in the Williams lab focuses on the molecular biology/genomics of parasites that cause neglected tropical diseases (NTDs) in humans (particularly lymphatic filariasis and soil-transmitted helminths). Many of the lab's research objectives involve PCR-based diagnostics, molecular xenomonitoring using insect vectors, drug development and studies of gene expression coupling bioinformatics and wet lab experimentation. The Williams lab also conducts research on parasites of marine mammals that will be crucial to the maintenance of healthy wildlife populations. Information about the Williams lab can be found at http://www.science.smith.edu/sawlab/.

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Submit application at http://apply.interfolio.com/48740 with a cover letter, curriculum vitae, a statement of research interests, a teaching statement, three representative publications, and contact information for three references. Review of applications will begin on March 1, 2018.

Located in Northampton, MA, Smith College is the largest women's college in the country and is dedicated to excellence in teaching and research across the liberal arts. A faculty of outstanding scholars interact with students in small classes, as advisors, and through student-faculty research projects. The College is a member of the Five College Consortium with Amherst, Hampshire and Mt. Holyoke Colleges, and the University of Massachusetts Amherst. Students cross-enroll and faculty cross-teach across the Five Colleges. Details about the Department of Biological Sciences may be found at http://www.smith.edu/biology/ . Diversifying the student body, faculty, administration, staff, and curriculum is crucial to the mission of and vision for the College. We are committed to providing access and reasonable accommodation in the application process for individuals with disabilities and encourage applicants to request any needed accommodation(s). We value and are committed to a host of diverse populations and cultures, including, but not limited to, those based on ability, age, ethnicity, gender, gender identity, national origin, race, religion, sexual orientation, and veteran status.

Smith College is an EO/AA/Vet/Disability Employer. Women, underrepresented racial groups, veterans and individuals with disabilities are encouraged to apply.

Laura Katz <lkatz@smith.edu>

SmithCollege EukaryoticBiodiversity

The Department of Biological Sciences at Smith College invites applications for a postdoctoral research position focusing on the biodiversity of the microbial lineages within 'SAR' (Stramenopila + Alveolata + Rhizaria), to begin July 2018. This grant-funded position will be housed in Laura Katz's laboratory (http://www.science.smith.edu/departments/Biology/lkatz/Research.htm). The initial appointment is for one year, with the possibility of extending for additional years.

Candidates with experience involving genomics, bioinformatics and/or target lineages are encouraged to apply. Ph.D. in evolution, microbiology, genomics or related field is expected by time of appointment. More information can be found below and at: http://apply.interfolio.com/48449 . *****

The goals of the project are to characterize the biodiversity of lineages within SAR through a combination of community and genome analyses, including high-throughput sequencing of communities and specific lineages, bioinformatic analyses of resulting data, and some microscopy of target lineages. The project is collaborative with Chris Lane at the University of Rhode Island (http://cels.uri.edu/bio/lanelab/) and Charles F. Delwiche at the University of Maryland (http://www.life.umd.edu/labs/delwiche/home.html). The Katz lab will focus initially on under sampled lineages within Ciliophora and Rhizaria.

Research in the Katz lab aims to elucidate principles of the evolution in eukaryotes through analyses of microbial groups, and to assess how these principles apply (or fail to apply) to other organisms. Currently we focus on three interrelated areas: (1) Characterizing evolutionary relationships among eukaryotes; (2) Exploring the evolution of ciliate genomes; and (3) Describing the phylogeography of coastal marine ciliates. Resources for the department include the Centers for Microscopy and Imaging, Molecular Biology, and Proteomics, in addition to the Young Science Library and MacLeish Field Station (http://www.smith.edu/biology/resources.php).

APPLICATION INSTRUCTIONS Submit application at http://apply.interfolio.com/48449 with cover letter, C.V., a statement of research interests, three representative publications, and contact information for three references. Review of applications will begin February 15, 2018.

Diversifying the student body, faculty, administration, staff, and curriculum is at the heart of our mission and vision for the College. We are committed to providing access and reasonable accommodation in the application process for individuals with disabilities and encourage applicants to request any needed accommodation(s). We value and are committed to a host of diverse populations and cultures, including, but not limited to, those based on ability, age, ethnicity, gender, gender identity, national origin, race, religion, sexual orientation, and veteran status.

lkatz@smith.edu

StockholmU PlantEvolutionaryGenomics

Postdoc position in Plant Evolutionary Genomics at Stockholm University

Closing date: 2 March 2018.

We have an opening for a highly motivated postdoctoral fellow to work on the research project “Genome evolution in parasitic plants” in the group of Dr. Gitte Petersen at Stockholm University.

The complete ad with information on how to apply is available on the Stockholm University webpage: http://www.su.se/english/about/working-at-SU/-jobs?rmlang=UK&rmpage=job&rmjob=4625 Project description The position will be associated with the project Genome evolution in parasitic plants. Several groups of angiosperms are parasites, which makes them more or less dependent on a host for nutrient supply. The overall aim of this project is to understand evolution and consequences of host-parasite interactions at the genomic level, by using comparative methods to reveal unique or shared evolutionary pathways leading to a fully parasitic way of life. While current research is focused on organelle genome evolution, this project will shift emphasis to the nuclear genome e.g., by integrating data from transcriptomics and targeted sequencing into the framework.

Main responsibilities The research associated with this position includes analysis of existing data as well as molecular laboratory work to generate new data. The successful candidate will use a suite of bioinformatics tools for processing, characterizing and analyzing data.

Qualification requirements Postdoctoral positions are appointed primarily for purposes of research. Applicants are expected to hold a Swedish doctoral degree or an equivalent degree from another country.

Assessment criteria The degree should have been completed no more than three years before the deadline for applications. An older degree may be acceptable under special circumstances, which may involve sick leave, parental leave, clinical attachment, elected positions in trade unions, or similar. In the appointment process, special attention will be given to documented proficiency in the use of Next Generation Sequencing techniques and application of bioinformatics tools for downstream analyses including phylogenetic analysis. A good knowledge of plant systematics is desirable. In addition, we expect the candidate to have excellent team-working and communication skills.

Terms of employment The position involves full-time employment for a maximum of two years, with the possibility of extension under special circumstances. Start date 2018-09-01 or as per agreement. Stockholm University strives to be a workplace free from discrimination and with equal opportunities for all.

Contact Further information about the position can be obtained from the Head of the Department, Professor Ove Eriksson, telephone: +46 8 16 12 04, ove.eriksson@su.se or directly from Gitte Petersen, gittep@snm.ku.dk.

Application Apply for the position at Stockholm University's recruitment system by clicking the "Apply" button. It is the responsibility of the applicant to ensure that the application is complete in accordance with the instructions in the job advertisement, and that it is submitted before the deadline. Closing date: 02/03/2018

gittep@snm.ku.dk

Toulouse CNRS 4mnth PlantsEvolutionaryEcol

A short time postdoctoral research associate position is available for 4 months in the laboratory of Benoit Pujol at CNRS in Toulouse (France) to study connectivity in wild populations of Antirrhinum majus, the snapdragon plant. The postdoctoral associate will work as a member of the ERC-funded ANGI project and will organise the field-trip, conduct the survey, record the data, manage the data (including molecular biology). A manuscript is to be prepared during the time of the contract. The aim is to understand the connectivity of wild populations and habitats. The successful candidate will be part of a team of scientists studying the evolutionary ecology and the adaptive potential of plant populations.

We are looking for a candidate with experience in plant wild population surveys. Previous work on Antirrhinum majus would be an advantage. French is not mandatory. A Ph.D. in evolutionary ecology, quantitative genetics, or closely related field is required. We seek applicants with postdoctoral research experience. The appointment is for four months. Position starting as early as April 2018. To apply, please send (1) a brief cover letter explaining your interest in the position, (2) a CV, and (3) contact information (phone number and email) for three references to benoit.pujol@univ-tlse3.fr Closing date for application: February, 15th, 2018 SALARY: monthly salary after tax around 2000 euros

– *Benoit PUJOL* Researcher in evolutionary ecology at CNRS, France Quantitative genetics in the wild and non genetic inheritance

Lab. Evolution & Diversité Biologique (EDB) Office 104, Bat. 4R1, Université de Toulouse Paul Sabatier, 118 Route de Narbonne 31062 Toulouse Cedex 09 Mail: benoit.pujol@univ-tlse3.fr Follow me on twitter: @BenoitPujol

Benoit PUJOL <benoit.pujol@univ-tlse3.fr>

UArizona ProteinEvolutionBioinformatics

Postdoc position: long-term trends in protein evolution

A postdoc position is available with PI Joanna Masel (http://eebweb.arizona.edu/faculty/masel) at the University of Arizona in Tucson. A popular tourist destination surrounded on all four sides by mountainous national and state parks, Tucson is a vibrant city of nearly a million people with an attractive climate. The EEB department was ranked in the top 10 by US News & World Report.

We recently found that genes of different ages encode proteins with different computationally predictable structural properties, forming an extraordinarily long-term trend (see https://doi.org/10.1101/176867). This project will use bioinformatics techniques to discover whether these long-term trends are really a consequence of evolution by descent with modification that continues for long periods of time in a consistent direction. It will also provide a major new annotation of genes based on homology, in order to begin removing the problem of phylogenetic confounding within gene families from "correlomics".

Techniques used may include phylostratigraphy (assigning ages to gene families), ancestral sequence reconstruction, and porting macroevolutionary techniques for studying speciation and extinction to the study of gene duplication and loss. A high level of statistical sophistication is required throughout.

Excellent computer programming skills are strongly preferred, ideally with bioinformatics / genomics and statistics experience. Exceptionally strong candidates who come from a more experimental background within evolutionary biology, and who now wish to retrain as bioinformaticians, will also be considered. A background in evolutionary biology is also strongly preferred, although again, exceptionally strong computational scientists from highly quantitative backgrounds outside evolutionary biology will also be considered. Statistical knowledge, and knowledge about protein structure and folding, are advantages. Start date is negotiable, and the position is renewable, with funding secured through July 2020.

Contact Joanna Masel at masel@email.arizona.edu for more information and to apply.

masel@email.arizona.edu

UBasel Switzerland HostParasiteEvolutionaryGenetics

University of Basel, Switzerland Department of Environmental Sciences, Zoology

Postdoc position in host-parasite population genetics and genomics

A postdoc is available in the research group of Dieter Ebert, at Basel University in Switzerland. I am looking for a highly motivated post-doc with interest in the (co-) evolutionary genetics of host-parasite interactions. This position is funded to work on the genetics/genomics of Daphnia and its microparasites. A background in evolutionary genetics, molecular genetics and bioinformatics skills is welcome. Excellent written, verbal, and interpersonal skills, a superb work ethic, and the ability to think creatively and critically are desired. The project is in parts a continuation of the work described by Bento et al 2017 (PLoS Genetics, DOI:10.1371/journal.pgen.1006596).

Starting date isnegotiable (any time from April 2018 onwards). The working language in the group is English. Speaking German is helpful in every day life in Basel, but is not a requirement. A PhD degree is required. The position is initially for 2 years, but can be extended.

Please send your application by E-mail (all material in one PDF please) to Dieter Ebert. Applications should include a motivation letter, a CV, a list of publications and a 1-page statement about research interests. Please give names and email addresses of two persons who are willing to write a letter of recommendation. Application deadline is 1. March 2018.

Further information and address for application: Prof. Dr. Dieter Ebert, University of Basel, Department of Environmental Sciences, Zoology, Basel, Switzerland, Email: dieter.ebert@unibas.ch <mailto:dieter.ebert@unibas.ch>Tel. +41-(0)61-207 03 60.

Web:http://evolution.unibas.ch/ebert/ Dieter Ebert <dieter.ebert@unibas.ch>

UCalifornia Berkeley PathogenEvolutionaryGenomics

A postdoctoral researcher position for a highly motivated young scientist is available in the group of Rodrigo Almeida in the Department of Environmental Science, Policy and Management, at the University of California, Berkeley, to study the dynamics of plant pathogen epidemics, host adaptation, and specialization. The position is funded by a Horizon 2020 collaborative project dedicated to the emerging plant pathogen Xylella fastidiosa. Topics of interest include, but are not limited to: identification of genes underpinning pathogen host adaptation and specialization, exploration of pathogen genetic diversity and selection forces leading to disease emergence. Within the broad scope of the project, developing novel research questions will be encouraged.

Requirements

Applicants must have a Ph.D. in an area related to microbial genomics, evolution, or population genetics; computational, programming, and quantitative skills are required. The successful candidate will be independent and have good writing skills, yet be able to work in an interdisciplinary environment where collaboration and synergistic interactions are expected.

Responsibilities

Researcher will be responsible for experimental design, data analyses, preparation of research manuscripts and project reports. Post-doctoral researchers in our group are also expected to help mentor and work with students and peers when necessary.

Appointment

One year renewable to two years based on satisfactory performance. Salary commensurate to experience; starting annual salary for UC Berkeley postdoctoral researchers immediately after obtaining a PhD is US$48,216 'V salary scale follows NIH/NRSA stipend. Start date is negotiable, but strong preference will be given to candidates that can start by early Summer 2018.

Application

Prepare a single PDF with i) a 2-page CV that lists publications and computational skills, ii) a research statement (up to 2 pages), and iii) three references who could be contacted. Position will remain open until filled; applications will be reviewed immediately upon receipt. We hope to close the position by March 31st, 2018. Send PDF directly to Rodrigo Almeida: email-*rodrigoalmeida@berkeley.edu*

Rodrigo Almeida <rodrigoalmeida@berkeley.edu>

UCalifornia Riverside MicrobialEcology DataViz

Postdoc: Interactive and Exploratory Data Visualization Tools for High-Throughput Omics Datasets

2.5 year postdoctoral position at the University of California, Riverside focused on the development of data visualization tools for microbial ecology and -Omics datasets

Phinch (http://phinch.org) is an open-source framework for visualizing biological data, funded by a grant from the Alfred P. Sloan foundation. This project represents an interdisciplinary collaboration between Pitch Interactive (http://pitchinteractive.com/ - a data visualization studio in Oakland, CA) and the Bik Lab at UC Riverside (https://biklab.github.io). Phinch currently supports data import in the BIOM format, the standard file output from microbial ecology pipelines such as QIIME. Typical user applications for Phinch include environmental rRNA amplicons or shotgun metagenomic data, although this framework is being expanded to support any type of sample/observation data represented in a standard format (RNA-seq, gene variants, phenotype character matrices, etc.). The appointed candidate will work with the Pitch Interactive studio to implement novel and interactive visualization features, develop statistical tests as visual plugin tools (e.g. via R shiny apps), and implement new phylogenetic visualizations for microbial ecology datasets. The postdoctoral scholar will also contribute to software documentation and end user training workshops as needed.

Prospective applicants should review project aims outlined in the funded grant proposal (https://doi.org/-10.6084/m9.figshare.5471809.v1) as well as these other related resources:

* Phinch GitHub Wiki https://github.com/-PitchInteractiveInc/Phinch/wiki * Bik HM, Pitch Interactive (2014) Phinch: An interactive, exploratory data visualization framework for Omic datasets, bioRxiv, doi: http://dx.doi.org/10.1101/009944 (preprint)

Minimum Qualifications:

Postdoctoral applicants should possess a Ph.D. in a biological or computational discipline, demonstrate a strong publication record and ability to conduct independent research. All applicants are expected to develop strong written and verbal communication skills, as well as assist in mentoring undergraduate and graduate students. Exceptional candidates with M.S degrees and an appropriate skill set may also be considered for this position.

Desirable Qualifications:

Proficiency in a standard programming language (Python and/or Javascript preferred), experience in biological data visualization (e.g. knowledge of R packages such as ggplot, phyloseq, etc. or other visualization specific programming languages such as D3.js), and knowledge of common Omics data types and workflows (e.g. analysis of rRNA amplicon datasets in QIIME, experience with binning/assembly/functional analysis of shotgun metagenomes, large phylogenomic analyses, etc.). Applicants with expertise in phylogenomics, comparative phylogenetics, and/or ecological statistics in R or Python are especially encouraged to apply.

Application and Appointment:

All appointments are initially for one year, and renewable based on performance. Salaries are commensurate with experience and based on minimums set by the University of California postdoctoral union. To apply, submit a curriculum vitae, a 1-page statement of research interests, and contact details for 2-3 academic references to holly.bik@ucr.edu. Review of applications will begin immediately, and will continue until the position is filled.

Please contact Holly Bik (holly.bik@ucr.edu) with any questions.

– Holly Bik Assistant Professor Department of Nematology University of California, Riverside 3401 Watkins Drive Riverside, CA 92521 Email: holly.bik@ucr.edu Phone: (+1) 951-827-4230

Web: http://biklab.github.io Twitter: https://twitter.com/hollybik "holly.bik@ucr.edu" <holly.bik@ucr.edu>

UCalifornia SantaCruz 2 eDNA Biodiversity

We are hiring two post-docs as follows:

1. UCSC-based HHMI Post-Doctoral Scholar in Environmental DNA Research, Education, and Outreach

HHMI Post-Doctoral Scholar in Environmental DNA Research, Education, and Outreach

University of California 'V Santa Cruz

Summary:

UC Santa Cruz department of Ecology and Evolutionary Biology (EEB) is recruiting one full-time postdoctoral scholar to perform environmental DNA (eDNA) research and science education outreach. The position is ideal for a candidate with a background in molecular biology. In collaboration with project partners in the department of Ecology and Evolutionary Biology (EEB) at UC Los Angeles, the postdoctoral scholar will help establish a new education program called eSIE: environmental DNA for Science Investigation and Education, supported by a grant from the Howard Hughes Medical Institute (HHMI) jointly awarded to UCSC and UCLA. The scholar will work with a team of researchers and science education experts on eDNA research that connects to the eSIE program.

