EvolDir

February 1, 2019

Month in Review

Foreword

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

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

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

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Conferences

Canberra EvidenceSynthesisHackathon Apr8-10

Registration for interest in the second Evidence Synthesis Hackathon - to be held from April 8th-10th in Canberra, Australia - is now open

What: This event is co-organised by a number of Evolutionary Biologists who are interested in promoting research synthesis in the fields of Ecology and Evolution.

We want to make it easier to synthesize studies that can inform eco/evolutionary theory and environmental management. The Evidence Synthesis Hackathon will bring together researchers and programmers, to discuss barriers to effective research synthesis and develop tools and discuss ideas on how to remove those barriers.

Website: http://evidencesynthesishackathon.com/
When: Monday 8th to Wednesday 10th April

Where: UNSW Canberra & Australian National University

Cost: $100 for full registration, $50 for students. Food included. Attendees can apply for funding to help with costs.

Who: The event is capped at 60 people. Organising committee: Neal Haddaway (Stockholm Enviornment Institute), Shinichi Nakagawa (University of New South Wales) Daniel Noble (Australian National University) Martin Westgate (Australian National University)

Confirmed presenters: Adam Dunn (Macquarie University) Kerrie Mengersen (Queensland University of

Technology) Gillian Petrokosky (University of Oxford) Wolfgang Viechtbauer (Maastricht University) Vivian Welch (Campbell Collaboration).

If this event interests you then please apply, and we hope to see you there!

Shinichi Nakagawa E : s.nakagawa@unsw.edu.au W: http://www.i-deel.org/ Daniel Noble E : daniel.noble@unsw.edu.au W: www.nobledan.com Rose O'Dea <rose.eleanor.o.dea@gmail.com>

Gainesville FL LifeDiscovery Mar21-23

5th Life Discovery - Doing Science Education Conference March 21-23, 2019 Microbiomes to Ecosystems: Evolution and Biodiversity across Scale, Space, and Time Gainseville, Florida

Early Bird Registration deadline: Feb 15, 2019 Travel Award Application deadline: Jan 31, 2019

Announcing Travel Awards for the 5th Life Discovery - Doing Science Education Conference. Applications are due on Jan 31, 2019. To increase the diversity of participants and institutions, funds are available to support educator travel and conference registration to the 2019 Life Discovery V Doing Science Education conference (LDC) These travel awards are made possible through support from our sponsors.

Priority will be given to faculty from high schools, community colleges, primarily undergraduate institutions and minority-serving institutions (colleges and universities) as well as faculty from underrepresented minority backgrounds at any institution. Faculty must be teaching at a US based institution.

All awardees are expected to submit a proposal for the Education Share Fair Roundtable session V a unique format for friendly, informal peer feedback of teaching ideas at any stage of development. Call for proposals are still open!

For full details, please visit, www.esa.org/ldc . Forwarded by:

Richard M. Kliman, SSE Rep to the Life Discovery Conference

Professor and Chair, Department of Biological Sciences

Cedar Crest College, Allentown, PA

Richard Kliman <Rmkliman@cedarcrest.edu>

Granada Spain SalmonidEvolution May20-24

Granada_Spain.SalmonidEvolution.May20-24

Dear Colleagues,

The fifth international conference on Stream Salmonid Ecology will be held in Granada, Spain this May. Held every five years, this conference brings together international researchers working on the evolutionary, population, behavioural and conservation ecology of stream rearing salmonids. With single sessions daily, group dinners and field trips, the conference offers a rare opportunity for in-depth discussions.

Registration is open, and the early registration discount ends March 1st.

All relevant information about the conference, travel and accommodation is available on the conference website: http://www.salmonidsymposium.es On behalf of the organizing committee,

Kyle A Young <kay62@pitt.edu, kayoung1969@gmail.com>

kyle young <kayoung1969@gmail.com>

Hull UK FishEnvironmentalDNA Jul

Dear all, I just wanted to draw your attention on the extension of the abstract submission for the 2019 FSBI Symposium, to take place later this year in Hull, UK.

New deadline: Jan 25th Conference information: https://www.fsbi.org.uk/annual-symposia/symposium-2019/ twitter updates: @Boristhefish

Thanks,

Stefano Mariani, on behalf of the organising committee.

Mariani Stefano <S.Mariani@salford.ac.uk>

London KingmanSymposium Jan20

Kimura Motoo Award Ceremony

Time: 11:00-13:00, Sunday, January 20th, 2019

Place: Royal Society Kohn Centre and Marble Hall, London, U.K.

Program

11:00-11:20 Kimura Motoo Award delivered to Sir John Kingman FRS

11:20-12:00 Speech by Sir John Kingman FRS

12:00-13:00 Buffet Lunch

Accompanying Symposium to honor Sir John Kingman FRS, recipient of 2019 Kimura Motoo Award

Time: 13:00-18:00, Sunday, January 20th, 2019

Place: Royal Society Kohn Centre and Marble Hall, London, U.K.

Symposium Speakers

Dr. Peter Donnelly FRS

Professor, Wellcome Centre for Human Genetics, University of Oxford, Oxford, UK

Dr. Yun-Xin Fu

Professor, School of Public Health, University of Texas Health Science Center at Houston, Houston, TX, USA

Visiting Professor, National Institute of Genetics, Mishima, Japan

Dr. Takashi Gojobori

Professor, Computational Bioscience Research Center, King Abdullah University of Science and Technology, Saudi Arabia

Visiting Professor, Waseda University, Tokyo, Japan

Emeritus Professor, National Institute of Genetics, Mishima, Japan

Dr. Robert C. Griffiths FRS

Emeritus Professor, Department of Statistics, University of Oxford, Oxford, UK

Adjunct Professor in Mathematical Sciences at Monash University, Australia

Dr. Jotun Hein

Professor, Department of Statistics, University of Oxford, Oxford, UK

Dr. Hideki Innan

Professor, Graduate University for Advanced Studies, Hayama, Japan

Dr. Naruya Saitou

Professor, Division of Population Genetics, National Institute of Genetics, Mishima, Japan

Adjunct Professor, Department of Genetics, School of Life Science, Graduate University for Advanced Studies Mishima, Japan

Adjunct Professor, Department of Biological Sciences, Graduate School of Science, University of Tokyo, Tokyo, Japan

Dr. John Wakeley

Professor, Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA, USA

Dr. Ziheng Yang

Professor, University College of London; London, UK

Visiting Professor, National Institute of Genetics, Mishima, Japan

Symposium Program

13:00-13:05 Greetings from Kimura Fund (by Dr. Takashi Gojobori)

Session 1 (chaired by Dr. Takashi Gojobori)

13:05-13:35

Diffusion processes and Coalescent trees

Dr. Robert Griffiths

13:35-14:05

Recombination, meiosis, and the origin of a species

Dr. Peter Donnelly FRS

14:05-14:35

A simple application of coalescent modeling to phylogenetic data

Dr. John Wakeley

14:35-14:50 Tea Break

Session 2 (chaired by Dr. Naruya Saitou)

14:50-15:20

The multispecies coalescent and its applications

Dr. Ziheng Yang

15:20-15:50

The Coalescent and Recombination

Dr. Jotun Hein

15:50-16:20

Within individual coalescence

Dr. Yun-Xin Fu

16:20-16:30 Tea Break

Session 3 (chaired by Dr. Yoshio Tateno)

16:30-17:00

The coalescent in a cancer cell population

Dr. Hideki Innan

17:00-17:30

High-speed construction of gene genealogies using newly developed distance matrix methods

Dr. Naruya Saitou

17:30-18:00

An incomplete lineage sorting issue on Japanese Emperor's evolutionary study of goby fish populations

Dr. Takashi Gojobori

18:30-20:00 Dinner (invited people only)

$B:XF#@.Li(B <saitounr@nig.ac.jp>

Manchester MolecularGenomeEvolution Mar25

The 8th Manchester Molecular and Genome Evolution Symposium (#MaGE2019) will take place on Monday 25th March 2019. Registration and abstract submission are now open.

MaGE encompasses all aspects of molecular and genome evolution, ranging from genomic analyses or computational algorithm development, to molecular ecology, population genetics, and experimental evolution.

We are very pleased to have plenary talks from Diana Fusco (Cambridge) and Denis Larkin (Royal Veterinary College). We will also have a wide range of contributed talks from PhD students, post-docs and PIs.

MaGE is free to attend, but places are limited so please register at the URL below. Please submit a title and abstract if you would like to present a talk or poster. We are particularly keen to give PhD students and postdocs a chance to present their work. Contributed talks and posters will be considered for a prize, presented at the drinks reception following the symposium.

Hope to see you in March!

Registration and more information at: https://manchestermage.wordpress.com/ On behalf of the organisers: Danna Gifford, Dave Gerrard, Chris Knight and Sam Griffiths-Jones

danna.gifford@manchester.ac.uk

Manchester SMBE 2019 Jul21-25 CallForAbstractsAndAwards

We are delighted to announce that abstracts are now being accepted for SMBE 2019, at http://smbe2019.org/abstracts/. The deadline for abstracts is midnight GMT on Sunday 17 March 2019. Please be aware that the deadline will not be extended. Abstracts should be no longer than 2500 characters (~250 words), with a title no longer than 300 characters.

SMBE 2019 is taking place in Manchester, UK on 21-25 July 2019 at the state of the art venue Manchester Central. Full details on the symposia programme and confirmed keynote speakers can be viewed at http://smbe2019.org/scientific-programme/ . A range of awards can be applied for during Abstract submission, all of which require SMBE membership (costing only $10/$30 for 3 years for students/others at https://www.smbe.org/smbe/MEMBERSHIP.aspx) at the time of application.

Current graduate students and postdoctoral researchers who received their primary doctoral-level degree no earlier than one year prior to the start of the annual meeting of the society may apply for the Fitch Award (https://www.smbe.org/smbe/AWARDS/TheWalterMFitchAward.aspx). Extended abstracts are no longer required this year, just the conference abstract and a cv. Unsuccessful Fitch applicants will automatically be considered for Young Investigator and Registration awards.

Any graduate student or postdoc may apply for the Young Investigator Award (https://www.smbe.org/smbe/AWARDS/AnnualMeetingTravelAwards/YoungInvestigatorTravelAward.aspx), which substantially funds the cost of attending. Application materials are the same as for the Fitch, i.e. abstract and cv. Unsuccessful applicants for both will automatically be considered for Registration-only awards.

Undergraduates (including Masters students under a 3+2 system) can apply for the Undergraduate Travel & Mentoring Award (https://www.smbe.org/smbe/AWARDS/AnnualMeetingTravelAwards/UndergraduateTravelandMentoringAward.aspx). In addition to presentation title and abstract, this requires a short explanation (250 words) 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. You also need to arrange to have a short letter of support (250 words) sent from your academic supervisor to masel@email.arizona.edu, confirming that you are undergraduate or a Masters student under 3+2, and that the research is your own.

The Carer Travel Award (https://www.smbe.org/smbe/AWARDS/AnnualMeetingTravelAwards/CarerTravelAward.aspx) can be applied for as part of conference registration rather than abstract submission, or by email to Nicolas Galtier nicolas.galtier@umontpellier.fr if an earlier response is needed. SMBE will make available up to $2000 to SMBE members with children or dependent adults (including adult children with a disability or elderly relatives) to spend as they wish to facilitate the members attendance at the annual SMBE meeting. Examples of eligible expenses include (but are not limited to) providing airfare for your child or for your caregiver to accompany you, flying a relative out to help with care at your home while youre at the meeting, or extra help paying for on-site daycare.

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

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

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

Manhattan Kansas ArthropodGenomics Jun12-14

Hi All: In 2019, the AGS returns to Kansas State University in Manhattan, Kansas.

The meeting begins Wednesday evening, June 12, with a Welcome Reception featuring our Keynote Speaker Denise Montell, Duggan Professor and Distinguished Professor from University of California Santa Barbara.

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

Featured Speakers Include: + Kerri Coons, University of Wisconsin-Madison, USA + Conor McMeniman, John Hopkins Bloomberg School of Public Health, USA + Shahideh Nouri, Kansas State University, USA + Luisa Orsini, University of Birmingham, UK + Mark Rebeiz, University of Pittsburgh, USA + Stephane Rombauts, Ghent University, Belgium + Nick Teets, University of Kentucky, USA + Yoshi Tomoyasu, Miami University, USA + Jamie Walters, University of Kansas, USA

Additional information about registration and housing for the symposium to follow in late January.

2019 AGS ORGANIZING COMMITTEE: Sue Brown, Neal Dittmer, Maureen Gorman, Mike Kanost, Berlin Londono, Jocelyn McDonald, Mary Ann McDowell, Kristin Michel, Yoonseong Park, Mike Pfrender, Hugh Robertson, Gene Robinson, Molly Scheel

Sent on the committees behalf by: Kascha Johnson, Event Coordinator K-State Arthropod Genomics Center Division of Biology, Kansas State University email: kascha@ksu.edu

Kascha Johnson <kascha@ksu.edu>

Marseilles EvolBiol Sep24-27

Dear all the early dead line for the 23rd evolutionary biology meeting at Marseilles September : 24-27 2019 is January 31 2019 see http://aeeb.fr/evolutionary-biology-meeting-2/ the programs of the 22 previous meetings are available < http://aeeb.fr/evolutionary-biology-meeting-2/ >

The meeting will be followed by several visits of the city and the calanques

see also https://twitter.com/pontarotti https://-

www.facebook.com/groups/203530083353767/ Pierre Pontarotti DR CNRS Evolutionary Biology team. Aix Marseille Univ IRD, APHM, MEPHI, IHU Méditerranée Infection,Marseille France

19-21 Boulevard Jean Moulin 13005 Marseille

tel 33 (0) 4 13 7 32425 https://sites.google.com/view/pontarotti/ < https://twitter.com/pontarotti >

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

Marseilles EvolBiol Sep24-27 EarlyDeadlineJan31

Dear all the early dead line for the 23rd evolutionary biology meeting at Marseilles September : 24-27 2019 is January 31 2019 12 PM Paris Time http://aeeb.fr/evolutionary-biology-meeting-2/ the programs of the 22 previous meetings are available < http://aeeb.fr/evolutionary-biology-meeting-2/> The meeting will be followed by several visits of the city and the calanques

see also https://twitter.com/pontarotti https://www.facebook.com/groups/203530083353767/ all the best

Pierre

< https://twitter.com/pontarotti >

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

Montpellier DomesticationEvolution Jun3-7

Dear Colleagues,

We are happy to announce that the registration is now open for the Third Harlan International Symposium, 3-7th June 2019 Montpellier France.

Please check out our website : http://www.harlan3symposium.org This symposium is dedicated to the Origins of Agriculture and the Domestication, Evolution, and Utilization of Genetic Resources. This rare event is a great opportunity to gather the community around the latest advances in the study of these topics : don't miss it !

Four sessions will dynamise the discussions about the following subjects : - History of agriculture - Diversity and adaptation - Mobilization of genetic resources - Agrosystems services and functioning A keynote speaker will open each session : Greger Larson and Yves Vigouroux have already confirm their presence.

In addition, we will have the pleasure to welcome additional speakers, who will address broader perspectives to the discussion, through a daily opening lecture: among them Rachel Brezner Kerr and Ford Denison.

Finally, the Call for Abstracts will open very shortly : stay tuned !

Anne-Céline Thuillet, On Behalf of the organizing committee

Dear colleagues,

The Call for Abstracts is now opened for the Third Harlan International Symposium, 3-7th June 2019 Montpellier France. We invite you to submit an abstract for an oral or a poster presentation using the online submission form. Please check out our website : http://www.harlan3symposium.org < https://www.alphavisa.com/harlan/2019/abstract-submission/ >

The deadline for abstract submission is 15 March 2019.

The Scientific Committee will evaluate the abstracts and confirm the type of presentation (oral or poster) and session retained.

Preliminary program :

Please refer to the Abstract —Guidelines < https://www.alphavisa.com/harlan/2019/documents/Abstract-Guidelines.pdf > in order to get information about the preliminary program and other useful information.

This symposium is dedicated to the Origins of Agriculture and the Domestication, Evolution, and Utilization of Genetic Resources. Four sessions will dynamise the discussions about the following subjects:

Â History of agriculture Â Diversity and adaptation Â Mobilization of genetic resources Â Agrosystems services and functioning

We kindly ask you to forward this message to anyone who may be interested in the Third Harlan International Symposium.

We are looking forward to welcoming you to Montpellier in June.

Sincerely,

– Anne-Céline Thuillet For the organizing committee

Norway iBOL2019 Jun17-20

I would like to remind you all that the deadline for abstract submission to the upcoming iBOL Conference is January 15! Therefore, if you plan to attend, please submit your abstract as soon as you can: http://dnabarcodes2019.org/abstracts/. We need this early deadline in order to run a proper review process of all abstracts before publication in the journal Genome.

Although abstracts can be submitted before registration, please do not hesitate to register. Payment can be made by credit card or invoice: http://dnabarcodes2019.org/registration/ Interested in news about the conference? Check out our news section http://dnabarcodes2019.org/category/news/ and follow @norwbol on Twitter.

More on the program and invited speakers on our website: http://dnabarcodes2019.org/ Best regards, Torbjørn

Torbjørn Ekrem, PhD Professor of biosystematics NTNU University Museum,Department of Natural History

Torbjørn Ekrem <torbjorn.ekrem@ntnu.no>

Padova EvolAnthro CallForAbstracts

The bi-annual meeting of the Italian Anthropological Association aims at bringing together the various streams of Biological Anthropology in a three-day long international conference. In recent years a number of ground breaking discoveries have been made possible by several technological advances in the fields of ancient and modern genomics, isotopic analysis and virtual anthropology. Also, new developments in the field of applied anthropology have changed our approach to the study of living and past human populations. All these, and other topics, will be distilled in this year' conference, in search of what will be the next relevant research questions. In addition, a joint symposium with SIBE will promote a dialogue among invited speakers on "what is a population" and on communication of science.

The conference will be structured in four main sessions, harboring contributions from all fields of Biological Anthropology: 1) Hominids and Palaeolithic humans - covering all subjects up to the Palaeolithic 2) From prehistory to history - from the Neolithic and Bronze Age cultural revolutions and demographic expansions all the way to contemporary populations 3) Contemporary human populations - mostly based on living populations, with support from ancient data 4) Applied Anthropology - including biomechanics, biomedical, forensic and all other branches of applied Anthropology.

Please send your abstract to aaiconference2019@gmail.com using the template provided on the website (www.aaiconference2019.it) and specifying whether it is intended for a talk, a poster or either of them. Presenters will be notified by email about acceptance of their abstract and assignment to a talk/poster by 15/05/2019 Please note: only one abstract per registered presenting author will be considered. This also means that all presenting authors must pay the registration fee by the abstract submission deadline (31/03/2019) for their abstract to be considered.

Looking forward to seeing you all there, Luca Pagani, Researcher at the University of Padova, Italy on behalf of the organizing committee

Luca Pagani <lp.lucapagani@gmail.com>

Padua ItalianSocEvoBiology Sep1-4

Dear all, I would like to share the following first announcement about the 8'th Congress of the Italian Society of Evolutionary Biology

Dear all,

we are glad to announce that the 8th Congress of the Italian Society of Evolutionary Biology (SIBE-ISEB, http://www.sibe-iseb.it/) will be organized by the Department of Biology of the University of Padua and will be held on 1-4 September in Padua. The congress will be hosted in the wonderful locations of the historical Botanical Garden of Padua, the most ancient botanical garden in the world and UNESCO world heritage, and in the 'Galileo Galilei' Main Hall of the XVI century Palazzo Bo.

The symposia and the events scheduled for September

4th will be shared and organized in partnership with the Italian Anthropological Association (AAI).

During the congress, we will launch the first edition of the 'Luigi Luca Cavalli Sforza Award', established by the Italian Society for Evolutionary Biology. Such an initiative recognizes eminent personalities in the research fields of evolutionary biology. The ceremony and the Cavalli Sforza Lecture will take place on the afternoon of September 4th in the 'Galileo Galilei' Main Hall.

The congress will be structured in five sequential symposia promoted by SIBE-ISEB (1-3 September) and three symposia shared with AAI on September 4 th, with distinguished international invited speakers giving their contributions. The general subject of the symposia shared with AAI will be 'Population genetics and genomics', while the subjects of the SIBE-ISEB symposia will be selected very soon, with the aim of accounting for the existing broad spectrum of interests and approaches to the study of Evolution.

There will also be a poster session, a public round table focused on science communication, and a very rich and surprising programme of social events.

The Society is also pleased to offer a crash course in Molecular Clocks using BEAST, on the morning of September 1st, at the Botanical Garden.

The Call for abstracts and deadline for the early-bird registration will be published soon. We expect, and particularly hope for, the participation of many young researchers and students.

English will be the preferred language for both oral communications and posters.

Please save the dates and we look forward to seeing you all in Padua!

The President of the Italian Society for Evolutionary Biology

and the Organizing Committee

Best Regards

Silvia

Silvia Ghirotto, PhD Associate Professor in Genetics Department of Life Sciences and Biotechnology University of Ferrara via Borsari 46 I-44121 Ferrara Phone: +39 0532 455956 Fax: +39 0532 249761

Silvia Ghirotto <ghrslv@unife.it>

PalmSprings EvolutionMobileDNA Jun23-28

FASEB Mobile DNA is coming this summer!

As a previous attendee of a FASEB Mobile DNA meeting, please be aware that registration for the 2019 meeting is NOW OPEN. The Mobile DNA Conference: 25 Years of Discussion and Research June 23-28, 2019 | Palm Springs, California

For detailed information, visit https://src.faseb.org/-mobile-dna/ Important dates: Advance registration deadline Wednesday, May 8, 2019 Last day to register Saturday, June 1, 2019

Travel awards are available from FASEB and other sponsoring organizations. http://www.faseb.org/Science-Research-Conferences/Awards-and-Travel-Grants.aspx (Note: The Society for Molecular Biology and Evolution (SMBE) is sponsoring four travel awards, $500 each, to junior evolutionary biologists specifically for this conference.)

Organizers for this year's meeting are: David Ray - Texas Tech University Wenfeng An - South Dakota State University Victoria Belancio - Tulane University Stephane Boissinot - NYU Abu Dhabi Richard Cordaux - Centre National de la Recherche Scientifique

Please contact any of us if you have questions not answered at the website.

See you this summer!

–

David A. Ray

Associate Professor Department of Biological Sciences Texas Tech University Phone: (806) 834-1677 www.davidraylab.com www.crocgenomes.org/-david.4.ray@gmail.com

Even the best of us have bad days. "I am very poorly today and very stupid and hate everyone and everything." - Charles Darwin - Oct. 1, 1861

David Ray <david.4.ray@gmail.com>

Portland Oregon Sex Asex Jun2-4

Registration is now open for AGA2019!

Sex & Asex: The Genetics of Complex Life Cycles American Genetic Association President's Symposium 2-4 June 2019, Portland, Oregon

Many organisms across the tree of life have complex life cycles that include both sexual and asexual reproduction or are obligately asexual. These include those that sequentially switch between sexual and asexual forms (for example, Daphnia), those whose life histories can include both types of reproduction in the same generation (for examples, marine invertebrates capable of both sexual reproduction and clonal spread, many plants), and species that appear to have secondarily lost sexual reproduction, including some surprisingly ancient lineages. Recently, scientists have been applying both theory and empirical work, including genomic and genetic studies, to untangle the evolutionary effects of the amount and timing of sexual and asexual reproduction.

Join AGA President Maria Orive at beautiful McMenamins Edgefield. Confirmed speakers include:

Key Distinguished Lecturer Sally Otto Rebecca Zufall, University of Houston (Tetrahymena) Stacy Krueger-Hadfield, University of Alabama at Birmingham (Seaweeds) Matthew Hartfield, University of Edinburgh (Theory) Laura Katz, Smith College (Ciliates) Tanja Schwander, University of Lausanne, Switzerland (Stick insects) Curt Lively, Indiana University (Snails) Catherine Rushworth, Duke University (Boechera plants) Solenn Stoeckel, INRA Rennes, France (Theory) Karine Van Doninck, University of Namur, Belgium (Rotifers) Jennifer Anderson, Uppsala University, Sweden (Neurospora) Mercedes Burns, University of Maryland (Harvestmen arachnids)

Early discounted registration is open. There are registration and travel awards for students presenting posters. Details on the AGA website: http://www.theaga.org . "Cough-Schulze, Chantal" <ccough-schulze@cvm.tamu.edu>

Portugal EuropeanPhDEvolBiol May26-Jun1 reminder

The 25th edition of EMPSEB (European Meeting of PhD Students in Evolutionary Biology) will take place from May 26th to June 1st, in Pedrógão Pequeno, Portugal.

This meeting promotes a unique atmosphere for all its participants, giving them the opportunity to share and debate their projects with peers and with a group of invited international scientists, recognised as leaders in their scientific fields.

Additionally, this event also provides an excellent opportunity for early-carrer scientists to develop important soft skills and be exposed to distinct professional aspects that are intrinsically related to a carrer in science.

Abstract submission for EMPSEB25 is now oOPEN and will close on February 3rd 2019! There are still a few slots left, so don't forget to send in your abstract!

For more information please visit the official website for the event EMPSEB25 < http://www.empseb25.wixsite.com/pedrogao > and follow us on Twitter (@empseb25 < http://www.twitter.com/empseb25 >).

Kind regards,

The EMPSEB25 organizing committee

EMPSEB 25 <empseb25@gmail.com>

RBGKew UK PlantEvolution Apr3-5

3rd UK Plant Evolution Meeting April 3-5 2019, Royal Botanic Gardens, Kew Deadline for abstract submission: 1st March 2019 Deadline for registration: 31st March 2019 Webpage: https://www.kew.org/kew-gardens/whats-on/3rd-uk-plant-evolution-meeting Dear Colleague,

We are pleased to announce the 3rd UK Plant Evolution Meeting. The meeting brings together researchers from across different disciplines in plant evolutionary biology, and follows on from previous successful meetings at the Royal Botanic Garden Edinburgh and Cambridge University Botanic Garden. The programme will comprise a mixture of invited and contributed talks, and poster sessions.

Outline of meeting The meeting is divided into two parts:

Day 1: Symposium entitled ÂMonography: where are we and where are we going? This day provides the opportunity for participants to learn about and discuss approaches to contemporary monography and its applications.

Days 2 and 3: Conference on Plant Evolution This two-day conference will follow on Thursday 4 and Friday 5 April, and will be focused on the following four themes:

SESSION 1: Plant development and evolution SESSION 2: Plant traits involved in adaptation and domestication SESSION 3: Evolutionary drivers of plant diversity SESSION 4: Recent approaches to understanding macroevolution

Registration Full registration (3 days): pounds 80 (students pounds 40) One day registration (day 1 only): pounds 40 (students pounds 20) To attend this meeting register here: https://tickets.kew.org/WebStore/shop/ViewItems.aspx?CG=uk&C=pem Call for talk and poster abstracts We are inviting abstract submissions from researchers wishing to present a poster and/or talk. A prize will be awarded for the best student and early career researcher posters. The deadline for abstract submission is 1st March 2019.

Invited speakers Day 1: Prof. Alexandre Antonelli, Dr. Olwen Grace, Prof. Sandra Knapp, Dr. Gwil Lewis, Dr. Eve Lucas, Prof. Robert Scotland, Prof. Nina RÃÂnsted, Dr. Maria Vorontsova, Dr. Peter Wilkie.

Days 2 & 3: Prof. Jonathan Wendel (Keynote speaker), Prof. Robin Allaby, Prof. Scott Armbruster, Dr. Christine Bacon, Dr. William Baker, Dr. Sidonie Bellot, Dr. Anne Borland, Dr. Samuel Brockington, Prof. Liam Dolan, Dr. Charilaos Hyotis, Dr. Annaliese Mason, Dr. Edwige Moyroud, Dr. Mark N. Puttick, Dr. Alex Twyford.

Further details Full details of the event, registration options and abstract submission instructions can be found here: https://www.kew.org/kew-gardens/whats-on/3rd-uk-plant-evolution-meeting We look forward to seeing you at the meeting,

The Organising Committee

The Royal Botanic Gardens, Kew is a non-departmental public body with exempt charitable status, whose principal place of business is at Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AE, United Kingdom.

Michael Chester <M.Chester@kew.org>

RhodeIsland SSE Evolution2019 Jun21-25

Are you planning to attend the Evolution 2019 meeting in Providence, Rhode Island (ASN-SSE-ASB)? We are organising a Spotlight Session* on 'Evolutionary Biomechanics: Form, function and ecological interactions in animals and plants', and would like to invite you to submit a talk for this special session**.

Our goal is to mesh biomechanics with ecological and evolutionary studies towards a more integrated view of evolutionary biomechanics. We are particularly interested in organism-level studies in animal and plant systems, but we are happy to receive any suggestions from any interested speakers.

Invited speakers, so far, include: Beth Mortimer (Oxford; Animal perception and communication using vibrations); David Timerman (UToronto; Evolutionary biomechanics of windpollination); Callin Switzer (UWashington; Buzz pollination) and Casper van der Koi (UGroningen; Flower surface structure evolution). Topics include (but are not limited to): bioacoustics, flight and aerodynamics, locomotion, animal communication, plant biomechanics, pollination, predation, plant-animal interactions, macroevolution.

To apply: Email a title and brief summary (<200 words) of the talk you would like to present before 1st February 2019 to mario.vallejo@stir.ac.uk. Informal enquiries welcome. Speakers will be selected according to fit to the Session's topic and following the SSE's criteria for diversity and inclusion.

*A Spotlight Session consist of two consecutive 75 min sessions (separated by a coffee break). Spotlight talks have the same standard duration (15 min) as regular talks at the Evolution Meetings.

**Please note that (a) no funding is provided and (b) speakers at the Spotlight Session will be ineligible to give another talk at the meeting.

Mario Vallejo-Marin Biological and Environmental Sciences University of Stirling Stirling FK9 4LA United Kingdom

– The University achieved an overall 5 stars in the QS World University Rankings 2018 The University of Stirling is a charity registered in Scotland, number SC 011159.

mario.vallejo@stir.ac.uk

RoyalSocietyUK MolluscanGenomics Sep16-17

Mollusks! Molluscs! Genomes and Long-reads!

Save Sept. 16-17 for #pearls19 aka "Pearls of Wisdom", the first meeting focused on molluscan genomics, at the Royal Society of London's Chicheley Hall, UK. Co-organised by Dr Angus Davison, University of Nottingham (angus.davison@nottingham.ac.uk) and Dr Maurine Neiman, University of Iowa (maurine-neiman@uiowa.edu)

20+ confirmed speakers from around the world, full details to follow soon

https://royalsociety.org/science-events-and-lectures/-2019/09/pearls-of-wisdom/ https://twitter.com/-angus_davison/status/1082311754208739328 Dr Angus Davison | Reader and Associate Professor in Evolutionary Genetics School of Life Sciences | University Park | University of Nottingham | NG7 2RD +44 (0) 115 8230322 | angus.davison@nottingham.uk | @angus_davison | angus.davison.org

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

SouthernNewHampshireU GenomesEvol Jul14-19

How Genomes Illuminate Our Understanding of Ecological and Evolutionary Processes

July 14 - 19, 2019 Ecological and Evolutionary Genomics Gordon Research Conference

Registrations now open ***At least 8 talks will be selected from abstracts submitted by young investigators (trainees and PIs)***

Chairs :

Christian Landry and Angela Douglas

Vice-chairs :

Camille Berthelot and Sarah D. Kocher

See list of invited speakers and details here:

https://www.grc.org/ecological-and-evolutionary-genomics-conference/2019/ ***Note new location, closer to Boston (70 min) and Manchester (20 min) airports***

Southern New Hampshire University 2500 North River Road Manchester, NH, US

Meeting description Genomics tools have never been so powerful and accessible to biologists interested in how the interplay between ecological and evolutionary forces is shaping biodiversity. The 2019 Gordon Research Conference on Ecological and Evolutionary Genomics will explore how the genome-scale processes that underpin organismal phenotypes interact with ecological and evolutionary processes over multiple spatiotemporal scales. The meeting will be preceded by a Gordon Research Seminar (GRS), which will provide opportunities for early career researchers (students and postdocs) to present their projects and will include a special mentorship session.

Topics highlighted at the meeting will include: the ecological and evolutionary significance of novel genes and variation in genome architecture, including genomic conflicts; the role of hybridization and introgression as drivers of diversity; genome-scale perspectives on the role of the microbiome in host adaptations; and the increasing contribution of genomics to explanations of ecosystem function. This meeting will also bring the latest technological developments in genomics and genome manipulation, emphasizing their application to non-model species. Join us to participate in creative discussions in an inclusive social and scientific atmosphere, to empower the future research in the field.

Christian Landry <Christian.Landry@bio.ulaval.ca>

Tjarno Sweden SpeciationGenomics Jun17-19

Dear colleagues

We are pleased to announce the SMBE Satellite Meeting and Workshop on 'Identifying barriers to gene flow in the genome' to be held 17th-19th June 2019 at the Marine Biology Laboratory, TjÃÂrnÃÂ¶, Sweden.

Speciation genomics is a fast moving and rapidly changing field. Genome scans and demographic inference are popular tools for studying how barriers to gene flow evolve and how species diverge, but the field has only recently begun to take into account confounding factors that might bias these methods.

If standard approaches are insufficient for identifying barriers to gene flow and understanding the processes involved in speciation, where do we go next? One way forward is the use of sophisticated approaches to jointly infer signals of selection, gene flow and demographic history. We can also use efficient simulation to introduce greater statistical rigour to our approaches.

This three day workshop/meeting on speciation genomics will combine talks from invited speakers and participants, a discussion panel and a hands-on workshop to learn how to use a composite likelihood approach to infer selection, gene flow and demography from genome scan data.

Invited speakers include: * Reto Burri (University of Jena) * Jonna Kulmuni (University of Helsinki) * Kelley Harris (University of Washington) * Simon Aeschbacher (University of Zurich) * [Frederic Guillaume (University of Zurich)

The practical workshop will be led by Jerome Kelleher (Big Data Institute, Oxford) (the importance of simulations) and Konrad Lohse (University of Edinburgh). Some basic experience in Unix, and Python programming is necessary but we provide links to resources on our website: https://-smbespeciationgenomics.github.io/ There is space for approximately 40-50 participants. To apply, please register at https://smbespeciationgenomics.github.io//-register/. The deadline for applications is 25th February 2019.

It is free to register but attendance will cost $300 (US) to cover accommodation and food for the three days. Travel bursaries are available for MSc and PhD students wishing to attend.

We encourage participants from all backgrounds and levels to apply and we look forward to welcoming you to Sweden in June!

https://smbespeciationgenomics.github.io/ Mark Ravinet, Marina RafajloviÃÂ, Michael Matschiner, Simon Martin, Chris Jiggins & Markus MÃÂ

Mark Ravinet <mark.ravinet@ibv.uio.no>

Toulouse EcolBehaviour May19-24 AbstractSubmission

Abstract submission for Ecology and Behaviour 2019 is now open! The deadline is Friday 15 th February .

What: 14th meeting Ecology & Behaviour

Where: Toulouse, France

When: May 19-24 2019

For whom: students and researchers interested in evolutionary biology, ecology and behavior

The association “Rencontres Ecology & Behaviour” (AREB), founded in 2005 by a group of students, organizes each year an international conference about evolutionary biology, ecology, and animal behaviour . Fantastic invited researchers confirmed their presence:

* Intraspecific interactions: Charlotta Kvarnemo and Mike Wilson * Non-genetic heredity: Lucy Aplin and Etienne Danchin * Phylogeny and population genomics: Knud Jønsson and Ludovic Orlando * Cognition: learning and memory: Alice Auersperg and Audrey Dussutour * Conservation and global change ecology: Mike Bruford and Camille Parmesan * Interspecific interactions: Camille Bonneaud and Frédéric Santoul * Ecophysiology and ecotoxicology: Mathieu Giraudeau and Lieven Bervoets

To submit an abstract for an oral presentation or a poster, please login on our website [https://-eb2019.sciencesconf.org/] and go to “Submissions”. Abstracts should be written in English and not exceed 250 words.

As usual, we offer registration, accommodation and lunches to students exhibiting their work during the conference. Registration fees (including lunches) for postdocs and researchers are 70€and 130€, respectively. We also have a special deal for low prices accommodations on the university campus (100€for the week). Please visit our website or follow us on twitter (@EcoBehav2019) for more information. Do not hesitate to share this email with anyone you believe may be interested in attending.

We look forward to seeing you in the Ville Rose!

Maxime Pineaux, for the E&B organising committee (EDB lab, Toulouse)

pineaux <maxime.pineaux@univ-tlse3.fr>

UCambridge EvolutionaryGenetics Mar19

Dear Colleagues,

The annual Genetics Society "Evolutionary Genetics and Genomics Symposium" (EGGS) will take place on Tuesday 19th March 2019 at the University of Cambridge. The meeting is now pounds 1 to attend. We aim to bring together participants from a range of backgrounds, with a particular focus on work at the interface between genomics and evolutionary biology. This year we will be celebrating the 100th anniversary of the Genetic Society. EGGS 2019 will feature keynotes from:

The evolutionary history of M. tuberculosis: insights from ancient DNA

Professor Anne C. Stone

Regents' Professor, School of Human Evolution & Social Change, Arizona State University

Cancer Evolution and Immune Escape: TRACERx

Professor Charles Swanton FRCP FMedSci, FRS

Director, CRUK Lung Cancer Centre of Excellence, Senior Group Leader, The Francis Crick Institute

Flower evo-devo and the link to speciation

Professor Beverley Glover,

Director of Cambridge University Botanic Garden, Department of Plant Sciences, University of Cambridge

The meeting is free including a drinks reception. A subsidised lunch and dinner is available. Registration is now open and the deadline is 12/03/2019. Please register at

https://evolutionarygeneticsandgenomics.com/-registrationevolutionary-genetic s-and-genomics-symposium/

Abstract submission for talks is now open and the deadline is now 31/01/2019. If you are interested in presenting a talk, please submit your abstract via this link:

https://tinyurl.com/yao5nwaj With best wishes,

The organising committee.

Arunkumar Ramesh <ar885@cam.ac.uk>

UCambridge EvolutionEvolving Apr1-4

Early bird registration deadline for Evolution Evolving is Monday 7th January.

Evolution Evolving: Process, Mechanism and Theory Churchill College, University of Cambridge, UK 1-4 April 2019

Evolutionary biology is a vibrant field with a theoretical framework that itself evolves. The Evolution Evolving conference will focus on some emerging themes in the relationship between development and evolution. Topics include the evolutionary causes and consequences of developmental bias, plasticity, niche construction and extra-genetic inheritance V all of which contribute to an understanding of evolvability. The conference will feature a balanced program of talks and poster sessions spanning three days, and be a mix of empirical and theoretical work, as well as contributions to the history and philosophy of evolutionary biology.

Invited speakers include Alex Badyaev, Renee Duckworth, Laurel Fogarty, Jukka Jernvall, Alan C Love, Joanna Masel, Armin Moczek, Angela Potochnik, Sean Rice & Jessica Riskin.

Conference website: https://evolutionevolving.org/- Conference twitter: @EvoEvolving Conference email: evoevolving@st-andrews.ac.uk Organising committee: Prof Paul Brakefield, Prof Kevin Laland, Prof Tobias Uller, Dr Andrew Buskell & Dr Katrina Falkenberg

Katrina Falkenberg <kjf5@st-andrews.ac.uk>

UppsalaU AfricanHumanDiversity May22-25

Dear Colleagues,

The International conference:* 'Africa, the cradle of human diversity' will take place on May 22nd-25th 2019 at Uppsala University (Sweden)*. The conference will assemble 30 leading researchers from different fields to present and discuss state-of-the-art approaches to address long-standing questions about past and present human diversity in Africa. These questions include modern human origins in Africa, the history of farming expansions, admixture patterns, adaptation to new environments and cultural transitions. Conference contributions will span the fields of paleoanthropology, paleogenomics, evolutionary genetics, biological anthropology, archaeology, historical linguistics, and population genetics. Further, the conference will feature a keynote lecture from: Marlize Lombard (Professor and Director of the Centre for Anthropological Research, Department of Anthropology and Development Studies, University of Johannesburg, Johannesburg, South Africa).

The *registration is free*, including conference materials, coffee breaks and a cocktail reception. Registration is now open and the deadline is on April 22nd. Please register at https://goo.gl/forms/ND4ODgZKYQLrSsFi1 *Abstract submission for posters* is also open and the deadline is on March 22nd. If you are interested in presenting a poster, please register first and then submit your abstract via this link: https://goo.gl/forms/ZsYR6PS6BHLINwKy1 For *more informatio*n please visit the official website for the event https://africathecradleofhumandiversity.wordpress.com We are looking forward to welcoming you in Uppsala!

With our best regards, The organizers of 'Africa, the cradle of human diversity' Cesar Fortes-Lima, Postdoctoral researcher in Population Genetics, Ezekia Mtetwa, Researcher in Archaeogenomics, Cecile Jolly, Research Engineer, and Carina Schlebusch, Associate Professor and Group leader at Uppsala University

Cesar FORTES-LIMA <Cesar@eurotast.eu>

UYork ASAB Easter Apr3-5

There are just a few weeks left to submit your abstract to the ASAB Easter Meeting at York, 3-5th April. Abstracts are welcome in all areas of animal behaviour.

The ASAB (Association for the Study of Animal Behaviour) Easter Conference is aimed at postgraduate students and post-doctoral researchers studying animal behaviour, but is open to anyone with a keen interest in the field. The first day will focus on postgraduate training workshops, with the end of that day and subsequent two days involving plenary talks and conference talks.

Submit your abstract here: https://asabeaster2019.weebly.com We look forward to seeing you in York!

Dan Franks <daniel.franks@york.ac.uk>

Ventura Speciation Mar10-15

MEETING REGISTRATION ANNOUNCEMENT: REGISTRATION IS OPEN UNTIL 10 FEB 2019

We are pleased to announce SPECIATION 2019, the third Gordon Research Conference (GRC) dedicated exclusively to speciation research. The conference will be held at the Four Points Sheraton / Holiday Inn Express, Ventura, CA during the week of March 10 - 15, 2019, co-chaired by Rebecca Safran (University of Colorado, USA) and Katie Peichel (University of Bern, Switzerland).

The conference will be directly preceded by a two-day Gordon Research Seminar (GRS) on March 9 - 10, co-chaired by Martin Garlovsky (the University of Sheffield, UK) and Sheela Turbek (University of Colorado, USA), that offers opportunities for early-career scientists to get involved at the forefronts of modern speciation research.

Please follow this link to learn more about these conferences and to register.

https://www.grc.org/speciation-conference/2019/ Invited presentations and discussion sessions at both the GRC and GRS will cover a broad array of timely topics in speciation research.

Please send questions to Rebecca.Safran@colorado.edu

Sincerely

Rebecca Safran, Katie Peichel, Martin Garlovsky, Sheela Turbek

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

WashingtonDC RECOMB-Genetics May4

The 7th RECOMB Satellite on Computational Methods in Genetics will focus on current research at the intersection of genetics, computer science, statistics, and related fields in gathering and analyzing SNP and haplotype data and applying it to problems in medicine and basic research. Population genetics allows more refined understanding of the demographic history of our species, association analysis provides insights regarding the functional and molecular underpinnings of diseases and traits, while clinical applications suggest genetics as a trailblazer into personalized medicine. The complex bioinformatic questions arising range from inferring more nuanced statistical models of genetic information to algorithms that overcome the complexity challenges of analyzing millions of SNPs across millions of individuals, to systems level challenges of handling such Big Data repositories of genotypes and phenotypes.

RECOMB-GENETICS 2019 will be held in The George Washington University on May, 4th 2019.

https://recombgen.recomb2019.org/ Simon Gravel <simon.gravel@gmail.com>

YosemiteNatlPark Symbiosis May 17-19

Dear Colleagues,

Please SAVE THE DATE for the 9th Annual Yosemite Symbiosis Workshop!

The Ninth annual Yosemite Symbiosis Workshop will take place on May 17-19, 2019 at the Sierra Nevada Research Institute, Yosemite National Park.

Keynote speaker 2019: Dr. Martha (Molly) S. Hunter from The University of Arizona!

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 ninth 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 18-19, 2019, though we make accommodation arrangements available for attendees to arrive on Friday the 17th 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 We will soon open registration with abstracts likely being due in Mid March.

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 (up soon). We will only be able to accept credit card payments this year

Please direct any questions to the organizers:

Joel Sachs joels@ucr.edu

A. Carolin Frank cfrank3@ucmerced.edu

joels@ucr.edu

YosemiteNatlPark Symbiosis May17-19

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Register here: < https://t.co/i1hTGwqI15 > https://snri.ucmerced.edu/form/symbiosis-workshop-2019-registration Pay here: https://commerce.cashnet.com/cashneti/selfserve/EditItem.aspx?PC¯n03_W2-SYWK&ItemCount=1 Payment is required to confirm your registration.

Please direct any questions to the organizers:

Joel Sachs joels@ucr.edu

A. Carolin Frank cfrank3@ucmerced.edu

Joel L. Sachs *Professor & Vice Chair* Department of Evolution Ecology & Organismal Biology Department of Botany & Plant Sciences (Cooperating Member) Department of Microbiology & Plant Pathology (Cooperating Member) 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 Joel Sachs <joels@ucr.edu>

GradStudentPositions

AberdeenU 4 EvolutionaryBiol

Fully funded NERC QUADRAT funded PhD studentship (3.5 years)

“Effect of species range shifts on trophic networks in freshwater ecosystems”

This project will be supervised by DrLesley Lancaster of Aberdeen University, and Drs Paul Caplat and Sarah Helyar at Queens University School of Biological Sciences. The start date will be 1st October 2019.

https://www.findaphd.com/phds/project/effect-of-species-range-shifts-on-trophic-networks-in-freshwater-ecosystems/?p105126 Brief project outline: As climates warm in the 21st century, many species are shifting their geographic distributions towards higher latitudes and elevations. Previous studies have indicated that range shifting species may express greater metabolic and behavioural flexibility than species which have not recently undergone biogeographic shifts, with long-term implications for the structure and function of high latitude communities. For instance, research has already revealed that range shifting species often negatively impact species richness and biodiversity of areas where they become established. However, the processes by which community turnover occurs in colonised sites are little known, rendering future biodiversity predictions difficult. We propose to investigate how range-shifting species affect patterns of community composition, using pond damselflies (Odonata: Zygoptera: Coenagrionidae) as a model system. These species are rapidly range shifting in Britain under climate change, and are important, keystone predators in freshwater communities; the Irish species also have high conservation value. Our previous work has indicated that range shifts in Coenagrionid damselflies are associated with species turnover in high latitude freshwater ecosystems, but the effects on trophic interactions and resulting community resilience to future environmental change remain largely unknown.

To examine the ecosystem consequences of range shifts, the student will: 1) Relate the colonisation dynamics of range-shifting damselflies in Scotland and Ireland to changes in freshwater trophic network structure, accounting for land use and climatic variability across the study region, using hierarchical regression models. 2) Investigate differences in phenotypes, behaviour and metabolic rates under different thermal regimes in range-shifting vs. non-range shifting damselflies across the region, in order to identify alternative mechanisms mediating biotic interactions in range- shifting vs. non-range shifting populations. 3) Using data derived from Next Generation Sequencing approaches, identify genetic variants in range-shifting vs. non-range shifting damselfly species that are associated with particular trophic networks (Obj 1) and traits (Obj 2).

The project will contribute to our understanding of how communities are likely to respond to ongoing range shifts, and identify the mechanisms underpinning global homogenisation of biodiversity. The results also have the potential to make fundamental contributions to the development of the rapidly advancing field of functional community ecology.

The student will be based primarily at the University of Aberdeen, under the supervision of Dr Lesley Lancaster, who is a leading researcher in understanding evolutionary and community consequences of range shifts. The student will be co-supervised by Dr Paul Caplat at Queens University Belfast, who develops novel approaches to predict community patterns at multiple scales from life-history traits, climate and land use. Dr Sarah Helyar (Queens University) will supervise the genetic part of the work. There is potential for the student to establish links with NGOs responsible for freshwater restoration in Scotland and Ireland for application of the results. The student will form part of the QUADRAT doctoral training programme, which provides internationally cutting edge training in environmental management leadership.

Funding: This project is one of a number that are in competition for funding from the NERC QUADRAT Doctoral Training Partnership (DTP). For details of all the PhDs advertised for 2019 start please see: https://www.findaphd.com/phds/program/-quadrat-doctoral-training-partnership/?i2p4257 This studentship is available to UK and other EU nationals and provides funding for tuition fees and stipend, subject to eligibility. Candidates should have (or expect to achieve) a minimum of a 2.1 Honours degree in a relevant subject. Applicants who are classed as International for tuition fee purposes are not eligible for funding.

Deadline: Thursday 31st January 2019. Informal inquiries: lesleylancaster@abdn.ac.uk

Sarah Helyar <S.Helyar@qub.ac.uk>

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AgroscopeETH Switzerland AnimalBreeding

I am looking for a person interested in doing a PhD with the goal of breeding sustainable pigs at an agricultural research institute in collaboration with the ETH Zurich (Swiss Federal Institute of Technology in Zurich). I am particularly looking for a person who is interested in animal breeding, has an integrative biology mindset and enjoys wrangling with large datasets from a range of backgrounds (genetics, animal science, (evolutionary) biology, biochemistry, molecular biology, ...).

Breeding sustainable pigs: the genetic basis of nitrogen efficiency

Meat production contributes more to ecological hazards like global warming and environmental pollution than any other food type via the use of fossil energy, land and water, and in particular through the emission of greenhouse gases and nitrogen waste. Recently, it has been shown that a non-negligible part of the Swiss Large White pig population can cope with diets markedly reduced in essential amino acid content without displaying impaired growth, indicating variation in the efficiency to fix dietary protein in the body. This project aims to unravel the genetic basis of this improved efficiency using a two-fold approach: First, the candidate will use quantitative genetics analyses to estimate the heritability of this trait and potential genetic correlations with carcass and meat characteristics as well as performance and welfare traits. Second, SNP array and/or sequencing technology will be used to detect causal variants underlying improved protein efficiency with the ultimate goal to provide a tool to select for increased protein efficiency. This project will be carried out in collaboration with the ETH Zurich, several researchers and technical staff at Agroscope Posieux, and stakeholders in Switzerland.

Tasks - perform quantitative genetics analyses and genome-wide association studies using already available data and collect new phenotypic data at the animal research facility of Agroscope Posieux - perform Dual-energy x-ray absorptiometry measurements on carcasses as well as live animals, organize and help with blood and tissue collection at the slaughterhouse and extract DNA from blood samples in our laboratory - potentially assist with gene expression analyses, genomic prediction and method development for high-throughput phenotyping - collaborate with colleagues at Agroscope and ETH Zurich

Requirements - MSc in genetics, animal science, biology, biochemistry, or molecular biology - Strong interest in quantitative work - Motivated to work in the barn with the animals, in the laboratory and at the computer - Achievement-oriented, open-minded personality with the ability to work in a team but also independently - Good organizational and communication skills - Good IT skills, including statistical analyses in R, preferably experience with (or the willingness to learn) Linux - Working language is German, English or French; however, sufficient English (reading and writing) skills are necessary

Organisation Agroscope is an innovative research institute for agriculture and nutrition governed according to the principles of New Public Management. Agroscope is part of the federal administration and is attached to the Federal Department of Economic Affairs, Education and Research, EAER. It has research stations at a number of sites around Switzerland but its head office is in Bern (Liebefeld). The objectives of the Swine Research Unit are to optimize the use of phosphorus and protein in pig production by evaluating the genetic potential of pigs to develop breeding strategies as well as developing ecologically and economically viable feeding strategies, allowing the production of pork of excellent quality. The advertised project builds upon ample knowledge from previous work in pig nutrition of the host group.

We offer you a varied range of tasks and collaboration with specialized research teams as well as thorough initial training. Agroscope has excellent swine research facilities and well-equipped laboratories. You will enjoy flexible working hours and good employee benefits. The PhD project will be performed in collaboration with Professor Hubert Pausch at the ETH Zurich, who will be, together with Dr Claudia Kasper, your main supervisor.

Place of Work: Agroscope Posieux, 1725 Posieux, Switzerland. Salary Category: According to the guidelines of the Swiss National Science Foundation. Employment Level: 100%. Start date: April 2019 (negotiable), Duration: 3 years.

Application If this challenge appeals to you and you meet our requirements profile, we look forward to receiving your online application (sylviane.brasey-badoud@agroscope.admin.ch). Online applications consist of a single PDF containing an application letter, CV, copy of certificates (MSc &BSc) and email addresses of 2 referees. For further information and informal inquiries: Dr. Claudia Kasper, animal geneticist

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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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CharlesU AvianSpeciation

*A PhD position on **germline-restricted chromosome in songbirds** at Charles University in Prague *

Germline-restricted chromosome in songbirds: Understanding its genetic composition and potential role in reproductive isolation

A four-year PhD position is available from October 2019 Application deadline: 15th March 2019

Birds have the smallest genomes among vertebrates. This has been attributed to selection for smaller cells, which permits higher metabolic rate required for flight and more neurons to be packed in the brain. Recently, it has been shown that reduction of genome size in songbirds may be facilitated by elimination of genetic material dispensable for soma from somatic cells and its maintenance only in the germline, where it forms the so-called germline-restricted chromosome (GRC). The genetic composition and importance of this chromosome for gametogenesis is still largely unknown. The first aim of this project is to sequence the GRC in the Bengalese finch (*Lonchura domestica*), a songbird species where GRC represents the largest element of the karyotype, and to identify functional genes on this chromosome. This will be done by comparison of whole genome sequences of somatic and germinal tissues and by characterization of gonadal transcriptomes. Furthermore, given the highly variable size and genetic composition of GRC among species, the second aim is to study the potential role of GRC in speciation using crosses between different *Lonchura* species.

The project will combine genomic and cytogenetic approaches. The ideal candidate should have background in molecular genetics, cytogenetics and/or bioinformatics.

The selected candidate will work in a young independent research group of population and speciation genetics (http://web.natur.cuni.cz/~radkas/). The group is based at the Department of Zoology, Faculty of Science, Charles University, which belongs to the leading research institutions in the Czech Republic. The Faculty of Science is situated in the center of Prague, one of the world's most beautiful and monumental cities.

How to apply: If interested, please, send (1) CV including a list of publications, (2) motivation letter, and (3) contact details for 2'3 references to Radka Reifova (radka.reifova@natur.cuni.cz) by 15th March 2019. Besides this, it is necessary to apply for the PhD position through this web site: https://www.stars-natur.cz/phd-positions/-biology . – RNDr. Radka Reifová, Ph.D. Phone: +420 221 95 1852 E-mail: radka.reifova@natur.cuni.cz, radkas@natur.cuni.cz <radka.reifova@natur.cuni.cz> Web page: www.natur.cuni.cz/~radkas/ < http://www.natur.cuni.cz >

Department of Zoology Charles University Faculty of Science ViniÄná 7, 128 44 Praha 2

Katedra zoologie Univerzita Karlova PÅírodovÄdecká fakulta ViniÄná 7, 128 44 Praha 2

"RNDr. Radka Reifová, Ph.D." <radka.reifova@natur.cuni.cz>

CRAG Barcelona AncientDNA

PhD position available on Paleaogenomics of dog population in Europe.

The Botigue lab for "Genomics of ancient crops and domestication" in the Centre for Research in Agricultural Genomics (CRAG) in Barcelona is offering a PhD position under the La Caixa Foundation INPhINIT Programme to work on the genomic analysis of archaeological dog remains from Europe spanning from the Neolithic up to the Roman Period with the goal to understand population dynamics within the continent and gene flow during that period.

DEADLINE

6 February 2019 (Incoming modality)

27 February 2019 (Retaining modality)

TITLE: Genomic analysis of archaeological dog remains from Europe.

PROJECT DESCRIPTION:

The European continent has played a major role in dog domestication. A recent genomic analysis of Neolithic dogs from Germany, though revealing genetic continuity, showed complex admixture patterns, including gene flow from a population similar to modern Indian dogs. Additionally, studies examining the mitochondrial genome of ancient and modern dogs have detected a replacement in Europe that took place some time between the Neolithic and the Middle Age. In the present project we plan to unravel this complex demographic scenario of prehistoric European dogs by analysing the genome of twenty ancient dog samples from the Iberian Peninsula and Germany from a period of over 4,000 years spanning from the Neolithic up to the Roman Empire.

Analysis of the whole genome and the mitochondrial genome will be performed to determine the main demographic events that shaped dog populations during that period. Population structure and admixture will be studied in ancient dogs in the context of modern dog variation.

As a result, we will provide for the first time insights into the genetic structure, variability and admixture of dog populations in Europe over a period of 4 millennia, prior the generation of breeds. Results will elucidate demographic events surrounding dog prehistory in Europe and their relationship with humans migrating through the continent.

JOB POSITION DESCRIPTION

The dearth and the ambition of the current project are ideal for a PhD candidate. We are therefore looking for a highly motivated student seeking to pursue his doctoral studies and specialise in genomics and bioinformatics by analysing whole genome sequencing data, including that from archaeological samples. The student will receive extensive training in a broad range of skills, including theoretical population genetics and biostatistics. She will learn concepts such as population structure, admixture and adaptation, and be able to recognize the footprints these processes leave in the genome. Additionally, the student will also learn how to model demographic inference, gaining knowledge about coalescent theory and computational simulations. In order to analyse genomic data, the student will learn how to use and develop her own bioinformatic tools.

This project is an international collaboration with researchers from the United States and Germany, so the student will have the opportunity to perform research stays abroad, increasing her network of peers at an early stage of her career and learning new skills from renowned population geneticists. Opportunities to assist international meetings and present her research will also be granted throughout her PhD.

The PhD will be performed in CRAG'S Plant and Animal Genomics programme. During the first year of their studies, students receive teaching on state-of-the art technologies offered by the Core Units and Scientific Services of CRAG, such as genomics and next generation sequencing, proteomics, metabolomics, and bioinformatics. The student will also be able to attend internal and external seminars at CRAG and improve her oratory skills by giving seminars regularly.

By the end of her PhD, the student will have become a population geneticist specialised in the analysis of modern and ancient genomes with a strong computational background and a wide network of peers.

REQUIREMENTS

The doctoral fellowship programme INPhINIT "la Caixa" is devoted to attracting talented Early-Stage Researchers'of any nationality'who wish to pursue doctoral studies in Spanish or Portuguese territory.

The doctoral INPhINIT fellowships offer a highly competitive salary and complementary opportunities for training on transferrable skills (through the collaboration of leading entities such as Vitae and Oxentia), temporary stays in industry, incentives upon completion of the thesis, among other elements that make these fellowships some of the most attractive and complete in Europe.

CONTACT

For questions about the position and further information about the project, contact Laura Botigué, Email: laura.botigue@cragenomica.es

HOW TO APPLY

Applications should be done using La Caixa INPhINIT online application system . Please follow the link below to obtain further information

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GroningenInst NeuralEvolution

Job description

The Groningen Institute for Evolutionary Life Sciences (GELIFES < https://www.rug.nl/research/gelifes >*)* offers a 4-years NWO-funded PhD position for a project on the *Genetic dissection of a neuronal circuit under sexual conflict*, with *Drosophila melanogaster* as a model system.

The project is coordinated by Prof. Jean-Christophe Billeter < https://www.rug.nl/staff/j.c.billeter/ >, in collaboration with Prof. Yael Heifetz < http://departments.agri.huji.ac.il/entomology/yael_heifetz/index.html >, Prof Bregje Wertheim < https://www.rug.nl/staff/b.wertheim/ >*,* and Dr Philip Kohlmeier < https://www.rug.nl/staff/philip.kohlmeier/ >. The student will join a lively and highly international team of post-doctoral researchers, PhD and master students working on the neurogenetics of social and sexual behaviours in *Drosophila*, supported by laboratory technicians.

Sexual conflict (SC) shapes the evolution of reproductive behaviours. It manifests itself in male traits that limit female reproductive choices, generating selection for female counter-adaptations. This sexual conflict is a hot topic in evolutionary biology because it is hypothesized to fuel fast and exaggerated evolution of neural, behavioural and morphological traits that mediate male-female competition.

This projects aims at investigating how a sexual conflict has shaped brain functioning in the fruit fly *Drosophila melanogaster*. During mating, males transfer pheromones in their ejaculate that render a mated female less attractive to other males. As a counter-adaptation, females eject that ejaculate which restores attractiveness and facilitates faster remating. We are now interested in identifying the neuronal circuit that modulates ejaculate ejection and to reveal potential counteradaptations of the male. In particular, the PhD student will apply 1) optogenetics and intersectional methods to parse the function of single neurons in female ejaculate ejection, 2) mutant analysis and transcriptomics to identify sensory input 3) trans-synaptic marking and circuit modelling to reconstitute neuronal circuitry and 4) sperm-competition and female sexual receptivity assays to identify the selective drivers that shape the current state of the sexual conflict.

Qualifications

We are looking for an enthusiastic and talented PhD candidate with a Master's degree (or equivalent) in Biology with a strong interest in neurogenetics and behavioural neurosciences, and with an appreciation for evolutionary biology. The ideal candidate has experience with at least some of the following techniques: *Drosophila* genetics, *Drosophila* neuroanatomy, behavioural analysis, confocal microscopy and molecular genetics. We also ask for excellent communication and writing skills in English. Other helpful competences include statistical proficiency (ideally in the R software environment) and bioinformatics.

Conditions of employment

The University of Groningen offers a salary of 2,325 gross per month in the first year to a maximum of 2,972 gross per month in the final year (salary scale Dutch Universities as of Feb 1, 2019), based on a fulltime position (1.0 FTE) excluding a 8% holiday allowance and a 8.3% end of the year bonus.

The position is limited to a period of 4 years. A PhD training programme is part of the agreement and the successful candidate will be enrolled in the Graduate School of Science and Engineering. The successful candidate will first be offered a temporary position of one year with the option of renewal for another three years. Prolongation of the contract is contingent on sufficient progress in the first year to indicate that a successful completion of the PhD thesis within the next three years is to be expected.

The preferred starting date is between April and June 1st 2019. Organisation

Founded in 1614, the University of Groningen enjoys an international reputation as a dynamic and innovative institution of higher education offering high-quality teaching and research. Flexible study programmes and academic career opportunities in a wide variety of disciplines encourage the 30,000 students and researchers alike to develop their own individual talents. As one of the best research universities in Europe, the University of Groningen has joined forces with other top universities and networks worldwide to become a truly global centre of knowledge.

Application Application should include:

a letter of motivation to apply for this position

a curriculum vitae

a one-page statement of research interests, for instance description

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GulbenkianInst Portugal EvolutionaryDynamics

Individuals with any scientific background (i.e., including evolutionary, molecular, or systems biology, mathematics, physics, chemistry, computer science, statistics, and its hybrids) with a genuine interest in evolutionary questions and quantitative approaches are welcome to apply to the available ERC-funded junior and senior postdoc positions under the project “FIT2GO – A toolbox for fitness landscapes in evolution”.

Lab

Building on evolutionary theory, research in the lab revolves around quantifying epistasis across levels of biological organization and across environments, and to study its impact on the population genetics of adaptation and hybridization. We approach these questions through a combination of mathematical modelling, computer simulations, statistical method development, experimental evolution, and data analysis and interpretation. The long-term goal lies in understanding how ecology, evolution, and molecular constraints shape genomes.

Projects

PhD projects will be developed in collaboration with the respective candidate and may be focused on either or several of the following topics:

- develop mechanistic and statistical models of fitness landscapes across environments - quantify intra- and intergenic epistasis and its consequences for adaptation - infer distributions of fitness effects across genetic backgrounds and environments (experimentally and theoretically) - quantify population dynamics and genetics under clonal interference and epistasis - develop statistical methods for experimental-evolution data analysis - study the effects of epistasis on diversity and divergence - develop approaches to predict the cost of antibiotic resistance across environments (in collaboration with Isabel Gordo, IGC) - test predicted mechanisms of drug resistance in influenza experimentally (in collaboration with Maria Joao Amorim, IGC)

Application procedure

Applications should be sent by email to evoldynamics@gmail.com and include a letter of motivation, a CV, and names and contact information of at least two referees. The anticipated starting date is 1 September 2019. The student will be associated with the IGCs PhD Programme in Integrative Biology and Biomedicine and has to fulfill the according selection criteria; parallel application to the PhD Programme through the respective online platform is encouraged but not necessary: http://www.igc.gulbenkian.pt/education/phdprogrammes .Review of applications will begin on February 15, and the call remains open until the position is filled.

Location

The Gulbenkian Science Institute is a private research institute located on the coast just west of Lisbon, Portugal, which provides for both a top-level scientific environment and excellent quality of life. The IGCs mission is to meet sciences global challenges: to make groundbreaking discoveries in the Life Sciences, to innovate in training, to incubate the next generation of future leaders, and to place science at the heart of society. Potential applicants are encouraged to scroll through the lab and institute websites and to informally contact us to learn more about IGC and the Evolutionary Dynamics Group: https://evoldynamics.org/ Dr. Claudia Bank Principal Investigator Evolutionary Dynamics Group Instituto Gulbenkian de Cio̱ncia Oeiras, Portugal

Claudia Bank <evoldynamics@gmail.com>

HongKong MarineAdaptationTranscriptomics

*Acclimation and Adaptation to Climate Change in Marine Organisms *

Applications are invited for a funded Ph.D. position in Molecular Ecology in the School of Biological Sciences at the University of Hong Kong (https://www.hku.hk/), to commence as soon as possible. The University is a long-standing English-speaking institution and ranks as one of the top Universities in Asia.

We are looking for a curious, ambitious and enthusiastic Ph.D. student to take part in establishing a new lab led by Dr. Celia Schunter to work on marine acclimation to climate change. *Research topics span from molecular, neuronal and behavioural impacts of climate change to parental effects and transgenerational acclimation in fishes and other marine organisms (www.celiaschunter.com).* The lab is associated with the Swire Institute of Marine Science, also known as SWIMS (http://www.swims.hku.hk/), a beautiful research station in a remote area of the Island of Hong Kong.

The lab combines several disciplines ranging from *marine biology*, *behavior/physiology*, *molecular biology* to *computational biology* and prospective students should be interested in working in a cross-disciplinary environment. Generally, projects start with field work or aquarium experiments with measurements of e.g. behavior or other physiological traits, followed by molecular lab work to extract molecules of interest (e.g. RNA or proteins). Most projects are based on next-generation sequencing, subsequent bioinformatic analyses and writeup into scientific articles. The lab maintains long-standing international collaborations and travel might be required.

Additional requirements:

Â Willingness to work in a highly international and collaborative environment Â If no previous experience, the student must be eager to learn *bioinformatics*

Â Willingness to work in aquarium systems and/or field work in a marine environment.

A Postgraduate Scholarship will be offered, in addition to annual leave and medical benefits. Applicants who have a Bachelor's degree with honours will be considered for admission to a 4-year PhD programme, whereas those who already hold a research Master's degree (e.g. MPhil) will only be considered for admission to a 3-year PhD programme. Information about the PhD programme, including requirements for admission, can be found here https://www.gradsch.hku.hk/gradsch/ Interested candidates should send their CV, a cover letter summarizing research interests, career goals and contact information for three references to Dr. Celia Schunter (schunter@hku.hk). Review of applications will begin immediately and continue until the position is filled. The start date is flexible.

Celia Schunter <schunter@hku.hk>

KULeuven Belgium DaphniaMicrobiome

We invite applications for a PhD position to study the role of the gut microbiota in the evolution of stress tolerance in host organisms. The focus will be on thermal stress. The model host system will be the water flea Daphnia magna, of which we have clones in culture that evolved thermal resistance. These clones were obtained from resurrection ecology, experimental evolution and natural thermal gradients.

The PhD project includes controlled exposure experiments measuring heat tolerance and respirometry, metagenetic analyses of gut microbiota communities and gut microbiota transplant experiments between control and warm-adapted host clones. In addition, experimental evolution of stress resistance will be studied in the gut microbiome.

We are looking for a highly motivated student with an excellent academic record, a strong interest in evolutionary ecology, ecophysiology, genomics and microbiology, and a high ability for accurate lab work. A very good command of both spoken and written English is required. Proven microbiological skills are an asset, but training can be provided.

We offer a full-time job initially for a period of one year, but extendable to a total of four years pending good evaluation. Funding is available, but we request and give support for applying for your own scholarship.

You will be embedded in an international, enthusiastic and dynamic team with ample expertise in using aquatic invertebrates as model systems to address key questions at the intersection of ecology and evolution (https:/-

/bio.kuleuven.be/eeb/laeec/whoiswho/00034380). Our team has excellent research facilities including temperature-controlled rooms and well-equipped ecophysiology and microbiology laboratories. You will be co-supervised by Dr. Lizanne Janssens, Dr. Shinjini Mukherjee, and professor Ellen Decaestecker (https://www.kuleuven-kulak.be/nl/onderzoek/key-areas/onderzoeksgroepen/aquatische-biologie2/data/-persoonlijke-paginas/Prof_Ellen_Decaestecker) who have strong expertise in studying the gut microbiome.

Leuven is a beautiful historical university city with a very high and pleasant standard of living (https://www.kuleuven.be/english/living). Leuven is a 15-minute train ride away from Brussels International Airport and a 20-minutes train ride from Brussels itself. Brussels is one of the best-connected cities in Western Europe; Amsterdam, Paris and London are all reachable within 2 hours by train. The university, founded in 1425, has a top research and teaching standard (http://www.kuleuven.be/english). The KU Leuven features consistently in Europe's top-15 universities and has been elected by Reuters as most innovative university in Europe for three years in a row.

Interested? Please send your CV, a 1-page letter of motivation including relevant experience, a transcript of your bachelor and master study results, and the contact information of two referents as a single PDF to Professor Ellen Decaestecker (ellen.decaestecker@kuleuven.be) and Professor Robby Stoks (robby.stoks@kuleuven.be) with the subject 'PhD Application_NAME'. Shortlisted applicants will be interviewed. The application deadline is 15 February 2019. The starting date is 1st of April 2019 (can be negotiated).

Robby Stoks <robby.stoks@kuleuven.be>

Liverpool CanaryIslandReptiles

Students interested in applying for a Liverpool John Moores University scholarship for an evolutionary biology PhD supervised by myself (Richard Brown) should email me at r.p.brown@ljmu.ac.uk.

Reptiles and the Canary Islands have been central themes in my research but I am flexible so feel free to contact me with ideas that we can formulate as a PhD proposal.

Areas of particular interest include: 1) Conservation genomics: impacts of small population size on genomic diversity 2) Ecological divergence among contiguous vertebrate populations 3) The fitness consequences of colour pattern variation in the wild. 4) Reptile/amphibian phylogenetics and biogeography

Please see https://www.ljmu.ac.uk/about-us/staff-profiles/faculty-of-science/natural-sciences-and-psychology/richard-brown for a list of papers.

LJMU scholarships are for three years from October 2019 and 1) cover all University tuition fees, 2) provide £1500 p.a. (2018/19 figure) for consumables (and/or conference attendance etc) and 3) pay a stipend of ~£14777 p.a. (2018/19) to cover living costs. There are also opportunities to work as a demonstrator on undergraduate laboratory practicals/workshops, etc.

Applicants with a chance of success will be those that have a very good undergraduate degree, a Masters degree, some previous significant research experience and/or have authored/co-authored a scientific paper.

The closing date is 04/03/19: please get in touch well before this date!

"Brown, Richard" <R.P.Brown@ljmu.ac.uk>

Liverpool EvolutionAnimalBehaviour

I am looking for students with excellent CVs (first class degree and/or distinction at the Masters level, plus relevant experience and/or publication success in peer reviewed journals) to apply for a competitive 3 year doctoral scholarship in the school of Natural Sciences and Psychology at Liverpool John Moores University (https://www.ljmu.ac.uk/research/-phd%20scholarships).

Group living provides substantial advantages but may also engender conflict over reproduction or other resources. In order for groups to form and persist, animals must be able to manage this conflict. Across species, complex sociality involves an interplay between dominance hierarchies, aggression, submission, cooperation, and kinship. Understanding these dynamics is a major focus in social behaviour research. Much of the work done so far has examined primates and other mammals, however, conducting carefully controlled experiments in these species is often difficult. The cooperatively breeding cichlid fish, Neolamprologus pulcher, lives and breeds in highly complex permanent social groups. N. pulcher are small bodied and can easily be housed in aquaria where these remarkable fish will perform their full suite of social behaviour.

We will make use of a newly established N. pulcher breeding colony at LJMU. Social behaviours can be scored within these groups using both live observations and high definition video recordings. I am interested in understanding social behaviour from an integrative perspective, and thus neural, endocrine and/or molecular approaches may also be used. The specific details of the project are flexible and can be developed in collaboration with the successful candidate to align with his or her interests, skills, and expertise. This is an excellent opportunity for a keen student to develop their own project. The project will likely be primarily laboratory based, though field work in Lake Tanganyika may also be possible.

Preferred candidate characteristics include a keen interest in animal social behaviour; experience studying behaviour in the laboratory and/or the field; strong writing and analytical skills; knowledge of experimental design and statistical analysis. Previous experience working with fish is desirable but not essential. Full training will be provided. UK/EU nationals only.

The selected candidate will be put up for a competitive internal award (https://www.ljmu.ac.uk/research/-phd%20scholarships). If successful, the scholarship will cover all applicable fees for 3 years including a stipend at the standard UK rate (~£15000pa) and provides £1500pa in research funding

Please apply by email to a.r.reddon@ljmu.ac.uk with a CV, a brief statement outlining your interest, and the names and contact information for two references. Applications due to me by Feb 18. Please feel free to email me with any questions.

Adam R. Reddon, Ph.D. Lecturer in Behavioural Ecology Liverpool John Moores University Room 234A, James Parsons Building t: +44 (0)151 231 2034 www.adamreddon.ca A.R.Reddon@ljmu.ac.uk

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London Nagasaki PneumococcalPhylogenetics

Dear colleagues, We are seeking motivated applicants for a PhD position in PHYLOGENETIC INFERENCE OF PNEUMOCOCCAL TRANSMISSION IN VIETNAM.

This opportunity falls within the exciting new joint PhD programme between Nagasaki University, Japan, and the London School of Hygiene and Tropical Medicine (LSHTM), UK.

The transmission of S. pneumonae, particularly to infants, is not well understood. However, it is at the core of the highly topical debate around relying on herd protection from pneumococcal vaccines in order to reduce unsustainably high vaccine costs in low- and middle-income countries.

In Nha Trang, Vietnam, we have collected pneumococcal carriage samples from about 70% of the total infant and toddler population and their mothers in 2016 and 2018. All samples will have been deep-sequenced by 2019. This allows for a word-wide unique opportunity to study pneumococcal transmission among young children and their mothers, to identify prominent routes of transmission and characterise factors promoting ongoing paediatric infections.

The PhD candidate will use this data to develop, test and implement a robust methodology to infer pneumococcal transmission from genomic data and distinguish transmission events from close genomic proximity for other reasons (including an indirect transmission link via an intermediary), investigate who infects infants and toddlers with pneumococci using those techniques and will investigate the role of sub-dominantly carried serotypes for transmission.

As this project is at the forefront of research on the use of phylogenetics for pneumococcal transmission, a high degree of personal motivation is essential. Expertise in computer programming, ideally in R or Python as well as good command in English is required. Prior knowledge of molecular evolution and statistical proficiency are also desirable.

The student will learn about state-of-the art pneumococcal epidemiology and vaccinology, pathogen molecular evolution, genomic sequence analyses and phylogenetic inference.

Supervisory team LSHTM: Stéphane Hué, Stefan Flasche Nagasaki University (Pasteur Institute Nha Trang): Lay Mint Yoshida

More information on the Nagasaki-LSHTM joint PhD program is available here: www.lshtm.ac.uk/media/-10181 . If you are interested please get in touch directly with Stéphane Hué (https://www.lshtm.ac.uk/aboutus/-people/hue.stephane) and/or Stefan Flasche (https://-www.lshtm.ac.uk/aboutus/people/flasche.stefan). Applications close on 31 January 2019.

Stephane Hue <Stephane.Hue@lshtm.ac.uk>

MasseyU 2 PolyploidCytonuclearEvolution

Two PhD positions are available in the Tate lab < http://www.massey.ac.nz/~jtate/index.htm > at Massey University < http://www.massey.ac.nz/ > (Palmerston North, New Zealand) to study cytonuclear coordination in allopolyploids of the flowering plant Tragopogon (Asteraceae).

Eukaryotic cells must coordinate nuclear and organellar (mitochondrial and plastid) genomes to function properly. In plants, multiple genomes coordinate to generate energy (nuclear and mitochondrial) and conduct photosynthesis (nuclear and plastid). Successful coordination of these genomes is crucial for regular growth and development in all eukaryotes. Currently, we lack broad understanding of how nuclear and organellar genomes successfully integrate in allopolyploids, which form by hybridization between species and whole genome duplication.

Using our model polyploid system (Tragopogon) in which allopolyploids formed recently and recurrently, we aim to understand the coordination of the duplicated nuclear genomes with the haploid maternally inherited genomes using a variety of approaches. Depending on the interests of the students, the projects can involve different aspects of the larger project to include genomic, transcriptomic, proteomic, computational or physiological work. The project is funded by the Marsden fund < https://royalsociety.org.nz/what-we-do/funds-and-opportunities/marsden > and is in collaboration with Murray Cox < https://www.genomicus.com/ > at Massey University, Dan Sloan < http://www.biology.colostate.edu/people/dbsloan/ > at Colorado State University, and Doug and Pam Soltis < https://www.floridamuseum.ufl.edu/museum-voices/soltis-lab/ > at the University of Florida.

The PhD positions are funded for 3 years at $27,500 with fees also paid. The successful applicants will be enthusiastic and motivated, and have an MSc (or BSc Honours or equivalent) in Plant Biology, Genetics, Evolutionary Biology, Computational Biology, or similar. Candidates with non-standard backgrounds, but a clear fit to the project, are encouraged to apply. Opportunities for teaching experience are available and encouraged, but not compulsory. Students will be expected to attend and present their research at international conferences during their PhD.

To apply, please send a letter of interest, CV, academic transcript (unofficial is sufficient) and the names and contact details for three references to j.tate@massey.ac.nz with 'PhD scholarship' in the subject line. International applicants are welcome. See the Massey University postgraduate webpage < http://www.massey.ac.nz/massey/postgraduate/postgraduate_home.cfm > for additional entry requirements (including, where relevant, an English language proficiency exam). For full consideration, materials must be received by February 15th 2019. The starting date is flexible, but the project itself is funded from 1 March. Please feel free to email me (Jen Tate) with any questions about the project or the scholarship. This position offers an opportunity to experience New Zealand's unique natural and cultural environment. Located in Palmerston North, a university town with a large international community which offers a range of social and cultural amenities, the city is located close to mountains, rivers and the sea, and presents regular opportunities for hiking, skiing, surfing, and adventure sports.

Jennifer A. Tate, Ph.D. Senior Lecturer in Plant Systematics and Evolution Curator, Dame Ella Campbell Herbarium (MPN) < http://www.massey.ac.nz/herbarium > Massey University School of Fundamental Sciences Private Bag 11222 Palmerston North New Zealand

Phone: 64-6-350-5515 ext. 84718 FAX: 64-6-350-5682

Homepage < http://www.massey.ac.nz/~jtate/index.htm >

j.tate@massey.ac.nz

"Tate, Jennifer" <J.Tate@massey.ac.nz>

NorthDakotaStateU BehavioralSelection

The Dochtermann Lab in the Department of Biological Sciences at North Dakota State University is seeking to fill a PhD assistantship examining how selection shapes behavioral syndromes (behavioral correlations). The student will develop and pursue their own research topics while working within a broader NSF funded project.

In our lab we focus on evolutionary questions regarding the maintenance of variation within and among populations and the evolutionary implications of how traits are correlated.

The position will start Fall Semester 2019. The student will be housed and working in the Department of Biological Sciences (https://www.ndsu.edu/biology/) with their degree awarded through the NDSU Environmental Sciences and Conservation Program.

Requirements: Bachelors or Masters in ecology, evolution, animal behavior, or related field; experience collecting and analyzing data; ability to work independently and as part of a larger collaborative group.

Preferred: MSc preferred; experience conducting quantitative genetic experiments; field research experience

If interested please contact me at ned.dochtermann@gmail.com and provide a brief synopsis of your research interests.

Ned

– Ned A. Dochtermann Associate Professor / Department of Biological Sciences / NORTH DAKOTA STATE UNIVERSITY p: 701.231.7353 / f: 701.231.7149 / http://www.ndsu.edu www.neddochtermann.com ned.dochtermann@ndsu.edu

ned.dochtermann@gmail.com

OklahomaStateU EvolutionIntegBiology

M.S. AND PH.D DEGREE OPPORTUNITIES IN INTEGRATIVE BIOLOGY. The Department of Integrative Biology at Oklahoma State University is recruiting graduate students for Fall 2019 admission to join a collaborative and productive degree program. The Department of Integrative Biology takes an integrative approach to research in organismal biology, focusing on increasing our knowledge of organisms and their environments through studies ranging from the molecular to the ecosystem level.

We have three inclusive areas of study: evolution, ecology, and environmental stress, which we define quite broadly. Among other areas, we conduct studies in conservation ecology, genomics, neurobiology, behavioral ecology, environmental toxicology, science education, ecosystem studies, and physiology. Graduate Teaching Assistantships with competitive stipends are regularly available.

Oklahoma State University is located in Stillwater, a thriving college community with a low cost of living, diverse restaurants, a thriving music scene, air service through American Airlines, and close proximity to both natural and major metropolitan (Tulsa and Oklahoma City) areas.

Information on applying to our graduate program can be found here: http://integrativebiology.okstate.edu/-graduate-program/admission-procedure. For questions regarding the application process, please contact our departmental Graduate Coordinator, Dr. Jen Grindstaff (jen.grindstaff@okstate.edu). The application deadline is February 1, 2019. Evaluation will continue after that date, but students are encouraged to apply as early as possible.

waldman@snu.ac.kr

Prague MycorrhizalFungalCommunities

PhD position available from September 2019

Topic: Symbiotic efficiency of arbuscular mycorrhizal fungi in arable soils

Within a starting project, we seek a student interested in systematically exploring communities or arbuscular mycorrhizal fungi (AMF) in arable soils. These important plant symbionts are known to be negatively affected by conventional agriculture with respect to diversity and infectivity. However, their potential to contribute to crop growth in arable soils is unclear due to a lack of systematic research on their symbiotic efficiency in these conditions. We will conduct a series of greenhouse biotests in a wide range of representatively selected Czech arable soils along with evaluating AMF root colonization and diversity in field samples. Selected AMF communities from arable soils will be functionally compared to AMF communities from undisturbed grasslands to test whether arable soils select for lower mutualism. The student will participate at the establishment of the experiments, his/her main responsibility will be the collection and analysis of the experimental data: biomass parameters, root colonization (by microscopy) and diversity of AMF (by Illumina sequencing) and/or the costs and benefits of mycorrhiza (by isotope labelling).

The ideal candidate for this PhD position has experience with experimental plant cultivation and AMF-related methods, is willing to contribute both to greenhouse a laboratory work. Experience in the DNA lab is of advantage but not required. Ability to work independently and assume responsibility for partial tasks within the project team is essential as well as sound knowledge of written and spoken English. We also expect involvement into international collaborations and presentation at conferences.

The student will work under the supervision of Martina Janouskova in Department of Mycorrhizal Symbioses, Institute of Botany, Czech Academy of Sciences in Pruhonice, a suburban village close to Prague. The Department has excellent facilities for all the types of work required, good scientific reputation and a friendly atmosphere. Close collaboration with Laboratory of Fungal Biology in Institute of Microbiology, CAS, in Prague offers additionally scientific impulses and contacts.

To be eligible, the candidate must have obtained a degree equivalent to a biology diploma or M.Sc. by September 2019 (B.Sc. is not sufficient due to local legislation). Formally, the PhD studies can be conducted either at Faculty of Science of Charles University or at Faculty of Environmental Sciences of Czech University of Life Sciences, both in Prague - according to the student's preferences. Institute of Botany has a well-established, routine collaboration with both universities in supervising Ph.D. students. The position is available for up to four years, starting in September 2019. The PhD candidate's net monthly income will be about 18.000 CZK (ca 690 EUR, scholarship + partial employment in the Institute), which is sufficient to cover the living costs in Prague.

If interested, send a letter outlining your motivation for this position and specific experience, CV, list of publications or conference presentations (if available), abstract of Master thesis, and contact details of two senior scientist that can provide references on you to martina.janouskova@ibot.cas.cz until February 20, 2019. The selected candidate will be assisted in submitting an official application to the university of his/her choice for the PhD position.

Useful links Institute of Botany official web page https://www.ibot.cas.cz/en/ Department of Mycorrhizal Symbioses web page http://www.ibot.cas.cz/-mykosym/en_index.html Faculty of Science, Charles University https://www.natur.cuni.cz/eng?set_language=-en Faculty of Environmental Sciences, Czech University of Life Sciences https://www.fzp.czu.cz/en/ Martina.Janouskova@ibot.cas.cz

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Prague PlantPolyploidEvolution

PhD position in polyploid evolution of Cardamine amara (Brassicaceae) Dept. of Botany, Faculty of Science, Charles University in Prague, Czech Republic

We are seeking a highly motivated student to join a project focused on ecological and evolutionary consequences of genome duplication (polyploidization) in plants. Although polyploidization is a leading force in plant evolution including crops, we know little about evolutionary drivers promoting origin and coexistence of different ploidy levels within a species. By combining field surveys, cytogenomics, population genomics and crossing experiments, we aim to identify major forces shaping polyploid evolution in natural populations of Cardamine amara, a member of plant model family Brassicaceae. Specifically, the project will address following objectives: What was the role of ploidy (parallel) ecological adaptation in genetic divergence? Was ecological divergence linked with (parallel) whole genome duplication events? What is the strength of realized gene flow between diploid and tetraploid populations and do there exist intrinsic barriers restricting such gene flow? Had the genome of C. amara contributed to the formation of polyploid lineages in other species within the genus?

Biogeographic and biosystematics part will be lead by Prof. Karol Marhold (https://botany.natur.cuni.cz/-brassiploidy/). Population genomic analyses and experimental work will be done under co-supervision of Dr. Filip Koláø, group of Ecological genomics (https:/-/botany.natur.cuni.cz/ecolgen) and the cytogenomics in collaboration with Ass. Prof. Martin Lysak (http://-www.plantcytogenomics.org/). Additional training in population genomics will be provided under international collaboration with the Yant lab (University of Nottingham, UK).

The student will gain multi-disciplinary experience by addressing following tasks: - field surveys across European range of the species and in ploidy contact zones in central Europe - ploidy level estimation using flow cytometry complemented by cytogenomic techniques (GISH, chromosome painting) - crossing experiment between individuals of different ploidy - analysis of high-throughput sequencing data (RADseq, genome resequencing)

We offer - work in an inspiring student-dominated environment of two interconnected teams of Ecological genomics and Brassicaceae polyploidy - competitive salary topping-up the standard university scholarship (altogether monthly net income of 800 EUR) with rise in the following years when fulfilling additional PhD study duties - additional experience by international collaborations - work in the historical centre of the UNESCO heritage site of Prague city, Czech Republic, EU

We require - strong motivation for interdisciplinary research at the border of ecology, biosystematics and population genomics - a MSc degree in Biology or related fields (in summer 2019 at the latest)

Please send your CV, contacts for at least one reference person and a short motivation letter (max A4) to the project leader, Karol Marhold (Karol.Marhold@savba.sk). Review of the applications will begin on March 1st 2019 and will continue until the position has been filled. The position is available from September 2019.

Karol Marhold & Filip Kolar

Filip Kolar <filip.kolar@gmail.com>

QueensU Belfast 3 MolluscEvolution

Dear colleagues

We have funding to support up to three new PhD students working on great projects on living and fossil molluscs, between my lab in Queen's University Belfast and Alex Brasier in University of Aberdeen. Full funding is available only to EU and UK citizens.

The project based in the Queen's Marine Lab in Portaferry, N Ireland, is co-sponsored by Zeiss microscopy and would include an internship with them. There are other excellent opportunities for outside training with the other projects as well.

Application deadline is 31 January!

Project titles and links to more info and the application portal 1. Based in N Ireland, working on chiton aesthetes : "Bio-inspiration from molluscs: flexible armour with embedded sensing capacity" https://www.findaphd.com/phds/project/-bio-inspiration-from-molluscs-flexible-armour-with-embedded-sensing-capacity/?p105243 2. Based in Aberdeen, working on Jurassic bivalves: "Jurassic Lagoon: learning from the ancestors of the amazing mussels" https://www.findaphd.com/phds/project/-jurassic-lagoon-learning-from-the-ancestors-of-the-amazing-mussels-quadrat/?p105133 3. Based in Aberdeen, with fieldwork sites in N Ireland, working on protected reef building mussels in a marine protected area: "Sea-level change and conservation, past, present and future" https://www.findaphd.com/phds/project/-sea-level-change-and-conservation-past-present-and-future-quadrat/?p105131 Please circulate this message to anyone who may be interested, I would be very happy to hear from interested potential students.

Cheers,

Julia

– Dr Julia Sigwart Queen's University Belfast, Marine Laboratory

sabbatical address (2015-2018): University of California, Berkeley, Museum of Paleontology

www.qub.ac.uk/bb/People/DrJDSigwart/ Julia Sigwart <j.sigwart@qub.ac.uk>

QueensU MarineBiodiversity

Fully funded NERC QUADRAT funded PhD studentship (3.5 years)

"Harnessing the eDNA in tidal flows to assess marine biodiversity"

This project will be supervised by Dr Sarah Helyar of Queens University School of Biological Sciences and by Dr Alex Douglas of the University of Aberdeens School of Biological Sciences. The start date will be 1st October 2019.

https://www.findaphd.com/phds/project/harnessing-the-edna-in-tidal-flows-to-assess-marine-biodiversity/-?p105223 Brief project outline: For marine management to be effective, we need to have comprehensive data on the status of marine biodiversity. However, methods that can document biodiversity in our oceans are currently often extremely time consuming. Traditionally we have used specialist grabs and nets to survey marine communities, but marine environments can be very difficult to sample effectively. Rather than directly sampling these species, sampling the traces of DNA which are present in a body of water from skin, blood, faeces or mucous can be used to identify which species have recently been present in the local environment. Combined with recent advances in sequencing and bioinformatics, this environmental DNA (eDNA) offers a new means of sampling the biodiversity in aquatic ecosystems. Not only is sampling eDNA potentially faster and less expensive than traditional methods, it is also less destructive and has the potential to identify species that due to being rare, small, or able to avoid current sampling gear, are not reliably physically sampled in the environment.

Much of the current research looking at eDNA as a tool for sampling aquatic environments has been carried out in freshwater systems, with currently only a handful of published studies that have tested the approach in the marine environment. This project will take advantage of well characterised, natural, semi-enclosed waterbodies containing different habitat types, such as Strangford Lough, and asses the eDNA profile associated with each of those habitats. The effects of biotic and abiotic factors, such as persistence times, will also be investigated to determine if tidal flows can be harnessed to monitor biodiversity. Further technology development or oceanographic modelling may be included depending on the interests of the student.

The student will address a number of interlinked questions, including: 1) Define and ground truth eDNA profiles associated with known habitats.

2) Explore the effects of biotic and abiotic factors on eDNA samples across enclosed marine water bodies.

3) Determine the utility of single site sampling to assess the biodiversity of semi enclosed marine water bodies.

The project provides unique opportunities to work on in a range of stunning locations across Ireland and Scotland, combining fieldwork with state-of-the-art molecular genetic techniques (including high-throughput DNA sequencing and genotyping using second (Illumina) and third (Oxford Nanopore MinION) generation platforms). The student will be embedded within a dynamic, vibrant and supportive research group to gain training in field skills, bioinformatics, statistical and laboratory methods, and will have the opportunity to work with local stakeholder groups. Furthermore, the student will network with a broader cohort of DTP students to receive core and generic skills training in a multidisciplinary context to maximise employability.