Why eDNA?

eDNA is a highly sensitive molecular approach to catalog biodiversity in any ecosystem. The results can reveal a near complete diversity profile of the ecosystem from microbes to plants and animals, and can enable tracking biodiversity changes over time. UCLA and UCSC have pioneered cutting-edge methods to obtain eDNA data, from citizen science to packaged computational pipelines. Our goal with the eSIE program is to use the excitement and wide application of eDNA as a new gateway for students to enter research avenues in the environmental sciences.

The postdoctoral role in the eSIE program:

The postdoctoral scholar will help co-develop and manage eSIE program while receiving training focused on the advancement of science education. eSIE reaches a broad undergraduate constituency by involving hundreds of students annually in CALeDNA bioblitzes on UC Natural Reserves (www.ucedna.com). The postdoc will help select field sampling, ideally around research questions of their interest, and travel to do field collections at natural reserves around the entire state. eSIE will also launch a multidisciplinary flipped course to introduce undergraduates formally to STEM subjects through DNA and eDNA activities. The postdoc would co-design the course with the eSIE team, and receive training through the Center for Education Innovation and Learning in the Sciences (https://ceils.ucla.edu) at UCLA (remote learning possible). The eSIE program also supports students who enter research labs. The postdoc would be expected to occasionally work with student research interns.

Research scope:

The postdoc will be encouraged to pursue environmental science research that uses the eSIE-generated eDNA data and sample collections. They will join the lab group of Beth Shapiro < https://www.eeb.ucsc.edu/faculty/-singleton.php?&singleton=true&cruz_id=bashapir > (UCSC), who'Âs lab focuses on evolution, paleogenomics, and conservation genomics. They will also join the UC Conservation Genomics Consortium community that conducts many eDNA projects.

Preparation:

Candidates should have a PhD in biology or a related science field and molecular biology laboratory experience evidenced by a strong record of scholarship. The ideal candidate would have demonstrated interest or some experience working in science communication and education research, as well as undergraduate teaching or public outreach. Candidates should demonstrate strong written and verbal communication skills, interest in pedagogical innovation, educational assessment, and scholarship, excellent organization and management abilities, experience working with diverse groups. Candidates also should possess skills in mentorship. They must be willing to travel within California, including multiple trips per year between Santa Cruz and Los Angeles, and lead fieldwork excursions to collect eDNA on UC Natural Reserves. Candidates must have a valid driver'Âs license.

The postdoctoral position is a minimum two-year appointment starting Spring 2018, with salary commensurate with experience and following the UC salary scales. To apply submit a cover letter, CV, and contact information for three references here, or send all documents directly to Beth Shapiro (bashapir@ucsc.edu).

For inquiries about the position, please contact Robert Wayne (rwayne@ucla.edu) or Beth Shapiro (bashapir@ucsc.edu).

Review of applications will begin immediately and continue until the position is filled.

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, national origin, disability, age or protected veteran status. For the

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UCDavis EvolutionaryInnovations

Postdoctoral Positions in Developmental and Evolutionary Genetics

University of California - Davis

Postdoctoral positions are available in Artyom Kopp's lab in the Department of Evolution and Ecology, University of California - Davis, USA. — Our lab studies evolutionary innovations, sexual dimorphism, and the evolution of cell types and genetic regulatory circuits in Drosophila. — — We use a wide range of approaches including developmental biology, comparative genomics, phylogenetics, and quantitative/population genetics. — We are looking for creative and ambitious colleagues prepared to work both independently and in collaboration with other lab members. Initial projects are most likely to focus on (1) using genome editing and other transgenic manipulations to reconstruct the origin of new sex-specific structures, and (2) using single-cell sequencing and comparative genomics to investigate the evolution of tissue-specific regulatory networks. — Over time, postdocs will be encouraged to develop new research directions reflecting their own interests, within the broad field of developmental and evolutionary genetics.

Candidates should have demonstrated expertise in developmental biology, genomics, or evolutionary genetics. — Interdisciplinary training and interests are especially welcome. — Initial appointment is for one year, extendable by mutual agreement. — Our lab and the broader research environment at UC Davis provide a friendly and supportive atmosphere and many opportunities for collaboration with leading experts in genomics, evolutionary biology, and cell and developmental biology. — If interested, please contact Artyom Kopp (akopp@ucdavis.edu) with a CV, a statement of research interests and experience, and the names of three references.

– Artyom Kopp Professor, Department of Ecology and Evolution Director, Center for Population Biology University of California - Davis One Shields Ave Davis CA 95616 office (530) 752-8657 lab (530) 752-8328 fax (530) 752-9014 akopp@ucdavis.edu http://kopplab.ucdavis.edu/ "akopp@ucdavis.edu" <akopp@ucdavis.edu>

UCSantaCruz ComputationalGenomics

Post-Doctoral Scholar in Computational Genomics University of California - Santa Cruz

The UCSC Paleogenomics lab is seeking a post-doctoral scientist for an NSF funded project investigating past episodes of cross-species admixture, to begin in Spring 2018. The goals of the project are to develop methods for detecting admixture from modern, historic and ancient DNA samples and to interpret the biological consequences of this admixture as it relates to organismal biology and evolution.

The UCSC Paleogenomics lab is co-directed by PIs Beth Shapiro and Richard Green. It is a diverse group of ecologists, molecular biologists, geneticists, and computational biologists. Our lab has state of the art ancient DNA clean room facilities, sequencing facilities, and computational infrastructure. We are members of the UCSC Genomics Institute and collaborate with the community of genome scientists at UC Santa Cruz and the San Francisco Bay Area.

Qualified candidates will have experience in population genomics, analysis of high-throughput sequencing data, and facility with computational data analysis. A Ph.D. in computer science, computational biology, genetics, or equivalent is required. Candidates will demonstrate the ability to carry out a semi-independent research project by their record of publication.

The postdoctoral position is a minimum two-year appointment starting Spring 2018, with salary commensurate with experience and following the UC salary scales. To apply send a cover letter, CV, and contact information for three references to Beth Shapiro (bashapir@ucsc.edu). For inquiries about the position, please contact Ed Green (ed@soe.ucsc.edu) or Beth Shapiro (bashapir@ucsc.edu).

Review of applications will begin immediately and continue until the position is filled.

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, national origin, disability, age or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy see: http://policy.ucop.edu/doc/4000376/NondiscrimAffirmAct beth.shapiro@gmail.com

UEdinburgh 2 LifespanEvolution

Edinburgh Reply-To: WALLING Craig <craig.walling@ed.ac.uk>

Dear EvolDir,

Two research positions are available to join my lab (http://walling.bio.ed.ac.uk/) and the lab of Pedro Vale (http://pedrovale.bio.ed.ac.uk/) at the Institute of Evolutionary Biology, University of Edinburgh. These positions are part of a project to study the evolution of lifespan extension in response to dietary restriction in Drosophila melanogaster. Details of the positions can be found at the links below. Please note that the post-graduate position is only available to UK or EU nationals, sorry.

Three year post-doctoral research associate: https://www.vacancies.ed.ac.uk/pls/corehrrecruit/erq_jobspec_version_4.jobspec?p_id=042722 Two year post-graduate research assistant: https://www.vacancies.ed.ac.uk/pls/corehrrecruit/erq_jobspec_version_4.jobspec?p_id=042723 Please e-mail me at craig.walling@ed.ac.uk with questions/informal enquiries.

Best wishes Craig

– The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

WALLING Craig <craig.walling@ed.ac.uk>

UEdinburgh EvolutionaryQuantativeGenetics

A NERC-funded postdoctoral position is available in evolutionary quantitative genetics, specifically to investigate maternal effects in a wild mammal population, with Josephine Pemberton, Craig Walling and Susan Johnston at the University of Edinburgh.

Maternal effects are critical determinants of offspring fitness in animal populations, potentially as important as heritable genetic variation or ecological conditions. The study will involve analyses of (i) the genetic basis of maternal effect variation and its interplay with other key variables, (ii) new phenotypic measures to assess both maternal and offspring condition and (iii) the impact of maternal effects on the evolution of offspring traits.

The project will use the long-term study of individual life histories of red deer living in the North Block on the Isle of Rum, in which pilot analyses indicate maternal effects are large. A pedigree of >4000 individuals is available for study, and about 2,700 core individuals have been genotyped on a 50K SNP array, enabling genomic as well as genetic analyses.

Applicants should have (or nearly have) a PhD in evolutionary biology and be familiar with quantitative genetic concepts and analysis, ideally animal models. Experience in DNA extraction, genomic data management, pedigree reconstruction and GWAS would also be advantageous. The postdoc will work within the Institute of Evolutionary Biology, in the School of Biological Sciences. The Institute houses multiple research groups interested in evolutionary quantitative genetics and more widely, Edinburgh has a large community of quantitative geneticists working in biomedical research and on animal improvement.

More information and applications via: https://www.vacancies.ed.ac.uk/pls/corehrrecruit/erq_jobspec_version_4.jobspec?p_id=042909 or https://www.vacancies.ed.ac.uk and search for vacancy ref 042909 .

Informal enquiries to Josephine Pemberton, j.pemberton@ed.ac.uk

Closing date: 5.00 pm on Thursday 22/03/2018.

– The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

PEMBERTON Josephine <J.Pemberton@ed.ac.uk>

UGeneva Switzerland FloralColorEvolution

The Conservatory and Botanical Garden of Geneva (CJBG) and the department of Botany and Plant Biology from the University of Geneva is seeking an enthusiastic, independent postdoctoral researcher to work on an SNF-funded project on the ecological and molecular bases of flower color evolution.

The project aims to model the evolution of flower color and integrate comparative analyses of molecular evolution, gene expression, and anthocyanins production in a lineage of Neotropical plants, the Gesnerioideae. The amazing flower diversity present in this plant group and the frequent parallel evolution of bee, hummingbird and bat pollination will provide the necessary framework to identifying the role of pollinator- mediated selection on flower color evolution and to better characterize the biochemical and genetic mechanisms underlying color transitions. This project built on new transcriptomic resources available for the group, which will facilitate the identification of all genes involved in the anthocyanin biosynthetic pathway and their sequencing using target capture method. The CJBG/University of Geneva is recruiting a postdoc to: 1) collect data on floral reflectance (in the field and from cultivated plants) and assess the level of convergence of flower colors and their association with pollinator color vision; 2) identify the floral flavonoids in a large sample of species to determine the biochemical bases of flower color and evolutionary constraints imposed by the biosynthetic pathways; 3) characterize the anthocyanin genes using NGS and quantitative PCR to analyze their evolution in the Gesnerioidea radiation. This is a collaborative project with the Computational Phylogenetics Group of Prof. Nicolas Salamin at the University of Lausanne. We seek a collegial, self-motivated, independent, and intellectually curious individual. A PhD in evolutionary biology or related field is required. Applicants for this position must have strong bench skills and strong familiarity with bioinformatic analyses of next-gen sequencing data and/or comparative analyses. In addition, candidates must have demonstrated written and oral communication skills. The position is available for 24 months.

Applications should be sent by February 31, 2018 by email to Mathieu Perret (mathieu.perret@ville-ge.ch). Applicants are requested to send a single PDF file that includes a cover letter with names and contact information of three references, a CV and one or two representative publications. Preferred start date is April- May 2018.

Contact Dr. Mathieu Perret Conservatoire et Jardin botaniques Ch. Imperatrice 1 1292 Chambesy - Geneve Switzerland http://www.ville-ge.ch/cjb/pageperretm.php Mathieu.Perret@ville-ge.ch

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UGeorgia CropWildIntrogression

A postdoctoral position studying the genomic consequences of crop-wild hybridization in sunflower is available in the Burke lab at UGA. This position involves population genomic analyses aimed at documenting genome-wide patterns of introgression over the history of sunflower cultivation in North America. The results of this research will thus provide insight into the long-term fate of crop alleles/traits in the wild. Moreover, when coupled with the results of prior studies of selection in experimental hybrid populations, this work will enable an investigation of the reliability of experimental studies for predicting long-term, real-world evolutionary outcomes.

The ideal candidate will have a strong background in population genetics and experience handling and analyzing large, genomic datasets. Funds are currently available to support this position for up to two years, and the successful candidate will also be given the opportunity to develop independent lines of inquiry.

To apply, please send your CV, a brief statement of research interests, and contact information for three references to: jmburke@uga.edu

Informal inquiries are also encouraged. Applications will be reviewed on an ongoing basis until the position is filled.

Information on the plant science research community at UGA can be found at:

https://plantcenter.uga.edu/ Information about the UGA Department of Plant Biology can be found at:

http://plantbio.uga.edu/ And information on the Burke lab can be found at:

http://www.theburkelab.org/ – John M. Burke, Ph.D. Tel: 706.583.5511 Fax: 706.542.1805 http://www.theburkelab.org/ University of Georgia Department of Plant Biology Miller Plant Sciences Athens, GA 30602

"jmburke@uga.edu" <jmburke@uga.edu>

UGeorgia PlantEvolutionaryGenetics

Postdoctoral position in Plant Evolutionary Genetics/Ecology, Department of Genetics, University of Georgia

Jill Anderson's lab in the Genetics Department at the University of Georgia is currently searching for a highly-motivated postdoctoral associate to collaborate on an NSF-funded study of the evolutionary consequences of climate change for natural plant populations. Our lab studies the extent to which climate change imposes novel selection and disrupts long-standing patterns of local adaptation, using the subalpine mustard, Boechera stricta, as our focal species. Our field, growth chamber, and greenhouse studies also examine whether increased temporal variability under climate change will favor phenotypic plasticity. You can find additional information about research in the Anderson lab here: http://andersonlab.genetics.uga.edu The position is for one year, renewable for up to two additional years contingent upon performance. The anticipated start date is flexible, and could be as early as April 2018. The successful candidate will contribute to ongoing experiments, develop research on the genetic basis of climatic adaptation, and evaluate whether gene flow could facilitate adaptive response to climate change. This position includes a combination of fieldwork at the Rocky Mountain Biological Laboratory (Gothic, Colorado), field collection trips throughout the western U.S., and laboratory work at the University of Georgia (Athens, GA). The postdoctoral scholar will analyze existing datasets, write and publish peer-reviewed manuscripts, and present results in seminars at UGA and scientific conferences. The postdoc will also have opportunities to develop additional research programs related to the overall objectives of the project and to gain experience mentoring undergraduate and graduate students.

Candidates must have a Ph.D. in evolutionary biology/genetics (or a related field) from an accredited university. Preference will be given to candidates with one or more of the following: (a) experience in quantitative genetics and statistical modeling, (b) experience generating and analyzing next generation sequence data, (c) successful publication record, including first-authored publications, (d) experience mentoring students and technicians, and (e) laboratory and database management skills. We value diversity in background and perspective, and we seek to promote safety in the lab and field.

TO APPLY: Please submit a single PDF that includes (1) a cover letter describing past research experience and qualifications for this position, (2) a current CV, and (3) contact information for 3 references, as well as separate PDFs of up to 3 manuscripts (published, in review, or in preparation), to posting number S00409P here: https://www.ugajobsearch.com/postings/17524. Review of applications will begin immediately and continue until the position is filled. Feel free to email Dr. Anderson (jta24@uga.edu) with questions.

Jill T Anderson <jta24@uga.edu>

UGuelph 5 BiodiversityGenomics

The Centre for Biodiversity Genomics (CBG) at the University of Guelph has global leadership in the development and application of DNA-based identification systems for eukaryotes with a focus on the animal kingdom. Based in a 50,000 ft2 facility, its unique research capacity reflects the coupling of one of Canada's largest genomics platforms with a workforce that includes world-class expertise in biodiversity science, DNA sequencing, and informatics (visit biodiversitygenomics.net for further details). The CBG seeks five highly qualified postdoctoral fellows to join and strengthen a vibrant research and innovation group. Applicants for these positions must possess a passion for problem solving, the ability to work in a team, and a strong publication record. Ideally, candidates should bring prior experience in biodiversity genomics and in scripting (e.g. Perl, Python, R). These positions have the potential for extension beyond an initial two-year term, subject to annual performance reviews. Applications will be reviewed as they are received. Please send your curriculum vitae, the names of three potential referees, and PDF copies of your two most relevant publications to: CBGfellowship@biodiversitygenomics.net

Multi-species Population Genetics/Genomics High-throughput sequencing (HTS) of taxon assemblages makes it possible to test hypotheses relating to regional patterns of demographic stability, isolation, and admixture. The successful applicant will join a team developing multi-taxa population genomic models to understand community assembly, colonization, and vicariance based on population-level sequencing data collected across entire taxonomic assemblages. Desirable Background: proficiency with methods in community population genetics; statistical skills; experience in analysing large-scale genetic/genomic data.

Species Distribution Modelling and Spatial Mapping Large data sets generated by HTS can address current challenges in Species Distribution Modelling while extended matrix regression models (e.g. generalized dissimilarity modelling) can analyse and predict spatial patterns of turnover in community composition. The successful applicant will have a unique opportunity to combine metabarcoding results with ancillary information, such as trait data, to develop process-based models that can identify the functional composition of any location and map expected distributions of ecosystem functions and services. Desirable Background: proficiency with GIS software (ideally ArcGIS); statistical analysis in R; experience in distribution modelling and with predictive algorithms.