Funding: This project is one of a number that are in competition for funding from the NERC QUADRAT Doctoral Training Partnership (DTP). For details of all the PhDs advertised for 2019 start please see: https://www.findaphd.com/phds/program/-quadrat-doctoral-training-partnership/?i2p4257 For eligible students, the studentship will provide funding of fees and a stipend which is currently GBP 14,777 per annum for 2018-19. Applicants who are classed as International for tuition fee purposes are not eligible for funding.

Deadline: Thursday 31st January 2019.

Informal inquiries: s.helyar@qub.ac.uk

Sarah Helyar <S.Helyar@qub.ac.uk>

StockholmU Speciation

PhD position in Speciation at Stockholm University APPLICATION DEADLINE: February 15, 2019 The evolution of gametic isolation

A fully funded 4-year PhD position on the evolution of reproductive isolation is available in Rhonda Snooks group, Department of Zoology, Stockholm University.

Speciation is a fundamental evolutionary process requiring the evolution of barriers to gene exchange and therefore understanding how these barriers evolve is critical to understanding speciation. Barriers occurring after mating but before fertilization (gametic or postmating prezygotic (PMPZ)) may act early during speciation in response to rapid evolution between male and female reproductive traits. However, relatively few studies of early PMPZ barriers have been performed. This project aims to fill this gap by determining how the coevolution of male ejaculate and female reproductive tract traits within populations contributes to PMPZ RI between populations. The student will engage in an integrative research approach, combining phenotypic, proteomic and genomic work, on populations of Drosophila montana that vary in whether, and the extent to which, PMPZ RI between populations occurs.

The successful applicant will be enthusiastic about evolutionary biology with a good understanding of population genetics and/or are skilled in molecular genetics, along with enjoying the process of scientific discovery. The successful applicant must hold a master of science (or equivalent) in Biology/Ecology or a related field.

Stockholm Universitys Department of Zoology is a vibrant international and interactive community. Working language in the lab is English.

For informal queries, contact Rhonda on rhonda.snook@zoologi.su.se

Details about research in Rhonda Snooks lab can be found here: https://www.su.se/english/-profiles/rhsn2867-1.348903 Details to apply, including more about the project, are available here: https://www.su.se/english/about/working-at-su/-phd?rmpage=job&rmjobx29&rmlang=UK Rhonda Snook <rhonda.snook@zoologi.su.se>

SwedishU eDNApikeMonitoring

PhD position on the development of eDNA approaches for fish monitoring

A PhD position is available development eDNA approaches for fish monitoring by joining the research group of Prof. Anti VasemÃÂgi at the Institute of Freshwater Research, Department of Aquatic Resources, Swedish University of Agricultural Sciences. Research in the VasemÃÂgi group focuses on understanding the connectivity of aquatic organisms, relationships between genotype and phenotype, the genetic basis of adaptation and how contemporary natural- and human-induced selection works on ecological time-scales. Other researchers involved in the project include Dr. M. Ogonowski, Dr. G. Sundblad and P. Bohman.

eDNA is a rapidly developing tool for science-based management of aquatic environments. However, methodological issues remain before quantitative eDNA can be used practically. The northern pike is one of the most important recreational fish species in Sweden, as well as a keystone predator important for ecosystem health and functioning. Despite its ecological and socioeconomic importance, pike has been neglected in monitoring. One reason being the low catchability of pike using traditional monitoring methods. This PhD project will focus on developing and evaluating the performance of eDNA-based methods for monitoring northern pike. The position entails planning and executing a combination of controlled laboratory and outdoor experiments in fish tanks and ponds, fieldwork (including electrofishing and rod-fishing) and modern molecular genetic techniques to develop and systematically evaluate the usability of an eDNA approach to provide non-invasive quantitative estimates of northern pike abundance.

We are looking for a motivated and enthusiastic person with an interest in molecular ecology, ecological genomics, fish monitoring and aquatic biology. Preferably, the applicant's university degree focuses on genetics, molecular biology, ecology or fish biology. The applicant is expected to be fluent in English, both in speech and writing. Emphasis will be placed on personal skills, such as the ability to work independently as well as in a group, attention to detail and an ability to prioritize and multitask. Documented experience of practical work with molecular methods or in experimental ecology is an advantage.

Place of work: Drottningholm, Stockholm. Forms for funding or employment: Employment 4 years.

Starting date: 1 April 2019 or as agreed. Application: We welcome your application no later than 2019-03-01, use the link below. A person has basic eligibility for third cycle education if he or she has taken a second cycle qualification or has completed course requirements of at least 240 higher education credits, including at least 60 higher education credits at second cycle education. Upper secondary school grades equivalent to English B/English 6 are a basic requirement. Selection among applicants meeting the requirements is made with reference to written application including curriculum vitae, copies of degrees and transcripts of academic records, one copy of the dissertation for masters or undergraduate degree, a list of at least two references familiar with the applicant's qualifications, certified knowledge of the English language and an interview. Please observe that applicant/s chosen to participate in an interview shall hand in certified true copies of certificates, diplomas and transcripts from previous studies at an internationally recognized higher education institution (university or university college) and transcripts in connection to the interview. If the applicant is a foreign citizen we require a certified copy of the page in your passport with your personal data and photography.

Read about the PhD education at SLU at www.slu.se/-en/education/postgraduate-studies/ We at the Department of Aquatic resources (SLU Aqua) are passionate about our vision "Viable fish stocks in healthy waters ". We Âre expanding, searching for employees who want to develop themselves and make a difference together with us. The Department of Aquatic Resources conducts environmental monitoring and assessment, consulting, research and education in aquatic ecology with focus on fish and shellfish. The department is SLU's largest and has more than 180 employees at three main locations: Lysekil, Ã regrund and Stockholm (Drottningholm), as well as four field stations. The department is highly focused on data collection and analysis of fish, fisheries and ecosystems, and is characterized by intensive collaborations with industry, public agencies and NGO:s. This creates a vital research environment and gives us unique opportunities to develop knowledge with high societal impact. For more information about the department: https://www.slu.se/en/departments/aquatic-resources1/

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Switzerland EvolutionaryEcol

Eawag, the Swiss Federal Institute for Aquatic Science and Technology, has an open PhD position in Evolutionary Ecology of Ecosystems, at the Center for Ecology Evolution & Biogeochemistry (CEEB).

The position is fully funded for 4 years, and will be based in the group of Blake Matthews. The successful applicant will be a student at the University of Bern, and be co-supervised by Prof. Ole Seehausen (Institute of Ecology and Evolution, Bern).

The project will explore 15,000 years of evolution and ecosystem dynamics in Lake Victoria, East Africa, as reconstructed from sediment cores, fossils and ancient DNA. This Swiss NSF Sinergia project is a cooperation between U Bern, Eawag, the Centre for Geogenetics at U of Copenhagen, Denmark, the Tanzania Fisheries Research Institute, U of Arizona, U Massachusetts and others.

The group of Blake Matthews focuses on phenotypic evolution in a community and ecosystem context. The open PhD position will investigate how the community composition and phenotypic diversity of zooplankton has changed over time in Lake Victoria. To this end, the student will analyze subfossil remains of zooplankton from sediment cores spanning hundreds to thousands of years of ecosystem and evolutionary history. This is one of 4 PhD positions funded by the project. In close collaboration with ecologists, paleo-ecologists and paleo-genomics researchers, we want to address how the evolutionary diversification of the cichlid fish along with other ecosystem changes (e.g. eutrophication), have interacted with the plankton community of Lake Victoria.

Ideally, the candidate has some prior experience in invertebrate taxonomy (ideally with zooplankton) and/or paleolimnology. The candidate is motivated to learn about evolutionary ecology in general, and about paleolimnology and zooplankton in particular. The groups working language is English. Knowledge of German or French is not required.

Eawags CEEB is located on the shore of Lake Lucerne and is a strong nucleus of Eawag research groups aimed at integrating evolutionary biology, community ecology, and ecosystem science http://www.eawag.ch/forschung/cc/ceeb/index_EN. The PhD student will interact with a diverse range of researchers studying community ecology, evolutionary biology, ecological genetics, ecosystem science, and applied environmental science.

Review of applications will start Feb 11th and continue until the position is filled.

Please send one pdf file only, with CV, letter of motivation, and contact details of three referees to Dr. Blake Matthews (blake.matthews@eawag.ch).

Lab homepage: http://homepages.eawag.ch/~matthebl/Welcome.html Publication list: https://scholar.google.ch/citations?user=KPOcG_sAAAAJ&hl=en Matthews, Blake blake.matthews@eawag.ch http://homepages.eawag.ch/~matthebl/Welcome.html Eawag, Aquatic Ecology Department Center for Ecology, Evolution & Biogeochemistry Seestrasse 79 6047, Kastanienbaum Switzerland

“Matthews, Blake” <Blake.Matthews@eawag.ch>

UAberdeen SpeciesBiogeography

Fully funded PhD project at the University of Aberdeen: Effect of species range shifts on trophic networks in freshwater ecosystems

Closing date:

31/1/2019

Eligibility:

UK nationals and EU residents in the UK. Minimum 2.1 degree qualification.

Link to apply:

https://www.findaphd.com/phds/project/effect-of-species-range-shifts-on-trophic-networks-in-freshwater-ecosystems/?p105126 Overview:

This is a joint project run between the University of Aberdeen (Scotland) and the University of Belfast (N. Ireland), as part of a new Natural Environment Research Council funded doctoral training program. You will be part of a large and dynamic cohort of students, and the training will integrate project work with dynamic and intensive core training in ecology skills such as fieldwork, policy, and interface with stakeholder groups. The position is fully funded and includes all tuition, fees, research expenses, and a living expenses stipend for 4 years of study.

Supervisory team:

Dr. Lesley Lancaster (U. Aberdeen, expertise in biogeography and community dynamics, ecological genomics), Dr. Paul Caplat (U. Belfast, expertise in environmental and ecological modeling, community dynamics), Dr. Sarah Helyar (U. Belfast, expertise in ecological genomics, population genetics), and Dr. Pierre Bize (U. Aberdeen, expertise in physiological ecology and genetics).

Project description:

As climates warm in the 21st century, many species are shifting their geographic distributions towards higher latitudes and elevations. Previous studies have indicated that range shifting species may express greater metabolic and behavioural flexibility than species which have not recently undergone biogeographic shifts, with long-term implications for the structure and function of high latitude communities. For instance, research has already revealed that range shifting species often negatively impact species richness and biodiversity of areas where they become established. However, the processes by which community turnover occurs in colonised sites are little known, rendering future biodiversity predictions difficult. We propose to investigate how range-shifting species affect patterns of community composition, using pond damselflies (Odonata: Zygoptera: Coenagrionidae) as a model system. These species are rapidly range shifting in Britain under climate change, and are important, keystone predators in freshwater communities; the Irish species also have high conservation value. Our previous work has indicated that range shifts in Coenagrionid damselflies are associated with species turnover in high latitude freshwater ecosystems, but the effects on trophic interactions and resulting community resilience to future environmental change remain largely unknown.

To examine the ecosystem consequences of range shifts, the student will: 1) Relate the colonisation dynamics of range-shifting damselflies in Scotland and Ireland to changes in freshwater trophic network structure, accounting for land use and climatic variability across the study region, using hierarchical regression models. 2) Investigate differences in phenotypes, behaviour and metabolic rates under different thermal regimes in range-shifting vs. non-range shifting damselflies across the region, in order to identify alternative mechanisms mediating biotic interactions in range- shifting vs. non-range shifting populations. 3) Using data derived from Next Generation Sequencing approaches, identify genetic variants in range-shifting vs. non-range shifting damselfly species that are associated with particular trophic networks (Obj 1) and traits (Obj 2).

The project will contribute to our understanding of how communities are likely to respond to ongoing range shifts, and identify the mechanisms underpinning global homogenisation of biodiversity. The results also have the potential to make fundamental contributions to the development of the rapidly advancing field of functional community ecology.

The University of Aberdeen is a charity registered in Scotland, No SC013683. Tha Oilthigh Obar Dheathain na charthannas cl?raichte ann an Alba, ?ir. SC013683.

"Lancaster, Lesley" <lesleylancaster@abdn.ac.uk>

UBern CichlidRadiation

We are seeking to fill a PhD position funded for 4 years in the group of of Ole Seehausenat the University of Bern and the Eawag Center for Ecology, Evolution & Biogeochemistry (CEEB), Switzerland.

We are looking for a commited and enthusiastic graduate student researcher to work with ancient DNA, subfossils and paleoecology to explore whether and how the adaptive radiation of cichlid fish and the unfoldingHolocene ecosystem of modern Lake Victoria interacted. The project is funded by a Swiss NSF Sinergia grant and involvesresearchersat U Bern, EAWAG (Swiss Federal Institute of Aquatic Science and Technology), the Centre for Geogenetics at U of Copenhagen (Denmark), the Tanzania Fisheries Research Institute (Tanzania), U of Arizona, U Massachusetts (USA) and others.

The Seehausen groupfocusses on the phenotypic and genomic evolution of Lake Victorias super-diverse cichlid fish radiation. This PhD in evolutionary biology and paleogenetics will investigate the evolution of the cichlid radiation through study of time series of subfossils and ancient DNA. Specifically, you will analyse subfossil remains of cichlid fish from long sediment cores. You will study their phenotypes and ancient DNA content and you will perform genetics on aDNA sequences. Extensive reference collections of modern cichlids and their genome sequences are available in the group to guide interpretation of fossil phenotypes and aDNA sequence data. We want to understand how the ecological and phenotypic diversity of cichlids changed through time, and how genetic variation arose and got assembled into new species in the course of the adaptive radiation. Ultimately, we want to ask if the radiation was affected by the Holocene changes in the ecosystem, and whether the radiation changed the ecosystem in turn. To this end, we collaborate in this project with ecologists, paleo-ecologists and paleo-genomics researchers. Yours will be one of 4 PhD positions, and there are also several Postdoc positions in the project. Your PhD will be supervised by Dr. Moritz Muschick and Prof. Ole Seehausen.

We are looking forcandidates that bringprior training in some or all of the following areas: molecular genetic lab techniques, statistical shape analysis, computational analysis of genomic sequence data. Most of all, you have a good grasp ofevolutionary biology,you are interested in howevolutionchanges ecosystems, and you are deeply committed to persuing a career in science. Interest in cichlid fish or African lake ecosystems will be a plus too. You will have to learn quickly and will have to often work independently. Our working language is English and fluency in writing and speaking is required.

Besides Uni Bern, youwill spend time at Eawags Center for Ecology, Evolution & Biogeochemistry, the CEEB. The CEEB is located at beautiful Lake Lucerne and is a strong nucleus of Eawag research groups aimed at integrating evolutionary biology, community ecology, and ecosystem science http://www.eawag.ch/forschung/cc/-ceeb/index_EN .Salary is at Swiss NSF PhD Fellowship level (47,000 to 50,000 CHF, 100%). The position is available from March 1, 2019 (for 4 years).

Review of applications starts on February11, 2019 and continues until the position is filled. Please direct inquiries to Prof. Dr. Ole Seehausen, ole.seehausen@iee.unibe.ch. Please applywith one pdf file only which containsthe following: your CV, a strong letter of motivation (be specific why you want this project),transcript of MSc with grades, publication list, and contact details of three referees. Pleasesend your application by email to therese.oesch@iee.unibe.ch

We look forward to receiving your applications

Ole Seehausen

ole.seehausen@iee.unibe.ch

UBern Switzerland PaleogenomicsLakeVictoria

Dear colleagues

We have funding from the Swiss National Science Foundation for two outstandingly motivated PhD students for reconstructing the evolution of a species radiation and its ecosystem using paleo-genomics, paleoecology and paleontology matched with experimental ecology and genomics of extant organisms.

Both graduate positions are based at the Institute of Ecology & Evolution, University of Bern and at the Eawag Center for Ecology, Evolution & Biogeochemistry in Kastanienbaum.

The advert texts follow:

1. PhD in Evolutionary Biology The position is fully funded for 4 years, and will be based in the Aquatic Ecology & Evolution group of Prof. Ole Seehausen at the University of Bern and the Eawag Center for Ecology, Evolution & Biogeochemistry in Kastanienbaum, Switzerland.

The project will explore 15,000 years of evolution and ecosystem dynamics in Lake Victoria, East Africa, as reconstructed from sediment cores, fossils and ancient DNA. This Swiss NSF Sinergia project is a cooperation between U Bern, EAWAG (Swiss Federal Institute of Aquatic Science and Technology), the Centre for Geogenetics at U of Copenhagen, Denmark, the Tanzania Fisheries Research Institute, U of Arizona, U Massachusetts and others.

The group of Ole Seehausen focusses on the phenotypic and genomic evolution of Lake Victoria's super-diverse cichlid fish radiation. The PhD in evolutionary biology and paleogenetics will investigate the evolution of the cichlid radiation through study of time series of fossils and ancient DNA. We want to understand how the ecological and phenotypic diversity changed through time, how genetic variation arose and got assembled into new species in the course of the adaptive radiation. This is one of 4 PhD and several Postdoc positions in the project. In close collaboration with ecologists, paleo-ecologists and paleo-genomics researchers, we want to address how the evolutionary diversification of the cichlid fish interacted with the Lake Victoria ecosystem. The student will analyse subfossil remains of cichlid fish from sediment cores for their morphology and ancient

DNA content. Extensive reference collections of modern cichlids and their genome sequences will be available to aid interpretation of fossil phenotypes and ancient DNA data. The PhD will be co-supervised by Dr. Moritz Muschick.

Ideally, the candidate has extensive prior training in molecular genetic techniques, statistical shape analysis, computational analysis of genomic sequence data, or evolutionary biology. The candidate is motivated to learn and apply advanced laboratory techniques and to work independently. The group's working language is English and fluency in writing and speaking is required. Knowledge of German or French is not required.

Besides Uni Bern, the student will spend time at Eawag's Center for Ecology, Evolution & Biogeochemistry. The Centre is located at Lake Lucerne and is a strong nucleus of Eawag research groups aimed at integrating evolutionary biology, community ecology, and ecosystem science http://www.eawag.ch/forschung/cc/ceeb/index_EN . Supervisor: Prof. Dr. Ole Seehausen, Institute of Ecology and Evolution Salary: Swiss NSF PhD Fellowship (47,000 to 50,000 CHF, 100%). The position is available from March 1, 2019 (for 3-4 years).

Review of applications starts on January 20, 2019 and continues until the position is filled.

Please direct inquiries to Prof. Dr. Ole Seehausen, ole.seehausen@iee.unibe.ch.

Please send one pdf file only, with CV, letter of motivation, if applicable transcript of MSc with grades, publication list, and contact details of three referees by email to therese.oesch@iee.unibe.ch.

2. PhD in Evolutionary Ecology of Ecosystems The position is fully funded for 4 years, and will be based in the group of Blake Matthews at the Eawag Center for Ecology, Evolution & Biogeochemistry in Kastanienbaum, Switzerland. The successful applicant will be a student of the University of Bern, and be co-supervised by Prof. Ole Seehausen (Institute of Ecology and Evolution, Bern).

The project will explore 15,000 years of evolution and ecosystem dynamics in Lake Victoria, East Africa, as reconstructed from sediment cores, fossils and ancient DNA. This Swiss NSF Sinergia project is a cooperation between U Bern, Eawag, the Centre for Geogenetics at U of Copenhagen, Denmark, the Tanzania Fisheries Research Institute, U of Arizona, U Massachusetts and others.

The group of Blake Matthews focuses on phenotypic evolution in a community and ecosystem context. The open PhD position will investigate how the community composition and phenotypic diversity of zooplankton has changed over time in Lake Victoria. To this end, the student will analyse subfossil remains of zooplankton from sediment cores spanning hundreds to thousands of years of ecosystem and evolutionary history. This is one

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UBielefeld Germany ZebraFinchSpermCompetition

PhD position in Evolutionary Ecology and Functional Genomics

One Postdoc or PhD position in evolutionary ecology and functional genomics is available at the Faculty of Biology at Bielefeld University in the Evolutionary Biology group (PD Dr Tim Schmoll, see http://www.uni-bielefeld.de/(en)/biologie/Evolutionsbiologie) in collaboration with the Department of Animal Behaviour (Dr Peter Korsten, see http://www.unibielefeld.de/biologie/animalbehaviour). The position is available immediately for 24 months (Postdoc) or until 31.12.2021 (PhD) and is funded by the German Research Foundation (DFG) within the collaborative research centre (SFB/TRR 212) A Novel Synthesis of Individualisation across Behaviour, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3).

The goal of this project (project B04 of the collaborative research centre) is to test how male Zebra Finches conform to their social niche as set by the prevailing level of sperm competition. This will allow us to understand how individual variation in sexual competition generates individual variation, and covariation, in both competitive traits and parenting behaviour. The successful candidate will closely work together with a PhD student to (i) quantify male social niche conformance by analysing adjustment of sexual competitiveness including behavioural (e.g. aggression) and ejaculate (e.g. sperm motility) traits; (ii) identify the underlying mechanisms of social niche conformance on the hormonal (via endocrinological profiling) and the gene expression (via RNAseq) levels; (iii) assess the adaptive significance of niche conformance under a niche match/mismatch paradigm; and (iv) test for trade-offs between investment in sexual competitiveness versus paternal care. A sub-project A will primarily focus on male social niche conformance through adjustment of behavioural traits and the hormonal mechanisms underlying niche conformance. A sub-project B will primarily focus on male social niche conformance through adjustment of ejaculate traits and the gene expression underlying niche conformance. Note that the position offered here is exclusively for sub-project B.

The collaborative research centre: The position will be embedded within a larger collaborative research centre (SFB) comprising 20 principle investigators, 15 postdocs and 18 PhD students based at Bielefeld University, the University of Münster and the University of Jena. The aim of the SFB is to produce a conceptual and empirical synthesis of individualisation across behaviour, ecology and evolution. The SFB will provide exceptional opportunities for interdisciplinary collaboration and academic networking, together with structured training, scientific exchange and early career support programmes. Full details of the SFB can be found at www.uni-bielefeld.de/-biologie/crc212 . Main responsibilities

* Research tasks (90%): - Designing and conducting laboratory experiments in which zebra finch males are exposed to different levels of sexual competition - Maintaining a zebra finch stock population and breeding of experimental birds - Processing of tissue samples for transcriptomic analyses - Bioinformatic processing of high-throughput sequencing data to quantify gene expression - Phenotyping sperm samples using a newly established computer-assisted sperm analysis system and other methods - Assisting in taking behavioural recordings - Statistical analyses of experimental data - Collaborating with other research groups in the collaborative research centre - Writing scientific publications for international peer-reviewed journals

* Organizational tasks in the research groups and collaborative research centre (10%)

Applicants' profiles

We are seeking a bright, highly motivated and creative student with - a PhD (for the Postdoc level) or university degree (for the PhD level) in a relevant discipline with specializations in one or more of the following fields: bioinformatics, transcriptomics/genomics, animal behaviour, behavioural ecology, behavioural physiology, evolutionary ecology, and/or veterinary science, - a keen interest in using molecular genetic methods to answer behavioural and life history questions, - experience with bioinformatic processing of high-throughput sequencing data or a keen interest in acquiring relevant skills (excellent training opportunities available), - experience with statistical analysis (preferably using R), - ability to work both independently and as part of a team, and - excellent oral and written communication skills in English.

The following qualifications would additionally be of advantage: - publications in peer-reviewed international journals, - experience with sperm phenotyping

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UCLouvain ArtificialEvolutionInDroplets

PhD in directed evolution of enzymes using microfluidics (fellowship from Marie Curie ITN EVOdrops)

The selected candidate will be granted with a prestigious Marie Curie ITN fellowship. This Innovative Training Network is called EVOdrops and is focused on the directed evolution of proteins in droplets (please see https://cordis.europa.eu/project/-rcn/218050/factsheet/en for a general presentation of the network).

The PhD will work at the Louvain Institute of Biomolecular Science and Technology in Louvain-la-Neuve at the UCLouvain and in the team of Prof. Patrice Soumillion. The objective of the research project is the development of a simplified darwinian process in microdroplets for the directed evolution of enzymes. The central idea is to couple the activity of a given enzyme to the replication of its gene. Monodisperse droplets generated by microfluidics will be used as small reactors for in vitro transcription and translation of enzyme encoding genes. Droplets that contain active enzyme will accumulate the product of catalysis that will be necessary for the replication of the gene. In that way, the genes encoding the most active enzymes within a combinatorial library will be selectively enriched in a darwinian process but without the need of any living cell.

For previous work, see:

G. Woronoff et al., Anal. Chem., 2011, 15, 2852-7

G. Woronoff et al., ChemBioChem 2015, 15, 1343-9

Selected candidate will benefit from networking with top-rated european teams in microfluidics and enzyme engineering and from excellent doctoral training at the UCLouvain (participation to workshops, advanced courses, conferences...).

Candidate must have a Master degree or equivalent with mention. Experimental skills in molecular biology and protein biochemistry are required. Skills in enzymology and/or microfluidic technology is an additional asset. Candidates must also be willing to work in an interdisciplinary project requiring collaborations with other researchers (such as engineers). The project will also involve international mobility for performing experiments or participating to training workshops within the Marie Curie network consortium.

Candidates can apply by sending a CV and motivation letter to patrice.soumillion@uclouvain.be

Belgian fellow cannot apply.

Patrice Soumillion <patrice.soumillion@uclouvain.be>

UFribourg 2 SocialImmunity

A 4-year PhD position is available in the research group of Professor Nathalie Stroeymeyt in the Department of Biology, University of Fribourg, to study the effect of group composition on disease transmission and relative investment in personal vs. social immunity in ants. BACKGROUND*/. /*Group living offers favourable conditions for the spread of infectious diseases, because high population densities and frequent social contacts facilitate pathogen transmission. To mitigate that risk, social animals have evolved a variety of defence mechanisms to prevent the entry and propagation of pathogens within the group, ranging from a raised investment in personal immunity to highly coordinated collective sanitary actions ('social immunity'). Recent studies have shown that social groups can also adopt organizational features, such as the subdivision into well-separated subgroups, which reduce epidemic risk through transmission bottleneck effects. However, the importance of organizational immunity features in disease risk management by real animal groups is still poorly understood. Our research adopts an empirical approach based on the experimental manipulations of garden ant colonies (/Lasius niger/) to (i) quantify the effect of social organization on disease transmission and test key predictions from network epidemiology, and (ii) evaluate the relative of importance of personal immunity, collective sanitary actions and organizational features under different environmental conditions and at different stages of development (for more detail see https://stroeymeyt-lab.ch/research). PROJECT. The goal of this PhD project will be to investigate how group composition (in particular colony size) influences the social network topology of ant colonies, and how this in turn affects disease transmission risk and the need for individuals to invest in personal immunity. The project will rely on automated behavioural tracking, social network analysis, simulation of disease transmission, monitoring of the transmission of pathogenic and non-pathogenic agents, fitness measurements, physiological assays and immune gene expression analysis. Among others, the project will address general hypotheses about the effect of group size on social organisation ('size-complexity' hypothesis) and immune investment ('density-dependent prophylaxis').//The project will be embedded within an overall project team consisting of two PhD students and two post-doctoral researchers (https://stroeymeyt-lab.ch/open-positions/) and will be fully funded for four years by an ERC Starting Grant. The salary will be set according to the guidelines of the University of Fribourg (c. 47'000 CHF per year). //PROFILE. We are looking for candidates with experience in quantitative behavioural analysis and programming, a good working knowledge in statistics and experimental design, and a willingness to apply a variety of approaches (behavioural tracking, writing own code to analyse the data, and lab work). Experience with social insects, insect immunity and/or molecular biology would be a plus. Candidates must be creative, motivated and passionate about science, have excellent oral and written communication skills, and be at ease working both independently and as part of a team. A Master's degree (or equivalent) will be required prior to taking up the position. LOCATION. The Department of Biology at the University of Fribourg is a highly dynamic, —international and interdisciplinary —environment, spanning a wide range of —research in evolution and ecology, behaviour, population genomics, and bioinformatics, —developmental genetics, neurobiology, biochemistry and proteomics, across 27 —groups (_https://www3.unifr.ch/bio/en/_). STARTING DATE. The starting date is flexible; the earliest possible start will be May 1^st , 2019. HOW TO APPLY. Please send your application by email to Nathalie.Stroeymeyt@gmail.com. Your application should consist of a single merged pdf file including a letter of motivation, a full CV and publication list, the names and contact details of at least two referees, and copies of your publications and/or your MSc thesis (if available). Evaluation of candidates will begin on February 15th, 2019, and continue until the position is filled.

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A 4-year PhD position is available in the research group of Professor Nathalie Stroeymeyt in the Department of Biology, University of Fribourg, to study the effect of prolonged pathogen pressure on long-term investment in personal and social immunity in ants. BACKGROUND*/. /*Group living offers favourable conditions for the spread of infectious diseases, because high population densities and frequent

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UFribourg EvoSociallyExchangedFluids

2 PhD positions in integrative biology LeBoeuf Lab, Dept of Biology, University of Fribourg, Switzerland

How do you build a social circulatory system? Our lab takes an integrative approach to understanding how socially exchanged fluids evolve and how they can be co-opted by evolution to influence physiology and behavior.

We use social insects as a model system because many (but not all!) social insects engage in the mouth-to-mouth fluid exchange behavior, trophallaxis. In species that do engage in this behavior, every individual in the colony is connected through this network of fluid exchange. The exchanged fluid is rich with proteins, hormones, RNA and small molecules (LeBoeuf et al. 2016 eLife). Some of these components, when fed to larvae by trophallaxis, can influence development! This provides a means for how some social insect communities can collectively decide on the colonys developmental progression V by sending cues and signals over the social circulatory system.

PhD position: Evolution of social fluids Involving ample travel and international collaborations, this project will combine fieldwork, proteomics and bioinformatic, orthology and phylogenetic methods to understand how trophallaxis behavior, its concomitant social fluid, and the proteins found within it have evolved their roles in the colonys social circulatory system.

You The ideal candidate is collaborative, hard-working and passionate about evolution and behavior, with experience in coding/bioinformatics. A masters degree (or equivalent) is required prior to taking up the position.

PhD position: Collective control of development in social insects This project will combine fluorescence microscopy, quantitative video tracking of animal behavior, developmental biology, social networks, and machine learning to better understand how social insects crowdsource control of the colonys development using the social circulatory system.

You The ideal candidate is collaborative, hard-working and passionate about how social/biological systems can self-regulate. Ideally you have experience coding and have some maker/DIY skills. Image processing (e.g. opencv) and/or machine learning experience are a plus. A masters degree (or equivalent) is required prior to taking up the position.

Lab values Creativity, interdisciplinarity, collaboration, open source, open access, inclusiveness, team mentality.

Positions Start dates are flexible, maximum 4 years (3.5 fully-funded). These positions are funded by the Swiss National Science Foundation (salary matches guidelines, 47K CHF/yr).

Submission Applications (in English) should include a cover letter (on your background and motivation), CV, and the names and contact details of two references. Applications should be sent as a single pdf to adrialeboeuf AT gmail DOT com. DEADLINE: February 15th, 2019. Applications will be reviewed until position is filled.

Dr. Adria C. LeBoeuf (http://leboeuflab.com) Department of Biology - Ecology and Evolution, University of Fribourg

Adria <adria.exists@gmail.com>

UGlasgow UEdinburgh AnthraxGenomicEpidemiology

"Leveraging pathogen genomics and phylodynamics to control endemic anthrax"

We are seeking applicants for a 4-year PhD position in One Health and genomic epidemiology, jointly supervised by investigators at the University of Glasgow and the University of Edinburgh.

Recent advances in sequencing technology have revolutionised our ability to track infectious disease dynamics using pathogen genomes, such as during outbreak investigations. However, these tools remain underutilised for addressing endemic disease threats, especially those affecting human and animal health in low-resource settings.

Anthrax is a classic example of a neglected bacterial zoonosis, affecting marginalised communities in many parts of the global south, including much of Sub-Saharan Africa. It causes significant mortality in people as well as livestock losses, but tends to be undiagnosed and underreported. Although vaccination of livestock plays a key role in preventing infection in both people and animals, it is often not affordable. Moreover, because the spores of the anthrax bacterium Bacillus anthracis can remain infectious within the environment for decades, it is not clear how long livestock vaccination would have to be maintained before a measurable reduction in infection risk is achieved. Obtaining genome data from detected cases, and incorporating genomic and epidemiological data into phylodynamic models provides a novel and powerful means to track residual anthrax transmission and to quantify progress towards elimination.

This project aims to create the necessary framework for guiding anthrax control programmes in endemic settings through the use of pathogen genomics and phylodynamic modelling. Building on robust partnerships and research platforms established in northern Tanzania by the Glasgow supervisors, including existing genomic data, our project will:

1) Extend current analytical tools and molecular clock models to accommodate the alternation between extended environmental persistence and periodic rapid replication typical for B. anthracis

2) Develop a simulation model combining genomic, spatial, temporal and epidemiological information to examine the effect of vaccination on B. anthracis genetic diversity and transmission in silico

3) Validate this model by generating genomic data obtained during a livestock vaccination program expected to start in the study area in 2019.

The project will be jointly supervised by Dr Samantha Lycett (Roslin Institute, University of Edinburgh) and Drs Roman Biek, Tiziana Lembo, and Taya Forde (University of Glasgow). The wide range of skills and expertise represented by the interdisciplinary supervisor team will provide excellent training opportunities for the student at the interface of microbial evolution and genomics, epidemiological modelling, and human/animal health.

Applicants will have a first or upper second class degree in a relevant scientific discipline (e.g. evolutionary biology, bioinformatics, epidemiology, computer science). A strong quantitative background, including demonstrable skills in computer programming and statistics, will be essential. Prior experience in mathematical modelling and molecular evolution will be considered an advantage.

Open to home, EU and international students. However, the tuition fee waiver will only cover Home/EU rates so international applicants from outside the UK/EU would need to have additional funding to make up the difference in tuition. The 4-year stipends will represent UKRI rates (estimated to be in the region of £15,000 for 2019/20).

This project is one of twelve One Health projects currently advertised by the Universities of Glasgow and Edinburgh. For more information on how to apply see

https://www.ed.ac.uk/studying/postgraduate/-applying/research/phds/edinburgh-glasgow-joint-phd-studentships/one-health Application deadline: 5.00pm, Monday 21 January 2019

For informal inquiries, please contact Roman Biek (roman.biek@glasgow.ac.uk).

Roman.Biek@glasgow.ac.uk

UGothenburg Speciation

PhD studentship in evolutionary genetics of speciation.

Department of Marine Science, University of Gothenburg.

Working with Roger Butlin, Kerstin Johannesson, Rui Faria and Marina Rafajlovic

At the Marine Science department there is a long tradition in working with marine snails of the genus Littorina as models for studies of local adaptation, hybrid zones and speciation. This studentship will be embedded in a larger project that focuses on ecotype formation and the subsequent evolution of barriers to gene exchange in L. saxatilis. This species forms multiple ecotypes but we concentrate on contrasting adaptations to crab predation and wave action that occur in many parts of its North Atlantic distribution, particularly comparing Spanish and Swedish contact zones. Recently, we have discovered multiple polymorphic chromosomal inversions that appear to contribute to ecotype formation but which may also experience balancing selection. The studentship will focus on understanding the origin and evolution of these inversions and particularly the way in which they contribute to the parallel formation of distinct ecotypes in many parts of the species range.

For more information and to apply, see:

https://www.gu.se/english/about_the_university/job-opportunities PhD student (48 months): ref. PAR 2019/51

Or email Roger Butlin on r.k.butlin@shef.ac.uk

– Roger Butlin

Professor of Evolutionary Biology Animal and Plant Sciences The University of Sheffield

Guest Professor Marine Sciences University of Gothenburg

r.k.butlin@shef.ac.uk

Roger Butlin <r.k.butlin@sheffield.ac.uk>

UGroningen BehaviourEvoDevo

*heading: *UGroningen.EcoEvoDevoAnimalPersonality

Fully funded 4-year PhD position on the eco-evo-devo of social personalities

We are looking for a talented and enthusiastic evolutionary or behavioural ecologist for a fully funded 4-year PhD position. The successful applicant will work on a multidisciplinary project aimed at understanding the emergence of social personalities, using an integrative approach which considers the interplay of ecology, evolution, and development. To this end, the PhD candidate will work with researchers from three different groups: Dr. Marion Nicolaus (Animal Ecology), Prof. Franjo Weissing (Theoretical Biology) and Prof. Ton Groothuis (Animal Behaviour), which are all embedded within the Groningen Institute for Evolutionary Life Sciences (GELIFES).

Description In most animals, individuals differ systematically in social competences and behaviour. The existence of such social personalities is intriguing both from an eco-evolutionary perspective (when does the local environment select for diversification in social behaviour?) and from a mechanistic perspective (how do personality differences emerge in individual development?). Using an integrative eco-evo-devo framework, the successful applicant will address three questions: How do the ecological conditions at different life stages lead to the development of social personalities (eco-devo)? How does the interplay of environment-dependent selection and developmental mechanisms affect the stability of social personalities (evo-devo)? What are the eco-evolutionary consequences of mechanisms like social niche choice or social niche construction (eco-evo)? These questions will be addressed by studies on three-spined sticklebacks (Gasterosteus aculeatus), both in the field and in a semi-natural environment (replicate series of ponds connected by corridors allowing dispersal and habitat choice). The empirical research will be complemented by theoretical modelling to derive testable predictions and to provide a framework for interpreting the empirical results. The PhD candidate will receive varied and cutting-edge research training, with ample opportunities for following advanced courses, workshops and conferences, complemented by training in transferable skills and teaching. The successful applicant is committed to conduct independent and original scientific research, to report on this research in international publications and presentations, and to present the results of the research in a PhD dissertation, to be completed within 4 years. PhD candidates are expected to contribute 10% of their overall workload to teaching.

Qualifications The ideal candidate is highly motivated, hardworking, ambitious, creative, and has affinity with empirical behavioural ecology research and with theoretical modelling. The successful candidate will have the following required qualifications: an MSc degree with specialization in biology (ecology, evolution and/or animal behaviour) or related disciplines; the ability to work independently and in a team; excellent command of the English language; excellent communication and presentation skills, both in word and in writing. Preferentially, the successful candidate has some experience with modelling and knowledge of a programming language (R, C++).

Conditions of employment The University of Groningen offers a salary of 2,266 gross per month in the first year to a maximum of 2,897 gross per month in the final year (salary scale Dutch Universities), based on a fulltime position (1.0 fte) excluding a 8% holiday allowance and a 8.3% end of the year bonus. The position offered is for four years. For more details see https://www.rug.nl/about-us/work-with-us/job-opportunities/overview?detailsThe preferred starting date is *15 April 2019*

Application Application for this position is open until 15 March 2019. To apply, please fill in the online application form (click on the Apply button below the advertisement on this link: https://www.rug.nl/about-us/work-with-us/job-opportunities/overview?details).

Applications for the position should include (as a single PDF file): a cover letter explaining the educational background of the candidate and the motivation to apply for this position; a detailed description of previous research experience, such as obtained in bachelor/master research projects (1-2 pages); a comprehensive curriculum vitae, providing details on bachelor and master degrees, work experience, and a publication list (if applicable); academic transcripts; contact details of two or (preferably) three academic references who can provide information on the candidates suitability for the position.

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UGroningen EvolPhilos

4-year PhD position at the University of Groningen, the Netherlands

Interdisciplinary PhD scholarship in biology and philosophy

Recent developments in molecular genetics and developmental biology have inspired a re-evaluation of the legacy of Jean-Baptiste de Lamarck. In this project, we aim to explore the Lamarckian nature of recent discoveries in the transmission of inherited traits and the evolution of organismal complexity. In this way, we aim to establish what modern biology can or cannot learn from the original ideas of Lamarck, and whether or not his works offer lessons that change the way we think about evolution.

This project brings together the disciplines of evolutionary biology and the history and philosophy of science. It combines theoretical studies (historical analysis of the writings of Lamarck and his contemporaries; insights from modern studies) with experimental work (using nematodes as a model system to test Lamarcks ideas). The project is a collaboration between Dr. Martine Maan (www.rug.nl/staff/m.e.maan) and Dr. Han Thomas Adriaenssen (www.rug.nl/staff/h.t.adriaenssen). Funded by the Young Academy of Groningen.

Qualifications: The ideal candidate has a background in both biology and the history and philosophy of science, a strong interest in evolutionary biology, and hands-on laboratory experience.

"m.e.maan@rug.nl" <m.e.maan@rug.nl>

UHelsinki SalmonEvolution

A PhD student position, is available at the University of Helsinki, Finland to work in Prof. Craig Primmer's research group (http://www.helsinki.fi/evolution-conservation-and-genomics). The position is a part of a 5-year ERC-funded research program aimed at understanding the molecular and ecological basis of sea-age at maturity in Atlantic salmon, and the consequences for adaptation (e.g. Barson et al. 2015; Czorlich et al. 2018). Funding is available for up to 4 years.

The PhD student will (depending on the interests and experience of the successful candidate) conduct behavioural, physiological and/ or quantitative genetic research on the research group's common garden salmon stocks to identify phenotypic trait variation linked with sea-age at maturity and the gene(s) controlling this trait, as well as investigate the potential influence of environmental factors (GxE).

The salmon stocks that will be the focus of this project are already established and are housed in recently built indoor facilities at the Lammi Biological Station (130km north of Helsinki) and the student will be required to regularly spend time at this facility. The group also employees several research technicians to assist with salmon stock maintenance.

Skills seen as advantageous for the position include: previous experience in behavioural and/or physiological experimentation, preferably in fishes; experience in quantitative genetic analyses and/or statistical analysis of evolutionary ecological data in any species, preferably in R; experience with fish husbandry; an interest in evolutionary genetics; ability to cooperate with a multi-cultural team of researchers working on related projects.

The position is available immediately, and the preferred starting date is March 15 2019, or earlier. The salary will be based on level 2 of the demands level chart for teaching and research personnel in the salary system of Finnish universities. In addition, the appointee will be paid a salary component based on personal performance with the overall starting salary amount being about 2200 EUR per month. A six-month trial period will be applied.

Please submit your application using the University of Helsinki Recruitment System via the link

Apply for the position. https://www.helsinki.fi/en/-open-positions/doctoral-student-in-salmon-behavior-physiology-genetics The deadline for applications is Sunday 10 February 2019.

Informal inquiries should be directed to Prof. Craig Primmer (craig.primmer(at)helsinki.fi).

Finland is a member of the EU, has high quality free schooling (also in English), generous family benefits and healthcare, and was recently ranked as the happiest country in the world. The University of Helsinki is a top 100 ranked university in most ranking lists, and is currently investing heavily in life sciences research (see https://www.helsinki.fi/en/helsinki-institute-of-life-science).

Relevant articles: Barson et al. (2015) Sex-dependent dominance at a single locus maintains variation in age at maturity in salmon. Nature 528:405-408.

Czorlich, Y., Aykanat, T., Erkinaro, J., Orell, P., & Primmer, C. R. (2018). Rapid sex-specific evolution of age at maturity is shaped by genetic architecture in Atlantic salmon. Nature Ecology and Evolution, 2, 1800-1807.

Pritchard, V. L., Mäkinen, H., Vähä, J. P., Erkinaro, J., Orell, P., & Primmer, C. R. (2018). Genomic signatures of fine-scale local selection in Atlantic salmon suggest involvement of sexual maturation, energy homeostasis and immune defence-related genes. Molecular Ecology, 27, 2560-2575.

Craig Primmer, Academy Professor PO Box 56 Organismal & Evolutionary Biology Research Program | Biotechnology Institute 00014, University of Helsinki, FINLAND Visiting: Room 3404, Biocenter 1C Mobile +358 503116374 craig.primmer@helsinki.fi Twitter @FishConGen http://www.helsinki.fi/-evolution-conservation-and-genomics "Primmer, Craig" <craig.primmer@helsinki.fi>

UHolar Iceland 2 SticklebackEvoDevo

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

Hólar University College, Iceland, seeks two PhD students for a Grant of Excellence (RANNIS) project to study the dynamics of *Ecological (ECO), Evolutionary (EVO) and Developmental (DEVO) processes* The phenotype, including developmental plasticity, is an important determinant of the dynamic interactions between ecological and evolutionary processes (eco-evolutionary dynamics) and the processes that shape biological diversity in face of global change. This project will study the interplay among ECO, EVO and DEVO to fill knowledge gaps in 1) the dual role of ecology in evolution (as driver of natural selection and phenotypic plasticity), 2) the molecular mechanisms underlying phenotypic variation, and 3) the feedbacks between phenotypic change and ecosystem function. The project takes a spatio-temporal perspective, using threespine stickleback (*Gasterosteus aculeatus*) from lake Mývatn, Iceland, as a model. The project is lead by Prof. Bjarni K. Kristjánsson (lead PI, Hólar University College, Iceland) and Dr. Katja Räsänen (Swiss Federal Institute of Aquatic Sciences, Eawag, Switzerland). It is part of a large collaboration across Hólar Univ. College (Prof. Skúli Skúlason), Eawag (Dr. Blake Matthews), Univ. of Wisconsin-Madison, USA (Prof. Anthony R. Ives), Univ. of Iceland (Prof. Zophonías O. Jónsson) and the Mývatn research station (Dr. Árni Einarsson). The students will have the opportunity to conduct part of their research at the collaborative institutions.

The two PhD projects will *focus on i) the determinants of phenotypic variation and ii) consequences of phenotypic and genetic variation for ecosystem processes. *Which of these aspects each student specifically focuses on will depend on their interests as well as expertise (to be stated in application, see below). These PhD student projects are an integral part of our integrative study that includes long-term field data, laboratory, mesocosm and field experiments, genomics and mathematical modelling.

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

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

The working language is English. The students have to be able to work independently as well as a part of a team. A valid driving license is a requirement.

Applicants should send an application letter, with a statement of research interests (and favoured topic of PhD) and relevant experience (max. 2 pages), curriculum vitae with a list of publications, copies of academic qualifications and the names and e-mail addresses of three referees, *as a single pdf* to ecoevodevo@holar.is latest *March 15, 201*9. *Preferred starting date is May 1st 2019.*

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

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

Bjarni Kristófer Kristjánsson <bjakk@holar.is>

UIdaho RedbandTrout

GRADUATE STUDENT POSITION ECOLOGICAL GENOMICS AND MODELING OF REDBAND TROUT UNIVERSITY OF IDAHO NSF-EPSCoR GEM3

We seek a highly motivated student for a Ph.D. position at the University of Idaho in the recently funded NSF-EPSCoR GEM3 program (https://www.idahogem3.org). The program seeks to understand how genetic diversity and phenotypic plasticity affect species response to environmental change, shaping both population response and adaptive capacity. The program is focused primarily on two taxa: redband trout, a subspecies of rainbow trout, and sagebrush. These taxa are integral to aquatic and terrestrial ecosystems across the American West and are central to land-use management decisions that drive the economy of the region. This advertised Ph.D. position is focused on redband trout.

The Ph.D. student will join an interdisciplinary cohort of postdoctoral researchers and students working at scales from genomic characterization of physiological traits in trout and sagebrush, to mapping and modeling of complex ecological, evolutionary, and social-economic systems. The Ph.D. student will have the opportunity to gain skills such as molecular population genomics, landscape genetics analysis, and agent-based and systems modeling.

The position is available to start in fall 2019 and will be co-advised by Lisette Waits (Fish & Wildlife Sciences) and Paul Hohenlohe (Biological Sciences). Students in the GEM3 program may choose from several degree programs at UI, including Natural Resources, Bioinformatics and Computational Biology, Environmental Science or Biology.

To apply, please submit a letter of interest, curriculum vitae, GRE scores, and contact information for three references to Paul Hohenlohe (hohenlohe@uidaho.edu). Review of applications will begin immediately; for full consideration please apply before February 22, 2019.

Paul Hohenlohe Associate Professor Institute for Bioinformatics and Evolutionary Studies Departments of Biological Sciences and Statistics University of Idaho http://hohenlohelab.github.io "Hohenlohe, Paul (hohenlohe@uidaho.edu)" <hohenlohe@uidaho.edu>

UKassel Germany EvolutionAntPlants

Dear all, I am looking for a highly motivated PhD student to participate in our project "Spatial-temporal evolution of Macaranga ant-plant lineages (Euphorbiaceae) in Southeast Asia". This is a fixed term-position for three years (part-time, 65 % of a full-time employee), funded by the German Research Foundation (DFG).

Project description: In this project, we will use next generation sequencing technology (genotyping-by-sequencing, GBS) to resolve phylogenetic relationships among and within myrmecophytic lineages of the Southeast Asian ant-plant genus Macaranga. While many Macaranga species facultatively attract ants, about 30 species from western Malesia (comprising Borneo, Sumatra, and the Malay Peninsula, collectively Sundaland) live in obligate symbiosis with nine species of Crematogaster ants. Based on GBS-derived analysis (sample material is already available), we will reconstruct the temporal-spatial evolution of myrmecophytism in the group and will elucidate when, where and under which circumstances morphological traits associated with myrmecophytism have been gained (and lost). Further, we will test the hypothesis that myrmecophytism enhanced diversification and speciation in Macaranga. In the second part of the project, general aspects of Sundaland biogeography will be addressed by a comparative phylogeographic approach including five widely distributed species with different ecological requirements and different associations to ants. We specifically aim to understand how past climatic and geographic settings in Sundaland influenced the population structure and gene flow patterns of western Malesian Macaranga.

Requirements: Successful candidates will have a Masters degree or equivalent in biology / molecular systematics / evolutionary biology or a related field, good knowledge/experience in molecular systematics, and an interest in tropical ecosystems. Candidates with strong interest (ideally with prior experience) in bioinformatics and next-generation sequencing analysis are highly desirable. The ideal candidate will have very good oral and written communication skills in English. Knowledge of German language would be an advantage, but is not obligatory.

For further information please contact Dr. Daniela Guicking, E-Mail: guicking@uni-kassel.de. Applications should include a cover letter describing the motivation, previous research activities and current research interests, the CV with copies of BSc and MSc certificates, and a list of publications if applicable.

To apply please visit: https://www.uni-kassel.de/uni/universitaet/stellenangebote/stellenangebot/post/detail/News/research-assistant-mfd-salary-level-eg-13-tv-h-systematics-and-morphology-of-plants/ Deadline is 2019-02-15.

Dr. Daniela Guicking University of Kassel FB 10, Faculty of Mathematics and Natural Sciences, Biology, Systematics and Morphology of Plants Heinrich-Plett-Str. 40 34132 Kassel, Germany

Tel: 0049-(0)561-8044170 Email: guicking@uni-kassel.de

"Guicking, Daniela, Dr." <guicking@uni-kassel.de>

UKiel MeioticDrive

*PhD position - meiotic drive of supernumerary chromosomes *

A PhD position is available for three years to study the *meiotic drive of supernumerary chromosomes *with the Max Planck research group "Environmental Genomics" headed by Prof. Dr. Eva H. Stukenbrock. The Max Planck group is affiliated with the *Max Planck Institute for Evolutionary Biology* in Plön and the *Christian-Albrechts University of Kiel* in the North of Germany. The position is compensated at 65% of TV-L 13 and candidates are expected to complete a PhD.

*Background***

Selfish genetic elements are widespread in all groups of organisms. They are likely to have shaped the evolution of diverse biological systems, including genome structure, sex determination, and meiosis. To date, surprisingly little is known about the exact processes that underlie the spread of these elements. This project focuses on selfish genetic elements that cause uniparental meiotic drive of supernumerary chromosomes in a fungal pathogen.

Recently we could show that the supernumerary chromosome of the commercially important wheat pathogen /Zymoseptoria tritici/ show a chromosome drive, i.e. are inherited to more progeny than expected by Mendelian segregation, and these chromosomes may therefore be considered selfish genetic elements. Interestingly this chromosome drive is restricted to chromosomes inherited from the female parent. We hypothesize that this drive is based on an additional amplification of unpaired chromosomes during meiosis. This project aims at understanding this previously unknown aspect of meiosis and its exploitation by selfish chromosomes using the model organism /Z. tritici/.It will involve the establishment of in vitro crosses and the identification of the genetic and epigentic traits responsible for the chromosome amplification.

Expectations and Requirements:

The candidate must have university degree (Master or equivalent) in biology or a related field. High competence in statistics, experimental design, and English writing is a must. Ideally, the candidate has comprehensive experience in molecular genetics, work with plant pathogens or performance of evolution experiments. The selected candidate will have the opportunity to collaborate in an interdisciplinary team of biologists (molecular biologists, evolutionary biologists and population geneticists) as well as to pursue unique research in the field of chromosome biology.

Kiel University aims at a higher proportion of women in research and education, and, therefore, specifically encourages qualified female scientists to apply. Female scientists will be preferentially considered in case of equivalent qualification, competence and achievements.

Kiel University specifically supports employment of severely handicapped people. Therefore, severely handicapped applicants will be preferentially considered in case of suitable qualification.

Kiel University specifically welcomes application from people with migration background.

Application

Applications should include a motivation letter (max. 2 pages long), CV, publication list, names and contact details of two referees (who are familiar with the applicant's work), and copies of certificates. Deadline for applications is 15. February 2019. Applications should be sent to:

Prof. Dr. Eva Stukenbrock, Botanisches Institut, Christian-Albrechts-Universität zu Kiel, Olshausenstr. 40, 24118 Kiel

or _preferentially as a single-PDF-document_ by e-mail to: office@bot.uni-kiel.de

We explicitly do not require application photos and therefore these shall be omitted.

Further information can be obtained from Prof. Dr. Eva Stukenbrock (estukenbrock@bot.uni-kiel.de). Please also check: http://web.evolbio.mpg.de/envgen/ Michael Habig <mhabig@bot.uni-kiel.de>

ULeicester DiseaseVariants

Applications for two PhD positions in Genetic Epidemiology at University of Leicester are now open! Informal enquiries to Dr Chiara Batini (cb334@le.ac.uk) and/or Prof Martin Tobin (martin.tobin@leicester.ac.uk) are welcome.

1. "Harnessing large-scale genomic sequencing data to understand smoking behaviour" supervised by Dr Chiara Batini and Prof Martin Tobin

In 2018 it has been announced that both whole exome sequences and whole genome sequences will be analysed in the 500K individuals in UK Biobank over the next two to five years. Recently the UK Secretary of State for Health and Social Care has launched the plan of the NHS to sequence up to 5M genomes over the next few years highlighting the importance of genomics in the future of medical care. Smoking is one of the leading risk factors of the top five causes of death worldwide, including heart and respiratory diseases, killing around 6 million people a year. The number of smokers varies among world regions, and of the 1 billion smokers worldwide, 80% live in low and middle-income countries. Genome-wide association studies have identified up to 14 loci associated with smoking behaviour, including genes for nicotine receptors, nicotine-metabolizing enzymes and proteins involved in neurotransmission. However, no study so far has used sequencing data to investigate the full genomic architecture of smoking behaviour. This project will aim at (i) understanding the contribution of rare variants to the genetics of smoking, with a special focus on nicotine dependence and smoking cessation; and (ii) fine-mapping causal variants in newly-discovered and previously described genetic loci associated with smoking phenotypes. Potential extensions, depending on skill development and progress, include (i) harnessing primary care data to derive nicotine dependence variables; (ii) extending this approach to other substance use disorders; (iii) evaluating the impact of ascertainment bias in GWAS of non-European populations by analysing sequencing data in non-European individuals living in the UK. You will join the Genetic Epidemiology Group, led by Prof. Tobin, which comprises 27 staff and students and has hosted award-winning PhD students and externally funded early career fellows. You will be expected to participate in the regular meetings of the group, departmental seminars, training courses and conferences relevant to human genomics in the UK and abroad to present your work and discuss it with collaborators.

For more information, see https://www.findaphd.com/phds/project/harnessing-large-scale-genomic-sequencing-data-to-understand-smoking-behaviour/?p104782 2. "Genetic variants associated with multiple diseases" supervised by Prof Martin Tobin and Dr Nick Shrine

As increasing numbers of genetic associations are discovered, it is becoming clear that some genetic variants are associated with more than one or human phenotype (including disease phenotypes). For example, the supervisory team has recently discovered genetic variants associated with respiratory disease and inflammatory diseases (Shrine et al, Nature Genetics in press). These associations have important implications for the development of treatments. Since genetic variants can mimic the effect of drugs, such associations help us to understand opportunities to repurpose drugs (to treat diseases other than their initial use). When in opposite directions, such associations can provide warnings about potential side-effects of drugs. Furthermore, variants associated with more than one disease can help us to understand the causes of development of multimorbidity to inform more effective prevention and management. You will join the Genetic Epidemiology Group, led by Prof. Martin Tobin. The group comprises 27 staff and students and has hosted award-winning PhD students and externally funded early career fellows. You will have an opportunity to learn techniques for genome-wide association studies and phenome-wide association studies, analyse linked healthcare data alongside study-collected data and contribute to new discoveries informing future drug development. You will be expected to attend internal and external training opportunities, conferences and meetings to develop statistical genetic and broader academic skills that underpin subsequent postdoctoral career development.

For more information, see https://www.findaphd.com/phds/project/genetic-variants-associated-with-multiple-diseases/?p104780 "Batini, Chiara (Dr.)" <cb334@leicester.ac.uk>

UMaine WildlifeDiseaseGenomics

* Please NOTE: the deadline for this position has been extended to January 18th, 2019.

Ph.D. Assistantship in Wildlife Disease Genomics

A graduate student position is available in the Kamath Lab (https://kamathlab.weebly.com/) at the University of Maine, starting in 2019 (Summer or Fall semester). The student will join a NSF-funded project on the evolution and transmission of Bacillus anthracis, the causative agent of anthrax, in collaboration with Drs. Wendy Turner at the University at Albany (www.wendyturner.org) and Henriette van Heerden at the University of Pretoria (https://www.up.ac.za/veterinary-tropical-diseases/article/1945572/h-van-heerden). The Ph.D. research project will focus on host-pathogen evolutionary dynamics and the genetic basis for heterogeneity in susceptibility to the B. anthracis bacteria in ungulate hosts of Etosha National Park, Namibia, and Kruger National Park, South Africa. This position will involve interdisciplinary research with strong field, laboratory and analytical components. Data collection will require international fieldwork.

The graduate student will also have the unique opportunity to be part of the interdisciplinary Center for One Health & the Environment (https://sbe.umaine.edu/school/center-for-one-health-the-environment/).

Location: University of Maine, Orono, ME

Salary: The student will be supported by a combination of research and teaching assistantships, which include a 12-month stipend ($21,333), tuition waiver, and 50% health insurance coverage.

Qualifications:

Required qualifications: Bachelor's degree in biology, ecology, evolution, epidemiology, microbiology, immunology, genetics, bioinformatics, or a related field. Candidates should have relevant research experience, be highly motivated, and have a demonstrated ability to work both independently and in a team.

Preferred qualifications: Master's degree in ecology, evolution, or a related field. Desired candidates will be accomplished in writing, statistics, molecular methods, population/ phylogenetic analyses, genomics, bioinformatics, and/or field skills.

To Apply/Questions: Interested qualified applicants should send a cover letter, current CV, unofficial transcripts, a publication or writing sample, and the names and contact information for three references to Dr. Pauline Kamath at pauline.kamath@maine.edu. The cover letter should describe interest in the project and in graduate study, relevant coursework, research experience, and other qualifications. Letters of reference may be requested for finalists.

Review of applications will begin on December 20th and will continue until the position is filled.

The University of Maine is an EEO/AA employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, sexual orientation, age, disability, protected veteran status, or any other characteristic protected by law.

– Pauline L. Kamath, Ph.D. Assistant Professor of Animal Health Animal and Veterinary Sciences School of Food & Agriculture 5735 Hitchner Hall, Rm 342 University of Maine Orono, ME 04469-5735 Phone: +1 207-581-2935 Email: pauline.kamath@maine.edu Website: https://umaine.edu/foodandagriculture/kamath2/ pauline.kamath@maine.edu

UManitoba SeaLampreyPopGenetics

Funded MSc position (2 years) Department of Biological Sciences, University of Manitoba

Assessing the population genetic structure of resident freshwater and western Atlantic sea lamprey populations

We are recruiting an MSc student to explore the spatial genetic structure of native western Atlantic and resident freshwater sea lamprey populations from within the Great Lakes, the Finger Lakes, and Lake Champlain. Our aim is to sample ~30 sea lamprey from ~20 Atlantic and freshwater sites and use genotyping-by-sequencing to genotype individuals for this work. The results of this analysis will contribute to our understanding of the sea lamprey invasion of the Great Lakes system and the management of those invasive populations. There will also be the opportunity to develop your own additional research questions using these and other available data.

The successful applicant should have an honours undergraduate degree and an interest in population genetics and species management. Experience with population genetic data analyses will be considered an asset but is not required, we can train you in the necessary skills. You will work closely with a postdoctoral fellow working directly on this project and with a broader team of professors (Colin Garroway, Margaret Docker, and Ken Jeffries), postdocs, and graduate students using genomic and transcriptomic tools to address sea lamprey management questions at the University of Manitoba.

Please do not hesitate to get in touch if you have any additional questions. If you are interested in applying send Colin Garroway (colin.garroway@umanitoba.ca): 1) a copy of your CV; 2) a brief letter (no more than 1 page) introducing yourself and outlining your general research interests and your interest in this position in particular; 3) email addresses and phone numbers for two references. We will arrange Skype chats with the 3-5 best matched applicants. Our ideal start date is summer 2019 but we may be able to accommodate an autumn start. Finally, if you have made it this far, but are looking for a PhD position rather than an MSc, please still get in touch. We may be able to work something out for the right fit.

Contact:

Colin Garroway Assistant Professor Department of Biological Sciences University of Manitoba Winnipeg, Manitoba tel: (1) 204-4748267 www.garroway-lab.com Colin Garroway <Colin.Garroway@umanitoba.ca>

UNeuchatel ModellingMicrobialInteractions

PhD position on Modelling Microbial Interactions

I am looking to recruit a PhD student to work on mathematical modelling of microbial interactions, including bacteria growth in biofilms, bacteria dispersal through fungal hyphae networks, and bacteria-fungi interactions under different nutritional conditions, in the University of Neuchâtel, Switzerland. The student will be co-supervised by Prof. Redouan Bshary and/or Prof. Pilar Junier.

Bacteria are powerful in breaking down chemicals and thus have great potentials in treating polluted soils, but they cannot disperse in the soil without water, and this limits the applications of bioremediation of polluted soils. Recently, it is found that bacteria can disperse in the liquid layer on the surface of fungal hyphae. The fungal hyphae networks are like a 3D highway system that connects vast areas in the soil, providing potentially a very efficient way for bacteria to disperse. But unlike the highways we're familiar with, the fungal highways are living organisms and they interact with bacteria in complex ways. In the PhD project we will find out how bacteria spread through fungal hyphae networks, and whether the interactions between fungi and bacteria promote or impede the dispersal. In addition, we will study how nutrients influence the interactions between fungi and bacteria. Our pilot experiments have already shown that the nature of interactions between fungi and bacteria can change with the concentrations of nutrients. As fungi and bacteria involve in many different types of interactions, they can cooperate and compete at the same time, it is interesting to find out how a mixture of different types of nutrients affect the interactions between fungi and bacteria. Understanding the effects of nutrients can help us find ways to manipulate fungi-bacteria interactions in the way that we want.

The PhD project involves both experiments (20%) and modelling (80%). The successful applicant should have a Master's degree in mathematics, physics, biology, or another related field. A prerequisite is a keen interest in both mathematical modelling and understanding real biological systems. Good quantitative skills are essential.

Experience in mathematical modelling and knowledge of a programming language is an advantage. Experience in microbiology experiments is preferred but not required, since the lab skills required by the experiments are basic and can be learned quickly. The candidate needs to be fluent in English.

To apply, please send an email to < li[AT]evolbio.mpg.de >. Please include in your email a statement including 1) your research interests and career plan, 2) a brief overview of your previous academic and research experiences, and explain how your background fits with the project, 3) a CV or resume, and 4) a list of 2 to 3 academic references with their names and email addresses.

The position is funded by the Swiss National Science Foundation with a competitive salary for 4 years. The starting time should be September 2019 or earlier. Applications will be reviewed continuously until the position is filled.

For specific information about the project, please send me an email.

Xiang-Yi Li (PhD) Institute of Biology University of Neuchâtel Rue Emile-Argand 11 CH-2000 Neuchâtel Switzerland

li <AT>evolbio.mpg.de

Xiangyi Li <li@evolbio.mpg.de>

UNewOrleans EvolutionaryPhysiology

Graduate Student (PhD) Position Available

I am seeking motivated applicants to our Integrative Biology Ph.D. program to begin in the Summer or Fall of 2019. The successful applicant will be supported by a research fellowship in the broad area of aquatic conservation biology, with particular emphasis on the evolutionary and ecological physiology of hypoxia tolerance in estuarine fish (see Townley et al. 2017. AJP 312: R412-R425, doi: 10.1152/ajpregu.00402.2016 and Rees & Matute. 2018. PBZ 91: 1046-1056, doi: 10.1086/699596 for recent research). Applicants should have previous research experience in these or related areas and strong analytical skills. Interested students should contact:

Dr. Barney Rees Department of Biological Sciences University of New Orleans brees@uno.edu 504-280-6743

See http://www.uno.edu/cos/biology/index.aspx for information on the department, faculty, and application procedures. The deadline for applications is February 1, 2019.

Bernard B Rees <brees@uno.edu>

UNorthDakota AncientPaleoecology

U. North Dakota. Ancient paleoecology.

The Laboratory of Human and Forensic Genetics at the University of North Dakota (www.und.edu) is inviting applications from highly motivated students who pursue a PhD degree.

A student will be engaged in a project on computational analysis of big oral and environmental microbiome data collected from diverse organisms across the American Midwest, Eastern Europe, and Madagascar. This cross-disciplinary project represents an opportunity to get intensive hands-on training in the methods of ancient DNA analyses including next-generation sequencing, computational biology and statistical modelling.

Candidates should demonstrate motivation for hard laboratory work and strong interest in genomics and computational biology. Preference will be given to candidates with a proven record of computational analysis and bioinformatics skills. Additional experience in high-throughput sequencing technologies is a plus. If you are interested, you need to apply to the University of North Dakota Biology Graduate Program using the regular procedure. Requirements and How to Apply procedure can be found in the UND Biology Graduate School website:

https://und.edu/programs/biology-phd/-requirements.html The additional information can be also found in the Biology Department website:

https://arts-sciences.und.edu/academics/biology/ The position starts in August 2019. To receive full consideration, applications and required materials should be received by the Biology Graduate Program by February 15, 2019.

Potential graduate students are strongly encouraged to make contact with Dr. Igor Ovchinnikov.

Contact information:

Dr. Igor Ovchinnikov Associate Professor Lab. of Human and Forensic Genetics Department of Biology Forensic Science Program University of North Dakota

Email: igor.ovtchinnikov@und.edu

Thank you.

Igor Ovchinnikov

Dr. Igor Ovchinnikov Associate Professor Lab. of Human and Forensic Genetics Department of Biology Forensic Science Program University of North Dakota 10 Cornell Street Grand Forks, ND 58202 Phone (office): (701) 777-4471 Email: igor.ovtchinnikov@und.edu

"Ovtchinnikov, Igor" <igor.ovtchinnikov@und.edu>

UPuertoRico Mayaguez BruchidHostSpecificity

The University of Puerto Rico Mayaguez Invertebrate Collection (UPRM-INVCOL) is seeking a M.Sc. student to fill a two-year position to investigate differential gene expression in Bruchidae seed pests. This is a fully funded USDA project to investigate host specificity in beetles. Funds include tuition, stipend, and funding for research project described below that if completed will serve as your thesis for a M.Sc. degree at UPRM.

Bruchids are a high-priority global pest to food security, as they are a stored grain pest on many varieties of legumes. We will be testing differential gene expression of larval bruchids on two different varieties of beans. The project aims to identify which genes, if any, are upregulated in response to resistant and non-resistant varieties of beans. With that we can begin to investigate how these genes evolve in bruchids and the underlying mechanisms of host specificity. This will be the students primary project, but we have a number of other projects at INVCOL which the student may also be able to participate. These include Curculionoid genome assemblies, meta-barcoding of leaf litter insects, and various phylogenomics projects. Please visit the INVCOL webpage to find out more about our research.

https://www.uprm.edu/invcol/ INVCOL is looking for a highly motivated student with a background in next generation sequencing analyses. The ideal candidate would be adept at Linux and R, especially Bioconductor. A general background in Entomology would also be greatly preferred as this skill set will transfer well to other projects, but students with a background in Biology, or Engineering would also be considered. The candidate should have a B.S. or similar by July 2019. Candidates with a B.S. degree and Senior B.S. students are encouraged to apply.

The position will start July 1, 2019.

Candidates should send 2-page CV along with a one page essay on their interest in Entomology related research, with three letters of recommendation e-mailed to Dr. Van Dam from your letter or reference writer with ^{o}Letter of Reference for Your Name± in the heading of their e-mail.

Application process will close on January 31, 2019.

If you have further questions don't hesitate to contact Dr. Alex Van Dam, Director of INVCOL, via e-mail: alex.vandam@upr.edu

Mr. Alex Van Dam, Ph.D. Assistant Professor Director of the UPRM Invertebrate Collection

University of Puerto Rico Mayag'ez Department of Biology

PO Box 9000

Mayag'ez, PR 00681-9000

website:

https://www.uprm.edu/invcol/ Alex R Van Dam <alex.vandam@upr.edu>

USherbrooke TroutEvolutionaryEcol

MSc project: Stocking of brook trout

We are seeking to recruit a student at the MSc level to join our research team at the Département de biologie, Université de Sherbrooke, starting in May or September 2019.

Our research aims at quantifying the effects of changes in thermal regime during brook trout production on growth and survival of young life stages following stocking in the wild. The candidate will participate in study conducted in 2019-2021 and will contribute to fieldwork each spring/fall. The candidate should ideally have skills in handling fish and a good knowledge of statistical analyses and evolutionary ecology.

Interested candidates should send a CV and a cover letter, as well as contact information of two references before 16 February 2019 to:

Dany Garant : Dany.Garant@Usherbrooke.ca See also: labogarant.weebly.com for more details on our research team.

Dany Garant <Dany.Garant@USherbrooke.ca>

UTartu Estonia aDNA

Institute of Genomics, University of Tartu (Estonia) seeks for

PhD student in ancient DNA (Institute of Genomics, Estonian Biocentre), University of Tartu, Estonia

Supervisors: Dr. Kristiina Tambets, University of Tartu Dr. Toomas Kivisild, University of Tartu/KU Leuven

Deadline: February 5th 2019

Who we are: The Institute of Genomics of the University of Tartu was formed in 2018 through a merger of the Estonian Genome Center and the Estonian Biocentre, bringing together world class expertise in medical, population and evolutionary genomics. We host the Estonian Biobank (www.geenivaramu.ee) which has 150,000 participants and is connected to national health registries for phenotypic information. Starting in May 2018, we opened a brand-new ancient DNA laboratory, we have a core facility for DNA/RNA sequencing and genotyping and have access to a High-Performance Computing Cluster (www.hpc.ut.ee). We publish widely in top journals and sport a vibrant and international research community of 70 researchers and students.

Web page of our institute: https://www.geenivaramu.ee/en and of Estonian Biocentre: https://www.geenivaramu.ee/en/about-us/estonian-biocentre Position Description: We are looking for a motivated PhD student with a background in archaeology and/or genetics who is interested in completing their PhD program at the University of Tartu and in being part of the research group of ancient DNA.

PhD project focuses on the Medieval and Early Modern time (13th- 18th cc AD) demographic history of Estonia using ancient DNA as the primary source of information. The Medieval period started in Estonia much later than in Central Europe and Scandinavia, in the 13th century AD. The crusades and conquest brought along vast social, cultural and economic changes that were also likely to have shaped the genetic structure of the local population. The main aim of the project is to compare patterns of genetic diversity in Estonian rural and urban populations in a broader context of differences in Eastern Baltic. Comparisons across time transects will be enabled by the availability of aDNA data from deeper time layers as well as the data of the present-day population through the biobank of Estonian Genome Centre, University of Tartu. The knowledge from aDNA (population structuration, kinship studies, description of the presence and frequency of pathogens etc.) can be potentially combined with the data of individual and societal health status, which gives us clues also for the understanding of the history of present-day health problems in the region. The outcome of the project will be used for: 1) filling one of the remaining gaps in the synopsis of the population history of the Eastern Baltic region in Europe with an example of Estonia and 2) for opening new opportunities associated with the studies of health and diseases through the aDNA perspective.

Duties and responsibilities: PhD student will be carrying out research activity in the field of ancient DNA including but not limited to generation of aDNA data from archaeological samples to genomic library stage, analysis of whole genome data and writing publications.

Required qualifications: MSc in archaeogenetics, bioarchaeology, biological anthropology, genetics, molecular biology or related subjects. Having some knowledge and experience of working in a cleanroom and of ancient DNA wet lab protocols as well as having basic knowledge and experience of ancient DNA bioinformatic analysis and of current software use would be ideal.

Required language skills: English and/or Estonian

Starting at September 1st 2019

Stipend (per month): 1,100-1,300 The position is funded for 4 years.

Application documents and notification of results: In order to be considered for the PhD student position, the candidate must submit an application to the Institute of Genomics, Estonian Biocentre (postal address: Riia 23b, 51010 Tartu, Estonia) OR e-mail to: kristiina.tambets@ut.ee, toomas.kivisild@kuleuven.be and merilin.raud@ut.ee) the following documents: 1) a letter of application/motivation; 2) a curriculum < http://www.ut.ee/en/curriculum-vitae > vitae; 3) a copy of a document (including its annexes) which shows the candidate to hold the required qualification (authorized translation into Estonian or English if the credential is not in one of these languages), or examination transcripts if the qualification is yet to be obtained. A candidate can be required to submit the original or a certified copy of the document (including its annexes) showing the candidate to hold the required qualification; 4) other materials considered relevant by the candidate.

Additional information:

— / —

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To read the entire message look it up at http://life.biology.mcmaster.ca/~brian/evoldir.html

UVienna AncientDNA

PhD position at the Department of Evolutionary Anthropology, University of Vienna, Austria

PhD candidate will join a newly established group by Dr. Elmira Mohandesan at the Department of Evolutionary Anthropology at the University of Vienna. The project will be conducted in close collaboration with Prof. Joris Peters (LMU Munich), and Prof. Ludovic Orlando (University of Toulouse and University of Copenhagen). Data generation and analyses will require traveling to both collaborators labs.

Project Description: Humans have been crossbreeding wild and domestic members of the family Equidae for millennia, as illustrated by archaeological, iconographic and written sources. First-generation equine hybrids are, however, generally sterile. Maintaining such stocks thus required considerable wealth, and detecting when and how such practices developed during history can provide important information about the organization of past societies. This project aim at elucidating local breeding practices and the contribution of hybrid equine populations exploited in Germany and Austria in pre-Roman and Roman times. It will apply a multidisciplinary approach combining standard morphology with Geometric Morphometrics (GMM) and state-of-the-art methods in ancient DNA research aimed at the detection of hybrids, and possibly, at the characterization of both parental stocks. For more information please see https://www.anthropology.at/news-press-releases/ . Candidate Background: We are seeking a highly motivated candidate with background in molecular biology, population genetics, bioinformatics or equivalent. Proficiency in written and spoken English is required. Bioinformatics skills (Unix, R, and Python languages) are highly desired. Direct experience with ancient DNA is highly desired. Ability to work in a highly-international and multi-disciplinary team. Prospective student should demonstrate a desire to learn, work independently, and multi-task.

Terms of employment: Science Fund: Austrian Science Fund (FWF) Duration: three years, provided that the first year is successful (trial period) Start: anticipated as June 2019

How to apply: To apply for this position, please send your CV, letter of interests and at least one letter of recommendation toelmira.mohandesan@univie.ac.at and elmira.mohandesan@gmail.com. The applications will be reviewed immediately, and after initial selection the successful candidates will go through either the MFPL PhD selection (www.mfpl.ac.at) or the internal selection at the Department of Evolutionary Anthropology at University of Vienna.

Elmira Mohandesan, PhD Department of Evolutionary Anthropology Faculty of Life Sciences University of Vienna Althanstrasse 14 1090 Vienna Austria

Elmira Mohandesan <elmira.mohandesan@gmail.com>

UWisconsin StevensPoint WalleyeGenetics

Master's position in the Larson Lab using genetics to investigate the reproductive ecology of walleye in northern Wisconsin

Description and responsibilities: The USGS Wisconsin Cooperative Fishery Research Unit at UW-Stevens Point is looking for a MS student to conduct research on walleye populations in northern Wisconsin as part of a collaborative effort between the Wisconsin Department of Natural Resources (WDNR) and UW-Stevens Point. Walleye populations have been declining in northern Wisconsin over the past decade, and previous studies have been unable to provide a mechanistic cause for these declines. This project will utilize genetics to construct pedigrees for two northern Wisconsin lakes with the goal of correlating various ecological metrics to individual fitness (i.e. reproductive success). The project will include both field and laboratory components. Laboratory work will consist of using a newly developed SNP panel to genotype thousands of walleye, and field work will consist of assisting WDNR with walleye sampling in the spring and fall. Data analysis will leverage a variety of statistical methods to investigate relationships between reproductive success and variables such as size, age, spawning location, and egg quality.

Qualifications: B.S. in biology, fisheries, or a related field, GPA of 3.0+, and GRE of 300+. Previous experience with fisheries ecology is desirable. A background in genetics is not required.

Salary: $16,000 per year (2 yr) plus health insurance and tuition waiver. Closing date: May 1, 2019.

Starting date: Position will start in September 2019 but there may be an opportunity to work in the Larson Lab during summer 2019 before the position starts.

Contact: Please send CV, transcript copies, GRE scores, and names and contact information for 3 references to Wes Larson (Wes.Larson@uwsp.edu).

Web Links: https://larsonlab.wordpress.com/- https://www.coopunits.org/Wisconsin_Fish/-People/Wes_Larson/index.html "Larson, Wes" <wlarson@uwsp.edu>

UZurich OrangUtanGenomics

Two 4-year PhD positions on orang-utan genomics available at the University of Zurich

Overview: I am seeking two highly motivated PhD students for my recently funded project °Orang-utan genomics in an evolutionary and conservation context± at the Evolutionary Genetics Groups of the Department of Anthropology, University of Zurich (UZH), Switzerland (https://www.aim.uzh.ch/de/-research/egg/groupmembers/kruetzenmichael.html). My group has broad interests in evolutionary genetics and genomics of primates and delphinids. The work will be conducted in close collaboration with Prof. Tomas Marques at University Pompeu Fabra, Spain, Dr. Logan Kistler (Smithsonian), and Prof. Verena Sch'nemann (UZH).

The work will entail a combination of genomic laboratory work (based on faecal and historic DNA samples) at UZH and fieldwork Sumatra, Indonesia. Both positions are for 4 years fixed term. Remuneration is according to Swiss PhD salary scales (CHF 48540 p.a. plus employer social security contributions). Starting date for the first PhD project will be 1. April 2019, and for the second PhD project 1. November 2019.

Background: Environmental mechanisms are some of the most important forces affecting the evolutionary history and distribution of species, yet the roles of these environmental forces in driving genetic diversity and local adaptation remain underexplored. Investigating the processes of how such mechanisms have shaped patterns of DNA variation in space and time has long been one of the most important goals of evolutionary biology. Such patterns are the result of both adaptive and non-adaptive processes, and the debate about the relative importance of natural selection and random genetic drift in shaping genetic diversity within and among species is still ongoing.

The project aims to investigate (among others) how different evolutionary forces have shaped patterns of DNA variation within and among extant orang-utan species. Orang-utans on each island experienced long-lasting environmental differences throughout their evolutionary history, leading to a number of well-documented differences in their physiology, morphology, among other. As a first for a great ape, this puts us into a unique position to evaluate detailed hypotheses about the occurrence and maintenance of genetic adaptations, and provides the unique opportunity to study how environmental differences shaped the genomes of one of our closest relatives in situ.

Requirements: Successful candidates will have a Diploma/Masters degree in a relevant discipline, a strong interest (ideally with prior experience) in bioinformatic and genomic skills, laboratory work, and some background in evolutionary genetics. The ideal candidates will have strong oral and written communication skills in English and the ability to work and share ideas in a collaborative environment. Knowledge of German language is not essential, but may help with everyday life whilst in Zurich.

The students will work in a dynamic research environment and have access to cutting edge next generation sequencing techniques. The Department of Anthropology and others at UZH host several seminar series with high-calibre international speakers. The two PhD positions will be embedded in the Zurich Life Science Graduate School's program in Evolutionary Biology (http://www.lifescience-graduateschool.ch/).

Applications: Interested students should send their application package to michael.kruetzen@aim.uzh.ch before 28. February 2019. The package must include, in one PDF file: A cover letter expressing research interests relevant to the position, a complete CV, and reference letters of two academic referees.

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

Informal enquiries can be addressed to Prof. Michael Kr'tzen, Email: michael.kruetzen@aim.uzh.ch.

Michael Kr'tzen <michael.kruetzen@aim.uzh.ch>

UZurich PopulationGenomics

Zurich, January 2019

A four year PhD position is available in the lab of Prof. Anne Roulin, Department of Plant and Microbial Biology - University of Zurich (https://www.botinst.uzh.ch/-en/research/evogenomics/roulin/open_positions.html) to investigate transposable element evolution in plants using population genetics/genomics approaches.

Background & Aims of the project Transposable elements are mobile DNA sequences that constitute the main component of most eukaryotic genomes. Because TEs can modulate gene expression and are activated by stress, they are especially prone to produce the raw diversity necessary for individuals to respond and adapt quickly to new or changing environmental conditions. Understanding to what extent TEs contribute to adaptation in comparison to classical point mutations constitutes an essential step in characterising their role in evolution.

Methodology Genome-wide scans of selection (GWSS) are efficient methods to identify polymorphisms under selection at a whole genome scale and in a large number of populations: new mutations that are beneficial leave clear marks in genomes as they tend to reduce genetic diversity, increase differentiation among populations, and lead to extended haplotypes in the vicinity of the locus under selection due to genetic hitchhiking. Using whole-genome sequencing data produced for more than 200 accessions of the grass Brachypodium distachyon from all over Europe, Middle-East and North-Africa, the project aims at using GWSS to detect adaptive TEs under selection across a large number of populations and to then functionally validate their impact on phenotypes. Side projects also involve to reconstruct the demographic history of B. distachyon populations since the last glaciations to further investigate the bases of local adaptation in this species.

You are' ' interested in population genetics, genome evolution, population history and experimental biology. You will be encouraged to come up with your own ideas and creativity in order to shape your PhD project according to your interests. The successful candidate must hold a master degree in biology (or in a related field).

*How to apply? * Send a PDF file including a cover letter, a CV, and contact information of 2 referees to anne.roulin@boinst.uzh.ch. Applications that do not follow the guideline will not be considered. Applications are welcome until the position is filled. Ideal start: from April to September 2019 (but negotiable). For more information or to visit the lab, dont hesitate to contact us.

Anne Roulin Assistant Professor of Plant Evolutionary Genomics Department of Plant and Microbial Biology University of Z'rich Zollikerstrasse 107, 8008 Z'rich - Switzerland Phone +41 (0)44 63 48398

anne.roulin@botinst.uzh.ch

VictoriaU AbalonePopGenetics

PhD position available V Kaikoura region abalone population genetics based on GBS-derived SNPs

The position - A 3-year PhD position is available in the laboratory of Prof. Jonathan Gardner (Victoria University of Wellington, NZ), working in conjunction with Dr. Tom McCowan (Paua Industry Council, NZ) and Rob Elshire (The Elshire Group, NZ). The PhD position has a start date of early/mid 2019 or soon thereafter.

The project - Our group has received full research-only funding from Seafood Innovations Limited for this abalone (Haliotis iris) population genetics SNPs project. In New Zealand, abalone are called paua.

The November 2016 Kaikoura earthquake had devastating effects on paua populations resulting in the ongoing closure of the fishery for this locally important species. The catch reductions resulting from the closure are worth approximately $3 million annually to the quota holders, as well as loss of customary and recreational fishing opportunities. It is critical that best available information is used to inform management decisions about when and at what level this fishery is re-opened to ensure its future sustainability. Research programs to monitor both adult and juvenile paua recovery are currently being undertaken to inform management decisions. A critical gap in the current monitoring is an understanding of where the new recruits come from that contribute to population recovery and the spatial scales that are biologically relevant for future management.

Development of next-generation molecular markers called SNPs (single nucleotide polymorphisms) for paua and subsequent genetic analyses will enable a greater understanding of the patterns and processes for paua population recovery. The recent development of genotyping-by-sequencing (GBS) means that SNP development is achievable, even for -model species such as paua. PopulationVspecific genetic diversity will be used to quantify the magnitude of genetic bottlenecks in northern South Island paua populations resulting from the earthquake, and in neighbouring populations outside the affected area. Analyses across different cohorts will enable sources of recruitments to be identified from within and beyond the affected region. Together these analyses will assist in reducing the risk in decision making around the appropriate levels and timing for the fishery to be re-opened, to recover commercial losses from the fishery closure and to provide for sustainable recreational and customary fishing.

The timing - We are looking for an outstanding candidate whom we can support through the VUW PhD scholarship application scheme, to ensure that the person secures a stipend and full fees remission. The next round of VUW PhD scholarship applications closes on 1st March 2019, so we aim to identify someone before that date.

The ideal candidate V We are looking for a student with a background in population genetics and/or bioinformatics and an interest in applying SNPs to a marine invertebrate coastal fishery. Because we will need to support the candidate through the VUW PhD scholarship application process we need an academically strong candidate (GPA of >85%). We will give preference to candidates with a Masters level degree and also with previous experience of working with GBS and/or SNPs data sets.

This PhD position is open to all nationalities (i.e., the successful applicant does not have to be a NZ citizen). However, an international student (i.e., non-NZ and non-Australian) will require a NZ student visa to be allowed to study in NZ. In the normal course of events this is not a problem given that the student in question will be supported by VUW. But the visa application process can take several weeks to a few months. We understand this, and this is not a problem. The actual start date is therefore negotiable if the student is and requires a student visa.

For candidates whose first language is not English, a TOEFL or equivalent exam pass is required. The work location V Most of the 3 year PhD position will be based in Wellington, but there will be an opportunity to work with Rob Elshire in Palmerston North, which is about 2 hours drive north of Wellington. On a day to day basis the successful candidate will be based at Victoria University of Wellington. The NZ Paua Industry Council (PIC) is also based in Wellington. An opportunity exists to visit the field sites and to help PIC divers collect paua samples.

For general enquiries please email V jonathan.gardner@vuw.ac.nz

Applications V Applications from suitably qualified individuals should be submitted to jonathan.gardner@vuw.ac.nz, before the closing date of 31st January 2019. Applications should consist of: A cover letter outlining why you are interested in the position and how you meet the candidate selection criteria (Masters level degree preferred;

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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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VirginiaTech SumacGenomics

M.Sc. assistantship available at Virginia Tech

The Holliday Lab in the Department of Forest Resources and Environmental Conservation at Virginia Tech is seeking an M.Sc. student for a funded project aimed at understanding genetic diversity, population structure, and hybridization in the endangered sumac Rhus michauxii.

R. michauxii occurs in the southeast United States, primarily in Virginia and North Carolina. The species is federally listed as endangered, and the goal with this project is to understand the degree of local population diversity, population connectivity, and the degree to which it hybridizes with a related, more widespread species (R. glabra). The project will involve participating in sampling efforts during summer of 2019 (i.e., prior to official enrollment, for which an hourly wage will be provided) and subsequent genotyping-by-sequencing library preparation and downstream analyses.

Candidates should have a background in biology, environmental science, ecology, or a related field, and be interested in learning the necessary computational and statistical tools to complete this project. Please note that some foreign nationals may not be eligible for this project due to the sensitive location of some of the field work.

Please send expressions of interest and CV to Dr. Jason Holliday (jah1@vt.edu).

"Holliday, Jason" <jah1@vt.edu>

WageningenU 2 ComparativeGenomics

WageningenU.ComparativeGenomicsFish

Dear All,

I would like to draw your attention to an exciting PhD project on comparative genomics of fish, at Wageningen University, The Netherlands.

(text and link to apply available online: https://www.wur.nl/en/Jobs/Vacancies/Show/PhD-student-in-the-area-of-functional-and-comparative-genomics-in-fish-health-and-immunology.htm)

We are looking for an enthusiastic PhD candidate, with a clear interest in one or more of the following research fields: epigenomics/genomics, bioinformatics, health and immunology, and comparative biology. The PhD will be employed at a newly funded H2020 project AQUA-FAANG, aiming to support the global Functional Annotation of ANimal Genomes (FAANG) consortium, with a focus on domesticated fish species. How are traits of animals encoded in their genomes, and how is that code triggered to become active? To help answer those questions, AQUA-FAANG aims to generate a wealth of functional genomic (e.g. expression) and epigenomic (e.g. chromatin structure) data from six fish species, including Atlantic salmon, sea bass, and common carp, for different organs and developmental stages. Special emphasis lies on fish health, as this is a major concern for economic loss and animal welfare in aquaculture. Cells and tissues involved in immune response can be easily studied, and easily triggered, and therefore serve as a good biological Âmodel trait'. Since there are so many economically important fish species, a comparative genomic approach will be applied to identify common themes in the functional genomics of fish health, such as how immune responses are regulated across species. Special emphasis will lie on the role of whole genome duplications, that have occurred several times throughout the evolution of the bony fishes.

All candidates should meet the following requirements: A Master's degree in a relevant biological field (genomics/epigenomics, bioinformatics, computational biology, comparative biology, immunology, or evolutionary biology), or in a quantitative field (statistics, data analytics).

The candidate should have:

- A proven affinity for computational analysis (e.g. experience with Python, R, Linux). - A strong interest in functional genomic and comparative/evolutionary biological analysis - A strong interest in fundamental and applied research. - Be creative and innovative.Good organisational and (written and spoken) communication - skills in English, as well as a proven ability to collaborate with others. - Willingness to travel internationally, to attend international project meetings and conferences and visit other institutes.

We offer you a challenging job for a period of 4 years at an international leading organization. The position is available within Wageningen University & Researchat the Aquaculture and Fisheries group, and Animal Breeding and Genomics group, both at Wageningen Campus. The organization has good and flexible employment conditions, including good education and training facilities for PhD students. Employment basis: Appointment for 38 hours per week for a period of 1.5 years with extension of 2.5 years after successful evaluation.. The gross salary is in according to the Collective Labour Agreement of Wageningen University and first year salary is 2.266, per month rising to 2.879, in the fourth year.

Additional information about the vacancy can be obtained from: Dr Hendrik-Jan Megens (hendrik-jan.megens@wur.nl) +31317482469 or prof. Geert Wiegertjes (geert.wiegertjes@wur.nl) +31317482732.

For further information about working at Wageningen University & Research, take a look at http://www.wur.nl/en/Jobs.htm Closing date for applications: 08-02-2019

- H-J Megens, PhD, - Assistant Professor - Animal Breeding & Genomics, - Wageningen University, - Wageningen, The Netherlands - LinkedIn: http://nl.linkedin.com/pub/hendrik-jan-megens/24/536/2b8 - Google Scholar: http://scholar.google.nl/citations?user=kGUIXOYAAAAJ ––

WageningenU.ComparativeEpiGenomics

Dear All,

I would like to draw your attention to an exciting PhD project on evolutionary and comparative epigenomics, at Wageningen University, The Netherlands.