Mito-nuclear Interactions Functional incompatibility between mitochondrial- and nuclear-encoded components of the co-adapted gene complex responsible for oxidative phosphorylation is increasingly recognized as an important cause of post-zygotic isolation. The CBG holds DNA extracts from nearly 400,000 species, providing an exceptional resource for examining nuclear-mitochondrial interactions among both closely allied and distantly related taxa. The successful applicant will use these DNA extracts and our genomics facility to extend understanding of the interactions between nuclear and mitochondrial gene products. Desirable Background: molecular background such as primer design and PCR optimization; HTS and sequence analysis; statistical skills; experience in analysing large-scale genetic/genomic data; experience with technologies such as genome skimming and target enrichment as well as combinations of both (e.g. Hyb-Seq).

Bioinformatics/Phylogenomics Our team has initiated a collaboration that will strengthen two informatics platforms (BOLD, mBRAVE) developed at the CBG with platforms to support phylogenetic analysis and global ecosystem modelling. The successful applicant will join the implementation team to develop methods for estimating divergence times from DNA barcodes, as well as multi-gene and genome-scale datasets as well as the empirical analysis of large molecular datasets to test hypotheses relating to rates of speciation and molecular evolution. Desirable Background: proficiency with phylogenetic and phylogenomic methods; statistical skills;

experience in analysing large-scale genetic/genomic data; proficiency in programming and the use of compute clusters; experience in other programming languages.

Molecular Evolution About 5% of known species possess deep 'intraspecific' divergences at mitochondrial markers (including the DNA barcode region). These cases have several possible explanations; each taxon may represent an assemblage of young species or the deep divergence may truly represent variation in a single species that has arisen as a consequence of the merger of phylogeographic isolates or through rate acceleration. The successful applicant will do broad scans of sequence divergence in the nuclear genome, advancing our understanding of species ages and boundaries thereby

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UHalle BeeViralEvolution

Postdoc on viral evolution in bees

A postdoctoral researcher is sought for a project on the evolutionary ecology of viruses in bees within Robert Paxton's lab at the University of Halle, Germany. The overarching goal of the research is to understand the role of viral epidemiology and evolutionary change for pathogen emergence and host switching; the project is embedded within the DFG's priority program: Ecology and Species Barriers in Emerging Viral Diseases (SPP 1596). Requirements sought: a highly motivated individual; experience in, or knowledge of, evolutionary modelling and bioinformatics; an interest in host-parasite interactions. Prerequisites also include evidence of strong oral and written communication skills and the ability to complete tasks in a timely and structured fashion. Opportunities exist to develop the research through lab and field-based experiments as well as molecular genetic analysis of bees and their viruses in the lab.

The working language of the lab is English. The neighboring group of Robin Mortiz makes for a strong profile in bee biology and genetics at the University of Halle. Funding is secure for the first 1 year and 5 months, with good opportunities for continuation funding. Though the start date is flexible, we seek a person to commence research during spring 2018. Halle is a delightful, historical city approximately 1.5 hours SW of Berlin. The salary is on the standard German postdoc scale E13, which translates to approximately Euro 51-57 K per annum (dependent on experience).

Further details of the position can be obtained from Robert Paxton (robert.paxton@zoologie-uni-halle.de), to whom applications should be sent by 15 February 2018 as a single pdf file to include: cover letter referring to 'position 5-12596/17-D', cv, list of publications, a statement of research interests and goals (maximum 1 page), and contact details of two referees. Interviews are planned for March 2018, with a start date in April or as soon as possible thereafter. Please note: this is an update/reminder of the advert sent out at the end of 2017.

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

ULausanne EvolutionaryModeling

Postdoc positions in Evolutionary Modeling and Phylogenetics

Job description

A postdoctoral position is available in the group of Nicolas Salamin in the Department of Computational Biology of the University of Lausanne. The overall aim of the project is to develop and improve current methods to estimate the rates of evolution of continuous phenotypic traits along phylogenetic trees.

Most of the developments of comparative methods have targeted the evolution of species mean phenotypes, whereas the treatment of intraspecific variability has received less attention. The first objective is to develop a novel model testing framework to further understand the evolution of the variance in phenotypic traits within a macro-evolutionary framework and to extend this estimation to multiple continuous traits. The second objective is to model the evolution of phenotypic traits across speciation events to better understand the relationship between macro-evolutionary models and micro-evolutionary processes.

Profile requirements

The ideal candidate should be an autonomous and ambitious person with enthusiasm for inter-disciplinary work, who will need to interact productively with evolutionary biologists, genome biologists and computer scientists, and read the corresponding range of scientific literature. Candidates must have completed their PhD degrees or equivalent in a relevant field.

The requirements include a strong mathematical or statistical and computer science background and deep interest in computational biology and theoretical aspects of evolutionary biology. Previous experience with evolutionary biology and/or computational biology is also expected.

The successful candidates will be part of the Department of Computational Biology of the University of Lausanne as well as the Swiss Institute of Bioinformatics. The Department of Computational Biology of the University of Lausanne offers a supportive and stimulating environment, with access to excellent computer and academic facilities.

Start date and contract length

- April 1st 2018 or to be discussed - contract length: 1 year, renewable for another 2 years

Contact details

To apply, please use the following link: https://goo.gl/-NzPLgm For any questions, contact

Nicolas Salamin (nicolas.salamin@unil.ch) http://-www.unil.ch/dbc http://www.unil.ch/phylo Nicolas Salamin <nicolas.salamin@unil.ch>

UManchester EvolutionaryBiol

The University of Manchester Presidential Fellowships in Evolutionary Biology

We are inviting the brightest academic talent to apply for The University of Manchester Presidential Fellowships. We're interested in early-career academics who can deliver world-leading research and teaching, and become the inspiring leaders of the future. Applicants should have a high academic standing, a growing reputation in research, and the specialist knowledge needed to develop exemplary research programmes and methodologies. We offer:

- - a highly competitive salary (pounds 31,604-pounds 49,149 for 3 years)

- - generous research and travel expenses (pounds 10,000 per annum)

- - access to world-leading technology platforms

- - outstanding networking, learning and development opportunities

We will also provide a supportive, vibrant and inspiring environment for you to pursue your research and teaching career. Our resources and mentorship will enhance your competitiveness for external awards. We are interested in candidates that map on to our areas of research strength (for more information see: https://www.brightest-minds.manchester.ac.uk/-areas-of-opportunity/biolo gy-medicine-and-health/).

We are particularly interested in recruiting new colleagues working in the following areas:

- - Evolution of genomes and allied informatics to understand biological function and genetic disease

- - Computational biology, Biological networks and dynamic systems

- - 'Omics technologies and their applications in biology and disease

- - Microbial evolution and metagenomics, and applications to anti-microbial resistance

For initial enquiries in any of these areas, please contact Prof Simon Lovell (Simon.Lovell@manchester.ac.uk) or Prof Simon Hubbard (Simon.Hubbard@manchester.ac.uk).

Dr Reinmar Hager

Evolution and Genomic Sciences | School Lead for International Postgraduate Research

School of Biological Sciences | Faculty of Biology, Medicine and Health | Michael Smith Building

The University of Manchester | Manchester M13 9PT, UK

Tel. ++44 (0)161-275-1550 | http://-hagerlab.lab.manchester.ac.uk/ Reinmar Hager <Reinmar.Hager@manchester.ac.uk>

UMaryland StatModelingMicrobiomes

Postdoctoral Researcher in Statistical Ecology / Spatial Distribution Modeling of Microbiomes

Bill Fagan's ecology lab at the University of Maryland in College Park, MD, has a new opening for a Postdoctoral Researcher in the Statistical Ecology / Spatial Distribution Modeling of Microbiomes. This dynamic lab group, which currently includes one associate research scientist, seven postdocs, four graduate students, and numerous undergraduates, is pursuing a wide variety of research projects in ecology. Much of this work is explicitly spatial in nature, drawing upon GIS, mathematical modeling, and statistical analyses. For examples, see http://www.clfs.umd.edu/biology/faganlab/ This advertisement is for a postdoctoral position on a DoD / MURI-funded project in collaboration with Johns Hopkins Applied Physics Lab, Johns Hopkins School of Medicine, and Duke University. The project focuses on the analysis of the human skin microbiome, with a particular emphasis on developing multi-scale models for understanding and predicting spatial variation in microbiome composition. The candidate should have expertise in species distribution modeling and/or the statistical analysis of spatially structured presence/absence and abundance data. In addition, very strong computational skills with knowledge in various programming languages (e.g., R, Python, Matlab) are required. Experience in microbial ecology and familiarity with sequencing data are highly desirable. Experience working with large datasets and/or hierarchical spatial models would be particularly helpful.

The successful candidate will have a PhD at the time of appointment, likely in quantitative ecology, microbial ecology, statistics, or a related field. Prior postdoctoral experience is beneficial, but not required.

The initial appointment will be for one year, but funding is already in place for up to two additional years pending good performance. Efforts to secure substantial long-term support via collaborative grant proposals would be encouraged and, when successful, could lead to appointment at the level of assistant/associate research scientist. Benefits are included and pay will be commensurate with experience. The start date is negotiable, but could be as early as March 2018.

Review of applications will begin immediately and will continue until the position has been filled. To apply for the position, please email a CV, reprints, and the names and email addresses of three references to:

Bill Fagan

Professor and Chair

Department of Biology

University of Maryland

College Park, MD 20742

bfagan@umd.edu

Eleanor Brush <eleanor.brush@gmail.com>

UMichigan PredationParasitism

Postdoc position: Influence of predators on ecological and eco-evolutionary host-parasite dynamics

Job Summary A postdoctoral position focusing on the impact of predators on the ecological and eco-evolutionary dynamics of host-parasite interactions is available in the laboratory of Dr. Meghan Duffy in the Department of Ecology & Evolutionary Biology at the University of Michigan. The Duffy Lab studies the ecology and evolutionary biology of host-parasite interactions, using the aquatic crustacean Daphnia and their microparasites as a model system. The successful candidate will have access to a vibrant intellectual community and state-of-the-art facilities in the brand new Biological Sciences Building at Michigan; the Duffy Lab will move to this building in April 2018.

More information on the Duffy Lab can be found at: https://duffylab.wordpress.com/ More information on the Department of Ecology and Evolutionary Biology at the University of Michigan can be found at: http://www.lsa.umich.edu/eeb/ Responsibilities The successful candidate for this position will be expected to carry out independent research relating to predation and parasitism, using Daphnia and their microparasites as a model system. The project involves lab experiments (at scales from beakers to buckets) in Michigan; setting up these experiments will involve some field work, especially to collect predators and water for experiments (though alternative arrangements could be made if the postdoc is not able to perform field work). Ideally, the successful candidate would also work on larger scale experiments in cattle tanks in Indiana for 3-4 months in summer-fall 2019, based out of Spencer Hall's lab at Indiana University in Bloomington.

Depending on interest and abilities, the postdoc will also have the ability to work on mathematical modeling of disease. There will also be the potential to develop additional projects building on the strengths, interests, and expertise of the successful candidate.

This position will also involve mentoring of undergraduate researchers in the lab.

How to Apply Interested individuals should send a CV, a brief description of research accomplishments and future goals, and the names and contact information for 3 references to Meghan Duffy by e-mail (duffymeg@umich.edu).

Review of applications will start on March 12, 2018 and will continue until the position is filled. The University of Michigan is an equal opportunity / affirmative action employer.

Required Qualifications PhD (by start date) with experience in aquatic ecology, disease ecology, community ecology, eco-evolutionary dynamics, and/or evolutionary ecology

Desired Qualifications Experience working with Daphnia would be beneficial, but is not required.

Other information Preference will be given to applicants who can start by mid-summer 2018, though start dates as late as Fall 2018 are possible. Funding is available for at least two years, but is contingent on satisfactory progress in year one. The salary for the position is $48,000 per year plus benefits.

Meghan Duffy <duffymeg@umich.edu>

URennes ModellingBiodiversity

Two-year post-doctoral position - UMR CNRS 6553 EcoBio, University of Rennes 1 (France) / Evolutionary ecology, statistics and modelling of biodiversity

A postdoctoral position in evolutionary ecology, associated to statistics and spatial modelling of biodiversity is available at the UMR CNRS 6553 EcoBio Department (University of Rennes 1, Rennes, France, https://ecobio.univ-rennes1.fr/). Our laboratory integrates population ecology and evolution, community dynamics and evolution, and ecophysiology. We are seeking an experienced candidate that could expand the expertise of our group to different topics including, but not limited to, the evolutionary effects of biological invasions on (bio)diversity at different organisational levels, species distribution models, (process-based and/or correlative approaches) and the elaboration of scenarios of biodiversity in changing environments (which include modeling of habitat suitability and species distribution).

The successful candidate will have strong skills in evolutionary biology, statistical ecology and spatial modelling, with experience in linking spatio-temporal data on the evolution of distribution of species and community composition to data on habitat structure, evolution of life history traits, and climate change. Within the framework of currently funded projects in the laboratory, we are particularly interested in studying (i) the role of environmental changes on evolution of populations and biodiversity in a variety of habitats and (ii) the spread of invasive species (invertebrates, plants) and the associated spatial sorting of populations along invasion gradients. The research questions concern terrestrial ecosystems, and datasets are assimilated since the 90s for some taxa.

The applicant should have completed his/her PhD in ecology and evolution, with strong skills in statistics and / or modelling. It is required that the applicant must have spent at least one year outside France over the past three years for eligibility. We seek candidates with excellent skills who are able to conceive, execute and complete research projects in an autonomous fashion and to think independently and creatively.

The position is funded for two years by Region Bretagne and the Institut Universitaire de France, depending on satisfactory annual reports. The gross salary is 2300 euros / month. Applications will be considered until the position is filled, but the desired starting date is April 1^st 2018. Applications must include a cover letter with a statement of research experience and interests, curriculum vitae, and have three researchers you collaborated with that send us reference letters. Please send versions of these files to Dr. David RENAULT at david.renault@univ-rennes1.fr

David RENAULT <david.renault@univ-rennes1.fr>

USDA ARS Delaware BehavioralGenetics

Postdoc position in Behavioral Genetics and Genomics

The USDA-ARS Beneficial Insects Laboratory is seeking a highly motivated individual for a three-year Post-Doctoral Research Associateship funded by the USDA-NIFA program. Salary will be $66,110 per year plus benefits. The postdoctoral associate will perform research on the genetics, genomics, and evolution of host specificity of parasitic wasps. This will include mapping genetic loci underlying differences in host specificity, analysis of parasitoid genomes and transcriptomes for sequence and expression differences that indicate divergent selection, and further characterization of divergent genes in relation to parasitism. The research will also involve analysis of tissue- and stage-specific expression of divergent genes and knockout of these genes to determine whether they indeed affect host specificity. The laboratory is located on the campus of the University of Delaware in Newark, DE, and has active government-university collaborations and direct access to contemporary genomic, informatics and imaging facilities. Newark is a small, tranquil, college town in northern Delaware, midway between Washington, DC (100 miles) and New York, NY (130 miles). The closest large towns are Philadelphia (45 miles) and Baltimore (60 miles). Applications will be accepted until the position is filled. Only U.S. Citizens and Permanent Residents seeking U.S. Citizenship are eligible. USDA/ARS is an equal opportunity employer and provider. To apply please send CV and names/contact information for three referees to Dr. Keith Hopper, email: Keith.Hopper@ars.usda.gov.

Keith R. Hopper, PhD USDA-ARS, University of Delaware, Newark, DE 19713

“Hopper, Keith” <Keith.Hopper@ARS.USDA.GOV>

USouthernMississippi FinfishGenomics

Location Gulf Coast Research Laboratory, Ocean Springs, Mississippi, USA Company University of Southern Mississippi Closing Date Open until filled $45,000 yearly salary + benefit; 4 years of funding available.

Qualifications A Ph.D in genetics, evolutionary biology, bioinformatics or related disciplines is required. A strong background in bioinformatics and computational biology is desired, experience with aquaculture research is preferred.

Description Participate in research on domestication and breeding of cultured marine species. Research activities focus on developing genomic resources for non-model species candidates for aquaculture, estimating quantitative genetic parameters for characters of interest and studying their genetic basis using genomic approaches. The position would also involve participating in population genomic studies of studied taxa. Work will be performed in connection with the aquaculture program that aims to develop methods to control the life cycle in captivity and domestication.

Contact Name Eric Saillant Contact Phone 228-818-8007 Contact Email eric.saillant@usm.edu

Eric Saillant <Eric.Saillant@usm.edu>

UVermont TeachingRes EvolBiol

The Quantitative and Evolutionary STEM Training (QuEST: https://www.uvm.edu/quest) Program at the University of Vermont invites applications for a postdoctoral opportunity involving teaching and research, aligned with a unique new graduate program.

This program’Xfunded by an NSF Research Traineeship (NRT) grant’Xis an innovative and evidence-based model for transforming STEM graduate education training. Areas of focus include ecological genomics, emerging infectious diseases, antibiotic and pesticide resistance, reduced crop yields caused by climate extremes and shifts, and how loss of biodiversity affects the environment, global health and food security. In each case, identification of successful solutions to these global challenges requires fundamental knowledge of evolutionary principles and quantitative approaches. QuEST aims to train these problem-solvers through an innovative graduate program.