(text and link to apply available online: https://www.wur.nl/en/Jobs/Vacancies/Show/PhD-student-in-the-area-of-epigenomics-of-chicken-and-pig.htm)

We are looking for an enthusiastic PhD candidate, with a clear interest in one or more of the following research fields: epigenomics/genomics,

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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

Jobs

AMNH NewYork AssistCuratorEntomology

The Division of Invertebrate Zoology of the American Museum of Natural History is seeking an outstanding researcher in insect systematics, with particular preference for candidates with a research specialty in Lepidoptera or Coleoptera, or in minor insect orders. This is a tenure-track appointment to be filled at the Assistant Curator and Assistant Professor level.

Since its founding in 1869, the Museum has advanced its mission to discover, interpret and disseminate information about the natural world and human cultures through wide-ranging programs of scientific research, education, and exhibition.

The primary responsibility of curators at the Museum is to perform and supervise original scientific research, as well as to curate any relevant collections. They are also expected to provide service to the Museum. This can include advising programs in exhibition, education, including participation in the Richard Gilder Graduate School, or other forms of public outreach, as well as undertaking fieldwork and building collections.

The Museum places a high value on scholarship, as well as other factors that include collegiality, institutional citizenship, diversity, equity and inclusion. The Museum is committed to building a diverse community throughout science and education. Therefore, the service statement should address these objectives. Applicants should request three letters of reference to be sent separately. (Others may be solicited during the search process.) All materials should be submitted through this system.

The closing date for applications is February 1, 2019; evaluation of applications will begin on February 2, 2019.

Applications should be in PDF format and include a cover letter, a curriculum vitae with a list of publications, a research statement of no more than five pages including figures and references, a statement addressing Museum service interests and relevant experience, and copies of five significant publications.

Inquiries about the position should be directed to James M. Carpenter, Chair of the Search Committee (carpente@amnh.org; (212) 769-5611).

Applications should be submitted here: https://careers.amnh.org/postings/1699 Susan L. Perkins, Ph.D. Curator and Professor Sackler Institute for Comparative Genomics American Museum of Natural History 200 Central Park West New York, NY 10024 www.susanperkins.net @NYCuratrix

Immediate Past President, American Society of Parasitologists

Susan Perkins <perkins@amnh.org>

BowdoinC Maine LabTech

A full time molecular laboratory technician position is available in my lab at Bowdoin College, in Brunswick, Maine. The existing funding is short term, through June, but it is also possible that it will continue for a few more months. The project focuses on diet analysis using next generation sequencing and paired isotope data. Candidates with demonstrated experience in a molecular ecology setting, and who work well independently, are encouraged to apply.

For additional questions, contact Dave Carlon at: dcarlon@bowdoin.edu

Description-

Responsible for day-to-day operations of a molecular ecology research laboratory at Bowdoin College. Prepares samples, DNA libraries, and generates DNA sequence data from using Sanger and Next Generation Sequencing technology. Provides technical expertise to students and staff. Maintains a safe and productive working environment for all end users. This is a benefit eligible position.

Education/Skills Requirements BS degree in Biology or related field.

Demonstrated expertise in the following areas is preferred: 1. DNA extraction from environmental samples, including preserved tissues and environmental samples. 2. Preparation of multiplex libraries for sequencing on the Illumina platform. 3. PCR and Quantitative PCR (qPCR). 4. Preparation of amplicons for Sanger sequencing. 5. Next generation sequencing bioinformatics.

Experience Requirements and/or Equivalents Minimum of 2 years work experience in molecular biology laboratory setting required. Excellent organizational and time management skills. Computer programming experience in bioinformatics strongly preferred.

Standard Work Days and Hours Up to 40 hrs/week. Monday-Friday, 8:30-5:00. This is a temporary position that is funded through June 30th, 2019.

If interested, you can apply by going to: http://careers.bowdoin.edu/postings/5713 “dcarlon@bowdoin.edu” <dcarlon@bowdoin.edu>

CarnegieMuseumNatHist AssistDirector

Carnegie Museum of Natural History - Assistant Director, Science and Research

Carnegie Museum of Natural History invites diverse applications for ASSISTANT DIRECTOR, SCIENCE AND RESEARCH. Successful candidates for this position will be detail-oriented and have experience and success in collaboration and communication, in addition to having advanced training in the natural sciences. Responsibilities will include project management, support in organizing activities in the department of Science and Research, and working with the Director, Science and Research in providing leadership in meetings and on emergent projects in the department.

Qualifications: Ph.D. in natural sciences or demonstrably equivalent experience with a minimum of three years of experience in project management of complex science and science communication projects. Given the museum’s distinguished history of research and collections focused on the evolution of form, function and phyologeny, a background in evolutionary studies is strongly welcomed. Excellent written and verbal communication skills; a collaborative, friendly approach, as well as a general knowledge and interest in natural history, the environment, and the Anthropocene. Exceptional organizational skills, ability to work independently, creatively, keep track of details, and to exercise good judgment. Research experience with an emphasis in conservation and interdisciplinary fields and good humor preferred.

Carnegie Museum of Natural History is one of the four Carnegie Museums of Pittsburgh, with a mission in original scientific research, preservation of collections, and public science education and engagement. The museum has approximately 22 million specimens and artifacts in its collections, has hired six new members to its curatorial staff in the past four years and endowed its collection manager positions. Carnegie Museum of Natural History is located in the bustling Oakland neighborhood of Pittsburgh, with easy access to shops, dining, transportation, major universities and cultural attractions. From the Visit Pittsburgh website, “Not only are its sports teams a mighty force to be reckoned with, but the city has overcome adversity in a big way. Pittsburgh’s affordable standard of living, top-notch health care facilities and cultural attractions combine to make it America’s ’Most Livable City.”’ For cost of living comparisons, visit: https://money.cnn.com/-calculator/pf/cost-of-living/index.html .Consideration of applications will begin January 20th and continue until a suitable candidate is identified. Applications can be submitted here: https://usr55.dayforcehcm.com/-CandidatePortal/en-US/car/Posting/View/799 Carnegie Museums of Pittsburgh is firmly committed to equal employment opportunity for all persons without regard to race, color, religion, creed, national origin, ancestry, sex, gender identity or expression, age, marital status, sexual orientation, citizenship status, veteran status, non job-related disability or genetic information as those terms are defined under applicable law.

“Tonsor, Steve” <TonsorS@CarnegieMNH.Org>

CCMAR Portugal Bioinformatician

JUNIOR RESEARCHER (M/F) IN BIOINFORMATICS - 1 VACANCY

Reference: CCMAR/ID/20/2018

The Algarve Centre for Marine Sciences (CCMAR) opens a call for a Junior Researcher (M/F), of any nationality, including stateless candidates. The indefinite period employment contract will be as part of the EOSC-Life Research and Innovation Action (RIA) ’Providing an open collaborative space for digital biology in Europe’ (INFRAEOSC-04-2018).

Job Summary and Duties:

The Junior Researcher will provide bioinformatic and computational expertise to develop a ’Demonstrator’ project for the European Open Science Cloud (EOSC) infrastructure.

1) Develop a web-based portal for the EOSC to enable access to marine genomic resources, including a inter-species software pipeline to compare and update gene annotations and ontologies. a) Develop programmatically a content management framework (e.g. Drupal) based on the Orcae platform (Online Resource for Community Annotation of Eukaryotes). b) Develop programmatically databases and software pipelines for genome curation, and annotation and ontology comparisons. 2) Provide general bioinformatic expertise to project managers.

Full job description here: https://ccmar.ualg.pt/en/-job/ccmarid202018-1-vacancy-junior-researcher-mf Informal enquires to: Cymon J. Cox cymon@ualg.pt

Cymon Cox <cymon.cox@googlemail.com>

CornellU FieldAssist PlantPollinatorEvol

The Geber lab at Cornell University seeks a highly motivated, detail-oriented assistant for summer 2019 field research in the Southern Sierra Nevada (May-July) and lab work in Ithaca, NY (July-August). We are studying four species of annual plants in the genus Clarkia and their specialist bee pollinators. Our research focuses on how pollinators may impact plant species evolution and coexistence. We also study the population biology of one of the four species throughout its range and have yearly population censuses to conduct.

Our research sites are located in the Kern River Canyon in Kern County, California. The lab rents a house on a property where other labs working in this system are also based in the summer. This field assistant would have a private bedroom, access to a shared bathroom and a communal kitchen, and wireless Internet access. Frequent trips are made into town (Lake Isabella and Kernville) for groceries and other supplies.

Successful applicants are expected to assist in data collection, data entry, and flower, seed, and bee collection in the field; work in Ithaca will consist of sample processing and data analysis. The assistant will work a 39-hour workweek. Weather conditions in the Sierras can be very hot and dry (100+ degrees F) in the summer, so assistants should be prepared to work in hot conditions. Applicants must be able to hike up and down steep hills for up to 1 mile at a time, stoop or kneel for extended periods of time, and work in proximity to bees and snakes. The work can be very physically demanding and tiring, and the research team typically collects data 7 days a week. A good sense of humor and a positive attitude are essential.

Qualifications: 1) Citizenship and availability: applicants must be US citizens and must be available to begin working in California as of May 1, 2019. The exact end date of the position in August is flexible. 2) Education: some undergraduate education in biology, ecology, or related field, or equivalent experience. 3) Experience: experience with and enthusiasm about working outdoors, and/or previous field research experience. Previous experience working with plants, bees, or insects is preferable but not required. 4) Tasks: perform repetitive tasks with attention to detail, daily hiking. 5) Personality: interpersonal skills and willingness to live and work in close quarters with other researchers in a house.

Compensation: transportation to and from California, a private room with Internet access in the field house, and pay ($13-$15 an hour depending on experience) will be provided. Applicants will be responsible for securing their own housing in Ithaca for July and August.

The deadline for applications is March 1, 2019. Applicants should submit: 1) a short (1 page maximum) cover letter describing their qualifications as well as future academic and professional goals; 2) a resume or CV outlining previous work experience and relevant courses (completed or in progress), extracurricular activities; and 3) two letters of reference. Letters of reference may be included with the cover letter and resume/CV or emailed directly by letter writers to the email address below with the applicants name in the subject line of the email.

Applications will be reviewed as they are submitted.

Cornell University is an affirmative action/equal opportunity employer. Cornell University and we in the Geber lab have a commitment to support equality of education and employment opportunity by affirming the value of diversity. We welcome and encourage scientists of all backgrounds to apply to work with us! *http://-blogs.cornell.edu/geberlab/ < http://blogs.cornell.edu/-geberlab/ >*

Email to: Monica Geber, Professor of Ecology and Evolutionary Biology mag9@cornell.edu

Kate Eisen <kee39@cornell.edu>

DukeU AssociateInResearch Biology

Job: DukeU.AssociateinResearch.Biology

*An Associate in Research position is available, starting in Spring 2019, in the Tung lab at Duke University. *

The Tung lab studies the relationship between behavior, the social environment, and genetics and genomics. We combine detailed phenotypic and demographic information with modern genomic data sets on gene regulation and epigenetics. Current projects focus on the epigenetic signature of early life ecological and social adversity; gene regulatory mechanisms linking social adversity and health in rhesus macaques; trade-offs associated with helper-breeder transitions in meerkats and mole rats; and the genomic and phenotypic consequences of hybridization in wild baboons.

The ideal candidate will have previous experience with cell culture and aseptic technique, and will be familiar with basic molecular techniques such as DNA/RNA extraction and library preparation for high-throughput sequencing. We are also interested in the ability to work independently and the ability to multi-task. Attention to detail and careful record keeping are essential.

In addition to performing wet lab work as described above, duties will also include responsibility for day-to-day logistics, such as ordering and receiving, working with trainees in the lab, and exporting/importing irreplaceable samples to/from our field sites.

Requirements: bachelor's degree, 1-2 years of experience in a research laboratory (not just a lab class), and familiarity with the fundamentals of molecular biology.

Position is for 40 hrs/week, and will last 12 months, with the possibility of renewal contingent on performance and availability of funding.

For more information about the lab and our work, see: http://www.tung-lab.org/ If interested, please apply via academicjobsonline.org (job #12885). You will need a copy of your CV, a cover letter, and contact information for 3 references.

Duke University is an Affirmative Action/Equal Opportunity Employer committed to providing employment opportunity without regard to an individual's age, color, disability, gender, gender expression, gender identity, genetic information, national origin, race, religion, sex, sexual orientation, or veteran status. Duke also makes good faith efforts to recruit, hire, and promote qualified women, minorities, individuals with disabilities, and veterans.

Tawni Voyles <voyles.tn@gmail.com>

EasternKentuckyU PlantEvolution

The Department of Biological Sciences at Eastern Kentucky University is accepting applications for a Botanist at the rank of Assistant professor. This is a 9-month, tenure-track position to begin August 15, 2019. Teaching responsibilities will include courses in the undergraduate Biology (BS), Wildlife Management (BS), and graduate (MS) programs. Primary courses to be taught include General Botany, Dendrology, Plant Systematics, and Aquatic and Wetland Plants. Additional courses may be assigned based on the candidate's expertise and departmental needs. The typical teaching load is 12 hours per semester, but new faculty can expect to teach 9 hours per semester during their first year.

The successful candidate will be expected to direct and advance the mission of the Ronald L. Jones Herbarium, the largest in the Commonwealth of Kentucky, which is housed in the recently completed (August 2017) Science Building. In addition, the incumbent will establish an active research program, mentor undergraduate and graduate (MS) students, and engage with conservation-oriented organizations such as the Kentucky Native Plant Society, the Office of Kentucky Nature Preserves, and US Fish and Wildlife Service. Knowledge of the flora of the eastern United States is essential. Areas of research may include, but are not limited to, computational biology, population biology, plant phylogenetics/systematics, and organismal diversity.

A Ph.D. is required from a regionally accredited or internationally recognized institution by the time of appointment; post-doctoral experience is preferred. Review of applications will begin March 4th and continue until position is filled. All interested applicants must apply via http://jobs.eku.edu/postings/9370. At the present time, EKU is unable to sponsor applicants for this position for work visas.

For detail regarding facilities, equipment, natural areas, and space directed toward research refer to our EKU Biological Sciences website: https://biology.eku.edu/ or contact Dr. Pat Calie, Search Committee Chair.

Jennifer Koslow, PhD Associate Professor of Plant Ecology Department of Biological Sciences Eastern Kentucky University 521 Lancaster Avenue Science Building 3238 Richmond, KY 40475

office: Science Building 4232 phone: 859-622-6258 jennifer.koslow@eku.edu

"Koslow, Jennifer" <Jennifer.Koslow@eku.edu>

GabonResearchBase Manager

Research manager for a scientific research base in Gabon

The Mandrillus Project (www.projetmandrillus.com), created in 2012 by a CNRS researcher (France), is a long-term scientific project to study the ecology and sociality of a Gabonese forest primate, the mandrill (Mandrillus sphinx). The study population consists of 180 individuals living in a large social group in the Lekedi private park, in southern Gabon, near the village of Bakoumba. The study population is monitored daily.

The Mandrillus Project is recruiting a research manager to supervise this research station, which employs between 8 and 10 full-time staff and regularly hosts students and researchers for short or long stays.

The tasks / activities related to the manager position are:

-behavioral data collection in the field and daily follow-up of the mandrills

-laboratory work for the management of biological samples collected in the field

-management of the scientific data sent regularly to researchers

-management of scientific protocols developed by researchers and students.

-administration (planning, payrolls and administration with the Gabonese authorities, budget management) and human resource management of a team of Gabonese and European field assistants

-welcoming and facilitating stays of students and researchers

-management of the car park

-management of scientific/telecom equipment

-writing of monthly reports on project events

-management of the relationships with local communities and employees of the Lekedi Park

Required skills for the manager:

-Previous experience in the field is mandatory (preferentially in Equatorial/tropical countries)

-Previous experience in the study of animal behavior is a real plus

-Experience(s) abroad and / or in isolated conditions

-Previous experience(s) in management / logistics is a plus

-Excellent communication skills

-Be physically and mentally resistant

-Be open to cultural differences

-Abilities to live in isolated areas

-Excellent level of French (mandatory)

-Excellent physical conditions (mandatory)

Desirable assets:

-Being in couple (to come and live in Gabon)

-Bachelor degree

-Skills in car mechanics and maintenance

-Scientific rigor

We are looking for a very organized, motivated and serious person. The recruited person must be ready to live in isolated conditions and in an Equatorial environment, in an intercultural context. Although weekly days off are scheduled, this position often requires a daily investment . The hired person must be ready to manage their time optimally for the project.

Because of the isolated conditions, we will give our preference to a couple . Both partners must be in excellent physical conditions, because the field is very rough, harder than expected!

The partner will be in charge of behavioral data collection and lab work (this is a full-time local position).

The person/couple will be housed on site, in the private park, in very good material conditions (house equipped with air conditioning, water and electricity). The Lekedi Park is located 7kms away from a small Gabonese village, Bakoumba, and an hour away from a small town, Moanda.

Although a couple is strongly desired , we will also consider single applicant. If a couple is hired, arrangements for the significant-other are possible within the framework of the project.

Contract length:

1 renewable year (3 months probationary period) up to 2 times.

Salary and benefit :

Manager: CNRS tariff grid

Housing included

Local salary (=stipends) for the partner (full-time position)

An international round-trip (at the beginning and at the end) for both partners

Deadline for filing a file:

2019, January 31 th

Auditions of the selected candidates (in Montpellier V the transport to Montpellier is not included or by skype) and final answer:

First week of February 2019

Starting date:

May 1 st -15 th 2019 (not very flexible)

Application file:

Please send your CV (with names and addresses of three references for both partners) and a detailed and personalized letter of motivation (standard letters are not encouraged) by email only to:

projetmandrillus@gmail.com

– Marie

Marie Charpentier, Director of Researches, CNRS

ISEM UMR5554, Montpellier

Projet Mandrillus: www.projetmandrillus.com/

Visit my personal website and my opinion regarding the French granting situation:

www.mariecharpentier.net/publications.html Marie Charpentier <marie.charpentier@umontpellier.fr>

GeorgeWashingtonU FoundingChairBioinformatics

Tenured Professorship and Founding Chair, Department of Biostatistics and Bioinformatics, George Washington University

The Milken Institute School of Public Health is seeking a tenured faculty member as Professor and founding Chair of the Department of Biostatistics and Bioinformatics. We seek a dynamic and visionary individual to oversee the transition of biostatistical educational and research activities, currently located in the Department of Epidemiology and Biostatistics, into a new department with an innovative curriculum and cutting-edge scholarship. The successful candidate will have the opportunity to help shape the vision of and provide leadership to the development of the Department of Biostatistics and Bioinformatics.

Core responsibilities of the position will be to provide visionary academic leadership of the new Department, including curriculum development, budgeting, hiring and evaluation of faculty, assessment of the academic program as well as expansion of partnerships with other departments within the University to provide innovative and integrated educational experiences for all students. The Chair must be committed to the principle of diversity and inclusion in our students, staff and faculty. The position requires scientific leadership and experience.

The Milken Institute School of Public Health has a diverse and growing faculty, with a $90 million research portfolio. As the only school of public health in the nations capital, faculty and students have a unique opportunity to work closely with government agencies such as the National Institutes of Health, the US Department of Agriculture and the Food and Drug Administration, as well as the numerous non-governmental organizations that are headquartered in DC.

Basic Qualifications: We seek applicants with a doctorate in biostatistics, statistics, bioinformatics, health data science or a related field with strong written and oral communication skills; an established program of research; and a strong national or international reputation supported by a significant record of developing innovative statistical, data analytics or biostatistical methods. Applicants should also have a solid pedagogical record in one or more areas of teaching, advising, or mentoring and a demonstrated commitment to public health.

Application Procedure: Applicants should complete the online faculty application at http://www.gwu.jobs/postings/64164 and submit the following documents: 1) curriculum vitae; 2) letter of interest; and, 3) statement of qualifications. Only complete applications will be considered. Review of applications will begin on 1/18/2019 and will continue until the position is filled.

The university is an Equal Employment Opportunity/Affirmative Action employer that does not unlawfully discriminate in any of its programs or activities on the basis of race, color, religion, sex, national origin, age, disability, veteran status, sexual orientation, gender identity expression, or on any other basis prohibited by applicable law. Employment offers are contingent on the satisfactory outcome of a standard background screening.

Contact Keith Crandall (kcrandall@gwu.edu) for questions or informal inquiries.

Professor Keith A. Crandall, PhD Director, Computational Biology Institute < https://cbi.gwu.edu/ > Director of Informatics, CTSI-CN Department of Epidemiology &Biostatistics < https://publichealth.gwu.edu/departments/epidemiology-and-biostatistics > 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 < https://twitter.com/crandallkeith?lang=en > / LinkedIn < https://www.linkedin.com/in/keith-crandall-8a9b0a9 >

“Prof. Keith A. Crandall” <kcrandall@gwu.edu>

GulbenkianInst Portugal 2 Head Programmer

The Instituto Gulbenkian de CieÌncia (IGC) has an open call for a highly motivated and proactive PhD holder, with demonstrated experience in the field of Bioinformatics and Genomics, to act as a head of its Bioinformatics & Genomics Unit.

This will be a new facility at the IGC, following the merger of its Bioinformatics (http://facilities.igc.gulbenkian.pt/bioinformatics/bioinformatics.php) and Genomics UNITs (http://-

facilities.igc.gulbenkian.pt/genomics/genomics.php). This UNIT at IGC will provide its researchers with genomics services (Whole Genome Sequencing, Long-read Sequencing, Transcriptomics, Metagenomics, Genotyping, Single Cell Analyses, Nucleic Acid QC), services of consultation, support with experimental design, data processing, analysis and management and training courses. IGC also houses Biodata.PT/Elixir Portugal, the Portuguese distributed e-infrastructure for biological data and the Portuguese node of the European bioinformatics infrastructure - ELIXIR.

The Unit works under strong synergy with other facilities at IGC. Adding to its core mission above, this Unit aims also at providing services to external organizations and academic institutions with which the IGC has established collaborations. Thus we look for a candidate with experience/interest and strong motivation to collaborate with other institutions towards the transmural expansion of the services of IGC Bioinformatics & Genomics Unit.

GENERAL ADMISSION REQUIREMENTS *PhD *Know-how in bioinformatics and statistical data analysis; research and/or management expertise in NGS technologies, training experience *Record in grant proposal development will be a plus. *Leadership Capability *Ability to work in a team; *Ambition and Motivation for the exercise of the function; *Initiative and autonomy; *Planning and organization.

WE OFFER -Opportunity to lead an innovative UNIT -Competitive salary depending on the candidate's level of expertise -Continuous training -Career Development Perspectives -Dynamic work atmosphere

APPLICATION PROCEDURE Interested candidates should send an email to igcpositions@igc.gulbenkian.pt with a PDF file with Motivation Letter (maximum of 1 page), a vision for the Bioinformatics & Genomics UNIT (2 pages maximum), Detailed curriculum vitae, contacts of two references, with the subject "BioinfoGeno_name of candidate".

The deadline for submitting an application is 31st January 2019.

SELECTION PROCEDURE After a pre-analysis of the Curriculum Vitae, motivation letter, vision for the Bioinformatics & Genomics Facility and recommendations, the selected candidates will be contacted for an interview.

NON- DISCRIMINATION AND EQUAL ACCESS POLICY: The Instituto Gulbenkian de Ciencia of the Calouste Gulbenkian Foundation actively promotes a non-discrimination and equal access policy, wherefore no candidate can be privileged, benefitted, impaired or deprived of any rights whatsoever, or be exempt of any duties based on ancestry, age, sex, sexual preference, marital status, family and economic conditions, education, origin or social conditions, genetic heritage, reduced work capacity, disability, chronic illness, nationality, ethnic origin or race, origin territory, language, religion, political or ideological convictions and union membership.

I am posting this call on behalf of the IGC Direction. For further inquiries please contact: info@igc.gulbenkian.pt

Dr. Claudia Bank Principal Investigator Evolutionary Dynamics Group Instituto Gulbenkian de Ciência Oeiras, Portugal

Open positions in the Evolutionary Dynamics Group: evoldynamics.org/positions

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Individuals with strong programming skills and a genuine interest in evolutionary questions are welcome to apply to the available ERC-funded programmer position under the project "FIT2GO – A toolbox for fitness landscapes in evolution".

Lab

Building on evolutionary theory, research in the lab revolves around quantifying epistasis across levels of biological organization and across environments, and to study its impact on the population genetics of adaptation and hybridization. We approach these questions through a combination of mathematical modelling, computer simulations, statistical method development, experimental evolution, and data analysis and interpretation. The long-term goal lies in understanding how ecology, evolution, and molecular constraints shape genomes.

The programmer's missions will be the following:

- develop algorithms and code for lab projects - provide well-documented implementation of methods and simulations to be released as supplements or software packages - write methods, results, and manuals related to above-mentioned programming - manage the lab's computing resources - assist lab members regarding computing/computer questions

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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

HealthCanada Ottawa 2 Biostatistician

Looking to staff 2 senior bio-statistician positions at Health Canada in Ottawa Ontario.

Salary range $92,483 to $107,258.

2 permanent positions to be filled immediately.

Details and application: https://goo.gl/7sbohr Must apply using supplied URL. No email responses or applications.

Nicholas Petronella <bfssi.nicholas.petronella@gmail.com>

KewGardens UK EvolutionOrchids

A fantastic permanent research position at the Royal Botanic Gardens, Kew has just been advertised.

Research Leader - Sainsbury Orchid Fellow

You will work within the Integrated Monography team, specialising in the systematics, taxonomy and evolution of the most economically and ecologically important groups of plants, including the orchid family, Orchidaceae ' one of the most diverse, valuable and threatened plant families on Earth.

Kew's collections, which have been developed and refined by generations of experts, are vital to this research.

Kew's scientific vision is to document and understand global plant and fungal diversity and its uses, bringing to authoritative expertise to bear on the critical challenges facing humanity today.

Comparative Plant & Fungal Biology is one of Kew's six scientific research departments, with around 90 research staff, students and associates, generating authoritative and wide-ranging insights into the systematics, evolution and traits of major plant and fungal groups.

Hours of work: Full time

Contract type: Permanent

Salary: pounds 37,177 to pounds 40,737 per annum, depending on skills and experience

Closing Date: 05/02/2019

For more information and to apply please visit: https://careers.kew.org/vacancy/research-leader-sainsbury-orchid-fellow-374935.html —–

More details

Kew is the world's leading botanic gardens, at the forefront of plant and fungal science, a UNESCO World Heritage Site and a major visitor attraction. We want a world where plants and fungi are understood, valued and conserved ' because our lives depend on them.

We use the power of our science and the rich diversity of our gardens and collections to provide knowledge, inspiration and understanding of why plants and fungi matter to everyone.

The Integrated Monography team discovers and describes species on a global scale, uncovering the evolutionary dynamics and relationships of plants using taxonomy and -omics technologies. We aim to complete the tree of life for our focal plant groups and unlock fundamental biodiversity knowledge for the broadest audiences and applications, such as conservation, land management, and plants as resources for the future.

You will need to be qualified to PhD level with significant postdoctoral experience, with specialist knowledge in a field of science relevant to pursuing monographic research on the Orchidaceae. You will have sufficient skills and experience to plan and develop a world-class research programme on the orchid family, contributing to the collections at Kew (e.g. plant systematics, taxonomy, genomics, evolutionary biology, biogeography, ecology).

This will include the ability to motivate, manage and mentor a small team of researchers, which might include PhD and postdoctoral students. You will also have a good track record in securing research funding, and evidence of managing budgets. Your publication record should demonstrate a broad and deep knowledge of the systematics and evolution of the orchids, and a range of research skills.

The salary will be pounds 37,177 to pounds 40,737 per annum, depending on skills and experience.

We offer a fantastic range of benefits including a broad range of Learning and Development opportunities, with access to the Civil Service training curriculum, generous annual leave entitlement for new starters, family friendly policies, a choice of competitive pensions and flexible benefits scheme.

If you are interested in this position, please submit your application through the online portal, by clicking “Apply for this job”.

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

Olwen Grace <o.grace@kew.org>

Dr Olwen M. Grace Senior Research Leader | Integrated Monography | Comparative Plant & Fungal Biology Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AE, United Kingdom www.kew.org | www.researchgate.net/profile/Olwen_Grace

The Royal Botanic Gardens, Kew is a non-departmental public body with exempt charitable status, whose principal place of business is at Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AE, United Kingdom.

Olwen Grace <O.Grace@kew.org>

MARE CIBIO Portugal BioinformaticsEvolGenomics

- New Postdoctoral position in the field of Bioinformatics (Evolutionary Genomics) -

- Application deadline: February 8, 2019 -

We are looking for a motivated and skilled Bioinformatician to take on an active role in an international team working at the leading edge of genomics, environmental DNA (eDNA) metabarcoding and eDNA metagenomics, on a project recently funded by the Portuguese Science Foundation.

This position has an expected duration of 30 months, starting April 1, 2019, and will be based at the Research Center MARE, University of Lisbon, and/or CIBIO, University of Porto, Portugal. There will be plenty of opportunities to interact with scientists locally, and also internationally (Indiana State University and the Norwegian Sequencing Centre).

For more information on the project, contract details and application procedure, please visit: http://-www.eracareers.pt/opportunities/index.aspx?task=-global&jobId9624 and contact Hugo Gante at _hugo.gante@indstate.edu_ for more details.

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Hugo F. Gante, PhD

Assistant Professor Department of Biology TCGA - The Center for Genomic Advocacy Indiana State University Terre Haute, IN 47809, USA http://hugofgante.com Hugo.Gante@indstate.edu

MarineBiologicalLab EvolutionaryGenomics

The Josephine Bay Paul Center at the Marine Biological Laboratory (MBL) invites applications for a faculty position at the Assistant Scientist level in the area of evolutionary and functional genomics. The successful candidate will apply experimental and computational approaches to research areas including but not limited to: microbiome interactions, functional studies of host-associated marine microbial communities, evolutionary and ecological changes in marine systems, or genomic and transcriptomic studies of marine organisms.

The Bay Paul Center and the MBL have strengths in molecular evolution, functional genomics, microbial diversity and ecology, advanced imaging, and marine animal husbandry. The Center maintains state-of-the-art facilities for high-throughput sequencing and computational analysis. The MBL, an affiliate of the University of Chicago, has a distinguished history in fundamental biological discovery, now with a renewed focus on marine organisms, microbiomes, and the impact of environmental change on coastal ecosystems.

Qualifications: Applicants must hold a Ph.D. (or equivalent advanced degree) in a relevant field. The successful candidate will demonstrate strong potential for establishing a vigorous extramurally supported research program that can complement existing areas of strength across the institutions research and educational programs.

Applications: The MBL is an Affirmative Action/Equal Opportunity/Disabled/Veterans Employer and strongly encourages applications from candidates who would contribute to the diversity of its research community. Applications will be reviewed immediately upon receipt and will continue on a rolling basis until the position is filled. Those interested in the position should submit an application, including a CV, short summary of accomplishments and future research interests, and the names and contact information of at least three references to mbl.edu/ASSIS01024

For full consideration applications should be submitted by March 1, 2019.

dmarkwelch@mbl.edu David Mark Welch, Director of Research

David Mark Welch <dmarkwelch@mbl.edu>

Medellin Colombia 1yr MicrobiomeBioinformatics

A temporal research position is available at VidariumVNutrition, Health and Wellness Research Center in Medellin (Colombia). The position is to be occupied for one year, with the possibility of an extension for an additional year. The group focuses in understanding obesity and related cardiometabolic disorders through the analysis of gut microbiota datasets (16S rRNA, other amplicon sequences, qPCR, metagenomics, metabolomics). For more information, see www.vidarium.org/en or contact Dr. Juan S. Escobar at jsescobar@serviciosnutresa.com.

The researcher will contribute with the development of bioinformatic tools to analyze large datasets in the context of gut microbiota and health, and eventually support work at the molecular biology lab. The researcher will also have the freedom to contribute to other ongoing projects. Vidarium has an excellent collaborative network, offering potential interactions with local and international researchers from several universities.

Applicants should have at least a masters degree in computational biology, bioinformatics, or a related field. Applicants should have prior computational experience demonstrated through publications in scientific journals. Experience with gut microbiota datasets is advantageous.

We are a small team of young interdisciplinary researchers based at Medellin, Colombias second largest city. In 2012, our city deserved the title City of the Year, beating New York and Tel Aviv for its transformations during the past 20 years. At 4,900 feet above the sea level, culturally diverse Medellin is surrounded by the Andean Mountains, offering attractions for outdoor recreation. The area receives year-round sunshine and warm weather that give it the nickname of Spring City.

Please submit applications through

https://career4.successfactors.com/-sfcareer/jobreqcareer?jobId=-3930&companyÀ001139074P&username (Spanish only) or send your C.V. to jsescobar@serviciosnutresa.com.

Juan Sebastian Escobar Restrepo <jsescobar@serviciosnutresa.com>

NHM LosAngelesCounty InvertCurator

Curator, Marine Invertebrate Paleoecology

The Natural History Museum of Los Angeles County (NHMLA) seeks a Curator (Assistant preferred, but open to all ranks) to lead its research on invertebrate paleontology and paleoecology, to oversee the growth and care of collections of NHMLA's Department of Invertebrate Paleontology (IP), and to provide content for a variety of public programs. More specifically, the successful candidate will conduct collection-based research in late Cenozoic marine paleoecology, with the aim of contributing to NHMLA's program of long-term ecological change in Southern California.

NHMLA's vast IP collection (> 7 million specimens) spans half a billion years of biological and geological evolution in Southern California. It includes fossils of all major marine invertebrate groups as well as ichnofossils, and contains the world's largest collection of Cretaceous-Cenozoic mollusks from the Pacific Rim, the result of a century of research by NHMLA staff and amalgamation of collections from several Southern California universities. Half of this collection consists of fossils from the Pleistocene Epoch. Of the 3.5M Pleistocene specimens, 1.5M have been digitized, allowing this long-term dataset to bear on questions of Southern California's ecological past and present, in turn greatly augmenting the efforts of NHMLA's coastal biodiversity initiatives by incorporating a paleontological perspective.

The successful candidate will have a record of outstanding research, excellent communication skills, and a demonstrated ability to engage the public and stakeholders. A Ph.D., a strong record of peer-reviewed publications focusing on late Cenozoic marine invertebrate paleoecology and paleontology, and demonstrated ability to secure extramural funding are required. Experience in managing large natural history collections and active field programs are highly desirable. The Curator will be expected to build an active and publicly appealing research program, to lead continued improvement of the IP collections, to oversee all NHMLA's programs on invertebrate fossils, and to supervise staff and volunteers of the IP Department. Additionally, the successful candidate is expected to develop working relationships with local universities, mentor students and postdoctoral fellows, strengthen NHMLA's presence in key professional and governmental networks, and maintain research through competitive grants and/or other funding from external sources. The Curator will be expected to participate actively in a broad range of museum activities, including exhibits, education, community science programs, educator and volunteer training, public communications, media interactions, and fundraising activities. A vision and capability to build a research program that can be integrated with NHMLA's ongoing efforts to understand regional biodiversity, and to shape the collections and research in ways that activate both their scientific and public appeal, is paramount.

NHMLA is seeking applicants who have demonstrated experience and commitment working with a diverse community. This is a full-time position with a salary and title commensurate with experience.

Application deadline is February 15, 2019. The starting date is July 1, 2019. Applicants should send a cover letter, vision statement, curriculum vitae, and the full contact information of at least three professional references as a single PDF document to thayden@nhm.org, Marine Invertebrate Paleoecology Curatorial Search.

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

thayden@nhm.org

OakRidgeNatlLab MicrobialGenetics

http://bit.ly/2FI7Vyq The Biosciences Division (https://www.ornl.gov/division/bsd) of the Oak Ridge National Laboratory seeks a full-time technical professional staff member to perform genetic analysis and genetic modification of non-model microorganisms. The Biosciences Division is focused on advancing science and technology to better understand complex biological systems and their relationship with the environment. The division has expertise and special facilities in genomics, genetics, computational biology, microbiology, microbial ecology, biophysics and structural biology, and plant sciences. The Microbial Ecology and Physiology Group focuses on microbial ecology, genomics, and genetics of environmental and engineered organisms. The research is concerned with the basic science underlying bioenergy production, synthetic biology for bioproducts, carbon cycling and sequestration, and biosecurity.

Duties and Responsibilities:

* Collaborate with research teams to design, construct, and analyze biological and environmental samples. * Perform genetic analysis and genetic modification of non-model microorganisms, including targeted gene deletion and overexpression, as well as using library-based genetic approaches. * Work independently to develop, troubleshoot, and execute workflows for cultivation, manipulation, and characterization of non-model microbes. * Contribute to data management, visualization, and analysis as well as writing research publications. * Assist with project management activities. * Oversee instrument installation, maintenance, problem solving and training of new users. * Ensure compliance with environment, safety, health and quality program requirements.

Basic Qualifications

* PhD or MS in Biology, Biochemistry, Cellular and Molecular Biology, Microbiology, Chemistry or a related discipline * Significant contributions to peer-reviewed research publications * 2-4 years of relevant experience * Strong verbal and written communication skills are required to enable effective interaction with research scientists, postdoctoral researchers, and students * Outstanding organization skills, including the ability to coordinate and work productively on multiple projects * Demonstrated experience developing, executing, and troubleshooting molecular biology and molecular genetics experiments, including cloning, genetic modification, sequencing, PCR amplification and strain validation.

Preferred Qualifications

* Experience culturing diverse microorganisms (bacteria, archaea, or fungi) and performing genetic manipulation of multiple hosts systems * Project management skills * Experience with environmental, safety, health and quality programs

Benefits at ORNL: UT-Battelle offers a quality benefits package, including a matching 401(k), contributory pension plan, paid vacation, and medical/dental plan options. Onsite amenities include a credit union, medical clinic, cafeteria, coffee stands, and fitness facilities.

Relocation: Moving can be overwhelming and expensive. UT-Battelle offers a generous relocation package to ease the transition process. Domestic and international relocation assistance is available for certain positions. If invited to interview, be sure to ask your Recruiter (Talent Acquisition Partner) for details.

Josh Michener Staff Scientist, Biosciences Division Oak Ridge National Laboratory 1 Bethel Valley Road, Oak Ridge, TN 37830 https://michenerlab.org "Michener, Josh" <michenerjk@ornl.gov>

SanDiegoZoo SnrResearchCoord DeadlineExtended

The Conservation Genetics group at the San Diego Zoo Institute for Conservation Research is seeking a Senior Research Coordinator to contribute to the application of molecular genomic methods to address critical questions in evolution and conservation. This person will contribute to existing and ongoing research projects in conservation genetics.

Essential functions of this position include participating in collaborative research projects in genomics and bioinformatics; documenting research results and data analysis; contributing to papers in peer-reviewed scientific journals and popular literature; and giving presentations to professional groups and the public.

The minimum qualification for the position is a Masters degree in biology, genetics, bioinformatics or related fields. This position is appropriate for someone with a Masters degree and several years of research experience, or a recent PhD with minimal or no postdoctoral experience. Solid data analysis skills and bioinformatics background are required, as well as knowledge of population genetics and recent molecular genomic methods. Excellent communication and writing skills and the ability to work effectively with others is desirable. For inquiries, please email awilder@sandiegozoo.org. To apply: www.sandiegozoo.org/jobs. Deadline: 1/25/2019. AA/EOE.

– Aryn P. Wilder, PhD Researcher, Conservation Genetics San Diego Zoo Institute for Conservation Research 15600 San Pasqual Valley Rd Escondido CA 92027 760-291-5453

awilder@sandiegozoo.org

StonyBrookU VertebrateEvolution

TENURE-TRACK ASSISTANT PROFESSOR: VERTEBRATE EVOLUTION AND ITS ENVIRONMENTAL CONTEXT DEPARTMENT OF ECOLOGY AND EVOLUTION STONY BROOK UNIVERSITY

As part of a university-wide initiative involving the Turkana Basin Institute, the Department of Ecology and Evolution at Stony Brook University invites applications for a tenure-track faculty position at the rank of Assistant Professor whose research concerns vertebrate evolution and/or its ecological and climatological context. Areas of particular interest include, but are not limited to, phylogenetics, comparative vertebrate morphology, vertebrate paleontology, paleoecology, and paleo-community ecology.

This position is one of five faculty lines being created across campus for researchers whose interests intersect with the goals and resources of the Turkana Basin Institute. We seek a candidate with the potential to augment or build upon one or more of the Department of Ecology and Evolutions current research strengths, while taking advantage of Stony Brooks unique relationship with the Turkana Basin Institute and related programs across campus. The Turkana Basin is a premier site for the discovery and understanding of hominid and vertebrate evolution and the ecological and climatological context of these processes. Candidates need not at present have a research program in the Turkana Basin.

We seek a candidate who will be an effective teacher in undergraduate and graduate courses in the areas of ecology and evolution, and who will develop programs that will enhance the departments tradition of interdisciplinary research. Details of the departments areas of research emphasis and current facilities may be found at http://www.stonybrook.edu/ecoevo/ . The successful candidate must have a Ph.D. in ecology and evolution or closely related field at the time of appointment; preference will be given to those with related post-doctoral experience. The successful candidate must also have the clear potential to establish an internationally recognized, externally funded research program that would include mentoring of graduate and undergraduate students.

Applications are due by March 1, 2019 through AcademicJobsOnline.org at http://academicjobsonline.org/-ajo/jobs/13161 (Position ID: 13161). Applications must include a cover letter, CV, research and teaching statements and the names and contact information of three references. Applications should be addressed to Search Committee, Department of Ecology and Evolution, Stony Brook University, Stony Brook, NY, 11794-2100, USA. Questions should be directed to the Chair of the Search Committee, Prof. Jeffrey Levinton (Jeffrey.Levinton@stonybrook.edu).

Stony Brook University is an affirmative action / equal opportunity employer and educator. If you need a disability-related accommodation, please call the University Human Resources Services Department at (631)

632-6161 or the University Hospital Human Resources Department at (631) 444-4700. In accordance with the Title II Crime Awareness and Security Act, a copy of our crime statistics is available.

Robert Thacker <robert.thacker@stonybrook.edu>

SYSAAF France QuantGenetics

Job Offer: PROPOSAL FOR A "quantitative geneticist" PERMANENT POSITION (To be filled immediately)

Company: The SYSAAF is a non-profit private Research and Development umbrella organization exerting its mission through a delegation officially agreed by the French Ministry of Agriculture. SYSAAF staff has a large expertise in poultry and aquaculture breeding and, at present, provide technical support to around 40 breeding companies running selection programs of more than 30 different avian and aquaculture species. Presently, the SYSAAF employs 20 persons among which 10 highly qualified geneticists and three PhD students. The SYSAAF provide to its members a wide range of expertise ranging from design of breeding programs to implementation of innovative technologies in reproductive biology or domestication of new species. The SYSAAF invests an important part of its resources in developing methods of high throughput phenotyping and in developing methods of genetic and genomic evaluation adapted to high throughput selection data. The SYSAAF scientific and technical expertise evolves permanently through the involvement in research projects conducted in collaboration with scientific partners at the national and international levels and benefiting from National or European Commission (FEAMP, FP7, H2020) financial supports. The participation of the SYSAAF in these projects is a truly unique opportunity to not only be pioneer on the front lines of science but also to contribute to the development of breeding programs by integrating and implementing new scientific innovations and technologies in these programs.

Position: Quantitative Geneticist to head the Genetic Evaluation Group. More specifically, he/she will have to:

(1) initiate and contribute to the development of appropriate genetic and genomic evaluation tools and methods tailored to fit the specific needs of the SYSAAF and the particularities of avian and aquaculture species. He/she will also contribute to the validation of these tools and methods.

(2) participate in research and experimental programs in order to develop innovative strategies allowing the SYSAAF to answer SYSAAF and member company needs.

(3) perform routine genetic and genomic evaluations, as well as contribute to activities of collective interest.

This position requires an ability to work independently, but also an ability to share and collaborate within the SYSAAF and with private and scientific partners.

Profile: PhD or Post-doc in Quantitative Genetic (Professional experience is a prerequisite). Extensive theoretical and practical knowledge in quantitative genetics, genomics and statistics is essential. The candidate must be familiar with genetic evaluation tools based on the methodology of the mixed model using both frequentist and Bayesian methods of estimation (e.g. VCE, BLUPF90, WOMBAT, TM, ASREML). The candidate must also have good skills in the R statistical programming language. He/she will be mostly using Linux servers, ORACLE and ACCESS databases. Further, knowledge in poultry and/or aquaculture productions and skills in statistical modelling and in English will be highly appreciated. Proficiency in French is not a prerequisite for application, but the recruited candidate must learn French during his/her period of integration in order to be able to work efficiently with the SYSAAF national scientific and professional partners. Special interest in technology development and transfer of knowledge towards the SYSAAF member companies is essential.

Localisation: SYSAAF, Centre INRA - Val de Loire, UMR-BOA, 37380 Nouzilly, France.

Application: A CV together with a letter of motivation should be sent by email or postal mail to Dr. Daniel Guémené (SYSAAF Director) (+33 2 47 42 76 43 / + 33 6 62 69 19 58, daniel.guemene@inra.fr, Postal address SYSAAF, Centre INRA - Val de Loire, UMR-BOA, 37380 Nouzilly, France. Website: www.sysaaf.fr Romuald ROUGER

Romuald Rouger <Romuald.Rouger@inra.fr>

UBristol 4 EvolutionaryBiology

Four academic positions available in the School of Biological Sciences, University of Bristol, UK.

The School of Biological Sciences seeks four new academics at lecturer or senior lecturer level. Successful applicants will be research leaders with proven international track records commensurate with experience. They will drive influential research programmes that span the long-standing research strengths of the School: behavioural ecology and sensory biology, ecology and environmental change, evolutionary biology and plant and agricultural science.

Successful applicants will have strong interdisciplinary research portfolios and evidence of academic leadership along with strong commitment and aptitude for teaching at undergraduate and postgraduate level and roles across the spectrum of academic life.

A good fit to existing University Research Institutes and the Faculty of Life Sciences would also be an advantage.

For more details on the School and its research see:

http://www.bristol.ac.uk/biology/ < http://www.bristol.ac.uk/biology/ >

For informal enquiries please contact Prof Claire Grierson (headofschool-biology@bristol.ac.uk).