We are looking to add a talented postdoctoral fellow to our team, someone with a quantitative background (quantitative biology, statistics, computer science, applied mathematics or related fields) to aid in curriculum design and teaching for flagship courses in the graduate program. This would include a course designed to introduce first year QuEST PhD students to quantitative reasoning and methods applicable to various STEM-related disciplines (ecology, evolution, conversation biology, epidemiology, and others).

This postdoctoral fellow would also be expected to conduct independent research with with a QuEST faculty member (https://www.uvm.edu/quest/participating-faculty) in the areas of quantitative genetics, ecological genomics, marine biology, computational biology, bioinformatics, biostatistics or mathematical modeling.

The ideal candidate would have a record of success in teaching, be a willing mentor to graduate students in the program, and have a commitment to nurturing diversity in STEM.

Interested candidates should send a single PDF including a cover letter, CV (with names and contact information for three references), a short teaching statement (1 page), and a short research statement (1-2 pages) to Melissa Pespeni, Assistant Professor (Department of Biology) and Director of the QuEST program at mpespeni@uvm.edu.

The cover letter should contain several items:

(1) A discussion of the candidate'Âs interest in teaching, highlighting experience in curriculum design at any level

(2) A brief summary of the candidate'Âs research experiences, and what areas they might be interested in exploring further

(3) A discussion of the candidate'Âs long-term goals

Start date is July 1, but can be flexible. Review of applications will begin mid March and continue until a suitable candidate is identified. Informal inquiries prior to application are welcome.

Burlington is a hip, little city surrounded by the lakes and mountains of northern Vermont. The area thrives on local food, international culture, and outdoor activities year-round.

QuEST and the University of Vermont are especially interested in recruiting and supporting people who can contribute to the diversity and excellence of the academic environment. Women, LGBTQ, first-generation college, differently-abled people and people with veteran status and from underrepresented racial, ethnic, socioeconomic and cultural groups are strongly encouraged to apply.

"C. Brandon Ogbunu" <chike.brandon@gmail.com>

UVienna PDF PhD EvolutionGenomics

Title: UVienna.EvolutionGenomics

Dear Colleagues:

Applications are invited for one Ph.D. and one postdoc position in the group of Qi Zhou in the Department of Molecular Evolution and Development at University of Vienna, Austria. Both are supported by the European Research Council (ERC) grant, and planned for two years for postdoc, and three years for Ph.D. with possible renewal. The successful applicants will use bioinformatic and experimental methods to study the evolution of Drosophila sex chromosomes. Most model species' sex chromosomes, e.g., those of human and D. melanogaster bear few traces of their evolution, because they are too ancient and have become too repetitive in sequence for investigation. A fundamental question concerns evolution biologist is what are the causes and consequences of Y chromosome degeneration? We will be using Drosophila species with recently born sex chromosome ('neo-sex') systems to address: How does the Y chromosome become epigenetically inert? How does this universal evolution process drive the adaptation of small RNA defence systems? And how does such a male-specific arms race between parasitic transposable elements and small RNAs fuel the changes of the female genome? The candidates are expected to be independent and highly motivated. Essential qualifications include demonstrated experience either in Drosophila genetics experiments (transgenics, CRISPR/Cas9 mutagenesis, in situ hybridisation) or bioinformatic studies (RNA-seq, ChIP-seq and corresponding data analyses).

Successful applicants will receive very competitive salary and benefits (https://www.fwf.ac.at/en/research-funding/personnel-costs/), and enjoy the diverse and vibrant research environment of the Department and the University. The group members have frequent interactions with other neighbour labs of Drosophila neurobiology (Prof. Thomas Hummel) and developmental biology (Prof. Ulrich Technau), and have a chance to develop other collaborative research projects. The university is located in the city centre of Vienna, which houses numerous world's leading research institutes including Gregor Mendel Institute, Institute of Molecular Biotechnology and Institute of Science and Technology etc. The city now has gathered many great scientists in evolutionary biology (http://www.univie.ac.at/evolvienna/-?page_id=6), RNA biology (http://www.mfpl.ac.at/rna-biology/) and there is an encouraging plan to move the biology departments of the University near other institutes of Vienna Biocenter to form a new research cluster. Vienna has been voted as the world's most livable city for the eighth time, and is famous for its history and culture, and now also a modern and international lifestyle. Interested candidates please send her/his CV and contact information of three referees to Dr. Qi Zhou (qi.zhou@univie.ac.at). We will start reviewing the application immediately until the position is filled.

Qi Zhou

https://scholar.google.at/citations?user=-XwJHKgkAAAAJ&hl=en Qi Zhou <muntjaczhou@gmail.com>

YaleU EvolutionaryGenomics

Postdoc, NIH-supported position at Yale University starting any time. One year guaranteed, very likely two years. Looking for someone with experience in evolutionary genomics including GWAS. Our lab is studying the mosquito Aedes aegypti, performing evolutionary genomics including historical reconstruction of the species. Data collection includes microsatellites, SNPs from a chip, and complete genome sequencing. Studies on variation in the ability to transmit various viruses, especially dengue, provide data for GWAS using data from a SNP chip. Experience with large genetic data sets (sequences and SNPs) used for both population/historical reconstructions and GWAS preferred. Experience with mosquitoes is desirable, but experience with technologies and analytical procedures are more important than experience with the particular organism. Contact: jeffrey.powell@yale.edu

Recent publications from the Powell lab: Gloria-Soria et al. (2016) Mol. Ecol. 25:5371; Gloria-Soria et al. (2017) Proc. Roy. Soc. B 284:20171406; Kotsakiozi et al. (2017) PLOS Negl. Trop. Dis. 11:e0005653; Pless et al. (2017) PLOS Negl. Trop. Dis. 11:e0005718; Saarman et al. (2017) Evol. Appl. 10:1031.

jeff powell <jeffrey.powell@yale.edu>

YaleU EvolutionaryMedicine

Two Postdoctoral Fellowships in Global Health at Yale

The multidisciplinary academic program in Global Health at Yale seeks two Postdoctoral Fellows for the 2018-2019 Academic Year, with an option of renewal for the following academic year. Each Fellow will teach two undergraduate courses (one per semester) drawing on their respective areas of expertise in Global Health. They will also pursue research with a mentor of their choosing and participate in the interdisciplinary community provided by the Global Health Justice Partnership, directed by Professors Amy Kapczynski, Alice M. Miller, and Gregg Gonsalves. Participating Yale faculty in the program include members of Sociology, Anthropology, Women's Gender and Sexuality Studies, Biomedical Engineering, Medicine, Ecology and Evolutionary Biology, Public Health, History of Science and Medicine, Ethnicity Race & Migration. Successful candidates will also be granted a budget to host events that contribute to interdisciplinary conversations about Global Health.

Program Description

This program, administered by the Jackson Institute for Global Affairs and led by the Global Health Justice Partnership, develops the ability of Yale undergraduates to think critically and analytically about key challenges in global health today. Students balance their appreciation for biomedical and technical issues related to diseases, their treatment and prevention, with their growing understanding of the historical, social, economic and political concerns that are implicated in how health is determined and experienced in the 21^st century.

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Qualifications

Requirements: Ph.D. awarded between 2015 and June 15, 2018 in any field, or J.D.; demonstrated record of interdisciplinary engagement across biomedical and social sciences and humanities. Field or teaching experience in global health preferred.

Application Instructions

To apply, please submit a cover letter, Short Research Statement (1 page), CV, one writing sample (dissertation chapter or published article on which you are the primary author), 1-2 sample course syllabi, and 3 confidential letters of recommendation. Applicants are encouraged to identify potential mentors in their cover letter.

All materials should be submitted online through interfolio at http://apply.interfolio.com/48809 . For further information, contact Jackson Institute for Global Affairs Deputy Director, Larisa Satara at larisa.satara@yale and/or Co-Director of the Global Health Justice Partnership, Professor Alice M. Miller at alice.miller@yale.edu

To ensure full consideration, please submit all materials by Friday, March 16, 2018. Please be sure that your recommenders address your teaching abilities in their letters.

Equal Employment Opportunity Statement

Yale University is an Affirmative Action/Equal Opportunity employer. Yale values diversity among its students, staff, and faculty and strongly welcomes applications from women, persons with disabilities, protected veterans, and underrepresented minorities.

“Gonsalves, Gregg” <gregg.gonsalves@yale.edu>

WorkshopsCourses

AarhusU MethodsForGWAS Mar22

Understanding the genetic architecture of complex traits through SNP-based heritability analysis

Date: Thursday 22nd March 2018, 9.30-3.30pm *Location:* AIAS, Aarhus University, DENMARK *Tutor:* Dr Doug Speed *Cost:* Free, but advance Registration is REQUIRED

https://www.eventbrite.com/e/aias-short-course-methods-for-analysing-complex-trait-gwas-data-tickets-43197420648 *Background:* In recent years there has been great progress developing genome-wide statistical tools for detecting causal variants, constructing prediction models and better understanding the genetic architecture of complex traits. However these tools use regression models involving very large numbers of predictors, and strong modelling assumptions are required to tackle the consequent problem of over-fitting. The results can be sensitive to these assumptions, and also to the effects of population structure, genotyping errors and the extent to which rare SNPs are included.

Course outline: I will cover mixed-model association analysis (e.g., Fast-LMM, GEMMA), risk prediction (e.g., polygenic risk scores, BLUP and MultiBLUP) and heritability analyses (GCTA, LDAK, LDSC), both using individual-level genetic data and summary statistics. I will emphasise the common elements of these methods, highlighting a standard framework that has emerged for genome-wide SNP analysis, while also contrasting the differences in underlying modelling assumptions.

The practicals will provide step-by-step details for analysing genetic data, starting either with individual-level data (e.g., PLINK files or the output from IMPUTE2) or summary statistics (p-values from a GWAS). There will be a selection of worked examples; to take part in the practicals, participants should bring a laptop with either MAC or LINUX OS

Prerequisites: Participants should have a basic understanding of statistics, and would ideally be familiar with the idea of a Bayesian regression model. In genetics, knowledge of SNP genotypes and linkage disequilibrium will be assumed. Computer scripts and output will be discussed that assume some familiarity with scientific computing using Linux. Experience with PLINK would be helpful but is not essential.

Provisional Timetable: 09:30 - 12:00: Lecture 1 followed by Practical 1 Introduction to analysing GWAS data, including quality control, single-SNP analysis, polygenic risk scores, mixed-model analysis and gene-based analysis 12:00 - 13:00: Lunch (food will be provided) 13:00 - 15.30: Lecture 2 followed by Practical 2 Estimating heritability, confounding bias, bivariate correlations and enrichment of functional categories

Notes: If travelling from the UK, the closest airports are Aarhus and Billund (45 and 75 minutes away), which have direct flights to London Stansted. I wanted to charge an attendance fee, but was told “in Denmark, education is free” (puh!), so instead you can use the 30 to buy a Ryanair bacon sandwich.

Any questions, email doug@aias.au.dk

Doug Speed <doug.speed@ucl.ac.uk>

Barcelona IntroToBayesianInference Jun11-15

Dear colleagues,

Transmitting Science is offering a new course: Introduction to Bayesian Inference in Practice, June 11th-15th, 2018, Barcelona (Spain).

Instructors:

Dr. Daniele Silvestro (University of Gothenburg, Sweden) and Tobias Hofmann (University of Gothenburg, Sweden)

Course overview:

Bayesian methods have become standard practice in several fields, (e.g. phylogenetic inference, evolutionary (paleo)biology, genomics), yet understanding how it works is not always trivial.

The instructor will outline the relevant concepts and basic theory, but the focus of the course will be to learn how to do Bayesian inference in practice. He will show how to implement the most common algorithms to estimate parameters based on posterior probabilities, such as Markov Chain Monte Carlo samplers, and how to build hierarchical models.

The course will take a learn-by-doing approach, in which participants will implement their own MCM Cs using R or Python (templates for both languages will be provided).

After completion of the course, the participants will have gained a better understanding of how the main Bayesian methods implemented in many programs used in biological research work. Participants will also learn how to model at least basic problems using Bayesian statistics and how to implement the necessary algorithms to solve them.

Participants are encouraged to think of potential applications of Bayesian inference in their research, which we will discuss and try to implement during the course.

For more information please check the course webpage: http://www.transmittingscience.org/courses/-statistics-and-bioinformatic s/introduction-bayesian-inference-practice/

With best regards

Sole

Soledad De Esteban-Trivigno,PhD. Scientific Director Transmitting Science www.transmittingscience. org

soledad.esteban@transmittingscience.org

Berlin ComparativeGenomics Oct1-5

Course: Comparative Genomics

When: 1st - 5th October 2018

Where: Botanischer Garten und Botanisches Museum Berlin, Freie Universität Berlin, Königin-Luise-Straße 6-8, Berlin (Germany)

Instructors:

Dr Fritz J. Sedlazeck (https://fritzsedlazeck.github.io/)

Prof. Dr. Ingo Ebersberger (https:/-/scholar.google.com/citations?user=-LOOY3kYAAAAJ&hl=en)

Course overview

This course will introduce biologists and bioinformaticians into the field of comparative genomics. Different techniques will be introduced to identify single nucleotide polymorphism (SNP) and structural variations (SVs) as well as the annotation of these variations and the assessment for their functional impact.

Course format

The course is structured in modules over five days. Each day will include an introductory lecture with class discussion of key concepts. The remainder of each day will consist of practical hands-on sessions. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete individual exercises. After and during each exercise, interpretation of results will be discussed as a group.

TARGETED AUDIENCE & ASSUMED BACKGROUND

The course is aimed at researchers interested in learning how to compare genomes and what can be learned from genomic similarities as well as variations. It will include information useful for both beginners and more advanced users. We will start by introducing general concepts of comparative genomics. On this basis, we will then continue to describe all major analysis steps from the raw sequencing data via the identification of variations to an assessment of their impact on the phenotype.

Attendees should have a background in biology. There will be a mix of lectures and hands-on practical exercises using command line Linux. We will therefore dedicate one session to introduce basic and advanced Linux concepts for processing data on Amazon cloud (AWS). Attendees should have also some familiarity with genomic data such as that arising from NGS sequencing experiments.

LEARNING OUTCOMES

Identification of SNPs and SVs using de novo genome assembly and read mapping strategies Assessment of strengths and weaknesses of the different DNA sequencing technologies, Illumina, Pacific Bioscience, Oxford Nanopore, for the detection of variations Strengths and pitfalls of de novo assembly and mapping approaches for comparative genomics Hands on experience of state of the art methods to compare multiple genomes Annotation of variations and comparative genomics analysis

PROGRAM

Monday: Run your own de novo assembly

Lecture 1

General introduction File formats: FastQ, SAM, BAM Introduction in de novo assembly strategies, best practices and quality control

Lab 1

Setting up the computers/AWS instances Reads QC + trimming De novo assembly Computing General assembly statistics

Tuesday: Run a multi sample SVs comparison

Lecture 2

What are SVs and why are they important? Mapping of short and long reads Visualization SV calling

Lab 2

How to choose the appropriate short read mapper? Calling of SVs using de-novo and mapping based approaches Comparison of de novo based and mapping based results SV Visualization and quality control

Wednesday: Towards annotating the observed variations

Lecture 3

Gene prediction RNA-Seq mapping Repeat annotation Gene order analysis

Lab 3

QC and mapping of RNA seq data Annotate genome Visualize read mapping

Thursday: Identifying genes affected by SVs

Lecture 4

Gene order and their role in regulating gene expression The concept of shared synteny and regulation blocks Evolution of the gene set: Loss, duplication, fissions and fusion of genes

Lab 4

Annotation of variants Identification of orthologs/homologs across species

Friday: Predicting the functional consequences of genomic variations

Lecture 5

Assessment of gene function (e.g. GO analysis) Functional changes due to loss, SVs, cis-regulation Impact in pathways (e.g. KEGG)

Lab 5:

GO annotation and analysis Running your own pathway analysis

Lecture 6:

- Summary and discussion

For more information about the course, please visit our website: (https://www.physalia-courses.org/courses-workshops/course33/)

Here is the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR

info@physalia-courses.org

http://www.physalia-courses.org/

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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

Berlin LinuxForBiologists Mar12-16 DeadlineExtended

Dear all, The registration deadline for the course "Introduction to Linux and workflows for biologists" has been extended to the 16th of February.

Website: (https://www.physalia-courses.org/courses-workshops/course1/)

Where: Berlin (Germany)

When: 12th-16th March 2018.

Instructor: Dr. Martin Jones (founder, Python for biologists, UK) (https://www.physalia-courses.org/instructors/t1/)

OverviewMost high-throughput bioinformatics work these days takes place onthe Linux command line. The programs which do the majority of thecomputational heavy lifting genome assemblers, read mappers,and annotation tools are designed to work best when used with acommand-line interface. Because the command line can be an intimidatingenvironment, many biologists learn the bare minimum needed to get theiranalysis tools working. This means that they miss out on the power ofLinux to customize their environment and automate many parts of thebioinformatics workflow. This course will introduce the Linux commandline environment from scratch and teach students how to make the mostof its tools to achieve a high level of productivity when working withbiological data.

Intended audienceThis course is aimed at researchers and technical workers with abackground in biology who want to learn to use the Linux operatingsystem and the command line environment. No previous experience of Linuxis required.

For more information about the course, please visit our website: (https://www.physalia-courses.org/courses-workshops/course1/)

Here is the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

Best regards,

Carlo

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR

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http://www.physalia-courses.org/ Twitter: @physacourses

mobile: +49 15771084054

https://groups.google.com/forum/#!forum/physalia-courses "info@physalia-courses.org" <info@physalia-courses.org>

Berlin MetabarcodingMicrobialCommunities Apr16-20 update

Course "Metabarcoding of microbial communities"

https://www.physalia-courses.org/courses-workshops/course30/ When: 16th-20th April 2018

Where: Botanisches Museum, Königin-Luise-Straße 6-8, Berlin (Germany)

Instructors:

Dr. Anna Sandionigi (University of Milan Bicocca, Italy)

Dr. Bruno Fosso (Institute of Biomembrane,Bioenergetics and Molecular Biotechnologies, CNR, Italy)

Overview

This course will provide a thorough introduction to the application of metabarcoding techniques in microbial ecology. The topics covered by the course range from bioinformatic processing of next-generation sequencing data to the most important approaches in multivariate statistics. Using a combination of theoretical lectures and hands-on exercises, the participants will learn the most important computational steps of a metabarcoding study from the processing of raw sequencing reads down to the final statistical evaluations. After completing the course, the participants should be able to understand the potential and limitations of metabarcoding techniques as well as to process their own datasets to answer the questions under investigation.

Format

This course is designed for researchers and students with strong interests in applying novel high-throughput DNA sequencing technologies to answer questions in the area of community ecology and biodiversity. The course will mainly focus on the analysis of phylogenetic markers to study bacterial, archaeal and fungal assemblages in the environment, but the theoretical concepts and computational procedures can be equally applied to any taxonomic group or gene of interest.

Assumed Background

The participants should have some basic background in biology and understand the central role of DNA for biodiversity studies. No programming or scripting expertise is required and some basic introduction to UNIX-based command line applications will be provided on the first day. However, some basic experience with using command line and/or R is clearly an advantage as not all the basics can be thoroughly covered in that short amount of time. All hands-on exercises will be run in UNIX-environments (Linux, Mac) on remote servers. Statistical analyses will be run in R using RStudio.

Learning Outcomes

1) Understanding the concept, potential and limitation of microbial metabarcoding techniques.

2) Learning how to process raw sequencing reads to obtain meaningful information.

3) Obtaining experience on how to statistically evaluate and visualize your data.

4) Being able to make informed decisions on best practices for your own data.

For more information about the program, please visit our website: https://www.physalia-courses.org/courses-workshops/course30/ Here is the full list of our courses and Workshops: https://www.physalia-courses.org/-courses-workshops/ Best regards,

Carlo

Carlo Pecoraro, Ph.D

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https://groups.google.com/forum/#!forum/physalia-courses "info@physalia-courses.org" <info@physalia-courses.org>

Berlin Metagenomics Apr9-13

Dear all,

registration for our 'Metagenomics' course is now open! (https://www.physalia-courses.org/courses-workshops/-course33/)

Where: Berlin (Germany)

When: 9-13 April 2018

Instructors: Dr. Curtis Huttenhower (Harvard School of Public Health, USA)

Dr. Melanie Schirmer (The Broad Institute of MIT & Harvard, USA)

Dr. Kevin Bonham (The Broad Institute of MIT & Harvard, USA)

Overview

This course will provide a thorough introduction to microbial community data analysis (metagenomics, metatranscriptomics, and other culture-independent molecular data) through a balanced approach of lectures and hands-on lab sessions. Course participants will learn how to process data from raw meta'omic sequencing files through appropriate bioinformatic methods and approaches for subsequent integrative statistical analyses. Participants are invited to bring their own data to the practical session on the final day or can use publicly available data from the Integrative Human Microbiome Project (HMP2).

Format

This course is designed for researchers and students with interest in using culture-independent molecular data (particularly DNA and RNA sequencing technologies) to study microbial communities. This includes both the human microbiome in population studies and techniques generalizable to any microbial communities. The course will mainly focus on the analysis of meta'omic sequencing, including workflows for processing raw sequencing data, multivariate analysis of microbial profiles, and visualization techniques.

Assumed Background

The participants should have some basic background in microbiology and/or bioinformatics. Programming experience is advantageous but not required, and a basic introduction to UNIX-based command line applications and R will be provided. All labs/tutorials will be run using pre-built cloud instances provided to students. Statistical analyses and visualizations will also be run in R using RStudio.

Learning outcomes

- Familiarity with the goals of typical microbial community studies and common culture-independent molecular technologies used to assay them. - Metagenomic and metatranscriptomic data analysis for taxonomic, functional, and strain-level characterization of communities using reproducible workflows. - Learning how to perform multivariate statistical analyses, combine multiple measurement types in microbial communities, and how to visualize associated results. - Experience in integrative multi'omics analysis for large sets of human microbiome or environmental microbial community populations.

For more information about the course, please visit our website: (https://www.physalia-courses.org/courses-workshops/course33/)

Here is the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

Best regards,

Carlo

Carlo Pecoraro, Ph.D

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Berlin Metagenomics Apr9-13 deadline

Dear all,

the registration deadline is soon approaching and we have the last 6 spots left for our course "Metagenomics, metatranscriptomics, and multi'omics for microbial community studies"

[https://www.physalia-courses.org/courses-workshops/course33/]

Where: Botanischer Garten und Botanisches Museum Berlin, Freie Universität Berlin, Königin-Luise-Straße 6-8, 14195 Berlin (Germany

When: 9-13 April 2018

Instructors:

Dr. Curtis Huttenhower (Harvard School of Public Health, USA)

Dr. Melanie Schirmer (The Broad Institute of MIT & Harvard, USA)

Dr. Kevin Bonham (The Broad Institute of MIT & Harvard, USA)

Overview

This course will provide a thorough introduction to microbial community data analysis (metagenomics, metatranscriptomics, and other culture-independent molecular data) through a balanced approach of lectures and hands-on lab sessions. Course participants will learn how to process data from raw meta'omic sequencing files through appropriate bioinformatic methods and approaches for subsequent integrative statistical analyses. Participants are invited to bring their own data to the practical session on the final day or can use publicly available data from the Integrative Human Microbiome Project (HMP2).

Format

This course is designed for researchers and students with interest in using culture-independent molecular data (particularly DNA and RNA sequencing technologies) to study microbial communities. This includes both the human microbiome in population studies and techniques generalizable to any microbial communities. The course will mainly focus on the analysis of meta'omic sequencing, including workflows for processing raw sequencing data, multivariate analysis of microbial profiles, and visualization techniques.

Learning outcomes

Familiarity with the goals of typical microbial community studies and common culture-independent molecular technologies used to assay them. Metagenomic and metatranscriptomic data analysis for taxonomic, functional, and strain-level characterization of communities using reproducible workflows. Learning how to perform multivariate statistical analyses, combine multiple measurement types in microbial communities, and how to visualize associated results. Experience in integrative multi'omics analysis for large sets of human microbiome or environmental microbial community populations.

For more information about the course, please visit our website: [https://www.physalia-courses.org/courses-workshops/course33/]

Here is the full list of our courses and Workshops: [https://www.physalia-courses.org/courses-workshops/]

Best regards,

Carlo

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR

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https://groups.google.com/forum/#!forum/physalia-courses info@physalia-courses.org

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Berlin RStatistics Jun18-22

Getting started with R [https://www.physalia-courses.org/courses-workshops/course13/) 18-22 June 2018, Berlin (Germany) Application deadline is: May 20th, 2018.

Instructor: Dr. Alexandre Courtiol (Leibniz Institute for Zoo and Wildlife Research, Berlin (Germany)) https://www.physalia-courses.org/instructors/t40/) Overview: R is the statistical software the most used in the world. It is extremely powerful, free of charge and open source. Despite these benefits, many avoid R, or struggle with it, as writing computer code to do any operation – a requirement in R – is at first both difficult and intimidating.

This course aims at overcoming those challenges by providing solid basics in R. At the end of the course, participants should feel much more at ease writing a computer script in the R language which covers the entire spectrum of a statistical analysis: reading data, editing them, plotting them, and analysing them. Because linear models are the dominant statistical tool in many fields, the part of the course focussing on analyses per se (see schedule) will focus on those, but principles seen during the class should greatly help those interested in other kind of analyses as well. The course will be presented over five days and will mix explanations and guided exercises. Students are free to practice with their own datasets during the course.

Intended Audience & Assumed Background: This course is aimed at scientists from quantitative sciences (e.g. biology, epidemiology, psychology...). It has been created with biologists in mind but it should accommodate scientists from other disciplines. No previous experience with R is required. Participants should have a basic familiarity with statistical terms and concepts.

Session content Monday 18th 'V Classes from 09:30 to 17:30 Monday is DATA day This first day will be dedicated to the data. R is software dedicated to data analysis, so mastering the basics of data manipulation in R is essential for further steps. It will be explained how to import data into R and how to manipulate them (e.g. from adding or removing rows or columns, to merging tables and using pivot tables). This will be good practice for students to learn the basics of the R language. We will illustrate how to do everything using R base (that is R out of the box), but we will also introduce that allow users to perform some operations on large datasets a little faster.

Tuesday 19th 'V Classes from 09:30 to 17:30 Tuesday is PLOTTING day Plotting is a crucial part of any data analysis no matter how advanced you are in statistics. It is important to visualise the data before the analysis (e.g. to visually check the presence of potential errors and for getting a sense of the distribution of the data), during the analysis (e.g. to check the distribution of model residuals), and after the analysis (to communicate findings in the most efficient way). Therefore, knowing how to plot various kind of data matters a lot. We will thus show how to plot different types of data in R (points, distributions, rasters...) using different graphic environments (e.g graphics, lattice, ggplot2).

Wednesday 20th 'V Classes from 09:30 to 17:30 Wednesday is FUNCTIONS day As John Chambers – the grandfather of R – put it Everything that happens in R is a function call. That R allows for so-called functional programming is one of its great benefits: it allows the implementation of any workflow of statistical analysis as the succession of simple clearly identified steps. Each step is described by a function that takes an input and generates an output. The output of one function is often the input of the next. On this third day we will show that creating one's own function is very very easy (yes, even YOU can program!) and can be very very useful. As a first application we will create our own functions to implement a randomisation test. As a second application we will show how to create functions to perform a power analysis (the estimation of the probability of getting true positives when applying a test) for any statistical test.

Thursday 21st 'V Classes from 09:30 to 17:30 Thursday is LM day Many widely used statistical methods (t-tests, anova, ancova, linear regressions...) are just different type of Linear Models (LM), which is why LM represent the most useful statistical toolbox to be familiar with if you are in natural or social sciences. Fitting a LM in R is easy – but building models, checking model assumptions, interpreting the outputs, and plotting predictions correctly requires some know how. After refreshing the most important concepts surrounding LM, we will go through each of these steps in detail, working on real datasets. It is important to understand LM quite well before jumping into the more complex methods which we will see on the next day.

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Boston ArnoldArboretumSummer Jun11-22

Arnold Arboretum Summer Course 2018 'V Plant Morphology: Linking Phenotype to Development

This two-week short course (June 11 'V 22, 2018) will be taught by experts from around the world as an intense lecture, laboratory, and living collections learning experience. The course will be based at the Weld Hill Research Building at the Arnold Arboretum in Boston (Massachusetts), which offers a state-of-the-art microscopy laboratory for teaching and sits amid the 15,000+ living specimens of more than 2,200 species at the Arnold Arboretum.

This course will provide a working knowledge of tools and concepts that are central to understanding the developmental basis for the remarkable structural and functional diversity of plants. Topics include developmental dynamics, evolutionary diversification, and ecological and physiological function. Ultimately, this course aims to provide the skills necessary to interpret the vast array of morphologies that exist among plants. Each day will consist of lecture and laboratory sessions, with ample opportunity to explore the Arnold Arboretum.

There are no course fees, and funds are available to help defray costs of participant travel.

Course Instructors: Pamela Diggle (University of Connecticut), Peter Endress (University of Zurich), William (Ned) Friedman (Harvard University), Cynthia Jones (University of Connecticut).

Application Deadline: Applications must be submitted by 11:30 pm March 15th, 2018. Application instructions are available on the course website: https://www.arboretum.harvard.edu/education/aa-summer-course/ Eligibility: microMORPH summer short courses are open to postdoctoral researchers, graduate students, and undergraduates in their final year of study (who have been admitted to a graduate or professional program for the fall of 2018). Non-US-citizens are welcome to apply (but are responsible for obtaining the appropriate visa to be able to attend the course).

How to Apply: For full application instructions (including list of required documents) and to submit applications, please visit the microMORPH website (https://www.arboretum.harvard.edu/education/aa-summer-course/ . Questions or Comments? Contact Pamela Diggle at pamela.diggle@uconn.edu

Pamela Diggle

Professor Department of Ecology and Evolutionary Biology University of Connecticut

860-486-4788

diggle@colorado.edu

BuenosAires RevBayes Apr16-18

Subject: Call for Applications: “RevBayes Workshop: Bayesian Inference of Phylogeny and Diversification Rates” at the Museo Argentino de Ciencias Naturales (MACN) in Buenos Aires, to be held April 16-18, 2018.

*Objectives: *We are pleased to announce a new intensive short course on the use of RevBayes the new MrBayes focused on Bayesian phylogenetic tree inference and diversification rate estimation. The course will be free of charge, three full days in length and, and will take place at Museo Argentino de Ciencias Naturales (MACN-CONICET), Buenos Aires, Argentina from the 16th to the 18th of April, 2018. This course is primarily funded by the BAYLAT (Germany), with support from the MACN-CONICET. The course will be primarily taught in English. Applications may be written in English or Spanish and should be submitted online by March 15th, 2018 (

https://sites.google.com/view/revbayesargentina/página-principal). Preference will go towards students with background in phylogenetics and a compelling motivation for taking the course. Questions can be directed by email to hoehna@bio.lmu.de (Sebastian Höhna) or lpalazzesi@macn.gov.ar (Luis Palazzesi).

*Location: *Museo Argentino de Ciencias Naturales (MACN) in Buenos Aires, Argentina

Instructors: Sebastian Höhna, LMU Munich; and Luis Palazzesi, MACN.

For more information about the workshop and a link to the online application form, go to

https://sites.google.com/view/revbayesargentina/página-principal *Registration Fee: *There are no registration costs thanks to generous funding from *BAYLAT* < http://www.google.com/url?q=http%3A%2F%2Fwww.baylat.org&sa=D&sntz=1&usg=AFQjCNGh_M8GaT4klXdaXtA_so4WXnik6g > (Germany), with support from the MACN-CONICET.

Application deadline: March 15, 2018 (applications received after the deadline will be considered if space is available)

Sebastian Höhna <sebastian.hoehna@gmail.com>

DukeU EvolutionaryMedicineSummerInst Jun3-9

The Evolutionary Medicine Summer Institute (EMSI)

We invite students, faculty, public health practitioners, physicians and veterinarians to the first annual Evolutionary Medicine Summer Institute (EMSI) at Duke University from June 3 to June 9, 2018, organized by the Triangle Center for Evolutionary Medicine (TriCEM, http://www.tricem.org/). We also encourage applications from advanced undergraduates interested in evolutionary medicine, and graduate students in organismal biology who wish to apply an evolutionary perspective to human or animal health.

Evolution is largely absent from medical and public health training, yet it is vital to tackling our most urgent health challenges, including emerging infectious diseases, the evolution of microbial resistance, increasing prevalence of autoimmune diseases, the obesity epidemic, threats to food safety, neurodegenerative disease, and cancer.

The goal of EMSI is to introduce core evolutionary perspectives to a wide range of topics in human health and disease, and to train physicians and medical scientists in computational methods used in evolutionary and ecological research. EMSI will bring together internationally recognized experts in evolutionary biology with students and health practitioners who want to apply these perspectives rigorously to cancer, infectious disease, antibiotic resistance, brain sciences, autoimmune disease, the microbiome, and more. Mornings will feature lectures to instill a foundational understanding of core concepts in evolutionary medicine and evolutionary biology. In the afternoons, we will break into subgroups for training on specific evolutionary methods, including phylogenetics, molecular evolution, the microbiome, and epidemiology.

EMSI will also offer an opportunity for scientists and practitioners across disciplines to network and build collaborations. To facilitate networking, interested participants will form teams to write short papers that present evolutionary perspectives on specific diseases, which will be submitted as Clinical Briefs to the journal Evolution, Medicine and Public Health (http://emph.oxfordjournals.org/).

Applications are due by March 1, 2018. For more information, and to submit an application, please go to the EMSI website: sites.duke.edu/emsi/. Please direct questions to Melissa Manus (mbm40@duke.edu) or Charles Nunn (clnunn@duke.edu).

Charles L. Nunn

Department of Evolutionary Anthropology & Duke Global Health Institute

Director, Triangle Center for Evolutionary Medicine (TriCEM < http://tricem.dreamhosters.com/ >) Editor-in-Chief, Evolution, Medicine and Public Health < https://academic.oup.com/emph >

nunn-lab.evolutionaryanthropology.duke.edu

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clnunn@duke.edu

Greifswald GreifOlution MathematicsOfEvolution Sep16-22

Dear EvolDir users,

As part of the “Year of Mathematical Biology” we proudly announce GreifOlution, the 1st Greifswald Summer School on Mathematics of Evolution (kindly funded by the DAAD, the German Academic Exchange Service). The main focus of this summer school will be on mathematical models and methods for reconstructing phylogenetic trees and networks, but upon request we might also include some sessions on other related topics, e.g. from population genetics. — So if you are a mathematician or computer scientist with a strong interest in biology or a biologist who aspires to a deeper understanding of mathematical or statistical methods and— models, this summer school is what you need! — Greifswald University is one of the hotspots of mathematical phylogenetics and biomathematics in Germany - as the only German university which has been offering a biomathematics study program already for 20 years, the small town located directly at the Baltic Sea has attracted lots of renowned researchers over the years! So why not benefit from the presence of all these experts? Come and spend a week in summer at the beautiful Baltic Sea and deepen your knowledge on mathematical phylogenetics!