The closing date for applications is 11:59pm on Thursday 14th February 2019.

It is anticipated that interviews will be held during week commencing 1st April 2019.

For more details, please see:

http://www.bristol.ac.uk/jobs/find/details.html?nPostingId1774&nPostingTargetId1314&id=Q50FK026203F3VBQBV7V77V83&LG=UK&mask=uobext Jon Bridle <Jon.Bridle@bristol.ac.uk>

UCalifornia Davis RNAseqLabTech

The Ross-Ibarra (rilab.org) and Runcie (runcielab.ucdavis.edu) are looking to hire a technician to help out with a massive quantitative genetic analysis of RNA-seq in maize. We are especially interested in candidates with previous experience in library preparation and sequencing. Apply online at: https://www.employment.ucdavis.edu/applicants/jsp/shared/position/JobDetails_css.jsp Jeffrey Ross-Ibarra

Dept. of Plant Sciences 262 Robbins Hall, Mail Stop 4 University of California One Shields Ave Davis, CA 95616

Tel: 530-752-1152 @jrossibarra www.rilab.org Jeffrey Ross-Ibarra <rossibarra@ucdavis.edu>

UCambridge PlantEvolution

The title should be: University Lecturer - University of Cambridge (ecology and evolution) Link: http://www.jobs.cam.ac.uk/job/19419/ Text below: Applications are invited for the post of University Lecturer in Plant Sciences, to take up post in October 2019. Responsibilities include teaching undergraduates; research; supervision of graduate students; other duties associated with academic life. There is the opportunity for the successful applicant to become a Fellow of a College, we are operating a collaboration with Newnham College under the Trinity scheme for Joint Lectureships.

We welcome excellent candidates in all areas of Plant and/or Microbial Ecology including those with an interest in biodiversity conservation. The University has recently established a Conservation Initiative with the construction of the David Attenborough Building at the cost of £60M. This is a vibrant collaborative and interdisciplinary research hub that houses a number of academic groups and members of several NGOs based in Cambridge.

The appointee will teach undergraduates through lectures, ecology and evolution field courses, practical classes and small group supervisions, and will be motivated to further innovate our teaching methods. We expect the successful candidate to develop a research programme that complements and reinforces the existing Departmental research portfolio.

Candidates must have a PhD in a relevant field and an outstanding record of excellence in research that is reflected in their publications. They will have sufficient breadth and/or depth of specialist knowledge in the discipline, and of research methods and techniques to develop research objectives, projects and proposals.

Candidates should be able to teach to a high standard, manage a diverse workload, and have the ability to lead their own research programme.

Please include with your application a detailed CV (including an up-to-date publications list) and a covering letter indicating how you would contribute to teaching and research in the Department. The closing date is 3 March 2019.

Once an offer of employment has been accepted, the successful candidate will be required to undergo a health assessment.

To apply online for this vacancy, please click on the 'Apply' button below. This will route you to the University's Web Recruitment System, where you will need to register an account (if you have not already) and log in before completing the online application form.

Please note if you have not received any news 1 month after the closing date you should consider that on this occasion your application has been unsuccessful.

Please quote reference PD17290 on your application and in any correspondence about this vacancy.

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

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

"A.J. Tanentzap" <ajt65@cam.ac.uk>

UHouston TeachingEvolution

Job Description

Instructional Assistant Professor - Biology - (FAC000800) Organization : H0104 Biology Salary Commensurate with experience Description : The Department of Biology and Biochemistry at the University of Houston invite applications for an Instructional Assistant Professor to begin September 2019. The successful candidate will be responsible for teaching 3 courses/ semester in a highly collaborative setting. These courses may include, but are not restricted to, required courses in Genetics or Cell Biology, electives (e.g., Urban Ecology), and General Biology for non-majors. This is a 12-month, non-tenure track appointment with possibility for renewal. Applicants must have a Ph.D. in a relevant discipline.

Successful candidates will demonstrate broad training, skills in contemporary pedagogy, a strong interest in teaching undergraduates from diverse backgrounds, and a willingness to contribute to the development of student success initiatives and undergraduate programs in the biological sciences. Classroom teaching and course development experience is highly desirable. To apply, candidates should prepare a brief cover letter, names and contact information of three references, curriculum vitae, and a brief (1-2 page) statement of teaching interests and philosophy. Review of applications will start immediately and will continue until the position is filled.

The University of Houston is a Carnegie-designated Tier One research institution, as well as an Hispanic-Serving Institution (HSI). We are also an ADVANCE institution, one of a select group of universities to receive NSF funds in support of our commitment to increase diversity and the participation and advancement of women in STEM. The Department of Biology and Biochemistry is a vibrant unit of 44 tenured/tenure-track and 10 instructional faculty serving roughly 2,500 majors and an equal number of non-majors. As the fourth largest city in the U.S. and the most ethnically diverse city in the country, Houston is a vibrant city in which to live and work. It has multi-national industries, commercial centers, the largest medical center in the world, a robust arts community, professional sports, and is considered the world capital for petroleum exploration and energy.

The University of Houston, with one of the most diverse student bodies in the nation, seeks to recruit and retain a diverse community of scholars.

The University of Houston is an Equal Opportunity/Affirmative Action institution. Minorities, women, veterans and persons with disabilities are encouraged to apply.

Qualifications : Applicants must have a Ph.D. in a relevant discipline. Notes to Applicant: Official transcripts are required for a faculty appointment and will be requested upon selection of final candidate. All positions at the University of Houston are security sensitive and will require a criminal history check. Incomplete applications may not receive full considered.

Required Attachments by Candidate: Curriculum Vitae, Cover Letter/Letter of Application, Teaching Philosophy or Statement

Employee Status : Regular/Benefits Job Posting : Nov 30, 2018, 9:16:05 AM

UH Job Listing URL: https://uhs.taleo.net/careersection/ex2_uhf/jobdetail.ftl?jobÃºC000800&tz=GMT-06%3A00 Best,

Lisa M. Farmer, Ph.D. Instructional Assistant Professor Department of Biology and Biochemistry University of Houston 3455 Cullen Blvd., Houston, Texas 77204 Email: lmfarmer@uh.edu Office: (713) 743-8560

"Farmer, Lisa M" <lmfarmer@Central.UH.EDU>

UNAM Mexico DiseaseEvolution

Humana ante oculos foede cum vita iaceret in terris oppressa gravi sub religioni... Lucretius

The Universidad Nacional Autonoma de Mexico (UNAM) invites applications to fill a tenure-track Associate Professor position at the Departamento de Ecologia de la Biodiversidad, Instituto de Ecologia.

The successful candidate will be required to develop an independent research program on ecology and evolution of disease. It will be expected that she/he develops collaborations, primarily but not exclusively with members of the Department of Ecology of Biodiversity, lecturing regularly at undergraduate and graduate levels is compulsory.

Candidates should hold a PhD in Biology or Ecology and have a background in evolution, epidemiology, and ecology of disease. Mastering of genomic and bioinformatic tools is desirable. We will consider candidates with a strong publication record (> 10 high-impact peer-reviewed papers in the relevant area), a track record of securing competitive funds, and with verifiable experience teaching and supervising students. Fluency in Spanish to perform lecturing is a requirement.

Selection will be based on 1) the strength of the candidates Curriculum vitae, 2) a written research proposal (less than 10 pages) to study ecology and evolution of diseases to understand their dynamics under global change, 3) a brief outline of the research activities for the first year including teaching and student supervision, and 4) a two-page proposal for the following three years outlining how the candidate is planning to increase the scientific and social impact of his/her research project.

The application should include a letter addressed to the director of the Institute, Dr Constantino Macias Garcia stating the candidates reasons to apply, the Curriculum vitae, a brief description of current and future research interests, the documents indicated in numbers 2 to 4 (above), a copy of the PhD title, a copy of birth certificate, and the documents supporting the CV (only the first page of published papers, letters/e-mails indicating that papers have been accepted for publication, and evidence of teaching and theses supervision).

All documents should be sent electronically as a single PDF file to secacad@iecologia.unam.mx. The closing date is Feb 28th, 2019. Shortlisted candidates will be required to send the documents by post to: Instituto de Ecologia, UNAM, Ap. Postal 70-275, Ciudad Universitaria, Ciudad de Mexico, CP 04510, Mexico.

Dr. Juan Fornoni Secretario Academico Instituto de Ecologia, UNAM

maciasg <maciasg@unam.mx>

UTexas Austin REU2019 PlantEvolutionaryEcology

NSF Research Experience for Undergraduates in Plant Field Evolutionary Ecology ' Summer 2019

We seek a talented and diverse group of undergraduate students interested in conducting mentored independent research on the biology of switchgrass (*Panicum virgatum*) and its related genetic model, *Panicum hallii*. This is an exciting opportunity to participate in research studying switchgrass, an emerging biofuel candidate species at one of multiple locations across the United States.

Students will be immersed in a sustained research experience, focused primarily on the field biology of switchgrass. Research will mostly consist of intense field work with additional lab components. While all science majors are encouraged to apply, preference will be given to candidates with a strong interest and/or background in evolutionary ecology, environmental biology, quantitative genetics or agronomy.

How to apply?

- Please visit our website for details; *applications due Sunday February 25, 2019*: https://sites.cns.utexas.edu/juenger_lab/summer-research-opportunities *Who should apply?*

- All undergraduates not in their senior year are welcome to apply

- Must be a US citizen or permanent resident

Program description

- 10 week internship at one of several universities located across the US (see below for list of collaborating institutions), beginning the first week of June

- $4500 stipend + a housing and food allowance, and travel costs to and from host university

- A presentation – poster, lab meeting, or Powerpoint – on research must be completed at the end of the program

Collaborators

- Prof. Thomas Juenger, University of Texas

- Prof. David Lowry, Michigan State University

- Dr. Philip Fay, USDA ARS, Temple, Texas

- Prof. Felix Fritschi, University of Missouri

- Prof. Rob Mitchell, University of Nebraska

- Prof. Arvid Boe, South Dakota State University

- Prof. Yanqi Wu, Oklahoma State University

Robert Heckman <robert.heckman@utexas.edu>

UVictoria BritishColumbia EvolutionaryCellBiology

We welcome applications from evolutionary cell biologists.

The Department of Biology seeks applications for a Tier 2 Canada Research Chair (CRC) in Cell Biology. The successful applicant will be nominated by the University of Victoria for a Tier 2 CRC and, upon approval of the Chair by the CRC Secretariat, will be offered a tenure-track appointment at the appropriate rank. We are a diverse department that fosters a collegial and collaborative environment. Candidates who share this vision and can build tangible links to our departments strengths in developmental biology, cellular neuroscience and/or evolutionary biology/genetics are especially encouraged to apply.

Requirements

The successful nominee will have a PhD and/or post-doctoral training in cell biology. They will have demonstrated potential to develop an externally funded, independent and original research program that focuses on mechanisms of cell function. Candidates whose research has a component relating to human health are preferred.

Candidates will be evaluated against criteria set by the CRC program (www.chairs-chaires.gc.ca/-program-programme/nomination-mise_en_candidature-eng.aspx#s7). In accordance with regulations for the CRC program, Tier 2 CRC nominees must be within 10 years of receiving their highest degree when they are nominated to the Chair (expected nomination by April 2019). However, applicants who are more than 10 years from having earned their highest degree (and where career breaks exist, such as maternity, parental or extended sick leave, clinical training, etc.) may have their eligibility for a Tier 2 CRC assessed through the programs Tier 2 justification process. Please contact the Institutional Programs Office at the University of Victoria for more information (cfi@uvic.ca). Please consult the CRC website < http://www.chairs-chaires.gc.ca/home-accueil-eng.aspx > for full program information.

Candidates should submit a single PDF document that includes a cover letter outlining how the candidate meets the requirements of the position, a CV, and a 2-page description of their proposed research program (including how it complements current departmental strengths). Candidates must provide a 2-page statement on teaching experience and teaching philosophy, including how they have and will support diversity and inclusiveness in teaching and research. Candidates must also include the names and contact information for three referees.

Additional information

Faculty and Librarians at the University of Victoria are governed by the provisions of the Collective Agreement < http://www.uvic.ca/vpacademic/assets/docs/-Collective%20Agreement.pdf >. Members are represented by the University of Victoria Faculty Association < http://www.uvicfa.ca/ >.

Contact information

All application documents should be complied into one pdf file and emailed to: Chantal Lalibert (biology@uvic.ca) with the subject heading °Cell Biology position±. For questions regarding the position please contact Dr. Barbara Hawkins, Chair of the Department of Biology via email (biochair@uvic.ca) or phone (250-721-7091).

Application deadline

The committee will begin reviewing applications on Feb 8, 2019, however, applications submitted after this date will still be considered until the position is filled.

Equity statement

UVic is committed to upholding the values of equity, diversity, and inclusion in our living, learning and work environments. In pursuit of our values, we seek members who will work respectfully and constructively with differences and across levels of power. We actively encourage applications from members of groups experiencing barriers to equity. Read our full equity statement here:

www.uvic.ca/equitystatement . The University of Victoria acknowledges the potential impact that career interruptions can have on a candidates record of research achievement and encourages applicants to explain in their application the impact that career interruptions may have had on their record of research achievement.

Persons with disabilities, who anticipate needing accommodations for any part of the application and hiring process, may contact Francesca Pintucci, Faculty Relations Consultant in the Office of the VP Academic and Provost at (250) 472-5491 or frconsultant@uvic.ca. Any personal information provided will be maintained in confidence.

Steve Perlman Professor Department of Biology University of Victoria

Steve Perlman <stevep@uvic.ca>

Other

AGA EECG Research Awards Deadline Feb1

The American Genetic Association grants Evolutionary, Ecological, or Conservation Genomics (EECG) Research Awards to graduate and post-doctoral researchers who are at a critical point in their research, where additional funds would allow them to conclude their research project and prepare it for publication.

These awards are open to any PhD student or postdoctoral fellow who is a member of the AGA at the time of application - visit the AGA homepage for membership details.

The program is not intended to fund an entire research project, to initiate new research projects, or to provide salary support. Proposals addressing genome-scale questions, or ecological, evolutionary and conservation genetics questions best addressed with genome-scale data, will be given priority for funding. Awards will generally range from $5,000 to $10,000, awarded to the PI or institution (no overhead is provided).

To apply, visit https://www.theaga.org/ Anjanette Baker, AGA Manager

theaga@theaga.org

AGA SpecialEventsAwards Deadline Jan31

The American Genetic Association grants awards each year to its members for support of special events that advance the mission of AGA, particularly to support students to attend the event.

Eligible events include specialized workshops and short courses in topical areas of organismal genetics and genomics, but any event relevant to AGA's purpose will be considered, especially those that could lead to Journal of Heredity articles.

Awards are between $1,000-$15,000, with a total of $70,000 available for 2019. Funding is competitive, and applications must follow the guidelines.

To apply, visit https://www.theaga.org/ Anjanette Baker, AGA Manager

theaga@theaga.org

AMNH NewYork WomenSTEMfellowship

Dear Colleagues,

The BridgeUP: STEM program at the AMNH is excited to announce that the application for the Helen Fellowship is open. This fellowship is a one-year residency for post-baccalaureate, self-identifying females, to devote time immersed in computational scientific research and educational outreach at the AMNH. This fellowship is an initiative at the AMNH dedicated to increasing the diversity of the talent pipeline by providing underrepresented students access to the skills and tools required for the 21st Century.

To learn more about the fellowship and the application process, visit https://www.amnh.org/learn-teach/-higher-education/helen-fellowship . A colorful PDF flyer can be downloaded at this website.

Who is eligible to apply? The fellowship is intended for recent college graduates with a conferred bachelors or masters degree in computer science, natural sciences, applied mathematics, computational science, or other relevant majors prior to the fellowship start date in September.

What are the benefits? Fellows will receive an annual salary of $70,000 plus generous benefits. Funding is also available for research, travel and equipment expenses.

How do I apply? The online application is now open and is due by midnight of February 3, 2019. To learn more about application requirements, visit https://www.amnh.org/learn-teach/higher-education/helen-fellowship . With Regards,

The BridgeUP: STEM Team

Email: bridgeupstem@amnh.org

"BridgeUP:STEM" <bridgeupstem@amnh.org>

ASN FundingSupport RegionalMeetings

Call for proposals: American Society of Naturalists support of regional meetings.

The American Society of Naturalists (ASN) solicits proposals from organizers of regional meetings in the fields of ecology, evolution and behavior. The purpose of these small awards it to promote increased participation in regional conference meetings in the areas of ecology, evolution and behavior and use this support as a way of recruiting new membership to ASN. These awards typically provide subsidized registration for ASN members at these regional meetings. Applicants should submit a brief proposal including summary of the meeting focus, anticipated number of participants, venue and dates. For additional application details and previous awardees please visit: https://www.amnat.org/announcements/-CallRegionalWkshp.html Thanks, Courtney Murren murrenc@cofc.edu on behalf of the ASN Regional Society Liaison Committee

"Murren, Courtney J" <MurrenC@cofc.edu>

ASN StudentAwards LastCall

Applications for the 2019 American Society of Naturalists Student Research Awards are due tomorrow, 31 January.

The ASN Student Research Awards support research by student members that advances the goals of the society: the conceptual unification of ecology, evolution, or behavior. Each award consists of a $2,000 check to the candidate. An applicant must be a member of the ASN (membership is international), must hold a bachelors degree or equivalent, must have passed to candidacy in a Ph.D. program or equivalent, and must be at least one year from completing the Ph.D. Projects in all types of research (i.e., laboratory, field, theory) are encouraged. A total of ten proposals will receive awards. Proposals will be judged on originality, strength, and significance of the questions being addressed, prospects for significant results, and the match between the proposed research and the ASN mission.

For more information: https://www.amnat.org/announcements/AWAStuResearch.html Chris Eckert Department of Biology Queen's University Kingston, Ontario K7L 3N6 Canada chris.eckert@queensu.ca

Christopher Eckert <chris.eckert@queensu.ca>

Avian MoultPatterns data

Dear All,

Me and my colleague are currently working on meta-analysis concerning physiological and environmental factors affecting moult patterns in birds. We are interested in continuous as well as categorical data.

If you have any unpublished data concerning this topic, I would be very grateful if you were so kind to send me this information within the next two weeks.

Best greetings and thanks in advance!

Agnieszka Gudowska

agnieszka.gudowska@uj.edu.pl?

Agnieszka Gudowska, PhD Institute of Environmental Sciences Jagiellonian University Gronostajowa 7 30-387 Krakow, Poland

Agnieszka Gudowska <agnieszka.gudowska@uj.edu.pl>

CallForCollaboration SexRoleEvolution

Call for collaboration: Sex role evolution: testing the impacts of ecology, demography and genes

Sex roles (i.e., courtship, competition for mates, pair bonding and parenting) are among the most diverse social behaviour. Recent research is uncovering key elements of sex role variation, but significant gaps remain. Appropriate sexual behaviour is essential for reproduction, and thus understanding the causes and implications of sex roles are at the core of evolutionary biology and fundamental for the study of life history evolution, physiology and population biology. Understanding sex roles is also important for biodiversity conservation since disruptions to normal sexual behaviour due to environmental changes reduce the viability of wild populations.

Our team has been recently awarded an ELVONAL project of Hungarian Science Foundation to investigate sex role evolution in shorebirds (plovers, sandpipers and allies). The project is based at University of Debrecen (Hungary), and will be carried out between 2018 and 2022. Shorebirds exhibit an unusual diversity of sex role variation, and they provided some of the textbook examples of mating behaviour, parenting and breeding systems. Provisional results suggest that some of this variation is related to adult sex ratios, i.e. the ratios of adult males to adult females in the local population.

To achieve the objectives of this ambitious project, we are seeking collaborators willing to study behaviour, ecology and/or demography of any breeding shorebird population on the planet. To progress, we have developed a data collection protocol that explains field methodology to gather the information we are seeing in this project. We hope the ELVONAL project will lead to joint research publications, and in addition, to exchange of ideas, discussions and follow-up research. We also anticipate that our project will have training and capacity building components, and will impact on conservation for the benefits of shorebirds and people worldwide.

Find out more at: https://elvonalshorebirds.com/ or contact Dr Vojtech Kubelka kubelkav@gmail.com

Tamas Szekely <bssts@bath.ac.uk>

CornellU MicrobialFriendsFoes REU

The Cornell Institute of Host-Microbe Interactions and Disease (CIHMID) is accepting applications for the NSF-funded Microbial Friends & Foes Research Experience for Undergraduates (REU) Summer Program: http://cihmid.cornell.edu/reu-mff.html. Applications are due February 21, 2019.

The Microbial Friends & Foes Program will take place from June 3rd to August 9th, 2019. The program will provide training in the concepts and experimental approaches central to understanding microbial interactions with eukaryotic hosts. Students will learn about broad diversity of microbe-eukaryote interactions through conducting independent research projects, participation in weekly research group meetings, seminars presented by CIHMID faculty, Microbial Friends & Foes Synthesis Panels, CIHMID Summer Symposium, and Microbial Friends & Foes Poster Session. Emphasis will be placed on appreciation of the scientific method and developing effective strategies for conducting research as well as on the synthesis of concepts important to interspecific interactions across diverse systems. In addition, workshops in electronic database literacy, science citation software, research ethics, science communication, and planning for graduate study will be offered to the Microbial Friends & Foes program participants. More information about the program along with a flier can be found at http://cihmid.cornell.edu/reu-mff.html . Students will receive a stipend of $5750, travel subsidy, meal allowance and on-campus housing. Applicants will be asked to identify 3 laboratories of interest, and will be selected in a two-step review process by the program organizers and potential mentors.

WHO SHOULD APPLY

*All undergraduate students interested in understanding microbial interactions with eukaryotic hosts.

*Members of minorities underrepresented in science, undergraduates from small colleges, and first-generation college students.

*Applicants must be United Stated citizens or permanent residents and at least 18 years old.

Teresa Pawlowska <tep8@cornell.edu>

"Teresa E. Pawlowska" <tep8@cornell.edu>

EarlCoreAward PlantTaxonomy

Research proposals are now being accepted for the 2019 Earl Core Student Research Award from the Southern Appalachian Botanical Society. The award provides up to $1,200 in support of student research projects in plant taxonomy, systematics, or ecology. Undergraduate and graduate students are eligible to apply, but the student and advisor must be members of SABS to be considered. More details and the application can be found at http://sabs.us/awards/earl-core-student-research-award/ .Proposals are due by February 28, 2019 to be considered. Awards will be announced in April.

"Wallace, Lisa E." <lewallac@odu.edu>

EcoEvoRxiv

EcoEvoRxiv: We want your preprints! (and also postprints)

EcoEvoRxiv (EcoEvo"archive") is a not-for-profit, online repository for research papers related to ecology, evolution and conservation.

The archived papers can be empirical, theoretical, review or of any other research-related type.

The server can be used for freely and legally sharing of preprints (manuscripts before submissions to journals), postprints, reports, and datasets, which would transparency in ecology and evolution.

There are many benefits to submitting your work to EcoEvoRxiv , including improving the speed and discoverability of scientific findings, promoting interdisciplinarity which would better science and increase citation rate!

Also, EcoEvoRxiv integrates seamlessly with Open Science Framework (https://osf.io/) by the Center of Open Science (https://cos.io/).

For more details about EcoEvoRxov: https://www.ecoevorxiv.com/ For submitting a preprint at EcoEvoRxiv: https://ecoevorxiv.org/ Follow us on twitter:

@EcoEvoRxiv

fonti.kar@gmail.com

ESEB OutreachFund DeadlineMar15

ESEB Outreach Initiative Fund

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

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

The application form can be found on the ESEB website (http://www.eseb.org/prizes-funding/outreach-fund/). Applications will be accepted twice yearly (deadlines March 15, September 15) and should be submitted by email to Ute Moniatte (office@eseb.org; Subject: Outreach).

Dr. Ute Moniatte | ESEB Office Manager| office@eseb.org European Society for Evolutionary Biology | www.eseb.org office@eseb.org

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Finland VolFieldAssist AvianEvolEcol AprilJune

Volunteer field assistant/internship in avian evolutionary ecology

PERIOD: 22.4.-15.7.2019 with flexibility on the start and end dates LOCATION: Turku, Finland

PROJECT Maternal effects play a key role in shaping offspring development and are a source of phenotypic variation. Understanding the proximate mechanisms underlying maternal effects is crucial. I am looking for a volunteer field assistant/intern to a collaborative project on the role of maternal (egg) hormones shaping offspring development and fitness passerines. The work will be conducted in April-July in a nest-box population in Turku, Finland. It is possible to make part of the data collection into an intern project. It is also possible to contribute to labwork.

DUTIES The field assistant/intern will be conducting nest-box monitoring, tasks related to the experiments, ringing and measuring chicks (great tits and pied flycatchers), together with the rest of the team (international). Potentially also blood-sampling. The field work will include long days (sometimes in bad weather) and work during weekends, thus the candidate needs to be prepared for that.

QUALIFICATIONS Suitable candidates should be hardworking, independent and organized, possess good communication skills and good English. Candidates should have a valid driving lisence. Experience in field work with birds, and bird handling/ringing is a definite asset.

WE OFFER We will train the volunteer/student for the fieldwork and bird handling. Travel costs (from Europe) will be covered. The candidate will join an enthusiastic team of researchers and students (French, Finnish, Taiwanese).

If you are interested, please contact me asap and include your CV and a short motivation letter.

Suvi Ruuskanen (suvi.ruuskanen@utu.fi), Department of Biology, 20014 University of Turku.

Suvi Ruuskanen, Academy research fellow Department of Biology 20014 University of Turku, FINLAND

Mobile +358503256547

skruus@utu.fi

FortWorth Texas TwoPaidInternships GardenGenomics

PROJECT TITLE: Global Genome Initiative for Gardens: Genome-quality tissue collection and preservation in Texas, Summer 2019.

POSITION TITLE: Global Genome Initiative for Gardens Internship

TIMETABLE: 14 weeks, May ’ August 2019, expected

WHERE: Botanical Research Institute of Texas; Fort Worth, Texas

Payment: The selected applicants will receive a $2,000 stipend for their work with this project.

PROJECT DESCRIPTION: The Global Genome Initiative (GGI) is a Smithsonian-led international collaboration directed toward collecting and preserving genomic tissues from global biodiversity. The principle aim of GGI is to collect and preserve genome-quality tissue from specimens representing all families from the major branches of the tree of life and 50% of genera. To achieve these targets for global plant diversity, the Global Genome Initiative for Gardens (GGI-Gardens) was formed at the National Museum of Natural History in 2015. In August 2018, the Global Genome Initiative for Gardens (GGI-Gardens) moved its base of operations to the Botanical Research Institute of Texas (BRIT) in Fort Worth, TX. Here GGI-Gardens is building a network of preserved tissue collections from botanical gardens throughout Texas. During 14 weeks from May-August 2019, we will collect plant specimens and preserve genome quality tissues from the flora of Texas, emphasizing living collections in botanical gardens of Texas. The selected applicants for this internship will assist in this effort.

QUALIFICATIONS: Required: Enrollment (or recently graduated) in a program for Bachelor's degree in biology, botany, environmental/life science, or horticulture (or demonstration of equivalent experience). Minimum of one undergraduate- or graduate-level course in botany, plant science, plant ecology, etc. Ability to work outside for several hours, lift 30 lbs of field equipment, and collect plant specimens from herbs, shrubs, and trees in dense, wooded vegetation. A valid driver's license and willingness to drive in and around North/Central Texas.

Preferred: Experience with botanical fieldwork. Research experience in botanical sciences. Basic knowledge of plant taxonomy and major groups of the plant tree of life.

LEARNING OBJECTIVES: The selected, qualified applicant will be trained in the collection of genome-quality tissues from plants in the field and from greenhouses at botanical gardens in Texas. The applicant will receive training for fieldwork and tissue collection using field techniques as well as liquid nitrogen handling. The applicant will also be trained in database management and will have opportunities for basic molecular laboratory research and training.

TO APPLY: Please send the following to abyoung@brit.org with the Subject Line: "GGI Internship: LAST NAME, FIRST INITIAL."

APPLICATION DEADLINE: 15 February 2019

* Â A statement of interest (<800 words) in the position outlining your experience, qualifications, interests, and career and professional goals. * Â Your resume or curriculum vitae. * Â Arrange to have one letter of reference sent by an individual who can attest to your academic and/or professional qualifications for this internship.

If you have any questions, please contact GGI-Gardens Director, Dr. Morgan Gostel at mgostel@brit.org

Morgan Gostel, Ph.D. | Research Botanist | Botanical Research Institute of Texas (BRIT) | 1700 University Drive, Fort Worth, Texas 76107-3400 USA | Phone: 817-332-4441 x253 | BRIT.org | mgostel@brit.org

Morgan Gostel <mgostel@brit.org>

Gabon 2 ResFieldAssist Mandrills

Role description

The Mandrillus Project is a non-profit organisation aiming at longitudinally studying wild mandrills in Southern Gabon. We are currently recruiting Volunteer Field Assistants for our 2018-2019 field season. These positions combine practical research with training and are entirely field-based. The volunteers are trained by and work alongside local field assistants, field managers, sometimes students and researchers, contributing to the research activities of the Mandrillus Project. Following established protocols, the fieldwork will primarily involve daily follows of a natural population of mandrills on foot, collecting data on the behaviour of individually recognisable animals, together with the collection of non-invasive measurements and samples. Please visit the website of the project to get an idea of the scientific programs that are currently running ([http://www.projetmandrillus.com/research-and-conservation.html | http://www.projetmandrillus.com/-research-and-conservation.html]).

Positions available

Two Volunteer Field Assistant positions are currently available, each running for six months from March to August 2019.

What we cover

Once the volunteers arrive in the field site, the Mandrillus Project covers all their work-related costs, including accommodation (private equipped room with air-con and private bathroom, shared kitchen) and a stipend for meals (about

200âÂÂ¬/*month*).*Theassociationwillalsocoverthecostsof* [illegible] *e.Onthesuccessfulcompletionoffield*

Who are we looking for?

These positions are open to all with an interest in animal behaviour and ecology. We are particularly keen to hear from applicants who:

Â Are friendly, easy-going people, happy to live in small team at a remote field site

Â Are strongly motivated, reliable, honest and committed

Â Have good levels of physical fitness and stamina - you will be following the mandrills on foot several hours a day, 6 days per week, over mountainous terrain, in heat

Â Show good initiative, with a willingness to learn and show attention to detail

Â A good level in French is mandatory

What do volunteers get out of it?

Â An amazing opportunity to share the lives of wild mandrills in an equatorial forest landscape

Â An opportunity to learn new skills and gain experience, especially those relevant to research in behaviour and ecology

Â An opportunity to be involved in a long-term project on African wildlife, hosted by an international research institution

Â An opportunity to use this field experience with the Mandrillus Project as a stepping stone on to future Masters and PhD degree courses

Â Experience a new culture and share knowledge with local assistants

Further information

For further details about these positions, including the work involved, our living conditions in the field, preparations prior to departure, and what to bring with you, please see below (and additional information will be provided to successful candidates).

How to apply

If you would like to apply, please prepare a CV and a detailed covering letter that should explain why you would like to work on the project. The CV should include the names of two referees with e-mail contact details.

Applications must be sent at projetmandrillus@gmail.com by January 22 nd 2019. We will notify successfully shortlisted candidates few days after this deadline, and interviews will be held in Montpellier (for local successful candidates) or by skype the following week. Telephone/skype interviews will be possible for overseas applicants:

* * * * * *

The Study Site

Weather

Gabon has an Equatorial climate with little seasonality. Precipitations are important, almost every day from October to May, and days may be hot (up to 30 Â°C), although the Lekedi Park benefits from a cooler weather because of its altitude (600m). The long dry season, from June to September, is characterized by cool weather (temperatures can fall below 18 Â°C) with no precipitation.

Landscape

The Lekedi Park is characterized by a mix of savannas and gallery forests interspersed with rivers and riverbeds. Equatorial Marantaceae forests are found in the area.

Wildlife

The Lekedi park is home to a variety of wildlife including forest buffalos, several Apes (chimpazees, gorillas) and other primates (cephus, nictitans) and, of course, mandrills! Predators include, occasionally, leopards (but don't expect any encounter with them!). Birds and reptiles also abound.

Location

The Lekedi park is located in Southern Gabon. It is only a 1 hour drive from Moanda, the nearest town that comprises hotels, petrol stations,

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JMolEvol change

On January 1, 2019, the editorial leadership for Journal of Molecular Evolution changed, including a new Editor-in-Chief, a new collection of Senior Editors, and a large number of new Associate Editors. With it, the scope of Journal of Molecular Evolution is expanding to include more theoretical and computational work, including software for phylogenetic and other molecular evolutionary analysis, to include more (evolutionary) genomics, to now include molecular evolutionary ecology, and to include more reviews, in addition to chemical and biological evolutionary studies that are currently published.

The new senior editorial leadership is:

Editor-in-Chief

David Liberles, Temple University

Senior Editors

Belinda Chang, University of Toronto, Canada, Gene and Protein Evolution

Aaron Goldman, Oberlin College, Reviews and Perspectives Editor

Jody Hey, Temple University, Theory in Molecular Evolution

Michelle Meyer, Boston College, Chemical and Abiotic Evolution

Bill Murphy, Texas A&M University, Genome Evolution

Andrew Storfer, Washington State University, Molecular Evolutionary Ecology

Arndt von Haeseler, University of Vienna, Austria, Molecular Evolutionary Software and Computation

The new full editorial board can be found at:

https://www.springer.com/life+sciences/-evolutionary+%26+developmental+biology/journal/-239?detailsPage=editorialBoard The new journal description reads, “Journal of Molecular Evolution covers experimental, computational, and theoretical work aimed at deciphering features of molecular evolution and the processes bearing on these features, from the initial formation of macromolecular systems through their evolution at the molecular level, the co-evolution of their functions in cellular and organismal systems, and their influence on organismal adaptation, speciation, and ecology. Topics addressed include the evolution of informational macromolecules and their relation to more complex levels of biological organization, including populations and taxa, as well as the molecular basis for the evolution of ecological interactions of species and the use of molecular data to infer fundamental processes in evolutionary ecology. This coverage accommodates such subfields as new genome sequences, comparative structural and functional genomics, population genetics, the molecular evolution of development, the evolution of gene regulation and gene interaction networks, and in vitro evolution of DNA and RNA, molecular evolutionary ecology, and the development of methods and theory that enable molecular evolutionary inference, including but not limited to, phylogenetic methods.”

We hope you will consider submitting your work to Journal of Molecular Evolution.

David Liberles

jme1@temple.edu

Kalahari VolFieldAssist MoleRatEvolution

We are looking for voluntary field research assistants to assist us with our research on the completely subterranean, highly social Damaraland mole-rat in the Kalahari (South Africa). We are conducting a long-term field study, based at the Kalahari Research Centre, to investigate the life-history, social behavior, demography and microbiome diversity of Damaraland mole-rats (http://kalahari-meerkats.com/kmp/research-publications/damaraland-molerats-group/). Entire groups of mole-rats will be captured and individually marked. Morphological measurements, tissue samples, blood samples and gut-microbiome samples will be obtained before the release of the animals. The field work is physically demanding and weather conditions are challenging (heat during the day, cold during the night). Field work may make trapping during the night necessary. The assistants will mostly be working in small teams but will be embedded in a large research community. This position requires working independently and cooperatively in a remote location on free ranging animals. Research assistants must have a valid driving license. The field work starts in early March 2019 lasts for 3 months. Candidates need to be available for the entire period.

Accommodation is provided, and research assistants are paid a monthly allowance to cover their personal costs and food during the 3 months on site.

There is no formal application deadline and we will review applications as they arrive. We will aim to have the field team appointed by the end of January 2019.

Please apply by email (cover letter + CV) or contact for further information:

Dr Markus Zottl, Linnaeus University, Sweden Markus.zottl@lnu.se, +46722032818

Markus Zottl <markus.zottl@lnu.se>

LMU Munich GeobiologyPaleobiology

Applications for our Master's program "Geobiology and Paleobiology" (MGAP) from non-EU citizens for the winter semester 2019/20 can be submitted until 31 Jan 2019. EU citizens can submit their application from mid-Feb until 31 May 2019.

The Master's program "Geobiology and Paleobiology" (MGAP) is a consecutive, research-focussed, four-semester Master program at the Faculty of Geosciences, Ludwig-Maximilians-Universität Munchen, in collaboration with researchers of the Bavarian State collections under the umbrella of the GeoBio-CenterLMU.

The MGAP program is based on interdisciplinary, research-oriented courses in geo- and biosciences that address patterns and processes of the evolution of life and its habitats on our planet. Principal topics are evolutionary and environmental geobiology and paleobiology, supported by courses in complementary areas e.g., phylogenetics, bioinformatics, statistics.

Details about the curriculum and the application procedure can be found here: https://www.mgap.geo.uni-muenchen.de Dr. Oliver Voigt mgap@geo.lmu.de

"Voigt, Oliver" <o.voigt@lrz.uni-muenchen.de>

Malacologists Conchologists Grants

The Western Society of Malacologists (WSM) is proud to offer a financial stipend for students to study fossil or recent malacological collections to further their research. This award honors the late James H. McLean, Curator of Malacology at the Natural History Museum of Los Angeles County from 1964V2001 and Emeritus Curator until 2013.

*Eligibility: *Graduate, undergraduate, and exceptional high school students may apply. Those proposing to visit collections within daily commuting distance of their residence, university, or high school are ineligible for funding.

*Research Scope: *The student applicants research project must be collections-based and focus on extant or fossil western North American mollusks (freshwater, terrestrial, or marine).

Funding: The maximum award is $1000 (US dollars) and should be used to support travel and accommodation costs incurred by visiting one or more collections. Collection visits of two or more days are encouraged. Applicants need not apply for the full $1000 if it is not necessary.

*Museum(s): *Visits to any University-based or Natural History Museum collection (domestic or international) are eligible. Private collections are ineligible. Student applicants are responsible for confirming their projects feasibility and arranging visit logistics with the University or Museums collections manager and/or curator. Students may apply to visit more than one museum and collection in their proposal. Generally, visits to collections that are within a feasible driving distance away (up to 1.5 hours) from the home institution of the researcher will not be considered as having a high priority for funding.

Deadline: Proposals and recommendations are due *March 1st,* with announcement and notification of awardees in May or June. Funds are available for use until May 15th of the following year.

Proposal Submission: Proposals are to be sent electronically (as one document) to: Jann Vendetti at: jannvendetti@yahoo.com or jvendett@nhm.org, using the subject line: James McLean Student Grant

*Application: *Two pages (single-spaced) with a title, description of the planned research, specific collection(s)/institutions proposed to be visited and why, anticipated visit dates (and length), and a budget justification. Personal information including the applicants name, address, email address, and student enrollment status (where enrolled, major, degree program, anticipated graduation date) should be included.

One recommendation from one graduate, undergraduate, or high school advisor should be sent separately to jannvendetti@yahoo.com with OF APPLICANT: WSM McLean Student Grant in the subject line.

http://westernsocietymalacology.org/grants/james-h-mclean-student-grant-in-collections-based-research/
Conchologists of America (COA) Academic Grants, 2019 Deadline: February 28, 2019 Please see the website: http://www.conchologistsofamerica.org/grants/
Eligibility: - Degree-seeking students and anyone engaging in malacological research is eligible. Typically, 80V90% of applicants are degree-seeking students, and 80V90% of award recipients are degree-seeking students. - Persons of any nationality and country

of residence may apply. - Applicants from previous years may re-apply. - Recipients of previous years may re-apply, but must include a submitted manuscript to or published article in the American Conchologist based on the previous award. - Degree-seeking students must have a letter of recommendations by their advisor emailed to *jannvendetti@yahoo.com *by the Feb. 28th deadline with the applicant's name is the subject line.

* Rules & Guidelines:* - All submissions must be submitted via email as a .doc, or .pdf., preferably in one file. Keep file size under 3 MB. - The proposal must concern a malacological topic with any molluscan taxon or taxa as the focus, e.g., parasite studies should focus on the molluscan side of the interaction. All disciplines from autecology to zoogeography, including paleontology, are eligible. - The project must be self-contained. In other words, with the funding requested it must be possible to answer the question posed. However, the proposal may be a component of the applicant's overall research. - Permanent equipment is not an allowable expense. Time using a piece of permanent equipment (for example, SEM beam time) is allowable. - Institutional overhead is not permitted. - The maximum award is $2500 US. Smaller amounts can be requested and may be more likely to receive funding. Partial funding is possible at the discretion of the Academic Grants Committee. - If a grant is awarded, please consider options to avoid having to pay personal income tax on it (US citizens and residents must provide their

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MinnesotaChicago REUsAndInternshipsEchinaceaProject

Are you interested in gaining field research experience and learning about the ecology and evolution of plants and plant-animal interaction in fragmented prairie? The Echinacea Project is offering positions for students and soon-to-be graduates, including several NSF-funded summer REU positions at our field site in Minnesota, and a 12-month internship in Minnesota for the summer and at the Chicago Botanic Garden for the off-season. With the Echinacea Project, you will survey natural plant populations, measure plant traits in experimental plots, observe and collect insects, and assist in all aspects of research. Interns will have the option to do an independent research project. We have diverse potential projects for students with backgrounds in plant ecology, pollination biology, evolution, statistics, conservation, and computer science. In the past, researchers have conducted on a variety of topics including invasive species, prairie restoration, and plant-herbivore interactions.

No experience is necessary, but you must be enthusiastic, hard-working, and always willing to learn new things. Expect working in the tallgrass prairie for up to 8 hours a day. Housing is provided and there is a stipend. REU participants will do an independent research project.

Information about our positions for summer 2019 (starting in June) can be found at http://echinaceaproject.org/opportunities/. Review of applications will begin on February 28th for REU positions, and March 7th for other positions. Please feel free to email us with any questions you may have.

Michael LaScaleia Research Assistant Chicago Botanic Garden email: echinaceaproject@gmail.com http://echinaceaProject.org/flog/ http://twitter.com/TeamEchinacea Michael LaScaleia <mlascaleia@chicagobotanic.org>

mtDNA PopGenetics

Dear Colleagues,

Has anyone ever used mitochondrial tRNA sequences to investigate population differentiation or species delimitation?

I have some tRNA sequences resulting from the sequencing of a mitochondrial gene and I was wondering if they could be informative in terms of population structure and species difference. What strategies and methods have worked (or not) in your experience?

I'll be happy to share results in this mailing list.

Best,

Chiara

chiara.papetti@unipd.it

Chiara Papetti <chiara.papetti@unipd.it>

Phyloseminar NonTraditionalData FebMar

Here are the next 3 talks on http://phyloseminar.org :

Alexandre Bouchard-Côté University of British Columbia Advances in computational Bayesian methods and their use in large-scale single-cell tree reconstruction Wednesday, February 20, 2019, 10:00 AM PST

I will describe a Bayesian method to reconstruct single cell phylogenetic trees from copy number events such as those that arise in cancers with high genomic instability. The method is motivated by low-depth genome-wide data which can be obtained for increasingly large numbers of cells thanks to technologies such as Direct Library Preparation or 10x Single Cell Genomics. Computing the posterior distribution in this model at scale is challenging. I will describe how recent advances in the field of Bayesian computational statistics can be used to parallelize the posterior inference computation to an arbitrary number of cores, touching on topics such as non-reversible methods and change of measure approaches. The posterior inference methods described are available through an open source Bayesian modelling language called Blang, which can be used for a range of phylogenetic problems including more traditional phylogenetic models, as well as other Bayesian analysis problems. The motivating copy-number-based phylogenetic model is implemented in Blang and available in a cancer Bayesian phylogenetics and population genetics library we are actively developing. This library has been used to infer phylogenetic trees on >4000 cells using >60 cores.

Miriam Shiffman MIT Reconstructing probabilistic trees of cellular differentiation from single-cell RNA-seq data Tuesday, February 26, 2019, 9:00 AM PST

Recent advances in single-cell methods have made tangible how individual cell profiles can reflect the imprint of ephemeral or dynamic processes. However, synthesizing this information to reconstruct dynamic biological phenomena “ from data that are noisy, heterogenous, and sparse, and from processes that may unfold asynchronously ” poses a computational and statistical challenge. We develop a full generative model and inference for reconstructing a dynamic process (cellular differentiation) from many static snapshots (single-cell RNA-seq profiles), with calibrated uncertainties. Specifically, we define cell state by the latent parameterization of a distribution over gene expression space, and model these latent vectors as arising from bifurcating, self-reinforcing paths along a probabilistic tree “ necessitating the design of a new class of Bayesian tree models for data that arise from a latent branching spectrum. In this talk, I explore how our model fills a hole in the existing literature on probabilistic trees, and what having an explicit generative model buys us in the context of reconstructing trajectories to understand cell fate decisions in differentiation.

Aaron McKenna University of Washington Cellular phylogenetics - decoding the developmental history and relationships among individual cells Wednesday, March 6, 2019, 10:00 AM PST

Multicellular organisms develop by way of a lineage tree, a series of cell divisions that give rise to cell types, tissues, and organs. This pattern mirrors the evolutionary relationships between species, though our knowledge of the cell lineage and its determinants remains extremely fragmentary for nearly all species. This includes all vertebrates and arthropods such as Drosophila, wherein cell lineage varies between individuals. Embryos and organs are often visually inaccessible, and progenitor cells disperse by long-distance migration. We recently pioneered a new paradigm for recording cell lineage and other aspects of developmental history that has the potential to enhance our understanding of vertebrate biology. In brief, we engineer cells to stochastically introduce mutations at specific locations in the genome during development. The resulting patterns of mutations, which can be efficiently queried by massively parallel sequencing, can be used to reconstruct lineage using methods adapted from phylogenetics. We demonstrate our technique by tracing the lineage of tens of thousands of cells within individual Zebrafish and Drosophila, relating the lineage of numerous emerging tissue and organ systems.

– Frederick ”Erick“ Matsen, Associate Member Fred Hutchinson Cancer Research Center http://-matsen.fredhutch.org/ ematsen@gmail.com

PymatuningLaboratory GrantsFellowship

Pymatuning Lab of Ecology Grants in Aid of Research

The University of Pittsburghs Pymatuning Laboratory of Ecology (PLE) invites applications for Pape/Darbaker/McKinley Grants in Aid of Research. PLE is a vibrant research and education facility located on Lake Pymatuning in Northwest Pennsylvania. PLE's research facilities are spread across 350 acres and include access to a variety of aquatic and terrestrial ecosystems (http://www.biology.pitt.edu/-facilities/pymatuning/research). Its 10,000+ square feet of laboratory facilities include a field laboratory adjacent to an open field that can be used for large-scale replicated experiments, a modern molecular laboratory, and facilities for animal, plant and aquatic studies.

Pape/Darbaker/McKinley Grants are intended to support researchers in the early stages of their ecological and evolutionary research programs at PLE. Grant proposals are submitted each year in February and several awards are made, generally not exceeding $3,500. Most awards go to graduate students, but consideration will be given to recent Ph.D.s and more senior researchers interested in initiating new work at PLE. The due date for grant proposals is February 22, 2019.

Please visit our website for further details about the application process:

http://www.biology.pitt.edu/facilities/pymatuning/-research-grants Corinne L. Richards Zawacki, Ph.D. email: cori.zawacki@pitt.edu Associate Professor, Department of Biological Sciences and Director, Pymatuning Laboratory of Ecology University of Pittsburgh

"At night I went out into the dark and saw a glimmering star and heard a frog and nature seemed to say, well do not these suffice?" - Ralph Waldo Emerson

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PLE Schwartz Early Career Fellowship Pymatuning Laboratory of Ecology Summer 2019

The University of Pittsburgh's Pymatuning Laboratory of Ecology (PLE) is pleased to offer the Frank J. Schwartz Early Career Research Fellowship of up to $10,000 plus up to three months of station fees and residency costs for the primary investigator (PI). PLE is a vibrant research and education facility located on Lake Pymatuning in Northwest Pennsylvania. PLE's research facilities are spread across 350 acres and include access to a variety of aquatic and terrestrial ecosystems. Its 10,000+ square feet of laboratory facilities include a field laboratory adjacent to an open field that can be used for large-scale replicated experiments, a modern molecular laboratory, and facilities for animal, plant and aquatic studies.

This opportunity is open to researchers holding PhD degrees in any science discipline that can benefit from PLE's resources (http://www.biology.pitt.edu/-facilities/pymatuning). The purpose of the fellowship is to permit researchers to explore new projects or collect preliminary data. Fellowship funds can be used at the PI's discretion to facilitate the research but not for PI compensation. Preference will be given to individuals and projects with the potential to develop into long-term research activities at PLE. We especially encourage applications from individuals in the postdoctoral or early faculty phases of their careers working on projects involving fish, but researchers holding PhD degrees at all stages of their careers and working on projects involving other taxa are also encouraged to apply.

For more information about the fellowship program or research opportunities at PLE, please contact the Director, Dr. Cori Richards-Zawacki (cori.zawacki@pitt.edu).

Applicants should submit a single .pdf file including their CV, a 2-3 page proposal outlining the proposed research, a budget detailing how the fellowship funds will be spent, and planned dates of residence to cori.zawacki@pitt.edu, placing the words "PLE Schwartz Early Career Fellowship" in the subject line of the email.

Corinne L. Richards Zawacki, Ph.D. email: cori.zawacki@pitt.edu Associate Professor, Department of Biological Sciences and Director, Pymatuning Laboratory of Ecology University of Pittsburgh

"At night I went out into the dark and saw a glimmering star and heard a frog and nature seemed to say, well do not these suffice?" - Ralph Waldo Emerson

"Zawacki, Corinne Lee" <cori.zawacki@pitt.edu>

SMBE AwardNominations

This is a reminder that nominations are due January 25th, 2019.

Nominations Due for Prestigious SMBE Awards

Society for Molecular Biology & Evolution

smbe@allenpress.com

Dear SMBE Members,

In 2015, SMBE instituted four new awards for: Early-Career, Mid-Career, and Lifetime Research Achievements, and Service to the SMBE Community. We are now calling for nominations for these awards and ask you to consider nominating your colleagues.

The nominations will be due on January 25, 2019.

Briefly, the Junior Award for Independent Research is intended for nominees in tenure-track positions at the Assistant Professor level or equivalent; the Mid-Career Award is for the research contributions of faculty nearing promotion to Full Professor or in the early stages as a Full Professor; the Lifetime Contribution Award is for exceptional contributions to the published literature in the field of molecular biology and evolution; and the Community Service Award recognizes outstanding efforts on behalf of the Society and the broader scientific community. Awardees will receive a cash prize and a trip to the upcoming SMBE Annual Meeting in Manchester, United Kingdom (July 21-25, 2019).

Here are links to the pages describing these awards:

Allan Wilson Junior Award for Independent Research (https://t.e2ma.net/click/pv0gs/9yk2r1/lktc2f)

Margaret Dayhoff Mid-Career Award (https://t.e2ma.net/click/pv0gs/9yk2r1/1cuc2f)

Community Service Award (https://t.e2ma.net/click/pv0gs/9yk2r1/h5uc2f)

Motoo Kimura Lifetime Contribution Award (https://t.e2ma.net/click/pv0gs/9yk2r1/xxvc2f)

Nominations require a nomination letter, which should clearly indicate the award under consideration and also serve as a recommendation letter; a separate one-page summary of the nominees qualifications for the award; a CV of the nominee; and an additional letter of recommendation. Self-nomination is not allowed. The nominator need not be an SMBE member, but the nominee must be a member of SMBE to be considered for the award.

The materials should be compiled into a single PDF file, and should be emailed to smbe@allenpress.com.

Best wishes,

Laura Landweber Past-President, SMBE 2019 SMBE Awards Committee Chair

810 East 10th Street | Lawrence, KS 66044 US

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

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Community Service Award (https://t.e2ma.net/click/t6n5s/9yk2r1/xxv43f)

Motoo Kimura Lifetime Contribution Award (https://t.e2ma.net/click/t6n5s/9yk2r1/dqw43f)

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Best wishes,

Laura Landweber Past-President, SMBE 2019 SMBE Awards Committee Chair

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

Springer Genomics Books

The following first Population Genomics and Paleogenomics books have been published by Springer Nature.

Population Genomics: Concepts, Approaches and Applications (https://www.springer.com/us/book/9783030045876)

Population Genomics: Microorganisms (https://www.springer.com/us/book/9783030047559)

Paleogenomics: Genome-scale analysis of ancient DNA (https://www.springer.com/us/book/9783030047528)

Om Rajora <om.rajora@unb.ca> Om Rajora <om.rajora@unb.ca>

Survey Functional Traits

In June 2018, we led a workshop at the 5th European Congress of Conservation Biology entitled, “From fungi to flies: broadening the use of functional traits in conservation”. During this workshop, it became evident that researchers across disciplines define and use the terms “traits” and “functional traits” differently, with implications for communication across disciplines and collaborative research.

Now we would like your help to better characterize that diversity by asking you to fill out this 10-15 minute anonymous survey (https://tinyurl.com/ycrqo68q). We would be very grateful if you would take the survey, even if you do not typically work with traits as we are interested in how people interpret these terms in general.

The survey will be available until Friday 14th February.

The survey results will be analysed and included in a manuscript for publication illustrating and discussing the diversity in terminology and how it may affect research outputs and applications. Please do not hesitate to contact us if you have any questions or would like further information about the study.

Sincerely,

Samantha Dawson A. Bradley Duthie Carlos Pérez Carmona Manuela Gonzalez-Suarez Mari Jonsson

– The University achieved an overall 5 stars in the QS World University Rankings 2018 The University of Stirling is a charity registered in Scotland, number SC 011159.

Brad Duthie <alexander.duthie@stir.ac.uk>

Survey PreservingAvianDNA

Do you work with avian blood?

Please, share your experience by filling our survey ’Preserving avian DNA from the wild: your experience of blood sampling, DNA extraction and storage’.

https://www.surveymonkey.com/r/avian_blood_storage It is addressed to biologists and molecular ecologists handling blood samples collected from birds in the field and managing the long-term storage of blood and DNA extracts. We would like you to share with us your past and current experiences, along with the adversities you faced, both in the field and in the lab.

Sincerely,

Irene Di Lecce, Joanna Sudyka, David F. Westneat and Marta Szulkin (University of Warsaw and University of Kentucky)

Joanna Sudyka <joanna.sudyka@cent.uw.edu.pl>

Tenerife Spain VolResAssist ComparativeCognition

PARROT COGNITION (TENERIFE)

VOLUNTEER RESEARCH ASSISTANTS

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

The Max-Planck Comparative Cognition Research Group (CCRG) https://www.orn.mpg.de/Comparative-Cognition-Research-Group-von-Bayern invites applications for volunteer research assistants. The CCRG forms part of the collaboration between the Max-Planck Institute for Ornithology, Seewiesen, Germany, and the Loro Parque Fundación (LPF), Tenerife, Spain. We are currently running various comparative research projects on social and physical cognition in parrots. Interested candidates are encouraged to contact us to enquire about the ongoing projects. Successful applicants can expect to gain a solid insight in the field of Animal Cognition/Experimental Psychology and gain experience in working with psittacids in a dynamic, international research environment. The research is carried out on captive parrots of the LPF, which holds the largest parrot collection and gene reserve in the world (ca. 350 subspecies) for conservation and research purposes.

Logistics:

Voluntary research assistant position starts on 25 January 2019, but applications will be taken until the position is filled. The position requires a minimum of 4 months, but ideally 6 months, continuous commitment at the research station in Tenerife, Spain. Free accommodation in a shared student apartment can be provided. Successful applicants will be responsible for their own transportation expenses to and from the research station (Puerto de la Cruz, Tenerife, Spain).

Important skills/qualifications:

Successful candidates will have:

* completed a degree in Biology or any related field * a strong interest in comparative cognition * high motivation and commitment to the project * reliability, efficiency and an ability to work independently * confidence to interact with animals * previous research experience * good verbal and written English skills * initiative to develop the project * good team work attitude and social skills (potentially shared accommodation between 3 students)

To To apply:

Please send your CV and a cover letter reporting any relevant experience you have and motivation to participate in the project to Dr. Auguste von Bayern (avbayern@orn.mpg.de) and Dr. Matthew Petelle (mpetelle@orn.mpg.de). Contact details of 2 referees may be requested.

“Petelle, Matthew” <mpetelle@orn.mpg.de>

UNorthCarolina Greensboro REU2019 MathAndEvolBiol

REU Opportunity Summer 2019: “Research Experience for Undergraduates in Mathematics and Biology”

The University of North Carolina at Greensboro (UNCG) Department of Biology and Department of Mathematics and Statistics invite highly motivated undergraduate students to apply to our NSF-sponsored Research Experience for Undergraduates (REU) summer program.

Students will engage in one of multiple, co-mentored research projects at the interface of mathematics and biology. While exposure to both disciplines is desired, advanced expertise in both in not required because you will work in interdisciplinary teams.

Topics focus on virus transmission dynamics in honey bees and the evolution of recombination in bacteria. After a brief initial training period starting May 20, the students work on the research until July 26, 2019 and receive a stipend of $5000. Travel support and shared university housing will also be provided.

For more information, visit https://www.uncg.edu/-mat/bio-math/REU/ or contact Dr. Jan Rychtar (rychtar@uncg.edu) or Dr. Olav Rueppell (olav_rueppell@uncg.edu).

Olav Rueppell <o_ruppel@uncg.edu>

Yukon RedSquirrel FieldTechnician

We are looking for field technicians to assist with fieldwork that will run from March 1 to Oct 1 2019. We are looking for technicians for the following different time periods: (a) 1 March-15-May (b) 3 April-3 July, and (c) 20 August - 1 October.

The positions are part of a long-term study of red squirrel ecology, evolutionary biology and physiology. As a member of the study, technicians will be involved with monitoring the reproduction and survival of individual squirrels. Fieldwork will involve live-trapping and handling of squirrels, radio-telemetry, behavioural observation, and locating young in their nests. This is an excellent opportunity to gain experience working with a collaborative research team on a long-term study of a wild mammal.

All fieldwork is carried against the beautiful backdrop of southwestern Yukon, Canada. We will be staying at a rustic field station two hours from Whitehorse, and ˜30 min to the nearest town (Haines Junction). All food and accommodation are provided and technicians are provided with transportation (within reason) to and from the field site either through airfare or vehicles.

Training will be provided and no experience is necessary. Candidates should have an interest in a number of the following (the more the better!): ecology, evolutionary biology, wildlife, field biology, and animal behaviour. The field camp is remote and low tech (no showers, cell phone service, or internet), so successful applicants must enjoy the outdoors and be able to remain a positive and responsible team member under relatively isolated and demanding conditions. Candidates must be in good physical condition, have an enthusiasm for learning and a strong work ethic. KRSP aims to be a welcoming, safe, and inclusive research group and we strongly encourage applications from underrepresented groups.

If you wish to apply for one of these posts then please send a CV with a cover letter and contact details for three references (with e-mail addresses), by email kluaneredsquirrels@gmail.com by January 21 2018 (for positions starting on March1) but applications will continue to be accepted for the later positions. Please also indicate the time period(s) you are interested in.

“Lane, Jeffrey” <jeffrey.lane@usask.ca>

PostDocs

Arizona ComputationalPopulationGenomics

A postdoctoral research associate position is available in the Gutenkunst group, in the Department of Molecular and Cellular Biology at the University of Arizona. The group focuses on computational population genomics, with an emphasis on methods development, including recent forays into cancer genomics. For more information, see http://gutengroup.mcb.arizona.edu or contact Dr. Ryan Gutenkunst at rgutenk@email.arizona.edu.

The postdoc will contribute to an NIH-funded project to develop and apply methods for inferring novel models of natural selection from population genomic data. In particular, the postdoc will work on two-locus methods for inferring the distribution of fitness effects of new mutations, potentially including epistasis. The new methods will be applied to data from humans, Drosophila, and other model organisms. The postdoc will also have the freedom to contribute to other ongoing projects and to develop their own projects that mesh with the groups interests.

Applicants should have a Ph.D. in computational biology, bioinformatics, statistics, evolutionary biology, or a related field. Applicants should have prior computational experience and be motivated, creative, and collegial. Experience with statistical inference for complex models is advantageous. The University of Arizona has great strength in population and evolutionary genetics, offering potential interactions with Drs. Joanna Masel, David Enard, Joseph Watkins, Mike Barker, and others. Computational resources are similarly excellent. The campus is highly interdisciplinary and very collegial. The University of Arizona is an EEO/AA - M/W/D/V Employer.

At 2,500 feet above sea level, culturally diverse Tucson, Arizona is nestled among five mountain ranges in the beautiful Sonoran Desert and is surrounded by Saguaro National Park. Housing is affordable, quality of life is high, and outdoor recreation opportunities include the southernmost ski area in the United States and over 100 miles of bike trails. The area receives over 350 days of sunshine per year and enjoys average high/low temperatures of 82/54 degrees F.

Applications should include a C.V., cover letter, and contact information for three references. Please submit applications through https://uacareers.com/postings/34950. Application review begins Feb 18 and will continue until the position is filled.

rgutenk@email.arizona.edu

ArizonaStateU BiodiversityDataScience

The Biodiversity Knowledge Integration Center (BioKIC) at Arizona State University (ASU) invites applications for a postdoctoral research scholar position in biodiversity data science. The position is part of a new Biodiversity Data Science Initiative launched at ASU and led by Beckett Sterner and Nico Franz. The initiative will focus on building an innovative web platform that leverages theoretical advancements and prototype software for taxonomic concept alignment (https://doi.org/10.1093/sysbio/syw023), with the goal to establish a scalable taxonomic intelligence service that will carry value for scientific audiences, science publishers, government agencies, and environmental consulting firms. The platform will accelerate the growth of high-quality, reproducible biological data by driving the adoption of taxonomic intelligence metadata in scientific datasets and journals.

Position ad: https://sols.asu.edu/sites/default/files/job_12643.pdf This postdoctoral position will focus on connecting the taxonomic intelligence platform to users through designing high-impact use cases and front-end services for data discovery and integration. The position will also involve customer discovery to understand market demand and user specifications for taxonomic intelligence in order to validate and inform the underlying platform design. The successful candidate will therefore have a strong record of achievement in biodiversity informatics, such as implementing scalable queries for knowledge graphs, building data visualization tools, applying machine learning methods, and designing front-end systems. Experience working with external clients, digital curation of biological data, and research in the economic, social and ethical dimensions of data infrastructure are also preferred. Mentoring of students and co-/authorship of peer-reviewed publications, presentations, and of research proposals, will be strongly encouraged.

Exploratory e-mail inquiries are strongly encouraged. Interested applicants should send a one-page research statement, clearly indicating their qualifications and motivation to join the project, Curriculum Vitae, and contact information for three references to nico.franz@asu.edu and bsterne1@asu.edu. The review of applications is rolling until the search is closed. The start date is flexible, with a preference for early in 2019.

Salary is commensurate with experience, with a range of $55,000 to 75,000 annually, plus ASU benefits, for exceptionally well qualified applicants. Reasonable relocation funds are available.

Beckett Sterner <beckett.sterner@asu.edu>

ArizonaStateU EvolutionMedicine

The Center for Evolution & Medicine (CEM) at Arizona State University (ASU) invites applications for the Evolution & Medicine Research Scholars. The program brings talented researchers with a recently awarded M.D. or Ph.D. to the ASU campus to develop and extend their research agendas with opportunities to collaborate with CEM faculty and other members of their laboratories. Additionally, scholars will spend time working with their mentor to develop skills in the areas of outreach, education and grant writing. Possible research areas include, but are not limited to, Exploring how eutherian evolutionary traits, including invasive placentation, sex differences in the immune system, and sex-specific genomic structure results in common disease risk and generates sex differences in health and disease; Identifying evolutionary processes that buffer traditional populations from metabolic disorders, autoimmune diseases/allergies, cancer, and mental health; Leveraging evolutionary medicine insights in mitigating tolerance and resistance associated with the application of health interventions including prevention and treatment; Exploring the long-term evolution of pathogens in humans such as tuberculosis to allow a fine-grained assessment of the evolutionary dynamics affecting transmission and adaptation.

The successful scholar(s) will be an outstanding scientist with wide-ranging interests in evolutionary biology related to disease and health, and an appreciation for interdisciplinary research. Selections are based on academic achievement, creativity, and overlap of interests with multiple CEM faculty. Scholars 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 program. CEM does not support H1B visa status. A background check is required for employment.

Scholars will receive a salary of $60,000 and will have access to funding of up to $10,000 per annum to support their research, of which $1,500 may be allocated for moving expenses. The initial closing date for receipt of complete applications is March 15, 2019; applications will be reviewed weekly thereafter until the search is closed. The earliest anticipated start date is July 1, 2019; the latest is January 1, 2020. This is a full-time (1.0 FTE) benefits-eligible, fiscal year (July 1 - June 30) appointment. The award is granted for a period of two years, with a possible third year. Renewal for the second and possible third year is contingent on performance and the availability of resources. For additional information and policies regarding postdoctoral scholars at ASU, please see http:// provost.asu.edu/postdoc .

By the start date, candidates must have completed a Ph.D. in anthropology, biology, psychology or another natural science field that provides an extensive background in evolutionary biology, or an MD, DVM, DrPH or equivalent level health professional degree. Minimum qualifications include demonstrated proof of advanced degree listed above and research experience in the field of evolutionary medicine by the time of the appointment. Preference will be given to applicants interested in working in a multidisciplinary environment and prior research experience in co-evolution and infectious diseases, regulation of inflammation and other defenses, autoimmune disorders, cancer, genomics, reproductive health, lactation and factors that influence disease susceptibility.

To apply, please email a single pdf document to evmedsearch@asu.edu that contains posting # 12727:

a cover letter explaining your interest in this position and how it could advance your career plans, and please identify two faculty members within CEM that you would be interested in collaborating with. We are specifically looking for scholars that would interface with strategic projects already underway in the Center (see research areas above). a curriculum vitae names and Contact Information for three references

The Center for Evolution & Medicine is a university-wide Presidential Initiative directed by Randolph Nesse. Its mission is to improve human health by establishing evolutionary biology as an essential basic science for medicine, worldwide. It supports research that demonstrates the power of evolutionary biology to advance the understanding, prevention, and treatment of disease, as well as teaching and outreach initiatives. See http://evmed.asu.edu for details and information on Core Faculty. As an interdisciplinary unit, the CEM provides postdoctoral scholars with opportunities collaborate with faculty from a wide-range of disciplines including anthropology, biology, complex systems, computational

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Barcelona Transcriptomics

The candidate will join Marta Mels Transcriptomics and Functional Genomics lab within the Life Sciences Department at the Barcelona Supercomputing Center (BSC). The lab is interested in understanding how the information encoded in our genome determines gene expression variation across all cell types in our body. We ultimately want to understand how these expression changes in both coding and non-coding genes are associated with specific disease states. Expression datasets are accumulating at high speed and development of new and efficient computational tools to extract relevant biological information of large and interrelated data is crucial. Our lab uses novel computational tools and high-throughput functional assays to tackle these questions. The candidate will lead the analysis of a unique dataset of thousands of human transcriptomes in collaboration with researchers at the Broad Institute of Harvard and MIT. To this end, he/she will develop new tools to analyse expression and splicing variation across human tissues and develop statistical methods to find complex patterns across interrelated samples. Finally, the successful candidate will develop and analyse high throughput functional assays to address the question of how genetic variation alters gene expression and ultimately leads to disease.

Requirements

* PhD in Transcriptomics, Genomics, Bioinformatics, Computational Biology, or related fields * Strong publication record * Strong programming skills including proficiency in programming with bash, python, R, perl, or similar, and/or experience working in HPC clusters * Some experience with Next Generation Sequencing data analysis * Capacity to work as a team in a highly collaborative and diverse environment * Capacity to contribute to research projects with novel research ideas and analysis * Excellent communication skills in spoken and written English

Conditions

* The position will be located at BSC within the Life Sciences Department * We offer a full-time contract, a good working environment, a highly stimulating environment with state-of-the-art infrastructure, flexible hours, extensive training plan, tickets restaurant, private health insurance, fully support to the relocation procedures * Duration: Temporary - 1 year renewable * Salary: we offer a competitive salary commensurate with the qualifications and experience of the candidate and according to the cost of living in Barcelona * Starting date: as soon as possible

To apply, visit the site web: _https://www.bsc.es/join-us/job-opportunities/289lstfgr2_ and apply.

email: _recruitment@bsc.es_

– Marina Fernandez

/HR Support/

/Human Resources /

Barcelona Supercomputing Center - Centro Nacional de Supercomputacin

Tel. +34- 934054508

marina.fernandezl@bsc.es

www.bsc.es http://bsc.es/disclaimer Marina Fernandez <marina.fernandez@bsc.es>

Brittany France PopulationGenomicsAphids

Postdoctoral Researcher position in population genomics of asexuality in insects

A 18-month postdoctoral position is available in the team Ecology and Genetics of Insects (https://www6.rennes.inra.fr/igepp_eng/Research-teams/Ecology-and-Genetics-of-Insects), at INRA, Rennes, France, starting in June 2019.

INRA, the French National Institute for Agricultural Research, is an internationally recognized institute conducting research in different fields of biological, agricultural and environmental sciences. The team Ecology and Genetics of Insects, which is located at INRA Rennes research center in Brittany, France, has a strong involvement in adaptive genomics of insect crop pests and gathers experts in population genetics, functional genomics and bioinformatics. Our team has a particular interest in the genomic bases of sex loss in aphids, a group of insects which frequently shows coexisting sexual and obligatory asexual lineages in natural populations.

As part of a project recently funded by the French Research Agency (ANR, http://www.agence-nationale-recherche.fr/en/anr-funded-project/?tx_lwmsuivibilan_pi2%5BCODE%5D=ANR-17-CE20-0010), we are offering a 18-month postdoc position to identify genomic regions associated with reproductive mode variation in the pea aphid Acyrthosiphon pisum, for which important genomic resources (including a complete genome) and functional tools are available.

Highly motivated candidates with a PhD degree and having a strong background in population genetics and evolutionary biology are encouraged to apply. Previous experience with handling and analyzing high-throughput population genomic data is highly desirable. The candidates should also have good communication skills evidenced by scientific publications and oral communications in conferences. Ability to work in a team environment is required.

To apply for the position, please combine cover letter, CV, brief summary of previous research experience (max 1 page) and names and contact information of three referees in one PDF file and send it to Julie.Jaquiery@inra.fr and Jean-Christophe.Simon@inra.fr.

The closing date for applications will be 15th February 2019.

Contact:

Julie Jaquiery, Ph.D.

INRA, UMR Institut de Génétique, Environnement et Protection des Plantes (IGEPP), Domaine de la Motte, 35653 Le Rheu cedex - France

tel: +33 (0) 2 23 48 51 53

Julie.Jaquiery@inra.fr

Jean-Christophe Simon, Ph.D.

INRA, UMR Institut de Génétique, Environnement et Protection des Plantes (IGEPP), Domaine de la Motte, 35653 Le Rheu cedex - France

tel: +33 (0) 2 23 48 51 54

Jean-Christophe.Simon@inra.fr

Related publications:

Simon J-C, Rispe C., Sunnucks P. 2002. Ecology and evolution of sex in aphids. Trends in Ecology & Evolution, 17:34-39.

Jaquiéry et al. 2014. Genetic control of contagious asexuality in the pea aphid. PLoS Genetics 10: e1004838.

Nouhaud et al. 2018. Identifying genomic hotspots of differentiation and candidate genes involved in the adaptive divergence of pea aphid host races. Molecular Ecology.27:3287-3300.

Julie Jaquiery <Julie.Jaquiery@inra.fr>

BrownU EvoDevo

Postdoctoral Fellow: Cell and Developmental Biology, Brown University (Providence, RI)

Position type: Full time, at least for 2~3 years (or maximum of 5~6 years with annual renewal)

- Annual Stipend of $50,000 or higher. Insurance and benefits are separately provided.

- Qualification: PhD in the field of Cell and Developmental Biology.

-Project Description:

(1) Cell and Developmental Biology: Identifying how germline factors contribute to cellular functions and development, using sea urchin embryonic cells and human cancer cells.

(2) Evolutionary Developmental Biology: Discovering how the molecular evolution alters the developmental program and contributes to species diversity, using multiple echinoderm embryos.

-Required skills: Research record in Cell biology, Embryology and Live imaging (e.g. microinjection, optogenetics, and 4D-confocal imaging). Experience in Biochemistry and bioinformatics is also welcomed. The PI will provide necessary trainings both in experiment conducting and manuscript/grant writing.

We greatly appreciate ones independent thinking, creativity, curiosity, enthusiasm, and hard working. Interested individuals should contact the PI (Mamiko Yajima, PhD): mamiko_yajima@brown.edu <mailto:mamiko_yajima@brown.edu>. Please enclose your CV, Cover letter and reprints of your representative works (if any), and the contact information of your three referees. Reviews will begin immediately and continue until the position is filled.

Mamiko Yajima <mamiko_yajima@brown.edu>

Cornell MarineEvolutionaryGenomics

Postdoc in marine genomics

The Hare Lab at Cornell University is recruiting a postdoc with diverse skills to lead genomic aspects of an NSF-funded project to identify and spatially map balanced polymorphisms underlying oyster tolerance to low salinity. We are testing the hypothesis that short-term adaptive responses to environmental stress can involve distinct genetic architectures across a habitat gradient, even at spatial scales with high gene flow. These predictions are for the eastern oyster, a species in which high standing genetic variation and low linkage disequilibrium facilitate testing for polygenic architectures. A first goal for this study is to identify candidate genes for tolerance to low-salinity using whole-genome resequencing of experimental challenge before/after samples, supported by an available chromosome-level reference genome. Results will inform models of evolutionary response to environmental change as well as artificial selection strategies in breeding for aquaculture traits.

In general, this study is motivated by the expectation that dispersing genotypes in high fecundity species will have phenotype - environment mismatches resulting in strong viability selection. As a result, functional genetic differentiation is generated across small-scale habitat heterogeneities within each cohort. A second goal of this project is to measure candidate gene variation along the estuarine salinity gradient and test for associations with salinity variation. Field sampling of Delaware Bay eastern oysters will target larvae, newly-settled juveniles and adults to measure the extent and spatial/temporal pattern of recurrent within-generation selection. Environmental data will provide estimates of lifetime salinity exposures for oysters from different locations within the estuary, informing two replicate years of genetic-environment spatial correlation testing.

In addition to collection and analysis of genomic data at Cornell, this position will include summer work at the Rutgers Haskin Shellfish Lab in southern New Jersey to lead experimental challenge experiments. The ideal candidate will have experimental design experience that informs these experiments, but primary responsibility will be for bioinformatic and population genomic analyses of barcoded whole genome and sequence capture data. Laboratory molecular work will be minimal. The candidate also will be encouraged to develop a related, independent project according to their interests.

Qualifications: A PhD in ecological genetics, population genetics or related field is required. We are looking for a creative and productive scientist with strong computational and bioinformatic skills, good communication abilities, and a publication record commensurate with career stage. The ideal candidate will have previous experience with experimental design generally, or specifically with challenge and/or evolve and resequence experimental designs. Programming abilities are highly desirable.

The position is for 2.5 years with performance review annually. The start date is flexible, but sooner within 2019 is preferred. Information about salary and benefits at Cornell can be found here: https://postdocs.cornell.edu/postdoctoral-associates-benefits . Interested candidates should send a cover letter describing your relevant experience and interest, a CV, the contact information for three references to Matt Hare (mph75@cornell.edu). Review of applications will begin immediately and continue until the position is filled.

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

Matt Hare Associate Professor Department of Natural Resources 205 Fernow Hall Cornell University Ithaca, NY 14853 https://blogs.cornell.edu/harelab/ mph75@cornell.edu 607-255-5685

mph75@cornell.edu

GeorgetownU EvolutionaryGenetics

* Postdoctoral Position in Evolutionary Genetics of Vector Biting *

A postdoctoral position is available in Peter Armbruster's lab at Georgetown University (https://armbruster.georgetown.domains/) to study the evolutionary genetics of vector biting.The focus of the project is to conduct comparative genomics analyses between biting and non-biting lines/populations of three mosquito species: 1) the yellow fever mosquito, /Aedes aegypti/, 2) the northern house mosquito, /Culex pipiens,/ and 3) the pitcher-plant mosquito, /Wyeomyia smithii/.The project will leverage previous work on the genomics of biting in /W. smithii/ recently published in /PNAS/ (see https://bradshaw-holzapfel-lab.uoregon.edu/PDF/PNAS1.pdf). This is a collaborative project with the Bradshaw/Holzapfel lab at the University of Oregon and the Meuti lab at Ohio State University.The position will also include an opportunity to develop additional research projects. The initial appointment will be for two years, with the possibility of extension based on excellent performance and additional funding. Starting salary will be $47,400 per year with benefits. The start date is flexible, but April or May of 2019 would be ideal.

QUALIFICATIONS:

Candidates should have completed their PhD in evolutionary biology or a related discipline with a demonstrated record of research productivity and publication.The project will involve substantial insect husbandry, molecular biology and bioinformatics analyses.Candidates with expertise in two of these three areas will be given preference, and a desire to work in all three areas is essential.

APPLICATION:

Review of applications will begin February 1^st and continue until the position has been filled. Applicants should submit the following material to Peter Armbruster (paa9@georgetown.edu <mailto:paa9@georgetown.edu>) with 'postdoc application' in the subject line: 1) A CV including names and contact information of three references, and 2) A one-page research statement describing previous accomplishments and long-term goals. Informal inquiries prior to submission of a full application are welcome.

The Biology Department at Georgetown (https://biology.georgetown.edu/) is housed in the recently constructed Regents Hall, a state-of-the-art facility.The Biology Department is a vibrant academic community with a diverse set of research groups studying a range of topics in evolutionary ecology. Additionally, Washington D.C. provides exciting opportunities to interact with scientists at other institutions (i.e., NIH, Smithsonian Institution, George Washington University and University of Maryland, etc.).Washington D.C. is an outstanding place to live with world-class cultural attractions and numerous (underappreciated) opportunities for outdoor activities.Georgetown University values diversity and is committed to equal opportunity for all persons regardless of age, color, disability, ethnicity, marital status, national origin, race, religion, sex, sexual orientation, veteran status, or any other status protected by law.

Peter Armbruster, Ph.D. Davis Family Professor Dept. of Biology, Regents 508 Georgetown University 37th and O Streets NW Washington, DC 20057-1229

Office Phone: 202-687-2567 Lab Phone: 202-687-1741 Fax: 202-687-5662

http://www9.georgetown.edu/faculty/paa9/ Peter Armbruster <paa9@georgetown.edu>

HolarU Iceland FishFitness

One-year Post-doctoral position: Evolutionary ecology of Icelandic Arctic charr

Hólar University College, Iceland (Dr. Camille Leblanc and Pr. Bjarni Kristjánsson) seeks a Post-doctoral fellow to study how *Spatial and temporal variation in ecological resources affect fitness and phenotypic traits of multiple populations of small benthic Arctic charr.*

Numerous ecological and evolutionary processes contribute to the generation of biodiversity, and the complexity of their interactions has presented a challenge to our understanding of nature. Our knowledge of the roles of development, natural selection, genetic drift, and gene flow in shaping biodiversity is complicated by the spatial and temporal variability inherent in natural systems. A powerful approach to better understand such processes involves monitoring wild populations over generations and obtaining data including pedigrees, phenotype, and fitness, so that we can directly infer evolutionary parameters, particularly those describing selection and genetic variation. To approach such questions we study cave charr populations found in lava caves in Iceland, which are extensively replicated in space, and time. Seven years of data have been collected on individual fish from 16 populations, and preliminary results show important differences in survival, growth rate, shape, movement and ecology among these populations. The project is a collaboration between Hólar University College, University of St. Andrews in Scotland (Dr. Michael Morrisey), University of Guelph, Canada (Prof. Moira M. Ferguson) and EAWAG in Switzerland (Dr. Katja Räsänen).

We are seeking a talented candidate to conduct analyses of existing data from the previous seven years of field work, particularly analyses of spatial variation in size-dependent growth functions and size-dependent survival. The appointee will work closely with Dr. Michael Morrissey at the University of Saint Andrews in Scotland. The post doctoral fellow will have the opportunity to join the team conducting fieldwork in summer.

The project has been funded by two successive grants from the Icelandic Research Council RANNIS. *The position is funded for one year, *but there are opportunities for the post doctoral fellow to apply for more funding to continue this work.

LOCATION:

The home University is Hólar Univ. College (North Iceland) in the Dept. of Aquaculture and Fish Biology (DAFB - http://holar.is/en/-department_of_aquaculture_and_fish_biology). HUC is situated in the beautiful village of Hólar (Skagafjördur), with offices and research laboratories in the nearby town SauÃºárkrókur. DAFB is an active research centre composed by a dynamic international team of post-doctoral fellows, graduate students and faculty. The beautiful natural setting and easy travel allow both outdoor and cultural activities. This position will include a significant amount of work with the University of Saint Andrews.

QUALIFICATIONS:

The candidate must hold a doctoral degree and have the ability to conduct independent work. Suitable candidates will have a strong background in evolutionary biology as demonstrated by publications in relevant fields. Previous research experience in some or all of: analysis of natural selection, evolutionary quantitative genetics, analysis of longitudinal data from populations, mark-recapture analyses, and Bayesian statistics will be desirable but not essential. The position offers a highly competitive salary of up to one year according to the Icelandic regulation.

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

Applicants should send *a single PDF file named "Cave charr position 2019"* including an application letter with a statement of research interests (max 2 pages), a CV with a list of publications, copies of academic qualifications/transcripts, and the names and e-mail addresses of three academics references, to camille@mail.holar.is latest *March 01, 201*9. The position is available immediately.

For further information contact Camille A. Leblanc (Dept. of Aquaculture and Fish Biology, Hólar Univ. College) (camille@mail.holar.is) or Dr. Michael Morrissey (*mbm5@st-andrews.ac.uk*)

Camille Leblanc <camille@mail.holar.is>

Lisbon MetabarcodingGadflyPetrels

Research Scientist position at the cE3c, Lisbon, Portugal. Job Posting at http://www.eracareers.pt/opportunities/index.aspx?task=showAnuncioOportunities&jobId7754&idc=1 .Application Deadline is January 20, 2018. The cE3c (http://ce3c.ciencias.ulisboa.pt/j) is seeking a Research Scientist to join the team of a project which is focusing on understanding the mechanisms underlying allochronic divergence of NE Atlantic Gadfly petrels (Pterodroma sp).

The Postdoc will mainly focus on using metabarcoding tools to characterize the diet of the NE Atlantic Gadfly petrels and understand how niche specialization might be contributing to the allochronic divergence of Petrel taxa. The Postdoc is also expected to collaborate on other genomic tasks of the project. Other duties include leading authorship of publications, presenting research at conferences, and mentoring junior researchers at the lab.

Applications can be submitted by candidates holding a doctorate degree in Biological Sciences, and related fields, and have specialized expertise in Molecular Ecology and Evolution. General requirements include: 1. Experience in Omic analyses (particularly Metabarconding) and an understanding of the key issues and relevant analytical tools in the field, particularly if applied to the characterization of foodwebs in marine/estuarine ecosystems. Experience with DNA extraction from marine predator diet samples is useful but not essential; 2. Experience with phylogenetic analyses and population genomics analytical tools; 3. Knowledge of one or more programming languages; 4. Excellent writing and communication skills in English language;

The selection jury will only consider facts attested by documents issued by relevant people/authorities (copies of documents, reference letters, etc).

The project and the research position will be part of the Evolutionary Genetics group at the cE3c research center, Faculdade de Ciências, Universidade de Lisboa (http://ce3c.ciencias.ulisboa.pt/), which is a dynamic group studying speciation, population genomics and adaptation in natural and domesticated populations. Within FCUL there is scope for interaction with other groups that also apply Molecular Ecology tools to study the structure of foodwebs in marine and estuarine ecosystems.

Monthly remuneration to be paid is the one set by article 23 (3) of RJEC, corresponding to level 33 of the Single Salary Table, approved by Order no. 1553-C/2008 of December 31st, i.e. 2.128,34 Euros, plus holiday and Christmas allowances, and meal allowance.

All applications for consideration must be submitted online, more information can be found at http://www.eracareers.pt/opportunities/index.aspx?task=showAnuncioOportunities&jobId7754&idc=1 . For questions related to this opportunity, please contact Mónica C. Silva, mssilva[at]fc.ul.pt.

Monica Silva <mssilva@fc.ul.pt>

MARE CIBIO Portugal BioinformaticsEvolGenomic

- New Postdoctoral position in the field of Bioinformatics (Evolutionary Genomics) -

- Application deadline: February 8, 2019 -

We are looking for a motivated and skilled Bioinformatician to take on an active role in an international team working at the leading edge of genomics, environmental DNA (eDNA) metabarcoding and eDNA metagenomics, on a project recently funded by the Portuguese Science Foundation.

This position has an expected duration of 30 months, starting April 1, 2019, and will be based at the Research Center MARE, University of Lisbon, and/or CIBIO, University of Porto, Portugal. There will be plenty of opportunities to interact with scientists locally, and also internationally (Indiana State University and the Norwegian Sequencing Centre).

For more information on the project, contract details and application procedure, please visit: http://www.eracareers.pt/opportunities/index.aspx?task=global&jobId9624 and contact Hugo Gante at _hugo.gante@indstate.edu_ for more details.

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Hugo F. Gante, PhD

Assistant Professor Department of Biology TCGA - The Center for Genomic Advocacy Indiana State University Terre Haute, IN 47809, USA http://hugofgante.com Hugo.Gante@indstate.edu

MNS LouisianaStateU Systematics

Job Posting Title: Postdoctoral Researcher at the LSU Museum of Natural Science

Candidate will conduct research in coordination with one or more of the Curators. The candidate will also be responsible for helping with the laboratory supervision of graduate and undergraduate research assistants and management of the Museum molecular genetics core facility. Ongoing projects in the lab include systematics and population genetics studies of birds, fish, mammals, reptiles and amphibians.

Duties: 70% Conduct active lab research on a semi-independent basis. To prepare and publish scientific manuscripts under the direction of a Curator. To attend, contribute, and where necessary lead relevant meetings. To take the responsibility for planning and developing research methods and techniques within the framework of the research program. Bring new expertise to the research program. To undertake any other duties relevant to the program of research, including field work. To collaborate with research colleagues and support staff internally as appropriate to the research and to actively develop appropriate external contacts and networks relevant to the project and to future funding opportunities. The person in this position is expected to be part of the Museum's vibrant academic community, attending seminars, participating in journal clubs, etc.

30% Responsible for helping with the laboratory supervision and training of graduate, undergraduate, and high school research assistants, and management of the Museum's shared molecular genetics facility. Ongoing projects in the lab include systematics and population genetic studies of birds, mammals, reptiles and amphibians, and fishes. Monitor laboratory cleanliness and safety. Order general lab supplies for the department. Establish and enforce lab rules and regulations, and indoctrinate new staff/students in same at beginning of each semester. Attend regular meetings with the research team and investigators as required. Work with external collaborators as agreed with the investigators.

Min Quals: Ph.D. in Biology or related discipline; Experience in molecular methods, evolutionary biology, and computational biology, strong publication record, ability to manage an active laboratory

To apply, go to: https://lsu.wd1.myworkdayjobs.com/LSU/job/LSU—Baton-Rouge/Postdoctoral-Researcher_R00031615 Jake Esselstyn Museum of Natural Science Louisiana State University 119 Foster Hall Baton Rouge, LA 70803

phone: (225) 578-3083 fax: (225) 578-3075 https://esselstyn.github.io Want to support mammal research at LSU? Donate to the Alfred L Gardner and Mark S Hafner Mammalogy Fund at: https://securelb.imodules.com/s/1585/17/interior.aspx?sid85&gid=1&pgid“14&cid784 Jacob A Esselstyn <esselstyn@lsu.edu>

NatlU Singapore EvolutionaryPhotonics

A postdoctoral position is available in the Evolutionary Photonics lab (http://vinodal.weebly.com) of Vinodkumar Saranathan in the Department of Biological Sciences and Yale-NUS College to study the evolutionary and biophysical/optical basis of color production in butterfly wing scales.

The candidate will systematically identify, and structurally and functionally characterize independent mechanisms of color production in distinct lineages of butterflies, which have convergently evolved to produce certain colors (such as blues), in order to understand the evolutionarily independent coloration strategies Nature employs for the production of similar hues in butterflies. The candidate will also characterize the optical properties of the hierarchical features of scales by performing alterations (using nanofabrication tools) on wildtype butterfly scales and mutant scales, as well as assist with the synthesis of biomimetic reproductions for multi-functional applications, using nanopatterning and other techniques.

The position is initially for two years and can start immediately. The position can be extended up to 4 years. Salary will be competitive and commensurate with experience. Candidates with prior experience in studying biophotonic nanostructures, and familiarity with biomaterials characterization are especially encouraged to apply.

NUS/Yale-NUS offer world-class research labs and infrastructure and a convivial and collaborative environment. Singapore is a lush, green city offering tropical weather year around, a diversity of food, and nearby exotic locations.

Interested applicants should APPLY ONLINE using the NUS Careers portal:

https://nuscareers.taleo.net/careersection/-nusep/jobdetail.ftl?job You may contact me (yncvks@nus.edu.sg) with relevant queries. The deadline for submission of application is January 28th 2019 (Singapore Time)

vinodkumar.saranathan@aya.yale.edu

NIH Bethesda SystemsBiologyGenomeEngineering

The Intramural Research Program of the National Human Genome Research Institute (NHGRI) at the National Institutes of Health (NIH) is seeking a postdoc to join the newly formed Systems Biology and Genome Engineering Section (SBGE), in Bethesda, Maryland.

The sections focus is on genome functionalization: understanding how variation across the genome affects phenotypes. To tackle this question, we will be developing and applying new high-throughput methods. This includes harnessing the strengths of CRISPR, large scale oligo synthesis, and yeast genetics. Research in the SBGE involves both wet lab and dry lab components, giving postdocs the opportunity to develop and sharpen skills in either.

Postdocs in the SBGE will be joining the unique scientific environment at the NIH, with thousands of highly collaborative researchers working on topics spanning basic biology to clinical research. In addition, the Washington DC metro area is an exciting, cosmopolitan place to live, with excellent transit, schools, and attractions.

Qualifications: The successful candidate will have completed or be nearing the completion of their PhD, and have interests in genetics, evolution, or systems biology. The position will require strong oral and written communication skills, as well as fluency in English. It is important that the successful candidate be able to work semi-independently at developing and troubleshooting novel techniques, reading current scientific literature and applying it to their project, and presenting data and ideas through lab meetings, seminars, conferences, and written publications.

To Apply: Interested applications should send a detailed letter of interest to Dr. Meru Sadhu at meru@nih.gov. The letter should include the applicants motivation for joining the SBGE, as well as one or two project ideas that the applicant would be interested in pursuing. In addition, applicants should include their CV and the names of three potential references.

The NIH and SBGE are dedicated to building a diverse community in its training and employment programs.

“Sadhu, Meru (NIH/NHGRI) [E]” <meru.sadhu@nih.gov>

NorthDakotaStateU AvianEvolutionaryPhysiology

Position Description: An enthusiastic and highly motivated post-doctoral researcher is sought to join the lab of Dr. Timothy Greives (timothy.greives@ndsu.edu) in the Department of Biological Sciences at North Dakota State University (NDSU). This is a NSF funded position to study the relationship between reproductive hormones, daily behavioral rhythms and reproductive success in a wild Eurasian songbird (Parus major). The initial length of the contract will be for one year with the opportunity to renew for up to two additional years. This integrative project is being conducted in collaboration with Dr. Michaela Hau at the Max Planck Institute for Ornithology (Seewiesen, Germany). The post-doc will primarily reside in Fargo, ND, but will collaboratively conduct field research in Germany requiring extended stays of up to several months at a time. During this position, the post-doc will gain valuable experience in research design, avian field research techniques, endocrine and molecular techniques, international research experience, and mentoring graduate and undergraduate students. The post-doc is also encouraged to pursue independent lines of research related to this project. The start date is somewhat flexible, but ideally will begin around August 15, 2019.