This summer school aims at bridging the gap between mathematics and biology and providing both a broad introduction to various fields of biomathematics (e.g. biostatistics, bioinformatics and mathematical phylogenetics) as well as insights into state-of-the-art research. — We invite applications from PhD students, PostDocs and advanced graduate students of Mathematics, Computer Science or Biology (and related areas of study) who have a great interest in Biomathematics, in particular in Mathematical Phylogenetics. The school is free of charge. There are also no costs for the social dinner, the excursions and lunch during the summer school, but participants must cover their own accomodation and travel expenses. Foreign participants, however, may be eligible for funding (see the below for the DAAD reglementation concerning foreign participants).

For more details, please visit https://math-inf.uni-greifswald.de/institut/ueber-uns/mitarbeitende/-fischer/greifolution/ or contact us at greifolution@uni-greifswald.de

We would be pleased to welcome you in Greifswald in September 2018!

Kind regards, Mareike Fischer

(in the name of the organizing committee)

Prof. Dr. Mareike Fischer

Biomathematics and Stochastics

Institute for Mathematics & Computer Science Ernst-Moritz-Arndt University Walther-Rathenau-Str. 47 Office 3.15 17487 Greifswald GERMANY

+49 (0) 3834 420 46 43

email@mareikefischer.de

greifolution greifolution <greifolution@uni-greifswald.de>

HaGoshrim Israel SocialInsectGenomics Jul15-20

Call for applications. We are happy to announce that German and Israeli graduate students and postdocs are now invited to apply to the School. Please submit applications through the web form (link below).

German-Israeli Minerva School 2018: New Frontiers in Sociobiology and Sociogenomics July 15-20, 2018 HaGoshrim, Israel

A workshop on the frontiers of social insect research with an emphasis the application of omics (genomics, transcriptomics, proteomics) - Phylogenomics and comparative genomics in the study of evolution of complexity and novelty - Transcriptomics and regulatory networks in the study of SocioEvoDevo and indirect genetic effects - Socio-physiology: hormones and neurons as links between genes and social behavior - Emerging molecular technologies: CRISPR-Cas, epigenetics, miRNAs, microbiomes

Lectures will be accompanied with hands-on tutorials on the omics data analysis and a field trip. The School is primarily targeted at graduate students and postdocs. Travel and full board accommodations will be covered by Minerva for 20 students. German and Israeli graduate students and postdocs are invited to apply through the web form on School website: https://sites.google.com/-view/minerva2018 Application deadline: February 28, 2018

Organizers: JÃÂ¼rgen Gadau, Judith Korb, Eyal Privman, Guy Bloch Additional speakers to be announced

Eyal Privman <eprivman@univ.haifa.ac.il>

IndianaU TranscriptomeAssembly Apr30-May1

De novo assembly of transcriptomes using HPC resources workshop

Hosted by The National Center for Genome Analysis Support at Indiana University

The National Center for Genome Analysis Support, or NCGAS, at Indiana University is offering a National Science Foundation-sponsored, two-day workshop on high performance computing usage and de novo transcriptome assembly. It will take place April 30-May 1 on the IU Bloomington campus.

The workshop will include discussions, lectures, and hands-on tutorials to cover topics important to getting started constructing and analyzing transcriptomesâ euro “without the use of a genome. Material will cover both the availability and use of high performance computing (HPC) resources, alongside the task of assembling a new transcriptome, in order to provide a more comprehensive preparation for this and future bioinformatic tasks.

Transcriptome assembly will consist of using four separate assemblers (Trinity, SOAP de novo, Velvet Oases, and TransABySS), with multiple kmers, to be combined and curated with Evigenes. This combined assembly with multiple parameters is considered much more robust than simply using one assembler, and the NCGAS pipeline streamlines the process and allows for customization if desired.

While material will make heavy use of XSEDE and IU machines, the material is transferable to any cluster.

More information here: https://itnews.iu.edu/articles/-2018/s4es-de-novo-assembly-of-transcriptomes-using-hpc-resources-workshop.php To apply for the workshop and travel assistance, please fill out this form:£— https://redcap.uits.iu.edu/surveys/?s=93PLRF47MM Sheri Sanders Bioinformatic Analyst National Center for Genome Analysis and Support (NCGAS)

NCGAS is part of the Research Technologies division of UITS; Research Technologies is a PTI Cyberinfrastructure & Service Center.

ss93@iu.edu

LeedsUK EssentialComputingSkillsForMolBiol Mar21-23

Next Generation Biologists: Essential Computing Skills for Molecular Biology is a BBSRC-STARs programme-funded project to introduce and train researchers in the essential skills and best practices in scientific computing and bioinformatics. The format of the materials and the nature of the delivery is based on the successful “Software Carpentry’ (http://software-carpentry.org/) blended-learning model where students learn by developing skills through hands-on live coding and peer programming sessions led by experienced Software Carpentry instructors and supported by a small team of helpers. This is the third workshop in the series.

AUDIENCE The workshop is aimed at researchers with little or no experience in programming and data analysis who nevertheless need these approaches in their research in the life sciences.

ORGANISERS AND INSTRUCTORS

The main organisers of the workshops are Dr Mary J. O’Connell (@Evol_Molly), Dr Bede Constantinides, Dr Martin Callaghan (at the University of Leeds) and Dr Jarek Bryk (@jarekbryk, at the University of Huddersfield). Drs Callaghan and Bryk are Software Carpentry Instructors. The project is a joint initiative of the University of Leeds and the University of Huddersfield.

PRELIMINARY PROGRAMME Monday Introduction to the fundamentals of UNIX, command-line interface and shell.

Tuesday Introduction to fundamentals of R with R Studio, including data and analysis reproducibility, concluded with example analysis of high-throughput data.

Wednesday A "hackathon" day, during which participants will use skills learned in earlier days to solve a real-life data analysis problem of their choosing or a walk-through of an analysis of a real-life dataset using learned skills in shell and R.

DATE The workshop will be run on the 21-23rd March 2018 (Wednesday to Friday inclusive).

VENUE The workshop will take place at the University of Leeds, UK.

COSTS The workshop is free of charge for all BBSRC-funded researchers, as well as staff and students from the Universities of Leeds and Huddersfield. For all other participants a course fee of 170 will apply that will need to be paid before the workshop begins. Travel and accommodation costs are *not* covered by the organisers.

HOW TO APPLY To apply for a place on the workshop, prepare a maximum one-page long curriculum vitae and a 200 word statement detailing why this course if of particular importance to your current research. Please combine the two *into a single pdf file* and send it to Dr Bede Constantinides at b.constantinides[at]leeds.ac.uk *by midnight Monday 5th March 2018*. The selection committee will notify successful applicants by the end of 7th March. The workshop will be limited to 25 participants, who are expected to bring their own computers on the workshop.

More details about the project and the workshop are available on our website at http://nextgenbiologists.org. We are also on Twitter at @nextgenbiol (the "l" is important :-).

University of Huddersfield inspiring tomorrow's professionals.

Jarek Bryk <J.Bryk@hud.ac.uk>

MBL WoodsHole MolecularEvolution Jul19-29

Founded in 1988, the Workshop on Molecular Evolution is the longest-running workshop if its kind. The 2018 workshop will be held July 19-29, and this will be its 30th anniversary at the Marine Biological Lab in Woods Hole, MA. The Workshop is the premier program for integrating the methods, theory, and applications of molecular phylogenetics, statistical genetics, molecular evolution, and related disciplines. Students work closely with internationally-recognized scientists, receiving (i) high-level instruction in the principles of molecular evolution and evolutionary genomics, (ii) advanced training in statistical methods best suited to modern datasets, and (iii) hands-on experience with the latest software tools (often from the authors of the programs they are using). The material is delivered via lectures, discussions, and bioinformatic exercises motivated by contemporary topics in molecular evolution. A hallmark of this workshop is the direct interaction between students and field-leading scientists. The workshop serves graduate students, postdocs, and established faculty from around the world seeking to apply the principles of molecular evolution to questions of both basic and applied biological sciences. A priority of this workshop is to foster an environment where students can learn from each other as well from the course faculty.

As the course progresses, participants learn how to use the following software to address questions concerning the origins, maintenance, and function of molecular variation: ASTRAL, BEAST2, BEST, FASTA, FigTree, GARLI, IQTree, MIGRATE, MAFFT, MP-EST, RaxML, RevBayes, PAML, PAUP*, SNaQ, and SVD Quartets. Students will have the opportunity to work with software on their own laptops as well as receive training on how to use the same programs on a high performance computer cluster.

In 2018 the course instructors include Cécile Ané, Peter Beerli, Joseph Bielawski, Belinda Chang, Casey Dunn, Scott Edwards, Laure Eme, Deise Josely Pereira Gonçalves, Tracy Heath, Mark Holder, John Huelsenbeck, Lacey Knowles, Laura Kubatko, Michael Landis, Paul Lewis, Emily Jane McTavish, Bui Quang Minh, Suman Neupane, David Swofford, Noor White, Rachel Williams and Anne Yoder.

Deadline for applications is April 6, 2018: https://-

ws2.mbl.edu/studentapp/studentapp.asp?courseID=MOLE More information on the Workshop is available on the dedicated course website: https://molevol.mbl.edu/index.php/Main_Page The dates for the Workshop are designed to allow students to segue directly into the Strategies and Techniques for Analyzing Microbial Population Structures (STAMPS) course, though please note that applications must be submitted to, and are evaluated separately from, those submitted to the Workshop on Molecular Evolution.

For further information, please contact Workshop co-Directors: Joseph Bielawski (j.bielawski@dal.ca) and/or Mark Holder (mtholder@ku.edu)

"J.Bielawski@dal.ca" <J.Bielawski@dal.ca>

MexicoCity PhylogeneticComparativeMethods Jun26-29

The following is an announcement of a course on phylogenetic comparative methods to be taught in Mexico City in June. The English version of the announcement can be found below. The announcement is also available at http://www.phytools.org/mexico2018/ad/ . —

Curso de macroevolución y uso de métodos filogenéticos comparativos en R

Nos complace anunciar un nuevo curso intensivo, con modalidad de taller, destinado a estudiantes graduados / de posgrado, acerca del uso de métodos filogenéticos comparativos en R. Estos métodos tienen diversas aplicaciones en estudios macroevolutivos. El curso será gratuito, tendrá una duración de cuatro días, y se dictará en la Universidad Nacional Autónoma de México, Ciudad Universitaria, Ciudad de México entre los días 26 a 29 de junio de 2018. Este curso estará parcialmente financiado por la National Science Foundation (Estados Unidos), y contará con el apoyo adicional de la University of Massachusetts Boston y de la Universidad Nacional Autónoma de México. El financiamiento cubriría los costos de los pasajes de avión y del alojamiento de los alumnos que sean aceptados en el curso, si bien la totalidad de la cobertura podría estar sujeta a cambios, dependiendo de la localización geográfica de los postulantes seleccionados.

El curso se encuentra destinado a estudiantes avanzados, estudiantes de maestría o doctorado en ciencias biológicas o carreras afines, investigadores y profesionales interesados en la temática. Recibiremos solicitudes de cualquier país; sin embargo anticipamos que los postulantes mexicanos, centroamericanos, caribeños y de otros países latinoamericanos constituirán la mayoría de los estudiantes admitidos al programa. Los estudiantes provenientes de países más lejanos que resulten elegidos tendrán la posibilidad de recibir Ãºnicamente apoyo parcial para costear sus gastos del viaje.

Los temas que serán discutidos en el curso incluyen: una introducción al ambiente computacional de R, manipulación de árboles filogenéticos, mínimos cuadrados generalizados en un contexto filogenético, reconstrucción de estados ancestrales, modelos evolutivos de rasgos, análisis de diversificación filogenética, y visualización de filogenias y datos comparativos, entre otros. El curso estará a cargo de los instructores Dr. Liam Revell (University of Massachusetts Boston), Dr. Luke Harmon (University of Idaho), Dr. Michael Alfaro (University of California, Los Angeles) y Dr. Alejandro Gonzalez-Voyer (UNAM) contándose con la posible participación de instructores adicionales. El Dr. Alejandro Gonzalez-Voyer también será el coordinador de este curso.

El curso será dictado principalmente en inglés; sin embargo, algunos de los instructores y ayudantes de enseñanza del curso hablan español fluido. Las discusiones, los ejercicios, y las actividades del curso se harán en español e inglés.

Los interesados en solicitar la admisión deberán enviar su currículum vitae y una descripción corta (1 página) de sus intereses científicos, experiencia, y razones por las cuales quieren tomar el curso. El proceso de admisión será competitivo, y se dará preferencia a estudiantes con conocimientos de filogenética y que estén desarrollando investigaciones relacionadas a los temas del curso. Se espera que todos los estudiantes tengan un nivel básico de inglés científico. En la solicitud debe indicarse el aeropuerto de viaje preferido (si aplica). Las solicitudes pueden estar escritas en inglés o en español y deben ser enviadas por email a mexico@phytools.org antes del 1 marzo de 2018. Preguntas adicionales pueden ser dirigidas al Dr. Liam Revell (liam.revell@umb.edu) o al Dr. Alejandro Gonzalez-Voyer (alejandro.gonzalez@iecologia.unam.mx).

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Intensive short course on macroevolution and phylogenetic comparative methods in R

We are pleased to announce a new graduate-level intensive short course on the use of R for phylogenetic comparative analysis and downstream implementation in macroevolutionary studies. The course will be four days in length and free of charge, and will take place at the Universidad Nacional Autónoma de México in Mexico City from the 26th to the 29th of June, 2018. This course is partially funded by the National Science Foundation, with additional support from the University of Massachusetts Boston and the Universidad Nacional Autónoma de México. There are a number of full stipends available to cover the cost of travel and lodging for qualified students and post-docs. Applicants are

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Naples ELIXIRPopulationGenomics Apr21-27

Deadline on 05.02.2018 - only one week to go!

ELIXIR-IIB, in collaboration with the National Research Council Italy, is pleased to announce the upcoming training course on “Population Genomics: background and tools”.

IMPORTANT DATES

Deadline for applications: 5 February 2018

Chosen participants will be notified by: 28 February 2018

Payment deadline: 10 March 2018

Course date: 21-27 April 2018

A maximum of 28 candidates will be accepted in the course. Priority will be given to candidates from ELIXIR-IIB member institutions and ELIXIR nodes.

REGISTRATION FEE: 500 euro

Registration fee includes course material, coffee breaks and lunches.

VENUE

Biblioteca - Consiglio Nazionale delle Ricerche - Istituto di Genetica e Biofisica “Adriano Buzzati-Traverso” - via Pietro Castellino 111 - 80131 Napoli - IT

Full details at: https://elixir-iib-training.github.io/website/2018/04/21/PopGen-Napoli.html COURSE DESCRIPTION:

Study methods in population genomics have been profoundly reshaped in the last few years thanks to the growing availability of complete genomic sequences at population level. The rapid and recent growth of data and methods calls for new approaches to become routine in evolutionary genomics laboratories. The objective of this Practical Course is to give an overview of state of the art methods in population genomics combining lecturing from outstanding experienced population geneticists and software developers. All conceptual innovation will be presented in lectures and applied in practice both individually and in group work.

Practicals include computer exercises supervised by lecturers and training assistants. After attending the course participants will be aware of up-to-date concepts in population genetics, capable of running analyses using software based on whole genome data sequences and able to deal with basic aspects of any population genomics project. This Practical Course aims at evolutionary biologists who already have bioinformatics skills. PhD students and Post-Doc researchers will benefit the most out of this course, but applications from all candidates will be evaluated in their context.

COURSE SPEAKERS

§Aida Andrés, Max Planck Institute for Evolutionary Anthropology, Germany, balancing selection in humans and primates

§Andrew Clark, Cornell University, USA, population genetics

§Mathias Currat, Université de Genève, Switzerland, coalescent simulations in European populations

§Olivier Delaneau, Université de Genève, Switzerland, statistical genomics

§Pascale Gerbault, University of Westminster, United Kingdom, positive selection in humans

§Garrett Hellenthal, University College London, United kingdom, population structure and demography

§Andrea Manica, University of Cambridge, United Kingdom, population genetics, natural selection

§Ida Moltke, University of Copenhagen, Denmark, human evolution evolutionary medicine

§Martin Sikora, Natural History Museum of Denmark

Tweet #popgenELIXIR

Should you have any question, do not hesitate to contact the ELIXIR-IIB Training Team (elixir.popgen.2018@gmail.com)

Thank you for your interest,

The Organisers and the ELIXIR-IIB Training Team

Chiara Batini (University of Leicester, UK), Vincenza

Colonna (CNR, Napoli, IT) and Allegra Via (CNR, Bari, IT)

"Batini, Chiara (Dr.)" <cb334@leicester.ac.uk>

NorthCarolin Michigan Avida-ED Summer2018

We are currently soliciting applications for participants in a training workshop to teach faculty how to use Avida-ED, a free, web-based program designed to teach both principles of evolution and the nature of science, based on the research platform Avida.— This summer, we are holding two such workshops, **one at Michigan State University (in East Lansing) from August 1-3*, and* *one at the North Carolina A&T (in Greensboro) June 14-16*** .— Workshop participants will learn how to use this program, and incorporate it into courses that they teach.— We will give priority to applications submitted as teams of two, though *in a change from last year, we are also accepting applications from single individuals*.— Full details on the workshops, and information on how to apply, can be found at https://avida-ed.msu.edu/active-lens-train-the-trainers-workshop-2018-edition ; *the application deadline is March 19th*.— If you have any questions about this, please don't hesitate to contact me at mwiser@msu.edu

-Mike Wiser Postdoc in Evolution Education mwiser@msu.edu

Michael Wiser <mwiser@msu.edu>

ObergeriSwitzerland BEAST Jun17-22

Dear colleagues,

We are happy to announce that registration is now open for our summer school "Taming the BEAST".

Phylogenetics and phylodynamics are central topics in modern biology. Phylogenetic inferences reconstruct the evolutionary relationships between organisms, whereas phylodynamic inferences reveal the dynamics that lead to the observed relationships. These two fields have many practical applications in disciplines such as epidemiology, developmental biology, paleontology, ecology and even linguistics. However, phylogenetics and phylodynamics are complex and fast-evolving fields. As such, inference tools are not easily accessible to researchers who are not from a computational background.

Taming the BEAST is a summer school focusing on the BEAST2 software and consisting of a mix of invited talks, lectures and hands-on tutorials by leading and renowned experts in the field (including several of the core developers of BEAST2). The aim of this summer school is to equip participants with the skills necessary to confidently perform their own phylogenetic and phylodynamic inferences in Bayesian settings, while providing them with a firm grasp of the theory behind those inferences. Participants are also highly encouraged to bring their own datasets along and to engage with the organizers and speakers to address any problems specific to their own datasets/analyses.

REGISTRATION IS NOW OPEN. We welcome applications from graduate students and early-career scientists in the life sciences. Preference will be given to applicants who are not from a computational background and applicants who have already collected/assembled a dataset that they need to analyze.

Invited speakers: Alexei Drummond (University of Auckland) Vladimir Minin (University of California, Irvine) Alexandra Gavryushkina (University of Otago) Tanja Stadler (ETH Zurich) Sebastián Duchêne (University of Melbourne)

Dates: June 17th to June 22nd (Deadline for registration is March 25th).

Place: Oberägeri, Switzerland

Registration Fee: 900 CHF (Registration fee includes accommodation and meals).

For more information please visit the summer school website: https://www.bsse.ethz.ch/cevo/taming-the-beast/overview-2018.html For information on previous workshop programs, tutorials etc. please visit https://-taming-the-beast.github.io/ We hope to see you there, the Taming the BEAST organizing team

Tim Vaughan <timothy.vaughan@bsse.ethz.ch>

Plon EvolStructuredPopulatons Sep5-7

Dear Colleagues,

we are happy to announce the workshop “Evolutionary Models of Structured Populations: Integrating Methods” taking place in Plon on September 5 - 7th, 2018.

Speakers are: Annette Baudisch (University of Southern Denmark), Oana Carja (University of Pennsylvania), Hal Caswell (University of Amsterdam), Nicole Creanza (Vanderbilt University), Florence Debarre (Centre Interdisciplinaire de Recherche en Biologie), Andre M. de Roos (University of Amsterdam) and Bartlomiej Waclaw (University of Edinburgh).

Registration and abstract submission is open until April 30th: https://workshops.evolbio.mpg.de/event/-7/registrations/7/ Prior to the start of the workshop, Hal Caswell will give a tutorial about sensitivity analysis of demographic models for ecology and evolution in the morning of the first day (Sept 5th). It is meant mostly for junior scientists and researchers new to demographic modelling; some math background is assumed.

This tutorial is limited to 20 participants.

We hope to see you at the workshop! Please spread the word to potentially interested colleagues.

Best wishes, Stefano Giaimo & Laura Hindersin

–

Laura Hindersin PostDoc at Department of Evolutionary Theory Max Planck Institute for Evolutionary Biology August-Thienemann-Str. 2 24306 Plon, Germany 04522 763-576

Laura Hindersin <hindersin@evolbio.mpg.de>

Russia SummerSchoolBryozoa Aug18-31

Course: Russia.SummerSchoolBryozoa.Aug18-31

Dear colleagues,

Saint-Petersburg state university (SPbSU, Russia) invites master and PhD students and young researches to participate in the *International Summer School on Bryozoa:* diversity and evolutionary trends in colonial animals. The school will take place from August 18th till August 31st 2018 at SPbSU Educational and Research station “Belomorskaya” (White Sea).

The main objective of the school is to provide a detailed overview on bryozoan diversity gained through understanding various aspects of their biology, morphology and evolution, as well as their role in the freshwater and marine environment. The course is intended to serve those who wish to broaden their knowledge of bryozoans. Study sessions include lectures, field work and lab work. Working language is English.

The course fee is 18750 RUB (~250 ’Ã). It includes tuition, local transport at the White Sea and lodging.

For registration and more information please visit our website http://mbs.spbu.ru/en/education/international-summer-school-on-bryozoa-3/ . Please, forward this information to possible candidates.

*Registration deadline is March, 1th. *

Sincerely,

Ass.Prof. Natalia Shunatova

Dept. of Invertebrate Zoology

Bilogical Faculty, SPbSU

Olga N. Kotenko. Department of Invertebrate Zoology Faculty of Biology St.Petersburg State University E-mail: olgakotenko@gmail.com

olgakotenko@gmail.com

Serbia MolecularPhenotypicEvol Jun3-10

Dear colleagues,

On behalf of Serbian Evolutionary Society (SES) and European Society for Evolutionary Biology (ESEB), I am pleased to announce a seven-day workshop on Molecular and Phenotypic Evolution: theoretical and practical approaches (MolPhE 2018) that will take place from 3^rd to 10^th June 2018 at Petnica Science Center, Serbia. The workshop is organized for postgraduate and PhD students whose work focuses on evolutionary biology.

MolPhE 2018 will cover a wide range of issues in evolutionary biology with at least two overlapping thematic topics. First (molecular): genome evolution, phylogenetic comparative methods and population genomics. Second (phenotypic combined with molecular data): evolutionary morphometry and phylogeny (phylogenetic signals in morphometric data). The significance of the valid experimental design in solving various evolutionary questions will be discussed during the whole workshop with the special emphasis on experimental evolution approach. The participants will have the opportunity to interlink diverse theoretical concepts with cutting-edge methodology for their validation.

MolPhE 2018 is envisioned to help students in their professional development, as well as their networking opportunities. This is why a strong emphasis of the workshop will be focused on improving practical research skills, designing and presenting research projects, presenting own research and science popularization activities. Students are expected to take an active role in discussions on various topics.

We encourage you to promote this workshop to postgraduate students. We are convinced that this event will increase research excellence in the field of evolutionary biology in the region, help young researchers improve their academic careers and foster networking among young evolutionary biologists and senior scientists.

For more details regarding the workshop program, selected teachers, eligibility, application process and deadline please review the descriptions on our website (https://molphe2018.wixsite.com/home).

If you have any questions about the workshop, please do not hesitate to contact Mirko ??or??evi?? by email at molphe2018@gmail.com

Sincerely,

Prof. dr Biljana Stojkovi??

MolPhE 2018 <molphe2018@gmail.com>

ThunderBay Canada PracticalDNATraining May-Jun

Practical DNA Training Program:

A two-week (9 business days) intensive laboratory-based training program designed to teach participants the fundamentals of molecular techniques including DNA extraction, amplification (using PCR), sequencing and interpretation.

This training program is offered at various times throughout the year and we will work with you to find a suitable time for training. The cost of the training program is now $2500.00.

The next scheduled times for the Practical DNA Training Program is: May 7-17, 2018 May 29 - June 8, 2018 June 18-28, 2018

For more information please contact us at 807-343-8877 or email paleodna@lakeheadu.ca or visit our website at www.ancientdna.com and click on 'Training Programs'.

Thank you.

Karen.

Karen Maa Administrative Assistant Paleo-DNA Laboratory 1294 Balmoral Street, 3rd Floor Thunder Bay, ON P7B 5Z5

Telephone: 1-866-DNA-LABS

Karen Maa <kmaa@lakeheadu.ca>

UCalifornia LosAngeles ConservationBiol 2018 CallAppl

This annual workshop provides a comfortable, informal training environment for a small group of 20-25 motivated graduate students to explore how conservation problems can best be addressed with genomic-level data. Our goal is to provide hands-on experience in the efficient collection, troubleshooting, and analysis of large, genome-level data sets for conservation-relevant problems. We focus specifically on non-model systems, and how we can best study and protect endangered taxa with genomic approaches. One of the highlights of our workshop is active participation from members of several US and California governmental agencies who use actual genetic data in endangered species protection and management, providing a forum for exploring the most relevant aspects of conservation genomics to managers.

Please find more information in this link:

https://www.ioes.ucla.edu/project/conservation-genomics-workshop-2018-call-applications/ Conservation Genomics Workshop: 2018 call for applications ... www.ioes.ucla.edu This annual workshop provides a comfortable, informal training environment for a small group of 20-25 motivated graduate students to explore how conservation problems ... Best,

UCLA La Kretz Center for California Conservation Science

La Kretz Center <lakretz@ioes.ucla.edu>

UGroningen LifeHistoryTheory Mar11-16

PhD course on Life History Theory, Field station the Herdershut, Schiermonnikoog, March 11-16 2018

Life History Theory deals with species-specific adaptive schemes of the distribution of the reproductive effort over the life of an organism. The general theoretical problem is to predict which combination of traits will evolve under specific conditions. The concepts used are also relevant to study within species variation in life history traits. The one week course aims at giving an overview of the field and will discuss methodology and recent developments.

Contents & Structure

The subject will be worked out on the basis of lectures, case histories, discussion and literature. Attention will be paid to various groups of organisms such as birds, fishes, insects and plants. The contact with current research projects is guaranteed as concrete examples will be treated by scientists working in the field. In poster sessions work and/or plans of the participating students will be discussed with the whole group and we will use computers to illustrate some of the concepts.

Topics and Teachers:

Cost of reproduction and aging in a life history context (Simon Verhulst, GELIFES)

Life-history variation and population dynamics (Martijn van de Pol, NIOO)

Evolutionary genomics, Animal personalities (Kees van Oers, NIOO)

Age and size at maturity (Tom van Dooren, CNRS, France)

We are very happy to announce that this year we will have two special guest lecturers: Jonathan Wright and Yimen Araya Ajoy (both of the Norwegian University of Science and Technology, Trondheim, Norway). Professor Wright is a behavioural ecologist who is an expert on the evolution of cooperation, parental care, parent-offspring conflict, cooperative breeding in birds. Dr Araya-Ajoy is particularly interested in the causes of variation in labile traits and its consequences on population dynamics.

For more information on the programme and to register, please visit the course website < https://www.rug.nl/-research/ecology-and-evolution/phdcourses/-lifehistorytheory > : https://www.rug.nl/research/-ecology-and-evolution/phdcourses/lifehistorytheory The course will be held on the Dutch isle of Schiermonnikoog and starts Sunday night the 11th of March and ends Friday the 16th of March 2018. The registration fee is Â 350,- for all participants belonging to the RSEE and affiliated research schools (PE&RC, SENSE). All other participants pay Â 500,-. This includes lodging, meals, and the course material at the course venue.

For more information, visit the website or please contact the Course Organizers:

Prof. Christiaan Both (Conservation Ecology, Groningen Institute for Evolutionary Life Sciences, University of Groningen)

Dr. Corine Eising (Research School Ecology & Evolution)

Corine Eising <c.m.eising@rug.nl>

UK AdvancedPythonForBiologists May28-Jun1

Advanced Python for biologists (APYB02)

https://www.prinformatics.com/course/advanced-python-biologists-apyb02/ This course is running from 28 May 2018 - 1 June 2018 in Scotland

This course is being delivered by Dr Martin Jones, an expert in Python and author of two text books,

Python for Biologists [http://www.amazon.com/-Python-Biologists-complete-programming-beginners /dp/1492346136/]

Advanced Python for Biologists [http://-www.amazon.com/Advanced-Python-Biologists-Martin-Jones/dp/14952 44377/]

Course overview: Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. This workshop is aimed at people who already have a basic knowledge of Python and are interested in using the language to tackle larger problems. In it, we will look in detail at the parts of the language which are particularly useful in scientific programming, and at the tools Python offers for making development faster and easier. The course will use examples and exercises drawn from various aspects of bioinformatics work. After completing the workshop, students should be in a position to (1) take advantage of the advanced language features in their own programs and (2) use appropriate tools when developing software programs.

Monday 28th - Classes from 09:00 to 17:00 Module 1: Data structures in Python.

In this session we will briefly recap Python's basic data structures, before looking at a couple of new data types – tuples and sets – and discussing where each should be used. We will then see how we can combine these basic types to make more complex data structures for solving specific problems. We'll finish our discussion by looking at specialized data types that are found in the Python core library. This session will also be our first introduction to benchmarking as we talk about the relative performance of different data types. In the practical session we'll learn how to parse an input file into a complex data structure which we can then use to rapidly query the data. Core concepts introduced: tuples, sets, higher-order data structures, default dicts, Counters, big-O notation.

Module 2: Recursion and trees. In this session we will cover two very closely related concepts: trees (i.e. the various ways that we can store hierarchical data) and recursive functions (the best way to operate on treelike data). As recursion is inherently confusing, we'll start with a gentle introduction using biological examples before moving on to consider a number of core tree algorithms concerning parents, children, and common ancestors. In the practical session we'll look in detail at one particular way of identifying the last common ancestor of a group of nodes, which will give us an opportunity to explore the role of recursion. Core concepts introduced: nested lists, storing hierarchical data, recursive functions, relationship between recursion and iteration.

Tuesday 7th - Classes from 09:00 to 17:00

Module 3: Classes and objects. In this session we will introduce the core concepts of object-oriented programming, and see how the data types that we use all the time in Python are actually examples of classes. We'll take a very simple example and use it to examine how we can construct our own classes, moving from an imperative style of programming to an object-oriented style. As we do so, we'll discuss where and when object-orientation is a good idea. In the practical we will practise writing classes to solve simple biological problems and familiarize ourselves with the division of code into library and client that object-oriented programming demands. Core concepts introduced: classes, instances, methods vs. functions, self, constructors, magic methods.

Module 4: Object-oriented programming. Following on from the previous session, we will go over some advanced ideas that are common to most object-oriented programming languages. For each idea we'll discuss the basic concept, the scenarios in which it's useful, and the details of how it works in Python. This overview will also allow us to consider the challenges involved in designing object-oriented code. In the practical we will work on a simulation which will involve multiple classes working together. Core concepts introduced: inheritance and class hierarchies, method overriding, superclasses and subclasses, polymorphism, composition, multiple inheritance.

Wednesday 29th - Classes from 09:00 to 17:00

Module 5: Functional programming in Python. This session will start with a look at a few different concepts that are important in functional programming, culminating in a discussion of the idea of

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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

UK AnalysingBehaviouralData Mar19-23

PS statistics are running a course aimed specifically at analysing behavioural data and is therefor highly relevant to those studying the evolution of behaviour (both human and animal)

"Behavioural data analysis using maximum likelihood in R (BDML01)"

https://www.psstatistics.com/course/behavioural-data-analysis-using-maximum-likelihood-bdml01/ This course is being devilled by Dr Will Hoppitt and will run from 19th - 23rd March 2018 in Glasgow

Course Overview: This 5-day course will involve a combination of lectures and practical sessions. Students will learn to build and fit custom models for analysing behavioural data using maximum likelihood techniques in R. This flexible approach allows a researcher to a) use a statistical model that directly represents their hypothesis, in cases where standard models are not appropriate and b) better understand how standard statistical models (e.g. GLMs) are fitted, many of which are fitted by maximum likelihood. Students will learn how to deal with binary, count and continuous data, including time-to-event data which is commonly encountered in behavioural analysis.

1) After successfully completing this course students should be able to: 2) fit a multi-parameter maximum likelihood model in R 3) derive likelihood functions for binary, count and continuous data 4) deal with time-to-event data 5) build custom models to test specific behavioural hypotheses 6) conduct hypothesis tests and construct confidence intervals 7) use Akaike's information criterion (AIC) and model averaging 8) understand how maximum likelihood relates to Bayesian techniques

Full details and time table can be found at

https://www.psstatistics.com/course/behavioural-data-analysis-using-maximum-likelihood-bdml01/ We offer accommodation packages as well to make travel cheaper, easier and stress free.

Please email any questions to oliverhooker@PSstatistics.com

Also check out our sister sites, www.PRstatistics.com (ecology courses) and wwwPRinformatics.com (data science courses)

Other up-coming PS stats courses

Oliver Hooker PhD. PS statistics

Introduction to Bayesian hierarchical modelling using R (IBHM02) https://www.psstatistics.com/course/introduction-to-bayesian-hierarchical-modelling-using-r-ibhm02/ Behavioural data analysis using maximum likelihood in R (BDML01) https://www.psstatistics.com/course/behavioural-data-analysis-using-maximum-likelihood-bdml01/ Introduction to statistical modelling for psychologists in R (IPSY01) https://www.psstatistics.com/course/introduction-to-statistics-using-r-for-psychologists-ipsy01/ Social Network Analysis for Behavioural Scientists using R (SNAR01) https://www.psstatistics.com/course/social-network-analysis-for-behavioral-scientists-snar01/ PSstatistics.com facebook.com/PSstatistics/ twitter.com/PSstatistics

6 Hope Park Crescent Edinburgh EH8 9NA +44 (0) 7966500340

– Oliver Hooker PhD. PR statistics

2017 publications -

Ecosystem size predicts eco-morphological variability in post-glacial diversification. Ecology and Evolution. In press.

The physiological costs of prey switching reinforce foraging specialization. Journal of animal ecology.

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prstatistics.com/organiser/oliver-hooker/

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Oliver Hooker <oliverhooker@prstatistics.com>

UK EukaryoticMetabarcoding Jul23-27

Eukaryotic metabarcoding (EUKB01)

https://www.prinformatics.com/course/eukaryotic-metabarcoding-eukb01/ 23rd - 27th July 2018 in Glasgow

Delivered by Dr. Owen Wangensteen

Course Overview:

Metabarcoding techniques are a set of novel genetic tools for assessing biodiversity of natural communities. Their potential applications include (but are not limited to) accurate water quality, soil diversity assessment, trophic analyses of digestive contents, early detection of non-indigenous species, studies of global ecological patterns and biomonitoring of anthropogenic impacts. This course will give an overview of metabarcoding procedures with an emphasis on practical problem-solving and hands-on work using analysis pipelines on real datasets. After completing the course, students should be in a position to (1) understand the potential and capabilities of metabarcoding, (2) run complete analyses of metabarcoding pipelines and obtain diversity inventories and ecologically interpretable data from raw next-generation sequence data and (3) design their own metabarcoding projects, using bespoke primer sets and custom reference databases. All course materials (including copies of presentations, practical exercises, data files, and example scripts prepared by the instructing team) will be provided electronically to participants.

Intended Audience

This workshop is mainly aimed at researchers and technical workers with a background in ecology, biodiversity or community biology who want to use molecular tools for biodiversity research and researchers in other areas of bioinformatics who want to learn ecological applications for biodiversity-assessment. In general, it is suitable for every researcher who wants to join the growing community of metabarcoders worldwide.

Course Programme

Monday 23rd - Classes from 09:00 to 17:00

Session 1. Introduction to metabarcoding procedures. The metabarcoding pipeline. In this session students will be introduced to the key concepts of metabarcoding and the different next-generation sequencing platforms currently available for implementing this technology. The kind of results that we may obtain from metabarcoding projects is explained using examples from real life. We will outline the different steps of a typical metabarcoding pipeline and introduce some key concepts. In this session, we will check that the computing infrastructure for the rest of the course is in place and all the needed software is installed. Core concepts introduced: next-generation sequencer, multiplexing, NGS library, metabarcoding pipeline, metabarcoding marker, clustering algorithms, molecular operational taxonomic unit (MOTU), taxonomic assignment.

Session 2. Metabarcoding markers. Primer design. PCR and library preparation protocols. In this session students will learn about the various kinds of molecular markers that can be used for metabarcoding different kinds of samples and the quality of the information which can be retrieved from them. They will learn about the most commonly used primer sets for each target taxonomic group and how to use the software available for designing their own custom metabarcoding primers. They will know about sample tags, library tags, adapter sequences, PCR protocols and library preparation procedures. Core concepts introduced: metabarcoding marker, universality, specificity, taxonomic range, taxonomic resolution, primer bias, amplification errors, sequencing errors, in silico PCR, sample tags, library tags, adapter sequences, PCR, library preparation kits, PCR-free methods, avoiding contaminations, good laboratory practice.

Tuesday 24th - Classes from 09:00 to 17:00

Session 3. The OBITools pipeline. First steps and quality control. In this session, we will start to work with the OBITools software suite, using a real sequence dataset as example for testing our metabarcoding pipeline. We will outline the steps needed to start analysing raw data from next-generation sequencers. The students will learn about the different data formats used by OBITools for working with sequences and they will perform protocols for quality control, paired-end alignment, sequence filtering, removal of chimeric sequences, sample demultiplexing, format conversion and dereplication of unique sequences. Core concepts introduced: fastq, fasta and extended fasta formats, Phred quality score, paired-end alignment, demultiplexing, sequence filtering, chimeras, dereplication, unique sequences, reads.

Session 4. Clustering algorithms. Constant and variable identity thresholds. In this session, we will introduce different algorithms available for clustering sequences into molecular operational taxonomic units (MOTUs). We will learn the differences between constant and variable identity percent threshold for delineating the MOTUS.

We will run some of these algorithms with our example dataset and will analyse the

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UK IntroToPythonForBiolopgists May21-25

INTRODUCTION TO PYTHON FOR BIOLOGISTS http://www.prinformatics.com/course/introduction-to-python-f or-biologists-ipyb05/

This course will run from 21st - 25th May 2018 in Glasgow and is being delivered by Dr Martin Jones, an expert in Python and author of two text books, Python for Biologists [http://www.amazon.com/Python-Biologists-complete-programming-beginners/dp/1492346136/] Advanced Python for Biologists [http://www.amazon.com/Advanced-Python-Biologists-Martin-Jones/dp/1495244377/] . Course overview: Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. This workshop is aimed at 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 tackle problems in their own research and (2) continue their Python education in a self-directed way.

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.

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.

Curriculum:

Monday 21st Module 1: Introduction. We will start with a general introduction to Python and explain why it is useful and how learning to program can benefit your research. Some time will be taken to explain the format of the course. We will 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.â€Core concepts introduced: source code; text editors; whitespace; syntax and syntax error; and Python versions.

Module 2: Output and text manipulation. This session will show students how 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. We will 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.â€Core concepts introduced: terminals; standard output; variables and naming;â€strings and characters; special characters; output formatting; statements; functions; methods; arguments; comments.

Tuesday 22nd

Module 3: File IO and user interfaces. We will discuss about the importance of files in bioinformatics pipelines and workflows during this session, 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.â€Core concepts introduced: objects and classes; paths and folders; relationships between variables and values; text and binary files; newlines.

Module 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, at this point we will progress on to 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.â€We explore the use of loops and lists together to tackle some more difficult

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UK IntroToRemoteSensing May21-25

“Introduction to remote sensing and GIS for ecological applications (IRMS01)”

https://www.prinformatics.com/course/introduction-to-remote-sensing-and -gis-for-ecological-applications-irms01/

This course will be delivered from the 21st - 25th May 2018 by Prof. Duccio Rocchini and Dr. Luca Delucchi in Glasgow City Centre.

This course is aimed at anyone using remote sense (RS) data, for example those in the field of landscape genetics/genomics and will give a full overview of RS from an introductory level using R and Python

Course Overview:

The course will deal with different aspects related to the use of remote sensing and GIS in spatial ecology by using the Free and Open Source Software GRASS GIS coupled with R. By the end of this 5-day practical course, attendees will have the capacity to deal with ecological patterns and processes by using GIS and remote sensing algorithms. The increasing availability of open ecological and geographical data through networks such as the Global Biodiversity Information Facility (GBIF, http://www.gbif.org) or the Data Observation Network for Earth (DataONE) federated data archive (http://www.dataone.org) makes it increasingly possible to test cutting-edge ecological theories. In using a shared open-source code for testing these ecological theories, researchers can be sure that their results are reliable and also that the code they have used is robust. Attendees will be able to process spatial and ecological data by free and open source algorithms. The course will be mainly practical, but grounded on robust theory. All the analyses will be performed in GRASS GIS and the code will be shared with attendees.

Full details can be found at

https://www.prinformatics.com/course/introduction-to-remote-sensing-and -gis-for-ecological-applications-irms01/

Please feel free to share this email anywhere you see fit

Please email questions to oliverhooker@prinformatics.com

Other up-coming courses include

1. February 19^th - 23^rd 2018

MOVEMENT ECOLOGY (MOVE01)

Margam Discovery Centre, Wales, Dr Luca Borger, Dr Ronny Wilson, Dr Jonathan Potts

https://www.prstatistics.com/course/movement-ecology-move01/ 2. February 19^th - 23^rd 2018

GEOMETRIC MORPHOMETRICS USING R (GMMR01)

Margam Discovery Centre, Wales, Prof. Dean Adams, Prof. Michael Collyer, Dr. Antigoni Kaliontzopoulou

http://www.prstatistics.com/course/geometric-morphometrics-using-r-gmmr 01/

3. March 5^th - 9^th 2018

SPATIAL PRIORITIZATION USING MARXAN (MRXN01)

Margam Discovery Centre, Wales, Jennifer McGowan

https://www.prstatistics.com/course/introduction-to-marxan-mrxn01/ 4. March 12^th - 16^th 2018

ECOLOGICAL NICHE MODELLING USING R (ENMR02)

Glasgow, Scotland, Dr. Neftali Sillero

http://www.prstatistics.com/course/ecological-niche-modelling-using-r-e nmr02/

5. March 19^th - 23^rd 2018

BEHAVIOURAL DATA ANALYSIS USING MAXIMUM LIKLIHOOD IN R (BDML01)

Glasgow, Scotland, Dr William Hoppitt

http://www.psstatistics.com/course/behavioural-data-analysis-using-maxi mum-likelihood-bdml01/

6. April 9^th - 13^th 2018

NETWORK ANAYLSIS FOR ECOLOGISTS USING R (NTWA02

Glasgow, Scotland, Dr. Marco Scotti

https://www.prstatistics.com/course/network-analysis-ecologists-ntwa02/ 7. April 16^th - 20^th 2018

INTRODUCTION TO STATISTICAL MODELLING FOR PSYCHOLOGISTS USING R (IPSY01)

Glasgow, Scotland, Dr. Dale Barr, Dr Luc Bussierre

http://www.psstatistics.com/course/introduction-to-statistics-using-r-f or-psychologists-ipsy01/

8. April 23rd - 27th 2018

MULTIVARIATE ANALYSIS OF ECOLOGICAL COMMUNITIES USING THE VEGAN PACKAGE (VGNR01)

Glasgow, Scotland, Dr. Peter Solymos, Dr. Guillaume Blanchet

https://www.prstatistics.com/course/multivariate-analysis-of-ecological -communities-in-r-with-the-vegan-package-vgnr01/

9. April 30^th - 4^th May 2018

QUANTITATIVE GEOGRAPHIC ECOLOGY: MODELING GENOMES, NICHES, AND

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

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UNebraska EvolutionImmunity

"Immunity Across Scales" workshop

Location/Date: Glasgow, Scotland, May 28-29, 2018 with an opening dinner on May 27.

Leader: Clay Cressler, University of Nebraska

To apply: Submit your CV and a cover letter (1 page maximum) describing your interest in participating in this workshop. Please note that we are especially interested in contributions from researchers working on any aspect of immunity, from traditional mechanistic immunology, to wild immunology, to comparative immunology, and mathematicians working on developing models of the immune-parasite interaction. Please submit your application to: ccressler2@unl.edu by 31 March 2018.

** Accepted applicants will receive funding for transportation to/from Glasgow, accommodation and meals during the workshop, and the EEID conference registration fee. We strongly recommend early registration for EEID, as registration is capped. All costs will be reimbursed after the workshop and meeting.**

The immune response is perhaps the primary arbiter of a host's interaction with its parasites and pathogens, and its costs and benefits strongly influence the fitness of the host. It is well-established that the immune response is influenced by both the host's external environment (e.g., host diet, social interactions) and by its internal environment (e.g., interactions with other metabolic pathways, coinfection). At both scales, the environment creates trade-offs between immunity and aspects of organismal life history and physiology. The goal of this workshop is to bring together behavioral ecologists, disease ecologists, immunologists, and mathematical biologists to understand the emergence and implications of these trade-offs for ecological interactions, epidemiological dynamics, and, ultimately, the coevolution of the immune system with diverse parasites and pathogens. Researchers with relevant datasets, mathematical models, or statistical tools will give short talks and work in breakout sessions organized around focal questions generated by workshop participants, working to integrate the insights from ecological and mechanistic immunology and develop general mathematical and statistical models. Additionally, several workshop attendees will give talks during the EEID session, "Within-host dynamics: co-infection to wild immunity."

For more details please visit http://ideas.princeton.edu/future-workshops and http://eeidconference.org/2018/.

Clay Cressler <ccressler2@unl.edu>

UppsalaU AnalysingGenderedAssumptionsInEvolutionaryBiology Apr12-13

Dear EvolDir users,

We would like to invite you to the workshop Analysing Gendered Assumptions In Evolutionary Biology (https://genderedassumptions.xyz/), funded by ESEB's Equal Opportunity initiative. It will take place at Uppsala University on April 12-13. Description below:

In evolutionary biology research, we often approach questions on males and females differently. Sometimes there may be good reasons for this. However, it may also be an outcome of gender biased assumptions. For instance, in evolutionary biology we commonly study sex differences and how these result from natural selection. We study this from both genetic and environmental perspectives. We may, however, often times assume that males and females have fixed trait abilities determined by their past evolutionary history, despite the fact that evolution is an ongoing process. Emanating from what is considered well known patterns, our assumptions may turn out to be biased by our expectations of gender. Examples from this can be found in sexual selection research where we increasingly find diversity in how this force operates on males and females, which can be contrasted with more simplistic views that “males compete and females care” as an evolutionary rule (in this context, it should be noted that the Bateman gradient paradigm has been under debate for quite some time). Furthermore, in medical and scientific textbooks, gendered assumptions have been identified and analyzed. For example, gendered views are apparent in textbooks when depicting egg, sperm, cervix, mucus, and semen, with active wordings for the male part and passive, objectified words for the female part despite the fact that, scientifically, we know mucus activity is a vital part of the fertilization process. Similar gendered biases have also been found in sexual conflict studies. And when plasticity is found in male and female traits, there is a tendency to stick to firm sex differences despite contrary evidence - as, for example, in neuroscience. More recently we have seen in the news how, after DNA testing was conducted, the remains of a Viking leader were found to be those of a woman. This had been indicated previously but was not considered likely, probably due to pervasive gender biases. This provides an illustrative case of how researchers’ gender biased assumptions can affect scientific knowledge.

In this two day workshop we aim to identify and discuss such gender biased assumptions in scientific publications, as a gateway to more deeply analyze the way we make inferences in our scientific reasoning. Furthermore, we aim to constructively put forward guidelines on how we, as scientists and members of the general public, should handle gendered assumptions. We therefore hope, through this workshop, to address some important gaps in evolutionary biology research.

The workshop will take place at the Evolutionary Biology Center of Uppsala University, Uppsala, Sweden, on 12-13 of April 2018.

To participate, send an e-mail to Ingrid.Ahnesjo@ebc.uu.se before the 15th of March 2018 and provide a short motivation letter (150 words). Number of participants is limited to 25. Participants will have to arrange travel and housing themselves (for cheap accommodation, check https://www.hostelworld.com/).

Participants can apply for the ESEB congress attendance aid grants (http://eseb.org/prizes-funding/equal-opportunities-initiative/congress-attendance-aid-grant/) before 16 February 2018.

For more information, please visit https://genderedassumptions.xyz/ Or send an email to Ingrid.Ahnesjo@ebc.uu.se or Paula.Vasconcelos@ebc.uu.se

“paula.vasconcelos@ebc.uu.se”
<paula.vasconcelos@ebc.uu.se>

UTennessee Knoxville WomenMathBiology May16-18

Hello all,We are seeking undergraduate and graduate women in mathematics or mathematical biology to participate in a peer networking workshop at The University of Tennessee, Knoxville, coinciding with the Applications of Spatial Data: Ecological Niche Modeling tutorial taking place at NIMBIOS (National Institute for Mathematical and Biological Synthesis) from May 16th-18th.This workshop, fully funded by the Association for Women in Mathematics, will provide early-career women with the opportunity to meet with female mentors in a small group setting. During the workshop, participating students will collaborate to interview mentors and produce videos documenting their career trajectories and research. Mentors will be selected from faculty attending the tutorial, University of Tennessee - Knoxville faculty, and Oak Ridge National Laboratory researchers.If you or someone you know are interested in attending, please go to https://goo.gl/forms/3O9D9ijzwAikadwi1 to apply. Any questions regarding the event or application can be directed to jbeck10@vols.utk.edu. Applications are due March 30th.Thank you,Jessica Beck and Natalie Lemanski

natalie.lemanski@gmail.com

Virginia ConservationGenetics Aug19-29

Dear Conservation Genetics Community:

We are announcing the 2018 Recent Advances in Conservation Genetics (ConGen2018) Course (10 days) that will be held at the Northern Virginia 4-H Educational & Conference Center in Front Royal, Virginia (about 112 km from Washington, DC) between August 19-29, 2018. The venue is located on the outskirts of beautiful Shenandoah National Park and near the famous Appalachian Trail. The course will host 25-30 students dedicated to conservation of animals and plants and about 20-25 distinguished faculty from around the world.

The course will be directed by Dr. Stephen J. O'Brien, and taught by renowned scientists in methods, interpretation, and applications of genomic-based analyses for conservation of endangered species, who will also share a variety of their personal research experiences in this important and rapidly developing field. The ConGen2018 faculty represent an amazing group of people who come from all around the world and will be teaching, sharing their conservation stories, and interacting with students during the course.

Please fill out this form to be considered as one of the participants for the course.

Time: August 19-29, 2018

Address: 600 4h Center Dr., Front Royal, VA 22630, USA

Contact: congen2018@conservationgenetics.org webpage: http://conservationgenetics.org/congen2018 Direct link to the registration form: https://goo.gl/forms/ks4nF24xjN5OCrmR2

Taras K Oleksyk, Ph.D. Associate Professor of Biology University of Puerto Rico Mayaguez, PR 00680 taras.oleksyk@upr.edu

Taras K Oleksyk <taras.oleksyk@upr.edu>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.