Minimum: Candidates must 1) have a Ph.D. degree in biological sciences or a related discipline from an accredited institution; 2) have a demonstrated interest in research in physiological or evolutionary ecology; and 3) have strong oral and written communication skills, including an ability to work as part of team and collaborate with others, 4) ability and desire to work both in the United States and abroad in Germany.

Preferred: Preference will be given to candidates with demonstrated interest in 1) behavioral endocrinology; 2) biological rhythms; 3) evolutionary physiology and experience with: 4) avian field research 5) EIA hormone assays, 6) and automated behavioral monitoring, including automated telemetry and RFID monitoring, 7) and a valid drivers license and ability to operate a manual transmission vehicle.

Application: Applicants must submit a cover letter; a curriculum vitae; a description of research experience (2 pages maximum); and contact information (including telephone numbers and e-mail addresses) for three professional references. All application materials must be submitted online at: jobs.ndsu.edu position number 1800953

Review of applications will begin 5 March 2019 and continue until the position is filled.

Questions regarding the search may be sent to timothy.greives@ndsu.edu

Timothy J. Greives, Ph.D.

Assistant Professor

Department of Biological Sciences

North Dakota State University

p. 701.231.9461

"Greives, Tim" <timothy.greives@ndsu.edu>

NortheasternU EvolutionInChangingSeas

A Synthesis Postdoctoral Fellowship is available for the Research Coordinated Network for Evolution in Changing Seas. This is an excellent opportunity for the successful candidate to conduct cutting edge synthesis across disciplines and engage with a global network of researchers studying adaptation to ocean change. The postdoc will have the opportunity to develop their own research questions for synthesis and meta-analysis of existing data.

The fellow will be based at Northeastern University's Marine Science Center and will work closely with PIs Kathleen Lotterhos and Geoff Trussell. NUMSC 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.

Duration is for 24 months with an anticipated start date between January and December 2019.

Qualifications

Must have a Ph.D.; be able to undertake substantially full-time research or scholarship; work under the supervision of a senior scholar.

Specific requirements:

Applicants will be expected to develop and lead projects. Candidates are required to have a Ph.D. We welcome candidates from diverse research experiences. Candidates should have a strong track record of publication; have demonstrated an ability to manage and analyse large datasets; have strong organizational, written, and oral communication skills; and be able to work both independently and as part of a collaborative team. We think diversity is a component of excellence, and welcome applicants regardless of gender, ethnicity, sexuality, age or disability.

Application website: https://neu.peopleadmin.com/-postings/58943 To apply, please be prepared to attach the following materials in a single PDF (noted as cv in the application system):

Â A cover letter Â A CV with contact information for three references Â One peer-reviewed research publication (ideally your most significant or most relevant to this position)

The successful applicant will have many research opportunities through the RCN and Northeastern Marine Science Center. For more information on this job and opportunities that will be associated with the position, please contact Dr. Lotterhos k.lotterhos@northeastern.edu

We will begin reviewing applications on January 31st.

Kathleen 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

k.lotterhos@northeastern.edu

NTU Taiwan Bioinformatics

Postdoctoral Research Fellow Position in mycobacteria bioinformatics analysis Position in National Taiwan University, Taipei, Taiwan

Descriptions: This is a prospective four year funded project on the application of whole genome sequencing (WGS) in investigating transmission dynamics and the diagnosis of drug-resistant tuberculosis (TB) in southern Taiwan. We have a strong team including major medical centers, infectious disease epidemiologists, bioinformaticians, and public health sectors. We will combine genomic data and epidemiologic information to achieve the study aims. The use of WGS is anticipated to provide critical resolution and information for rethinking of TB diagnosis and management.

Qualifications for potential applicants: 1. Ph.D degree in bioinformatics or related fields 2. Familiarity with M.tb is a plus

Requirements: Candidates with independent research experience and good publication records will be given high priority

Commencement date of employment: Depends on the qualification check and approval from the National Taiwan University

Working location: College of Public Health, National Taiwan University, Taipei, Taiwan

Salary: USD25515/year-USD34790/year and is commensurate with qualifications and experience.

Application: Please contact Prof. Hsien-Ho Lin by email (hsienho@ntu.edu.tw), and attach following documents: (1) CV and personal statement (2) Other documents that support the qualification for this position.

jenny1004wu@gmail.com

OakRidgeNatlLab MicrobialHGT

The Biosciences Division of Oak Ridge National Laboratory (ORNL) has an opening for a microbiologist to investigate horizontal gene transfer in microbial communities. Horizontal gene transfer has the potential to disrupt microbial composition, function, and interactions. Through this research, we aim to improve our ability to predict and manipulate these processes.

In this position, you will use techniques from microbiology, genetics, molecular biology, and synthetic biology to measure, replicate, and apply horizontal gene transfer. You will be expected to collaborate with other labs at ORNL, including through the Plant-Microbe Interfaces project (https://pmiweb.ornl.gov/). You will also design and execute laboratory experiments, analyze quantitative data, write and communicate results to the scientific community.

Applications are accepted until the position is filled: https://jobs.ornl.gov/job-invite/219/ Duties and Responsibilities:

- Work with a diverse team of scientists. - Interface directly with internal and external partners in various disciplines. - Present research results at national scientific meetings. - Publish scientific results in peer-reviewed journals in a timely manner. - Participate in project planning and execution. - Maintain detailed and accurate records. - Acquire and analyze data in keeping with project scheduling. - Self-assess experimental research skill set and identify weakness and secure learning resources to address these issues. - Ensure compliance with environment, safety, health and quality program requirements.

Basic Qualifications

A Ph.D. in microbiology, bioengineering, evolutionary biology, molecular biology, or a related field is required. Applicants cannot have received the most recent degree more than five years prior to the date of application and must complete all degree requirements before starting their appointment.

Preferred Qualifications

- Expertise in microbial genetics and physiology, particularly with diverse non-model microbes - Familiarity with evolutionary processes in microbes - Expertise acquiring and analyzing high-throughput sequencing data - Effective writing and presentation skills demonstrated by a strong publication record from previous research - Desire to work both independently and collaboratively as part of a multidisciplinary team

Josh Michener Staff Scientist, Biosciences Division Oak Ridge National Laboratory 1 Bethel Valley Road, Oak Ridge, TN 37830 https://michenerlab.org "Michener, Josh" <michenerjk@ornl.gov>

OhioStateU InsectGenomics

A Post-Doctoral position is available focused on insect genomics and adaptation. The position is available for 1 year, with opportunities for renewal depending on progress and funding support. The position will focus on genomics of adaptation in the soybean aphid (Aphis glycines) and the fall armyworm (Spodoptera frugiperda). Specifically, the research projects will help identify insect genes responsible for overcoming resistance in plant hosts. Candidates with previous experience in bioinformatics, next-generation sequencing analysis, population genomics (including genome scans and QTL) and/or epigenetics are highly desirable. Questions can be sent to Dr. Andy Michel (michel.70@osu.edu, see https://entomology.osu.edu/-our-people/andrew-michel).

Please visit: http://www.jobsatosu.com/postings/92118 Deadline 02/10/2018.

The Ohio State University is an equal opportunity employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sex orientation, gender identity, national origin, disability status, or protected veteran status. EO/AA employer.

michel.70@osu.edu

Portugal GulbenkianInstitute 2 EvolutionaryDynamics

Individuals with any scientific background (i.e., including evolutionary, molecular, or systems biology, mathematics, physics, chemistry, computer science, statistics, and its hybrids) with a genuine interest in evolutionary questions and quantitative approaches are welcome to apply to the available ERC-funded junior and senior postdoc positions under the project "FIT2GO - A toolbox for fitness landscapes in evolution".

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Lab

Building on evolutionary theory, research in the lab revolves around quantifying epistasis across levels of biological organization and across environments, and to study its impact on the population genetics of adaptation and hybridization. We approach these questions through a combination of mathematical modelling, computer simulations, statistical method development, experimental evolution, and data analysis and interpretation. The long-term goal lies in understanding how ecology, evolution, and molecular constraints shape genomes.

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Projects

Postdoc projects will be developed in collaboration with the respective candidate and may be focused on either or several of the following topics:

- develop mechanistic and statistical models of fitness landscapes across environments - quantify intra- and intergenic epistasis and its consequences for adaptation - infer distributions of fitness effects across genetic backgrounds and environments (experimentally and theoretically) - quantify population dynamics and genetics under clonal interference and epistasis - develop statistical methods for experimental-evolution data analysis - study the effects of epistasis on diversity and divergence - develop approaches to predict the cost of antibiotic resistance across environments (in collaboration with Isabel Gordo, IGC) - test predicted mechanisms of drug resistance in influenza experimentally (in collaboration with Maria Joao Amorim, IGC)

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Application procedure

Applications should be sent by email to evoldynamics[@]gmail.com and include a letter of motivation, a CV, and names and contact information of three referees. The earliest starting date is 1 March 2019, and the anticipated duration of each position is 2-4 years (via postdoctoral fellowships or working contracts). Review of applications will begin on January 10, and the call remains open until all positions are filled.

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Location

The Gulbenkian Science Institute is a private research institute located on the coast just west of Lisbon, Portugal, which provides for both a top-level scientific environment and excellent quality of life. The IGC's mission is to meet science's global challenges: to make groundbreaking discoveries in the Life Sciences, to innovate in training, to incubate the next generation of future leaders, and to place science at the heart of society. Potential applicants are encouraged to scroll through the lab and institute websites and to informally contact us to learn more about IGC and the Evolutionary Dynamics Group.

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Dr. Claudia Bank Principal Investigator Evolutionary Dynamics Group Instituto Gulbenkian de Ciência Oeiras, Portugal

Website: https://evoldynamics.org/ evoldynamics@gmail.com

Prague EvolutionaryImmunology

Dear colleagues,

The Evolutionary and Ecological Immunology (EEI) group at the Faculty of Science, Charles University, Prague, is currently advertising a ~year (extandable) PostDoc position in avian evolutionary immunology with deadline for applications 17th February 2019.

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

PostDoc project: Diversified cytokine regulation of inflammation in parrots and passerine birds

Available from April/May 2019 to June 2020 (the starting date is flexible; the contract can be prolonged) Application deadline: 17th February 2019

Cytokines are protein signalling molecules that evolve to precisely regulate immunological processes in vertebrates. Several cytokines modulate inflammation, a well-known Âdouble edged sword' of immunity that can clear a pathogen infection as well as kill the host. Being soluble they have the capacity to systemically affect various tissues, including other physiological systems involved in self-maintenance and reproduction. In this project we are interested in describing the effect of inflammation on brain function and cognition in two related avian clades ' the passerine birds and parrots.

The objective of this PostDoc project is to characterise tissue-specific cytokine expression changes linked to local and/or systemic inflammation in the selected taxa of birds. A biodiversity-based approach will be adopted to reveal interspecific and intraspecific variation in the selected cytokine genes. The main model species of the research will be the budgerigar (Melopsittacus undulatus), the zebra finch (Taeniopygia guttata), the great tit (Parus major) and the house finch (Haemorhous mexicanus). Additional species will be included for interspecific comparison. Methods such as tissue-specific RNA-seq, RT-qPCR and proteomic analysis of cerebrospinal fluid through gel-free quantitative LC-MS/MS will be used (includes wet lab). 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 as well as to understanding the evolutionary processes forming immune defence in vertebrates.

Requirements: We seek for a researcher with experience in molecular genetics, evolutionary genetics, immunology and/or zoology - PhD degree in one of these or related fields and good English language skills (at least basic).

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, ~year contract starting from April-May 2019 (flexible), ending on 31.5. 2020 (flexible, can be extended based on mutual agreement). Salary: 26,000-34,000 CZK per month*# (320,000 CZK-400,000 12,500 ' 16,000 per annum; * standard local salary, fully sufficient to cover living costs in Prague; # the final salary will be adjusted at specific check points based on research productivity). The research fellow will be part of a young and enthusiastic interdisciplinary and international team (http://web.natur.cuni.cz/zoologie/-biodiversity/eei/people) and where she/he will be supervised by Dr. Michal Vinkler (http://web.natur.cuni.cz/-zoologie/biodiversity/eei/people/#post-73). We expect at least two articles being published in international peer-review journals in the period of two years from the beginning of the fellowship. Active participation at international scientific conferences will be encouraged and supported. The research fellow will also contribute to the supervision of students as needed.

Application: Please send (1) CV including a list of publications, (2) copy of PhD diploma, (3) motivation letter, and (3) contact details for 2'3 referees (references) to Dr. Michal Vinkler (michal.vinkler@natur.cuni.cz) by 17th February 2019.

About: Charles University was founded in 1348, making it one of the oldest universities in the world. Yet it is also renowned as a modern, dynamic, cosmopolitan and prestigious institution of higher education. It is the largest and most renowned Czech university, and it is also the best-rated Czech university according to international rankings. There are 17 faculties at the University, plus 3 institutes and 6 other centres. The Faculty of Science was established in 1920 as the fifth faculty of Charles University. It currently has 29 departments, 3 museums and a Botanical Garden. The Laboratory for Evolutionary and Ecological Immunology (team leader Dr. Michal Vinkler) at the Department of Zoology is oriented at research in animal defence against infectious

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Rennes France Bioinformatics

Postdoctoral position in bioinformatics at Agrocampus Ouest, Rennes France: Development of genomic resources on the invasive aquatic plant, water primrose.

The project is funded for 18 months by Region Bretagne Fund with the following eligibility criteria: The candidate must have spent a maximum of 18 months in France during the last 3 years as of May 28, 2018 (ie between May 28, 2015 and May 28, 2018).

Background : Our team is particularly interested in the invasive aquatic species water primerose, of which 2 species are present in France, Ludwigia grandiflora (decaploid, 10x = 80 chromosomes) and Ludwigia peploides (diploid, 2x = 16 chromosomes). These two aquatic species, which are widespread in the national water system, are also capable of invading wet meadows. In order to understand the adaptation of the water primrose to the terrestrial environment, genetic and epigenetic approaches are or will be developed on Ludwigia grandiflora. Since they do not have genomic resources in these two species, their development is essential to carry out such studies. This is why transcriptomic and genomic analysis are in progress to get data to carried out a reference genome and a reference transcriptome. Obtaining these genomic resources will support the genetic and epigenetic studies.

The role: The post doctoral researcher will in charge to generate genome and transcriptome references and to investigate the terrestrial adaptation of water primrose (evolution at short term) throught transcriptomic differential expression. This will include (1) generating de novo assembly from reads produced by new generation sequencing (NGS) from MiSeq and HiSeq technologies (Illumina) as well as MinION (Nanopore), to propose and implement strategies for assembling and annotating genomes or transcriptomes of non-model species, L. grandiflora and L. peploides, (3) to collaborate on the establishment of a methylome in L. grandiflora.

Required qualifications: We are looking for an enthusiastic candidate with a strong background in NGS data analyses (genome sequencing, RNA-Seq), in bioinformatics and statistical analyses (programming with languages R and Python or similar; knowledge in various informatic tools (Ensembl, IPA, cMAP, mirBase, ..) and methods for data analysis (Limma, GSEA). Knowledge in assembly and annotations of polyploid genomes as well as in biology will be appreciated. The successful applicant will possess at least an PHD in Bioinformatic, in systems biology, in informatic or related field. Additional information: The position is based at Agrocampus Ouest in Rennes in the Research unit Ecology and Ecosystem health (UMR ESE, https://www6.rennes.inra.fr/ese_eng/). Rennes (Brittany, Western France) is an historic and dynamic town less than one hour to the sea and two hours to Paris by train.

- Monthly gross salary is 3 145.20 (i.e. 1 781.39 monthly net salary) the six first months then 3 976.89 monthly gross salary (i.e. 2 267.62 monthly net salary)

- Beginning of project: between 01/04/2019 and 01/06/2019 - Deadline : 15/02/2019

To apply, please send an application letter detailing research background and your experience and skills fulfill the requirements listed above your CV and the contact of two references by e-mail to Dominique BARLOY (dominique.barloy@agrocampus-ouest.fr).

Dominique BARLOY <dominique.barloy@agrocampus-ouest.fr>

SaoPauloStateU Brazil AnuranColorationGenomics

The Herpetology Lab of the Sao Paulo State University (UNESP), campus of Rio Claro, Sao Paulo, Brazil, seeks a highly motivated candidate for a postdoctoral fellowship linked to the project "Colours hidden in the forest: evolutionary genomics of colour patterns in Neotropical frogs", funded by FAPESP. The successful candidate will live in Rio Claro, state of Sao Paulo, Brazil. Moreover, part of the project will be held at the University of Porto, Portugal, and the candidate should be willing to spend some seasons in Portugal. The initial duration of the postdoctoral position is 24 months.

The candidate must have obtained his doctorate within the last two years in Zoology and must have published at least one article from his doctorate in international and high impact journals. In addition, due to the interdisciplinary nature of the project, it is necessary for the candidate to have experience (proven through scientific publications) with high-throughput sequencing and morphological and bioacoustics analyzes of Neotropical anurans. Experience with family Hylidae *sensu lato *is highly desirable. One of the objectives of the project is the training of personnel, and it is essential that the candidate has prior experience with student mentoring. It is also desirable that the candidate has attended some kind of course or workshop in high-throughput sequencing and / or bioinformatics.

The candidate must have excellent verbal and written communication in English, and it is also necessary that the candidate can communicate in Portuguese and have experience with fieldwork in the Neotropical region. The project is a partnership between Brazil and Portugal, and it is essential that the candidate has had previous international experience curricularly demonstrated.

The vacancy is open to Brazilians and foreigners. The selected candidate will receive FAPESP Post-Doctoral Fellowship in the amount of R$ 7,373.10 per month (about US$ 2,000) and Technical Reserve equivalent to 15% of the annual value of the scholarship to meet unforeseen expenses directly related to the research activities.

Interested candidates should send the *curriculum vitae* to Professor Célio Haddad (haddad1000@gmail.com) with the subject, in the upper box: “APPLICATION FOR POST-DOCTORATE POSITION” until 23:59 (GMT -3:00) on February 25, 2019. The result will be announced within two weeks after the deadline for submissions, by e-mail.

The Project

The study of the evolutionary processes that originate phenotypic diversity is one of the most important endeavours in biology because it can offer insights into the process of adaptation in natural populations. Colouration patterns are remarkable traits for studying the mutational mechanisms underlying phenotypic diversity and how these affect patterns of evolutionary change. Among vertebrates, amphibians are one of the most interesting groups, exhibiting a vast variation in colouration, whose function has been mainly associated with thermoregulation, UV protection, conspecific communication, and predator avoidance. Despite significant advances have been made on this topic in both invertebrates and vertebrates, the genetic basis of colouration in amphibians is still surprisingly unknown. The South American leaf-frogs of the *Phyllomedusa burmeisteri* group, which have been widely studied by our research team, is a compelling case to study the evolution of colour pattern diversity in amphibians. First, they present striking variation in the patterns of bright colours at the hidden surfaces of thighs, which have been interpreted as a case of aposematism, one of the most widespread defensive strategy among Neotropical amphibians. Second, colour morphs variants coexist in some populations, offering, thus a unique opportunity for genetic mapping studies. Finally, these species meet in a well-defined contact zone, making this system an excellent model to understand the impact of colour polymorphism in the dynamics of speciation, and how selection shapes both phenotypic and genetic variation. The proposed research seeks to investigate the *genetic bases and evolutionary processes underlying colour variation in amphibians*. To this end, we will 1) perform a genome-wide association analysis using high-throughput DNA sequencing techniques, including exome capture and RNA sequencing; 2) study gene expression of associated genes in several developmental stages; and 3) investigate patterns of allele frequency change across the contact zone for causative loci and randomly chosen markers. Beyond these specific goals, we are convinced that the genomic data generated for the target species will be an important resource for further evolutionary studies, conservation efforts, and in particular for human medicinal research, since phyllomedusids are a rich source of peptides with great nanobiotechnological applications. With an International team of

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StanfordU Hybridization

Postdoctoral position - Stanford University - Evolutionary genetics

Description: The Schumer lab (https://schumerlab.com) has a postdoctoral position available for motivated and creative scientists with a background in population genetics, evolutionary genetics, or bioinformatics.

Our lab focuses on understanding the role of hybridization in evolutionary processes. A major goal of the lab is to understand the mechanisms of selection on hybrids, from identifying loci involved in hybrid incompatibilities or adaptive introgression to characterizing the impact of genetic processes such as recombination on hybridization. Research in the lab combines empirical and computational approaches with a particular focus on the genetics of natural hybridization. Possible projects include characterizing changes in the local recombination map in hybrids of several species and analyzing dense time-series data generated from natural hybrid populations.

Responsibilities: The successful candidate will lead the analysis of genomic datasets to address questions about hybrid genome evolution. The main responsibilities of this position include conducting research, leading the development of bioinformatics pipelines, working with large genomic datasets, working with other lab members and collaborators, and preparing results for publication. Other responsibilities include attending regular lab meetings and journal clubs, presenting research at scientific meetings, and being an active member of the Eco-Evo community at Stanford.

Minimum qualifications required at the time of application: - Completion of doctoral degree requirements except the dissertation in population genetics, evolutionary biology, or a related field. - Programming experience (Python/Perl, R or other programming languages) - Experience with genomic datasets

Additional qualifications: - PhD in population genetics, evolutionary biology, or a related field - Established track record of research productivity and independence - Experience with relevant theory or methods (e.g. analyses of admixture, construction of recombination maps, local ancestry inference) - Willingness to work closely with collaborators and lab members

How to apply: Applicants should submit the following materials to schumer@stanford.edu: 1) A curriculum vitae 2) One-page summary of research interests 3) Contact information for 3 references

Salary: This is a full-time position. Salary is commensurate with qualifications and experience.

The earliest start date is September 2019.

schumer@stanford.edu

StonyBrookU NY EvolutionaryGenomics

The Veeramah Lab at Stony Brook (http://life.bio.sunysb.edu/ee/veeramahlab/index.html) has an opening for a postdoctoral researcher to begin in April 2019 (earlier or later start dates may be negotiable).

The successful applicant will lead an NIH funded project using whole genome sequencing data to understand adaptation of marine Threespine Stickleback that have recently colonized freshwater lakes. We are studying the evolutionary trajectories of adaptive alleles by sequencing samples in time-series from young lake populations. The project will primarily involve bioinformatic processing, population and evolutionary genetic analyses of single sample and Pool-seq whole genome data, and some minimal sample preparation for sequencing.

The successful applicant should have or will shortly obtain a PhD in the areas of population, evolutionary or anthropological genetics, while at least some computer programming experience (particularly in python, equivalent or lower level languages) is required. Prior experience analyzing 2nd generation sequencing data and/or population genetic modeling is desirable.

Applications will be accepted until February 14th 2019. Applicants should a submit a State employment application, cover letter, resume, two references and a one page research statement through the official online application:

https://stonybrooku.taleo.net/careersection/post_docs/jobdetail.ftl?job04039&tz=GMT-05%3A00 The official REF# is: 1804039

Queries regarding this position can be made by email to: krishna.veeramah@stonybrook.edu

krishna.veeramah@stonybrook.edu

TempleU PlantReproductiveEvolution

The Spigler Lab in the Department of Biology at Temple University is looking to hire a Postdoctoral Fellow. The Postdoc will be involved in an ongoing project on pollinator-mediated selection of floral traits and have opportunities to design and implement new studies related to areas of active research in the lab, including: plant-pollinator interactions, mating system evolution, population genetics/genomics, demography, and floral nectar chemistry. There are also numerous opportunities to mentor undergraduates in research and to participate in outreach efforts. Additional information about the Spigler lab can be found at http://rachelspigler.weebly.com Candidates must have a PhD in Ecology, Evolutionary Biology, Botany, or related field; experience designing, conducting, and managing field and greenhouse studies; and strong quantitative skills. Ability and willingness to travel to field sites, for up to weeks at a time, during the summer flowering season is required. A demonstrated track record of publications, excellent communication and time-management skills, a strong work ethic, and attention to detail are also essential.

The position is anticipated to begin May 2019 and to last for one year, with the possibility of extension based on satisfactory progress and funding. Salary is commensurate with experience, and benefits are provided. Interested applicants should send the following as a SINGLE PDF file by email to Rachel Spigler (rachel.spigler@temple.edu): 1) a short statement (1-2 pages) on research interests, previous experience, and motivation for applying; 2) curriculum vitae, 3) contact information for three references. Review of applications will begin immediately and continue until the position is filled.

About the Biology Department at Temple University: Temple University is a large, comprehensive public research university in Philadelphia, PA, with more than 37,000 undergraduate, graduate, and professional students enrolled in over 400 academic degrees. The Biology Department at Temple (https://bio.cst.temple.edu/) represents an active research community with strengths in ecology, genomics, conservation, and evolutionary biology and is home to the newly formed Center for Biodiversity (http://cst.temple.edu/research/centers-and-institutes/center-biodiversity), Center for Computational Genetics and Genomics (https://bio.cst.temple.edu/~hey/CCGG/), and Institute for Genomics and Evolutionary Medicine (http://igem.temple.edu/).

Rachel Spigler <rachel.spigler@temple.edu>

UAberdeen SpeciationModellingSulwesi

30 month, full-time postdoctoral researcher in School of Biological Sciences, Aberdeen, UK

Forecasting biodiversity losses in Wallacea from ecological and evolutionary patterns and processes

We are seeking a highly motivated post-doctoral researcher in evolutionary modelling to join an exciting, NERC-funded project investigating the evolution and diversification of taxa on the Indonesian island of Sulawesi. The successful candidate will be one of two post-doctoral researchers working on this highly collaborative project with researchers at the University of Aberdeen, Bangor University and the University of Nottingham. The Research Fellow will join the School of Biological Sciences at University of Aberdeen and spend a portion of their time in Sulawesi.

Candidates should hold a PhD in evolution, ecology or genetics and have research experience either in (1) evolutionary biology, molecular ecology or a related discipline, preferably in relation to speciation or prokaryotic diversification or in (2) developing spatially-explicit individual-based models. The Research Fellow will be responsible for developing models incorporating both paleogeographic dynamics and speciation processes to deliver new understanding of the patterns of species diversity that are observed on Sulawesi today. They will work with the project team to develop and apply models for eukaryotes and prokaryotes and will be involved in work comparing model outputs with empirical patterns gained by other team members. Finally, the models will be used to forecast ecological and evolutionary futures for the island.

Experience in developing evolutionary and/or ecological theory and the ability to develop efficient computer simulation code are both desirable, as is the ability to work collaboratively on writing and analysis for publication. Experience in one or more of the following would also be useful: speciation (or prokaryotic diversification) modelling, high performance computing, geographic information systems, approaches for data-model integration.

This is a fixed term appointment until 13 November 2021. Starting Salary: £33,199 pa (Grade 6). Preferred start date is 01/04/19 or as soon as possible thereafter.

See https://tinyurl.com/yct4e7eh for further details and how to apply.

Closing date for applications: 07/02/19.

For informal enquiries contact Justin Travis (justin.travis@abdn.ac.uk)

Mae croeso i chi gysylltu gyda'r Brifysgol yn Gymraeg neu Saesneg

You are welcome to contact the University in Welsh or English

Rhif Elusen Gofrestredig 1141565 - Registered Charity No. 1141565

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

UBielefeld Germany FunctGenomicsSpermComp

Postdoc position in Evolutionary Ecology and Functional Genomics

One Postdoc or PhD position in evolutionary ecology and functional genomics is available at the Faculty of Biology at Bielefeld University in the Evolutionary Biology group (PD Dr Tim Schmoll, see http://www.uni-bielefeld.de/(en)/biologie/Evolutionsbiologie) in collaboration with the Department of Animal Behaviour (Dr Peter Korsten, see http://www.unibielefeld.de/biologie/-animalbehaviour). The position is available immediately for 24 months (Postdoc) or until 31.12.2021 (PhD) and is funded by the German Research Foundation (DFG) within the collaborative research centre (SFB/TRR 212) A Novel Synthesis of Individualisation across Behaviour, Ecology and Evolution: Niche Choice, Niche Conformance, Niche Construction (NC3).

The goal of this project (project B04 of the collaborative research centre) is to test how male Zebra Finches conform to their social niche as set by the prevailing level of sperm competition. This will allow us to understand how individual variation in sexual competition generates individual variation, and covariation, in both competitive traits and parenting behaviour. The successful candidate will closely work together with a PhD student to (i) quantify male social niche conformance by analysing adjustment of sexual competitiveness including behavioural (e.g. aggression) and ejaculate (e.g. sperm motility) traits; (ii) identify the underlying mechanisms of social niche conformance on the hormonal (via endocrinological profiling) and the gene expression (via RNAseq) levels; (iii) assess the adaptive significance of niche conformance under a niche match/mismatch paradigm; and (iv) test for trade-offs between investment in sexual competitiveness versus paternal care. A sub-project A will primarily focus on male social niche conformance through adjustment of behavioural traits and the hormonal mechanisms underlying niche conformance. A sub-project B will primarily focus on male social niche conformance through adjustment of ejaculate traits and the gene expression underlying niche conformance. Note that the position offered here is exclusively for sub-project B.

The collaborative research centre: The position will be embedded within a larger collaborative research centre (SFB) comprising 20 principle investigators, 15 postdocs and 18 PhD students based at Bielefeld University, the University of Münster and the University of Jena. The aim of the SFB is to produce a conceptual and empirical synthesis of individualisation across behaviour, ecology and evolution. The SFB will provide exceptional opportunities for interdisciplinary collaboration and academic networking, together with structured training, scientific exchange and early career support programmes. Full details of the SFB can be found at www.uni-bielefeld.de/-biologie/crc212 . Main responsibilities

* Research tasks (90%): - Designing and conducting laboratory experiments in which zebra finch males are exposed to different levels of sexual competition - Maintaining a zebra finch stock population and breeding of experimental birds - Processing of tissue samples for transcriptomic analyses - Bioinformatic processing of high-throughput sequencing data to quantify gene expression - Phenotyping sperm samples using a newly established computer-assisted sperm analysis system and other methods - Assisting in taking behavioural recordings - Statistical analyses of experimental data - Collaborating with other research groups in the collaborative research centre - Writing scientific publications for international peer-reviewed journals

* Organizational tasks in the research groups and collaborative research centre (10%)

Applicants' profiles

We are seeking a bright, highly motivated and creative student with - a PhD (for the Postdoc level) or university degree (for the PhD level) in a relevant discipline with specializations in one or more of the following fields: bioinformatics, transcriptomics/genomics, animal behaviour, behavioural ecology, behavioural physiology, evolutionary ecology, and/or veterinary science, - a keen interest in using molecular genetic methods to answer behavioural and life history questions, - experience with bioinformatic processing of high-throughput sequencing data or a keen interest in acquiring relevant skills (excellent training opportunities available), - experience with statistical analysis (preferably using R), - ability to work both independently and as part of a team, and - excellent oral and written communication skills in English.

The following qualifications would additionally be of advantage: - publications in peer-reviewed international journals, - experience with sperm phenotyping

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UCalifornia Berkeley WheatGenomics

A postdoctoral position in wheat genomics is available in the Krasileva Lab in the Department of Plant & Microbial Biology, UC Berkeley. Our research is focused on plant genomics and plant immunity. Plants are able to recognize and defend themselves against diverse pathogens. Plant immunity is innate, and therefore its diversity is specified on the population level rather than within a single organism. We study both natural and induced variation in wheat to understand how to enhance plant defense responses. Specifically, we are working with wheat mutagenized populations that have been screened against wheat yellow rust pathogen in the field. We have already identified mutant lines with enhanced resistance and are interested in isolating the causative mutations using genomics approaches, such as mapping-by-sequencing. We are also sequencing clusters of rapidly evolving disease resistance genes from natural wheat accessions, which will allow us to observe how domestication and polyploidization affected wheat immunity. The long-term goal of this project is to isolate specific nucleotide changes that enhance plant resistance and introduce them to crops using genome editing technologies. The candidate will work closely with PI and other lab members to design and lead research on wheat genomics and plant immunity. The candidate will be responsible for analyzing mapping by sequencing data to map causative mutations from mutagenized lines. In parallel, the candidate will conduct hypothesis driven research in the areas of comparative genomics looking at the evolution of plant disease resistance in polyploid wheat in comparison to its wild relatives, investigate the association between disease resistance genes and dangerous elements with the goal to determine how disease resistance genes proliferate in genomes and form new gene fusions. To do this, the candidate will write scripts, work in high performance computing environment, summarize data in figures and provide first drafts of publications. The candidate will have the opportunity to mentor undergraduate students and to provide guidance to graduate students.

Krasileva Lab, an interdisciplinary group of people who combine new technologies, basic and translational research. Our research program spans plant genomics and plant-microbe interactions. Our common goal is to understand plant innate immunity, a system that maintains plant health and to make an impact on agriculture and food security. We focus on evolution and function of plant immune genes, as well as the mechanisms that regulate genetic diversity. The postdoc will work closely with PI and other lab members to design and lead research on wheat genomics and plant immunity.

To read more, please visit Krasileva Lab website (https://krasilevalab.org/) and look through the Krasileva Lab Charter (https://tinyurl.com/ybvvq5zy).

Basic Qualifications

* Advanced degree or enrolled in advanced degree program at the time of application.

Additional Qualifications

* PhD (or equivalent international degree) required by the appointment start date. The candidate may have no more than four years of post-degree research experience by start date.

Preferred Qualifications

Demonstrated practical experience in next generation sequencing analysis and bioinformatics

Demonstrated theoretical understanding and practical experience in areas of mapping by sequencing, population genetics, comparative genomics

Demonstrated research effort in formulating testable hypotheses, experimental design, detailed description of data analysis, version-controlled code

Demonstrated ability to work independently and collaboratively as part of a team

Demonstrated ability to produce scientific results and to publish papers in international peer- reviewed journals

Demonstrated effective written and communication skills

Appointment:

The targeted start date for this position is early 2019. The initial appointment is for one year, with renewal based on performance and funding availability. This is a full time appointment.

Salary and Benefits

The annual salary range for this position is $50,760 to $59,100. Salary will be commensurate with

qualifications and experience. Generous benefits are included https://vspa.berkeley.edu/postdocs Interested individuals should include a 1-2 page cover letter that summarizes research interests and professional goals, along with a current CV and the names and contact information of three references. Letters of reference may be requested for finalists.

Questions regarding this recruitment can be directed to Ksenia Krasileva at kseniak@berkeley.edu

The total duration of an individual's postdoctoral service may not exceed five years, including postdoctoral service at other institutions.

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UCalifornia Davis PopulationGenomics

Postdoctoral Research Fellow Position in Population Genomics at the University of California, Davis

Description: The Vector Genetics Lab (VGL) at the University of California, Davis has a post-doctoral position available for a highly motivated candidate with a background in population genetics/genomics. The VGL is dedicated to research and training in the areas of population & molecular genetics, genomics and bioinformatics of insect vectors of human and animal disease. We have developed a program aimed at expanding knowledge that may be applied to improving control of disease vectors and that also addresses problems of interest in the field of evolutionary genetics. See details at: https://vectorgeneticslab.ucdavis.edu/ Ongoing projects include work on the following systems: - Island populations of Anopheles mosquitoes in islands off the coast of Africa - Invasive Aedes aegypti populations in California - Urban and island populations of Anopheles mosquitoes in India

Ongoing research topics include: - Interspecific hybridization and introgression as a mechanism for adaptation - The evolution of populations on isolated islands - Defining populations in urban centers as ecological islands - Development of new wgs-based methods to estimate population size and dispersal - Evaluating the behavior of gene drive systems via field trials

Responsibilities: The successful candidate will work on whole-genome sequencing data sets to decipher recent population history and evolution in mosquitoes that are vectors of human diseases.

Required Qualifications: - PhD in Population Genetics/Genomics, Bioinformatics, or related discipline (theoretical and/or applied) - In-depth knowledge of population genetics theory - Demonstrated record of research productivity and publications

Preferred Qualifications: - Experience working in Linux environment - Experience with genomic data analysis - Experience with coalescence/IBD methods - Programming experience (e.g. C/C++, Python/Perl, R) - Strong mathematical/statistical skills

Salary: This is a full-time position. Salary is commensurate with qualifications and experience.

How to apply: Applicants should submit the following materials: - A cover letter - A curriculum vitae - List of relevant publications - Contact information for 3 referees Send the above combined into a single PDF to Gregory Lanzaro (gclanzaro@ucdavis.edu). Review of applications will start immediately. This position will be open until filled. The appointment is for a duration of two years.

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy see: http://policy.ucop.edu/doc/4000376/NondiscrimAffirmAct . hschmidt@ucdavis.edu

UCalifornia LosAngeles ViralEmergence

POSTDOC: Cross-scale modeling of viral emergence risk

UCLA Department of Ecology & Evolutionary Biology

Lloyd-Smith lab

We seek a postdoctoral researcher to develop mathematical and statistical models of viral processes, linking data across scales to understand the determinants of zoonotic emergence risk. This position is linked to an exciting DARPA-funded project that brings together a world-class team of researchers across disciplines from virology to ecology to epidemiology, to study emergence risks from bat-borne viruses including Nipah and Hendra virus. The primary focus of this position is to design quantitative methods to integrate virological data collected in the lab and in the field, at scales from molecules to animals, with the goal of developing biological insight and practical predictors of the evolutionary and epidemiological risk posed by potential zoonotic viruses. The position offers the rare opportunity to interact closely with top empirical researchers in virology and allied fields, and to participate in designing on-going data collection to support future rounds of modeling. There will also be rich opportunities to collaborate with other groups on modeling zoonotic spillover, transmission dynamics and viral evolutionary dynamics.

The position is based in the lab of Jamie Lloyd-Smith at UCLA, where we combine diverse quantitative approaches with data to study the ecological and evolutionary dynamics of pathogen emergence (http://www.eeb.ucla.edu/Faculty/lloydsmith/). In addition to the rich intellectual environment of our lab, department, and broader UCLA campus, the postdoc will interact and collaborate with other members of the DARPA project team, across disciplinary boundaries, including virologists (Hector Aguilar-Carreno, Vincent Munster, Colin Parrish), ecologists (Raina Plowright (project PI), Peter Hudson, Hamish McCallum), immunologists (Aga Apple, Tony Schountz), physiologists (Liam McGuire), epidemiologists (Nita Bharti, Emily Gurley, Steve Luby), and quantitative biologists (Barbara Han, Megan Higgs, Olivier Restif). It is an extraordinary team working together to tackle important and ambitious problems.

We are looking for a dynamic and intellectually versatile person to join our team. The ideal candidate will have a PhD in a quantitative field, experience with data-driven modeling of biological systems, and a track record of research excellence. Strong quantitative and computational skills are essential, ideally including experience developing and analyzing mathematical models as well as the ability to collate, interpret and analyze diverse data sets. Excellent verbal and written communication skills are highly desirable, as is experience with infectious disease dynamics, virology, or systems biology. Finally, the successful candidate must be comfortable working both independently and as part of a larger interdisciplinary research team, and able to present findings clearly to experts from other fields.

UCLA has vibrant communities of researchers working on quantitative and computational biology, infectious diseases, and other related fields, and our research group has ties with the UCLA School of Public Health, School of Medicine, Institute of Quantitative and Computational Biology, and Institute of the Environment and Sustainability. The university is situated in a prime location in west Los Angeles, within minutes of mountains, beaches, and urban amenities. Quality of life is excellent V Los Angeles is a fascinating multicultural city with rich art, music and culinary scenes, and the region has a wealth of natural beauty and opportunities for outdoor pursuits.

The position is available immediately, and can be renewed for up to three years. To inquire, please contact Jamie Lloyd-Smith <jlloydsmith@ucla.edu> with your CV, a brief statement of interest in the project and relevant experience, and your potential start date. Review of applications is on-going until the position is filled. Salary and benefits will be competitive, and commensurate with experience and qualifications.

The University of California is an Equal Opportunity/Affirmative Action Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, sexual orientation, gender identity, national origin, disability, age or protected veteran status. For the complete University of California nondiscrimination and affirmative action policy, see: UC Nondiscrimination & Affirmative Action Policy (http://policy.ucop.edu/doc/4000376/NondiscrimAffirmAct).

– James O. Lloyd-Smith

Professor Department of Ecology & Evolutionary Biology Department of Biomathematics University of California, Los Angeles 610 Charles E Young Dr South Box 723905 Los Angeles, CA 90095-7239

Phone: 310-206-8207

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UChicago EvolutionaryBiochemistry

Postdoc position in evolutionary biochemistry, Thornton Lab, University of Chicago

We have an opening for a postdoc in protein evolution and functional molecular evolution. The labs goal is to characterize the evolutionary, genetic and biochemical mechanisms by which biological molecules acquired their present-day functions, structures, and biochemical properties. Most projects have combined computational approaches to reconstruct the historical trajectory of molecular evolution V particularly phylogenetics and ancestral sequence reconstruction V with detailed bench experiments to test hypotheses concerning the causes and consequences of those events. We also use high-throughput library-based methods and experimental evolution to characterize large ensembles of -have-been histories from ancestral starting-points to better understand why evolution followed the path it took.

A variety of projects are available, depending on the candidates interests, and we encourage creativity in developing new projects. We have studied the evolution of transcription factors, enzymes, ligand-binding and scaffolding proteins, and molecular machines. We have been particularly interested in the evolution of molecular specificity, complexity, catalysis, multimerization, and allostery, and in the causes and consequences of epistasis and the distribution of effect-sizes in shaping proteins evolutionary processes.

We are a highly collegial group that draws scientists and students from a variety of disciplines V evolution, biochemistry, molecular biology, computational biology, genetics, biophysics, and more. The University of Chicago is a fantastic place to do science, especially at the interface of evolution and the molecular biosciences. Chicago is a great city rich in high and low culture; it is a hipster heaven and, in the summer, a fun beach town. People in the lab are fun, funny, interesting, mutually supportive, and humane.

More information about the lab is at http://www.thorntonlab.org .We strongly encourage applications from scientists who are women and members of groups underrepresented in science.

To apply, please email a single PDF containing a CV and brief research statement, including why you are interested in our lab, to me at joet1@uchicago.edu. The start date is flexible.

Joseph W Thornton <joet1@uchicago.edu>

UCollege London EvolMulticellularity

The Thompson lab, based at University College London, is seeking a Research Fellow to work on understanding how gene network heterogeneity affects the evolution of multicellular development.

Recently, we found that cell-cell variation in cell cycle position facilitates symmetry breaking during development, as it primes cells to respond to different differentiation cues (Gruenheit et al, Developmental Cell, 2018).

You will perform single cell gene expression analysis to understand the molecular mechanisms underlying this cell cycle control of cell fate choice you. For this, you will utilise our recently generated single cell RNA-seq dataset in which gene expression in 1000s of single cells was generated at different times after receiving differentiation cues.

Your aim will be to reconstruct gene network dynamics to follow their temporal changes in gene activity in individual cells from different cell cycle positions as they differentiate along different linages. You will develop novel computational and statistical methods (e.g. gene network identification, pseudotime, machine learning) to characterize the dynamics of gene network activity, and capture temporal changes in gene network activity in individual cells from different cell cycle stages as they differentiate. Live imaging of transcription and molecular genetic approaches to modify network activity in genetically modified cells will be used to validate your findings. You will also develop predictive models to understand the mechanism controlling cell fate choice. This will include computer simulation of the molecular basis of cell cycle control of differentiation. High throughput live cell imaging to quantify the differentiation behaviour of cells at different cell cycle phases will be used to test these models. This framework will be fundamental in generating new hypothesis guiding future experiments.

You will join a multidisciplinary team led by Professor Chris Thompson. The approaches used in the lab include transcriptomics, functional genomics, molecular genetics, live cell imaging and mathematical modelling.

Candidates with extensive experience of using either computational genomic approaches or wet lab approaches to understand the molecular basis of gene networks will be considered. You should currently hold or be about to obtain a PhD in Computational, Cell, Molecular or Developmental Biology.

The post is funded by Wellcome and is available for 24 months in the first instance (with a possibility of extension).

Appointment at Grade 7 is dependent upon having been awarded a PhD, if this is not the case, initially appointment will be at research assistant Grade 6B (Salary £30,922 - £32,607 per annum) with payment at Grade 7 being backdated to the date of final submission of the PhD thesis.

https://www.jobs.ac.uk/job/BPE898/research-fellow-single-cell-transcriptomics-of-cell-cycle-heterogeneity-and-cell-fate-choice Informal enquiries are welcome to Chris Thompson (christopher.thompson@ucl.ac.uk)

Chris Thompson Professor of Evolutionary and Developmental Genetics Dept of Genetics, Evolution and Environment University College London Darwin Building, Gower Street London WC1E 6BT

Phone: 020 7679 4483 (int 34483)

lab website: http://thethompsonlab.wordpress.com Treasurer, British Society of Developmental Biology email: BSDB-treasurer@manchester.ac.uk website: bsdb.org

“Thompson, Chris” <christopher.thompson@ucl.ac.uk>

UExeter BacterialEvolution

The evolution of choosiness in bacteria. With Dr. Edze Westra, Prof. Angus Buckling, Dr Bram Kuijper and Prof. David Hosken. At the University of Exeter's Cornwall Campus (UK).

A full time post is available from 1 April 2019 on a fixed term basis until 31 March 2022. The starting salary will be from £35,211 up to £43,267, depending on qualifications and experience.

We wish to recruit a Postdoctoral Research Fellow to participate in a project aimed at understanding the evolution of CRISPR-based choosiness in bacteria. This Leverhulme Trust funded post is available from the 1st of April 2019 to the 31st of March 2022. You will carry out experimental evolution, and work in conjunction with a theoretician (Dr. Kuijper) and his PhD student, to explain what ecological conditions favour the evolution of choosiness, and the maintenance of choosiness, in bacterial populations exposed to mobile genetic elements. Evolutionary, ecological or microbial expertise/experience would advantageous.

The post will include designing and performing experiments, data analysis, and writing manuscripts in collaboration with Dr. Edze Westra, Prof. Angus Buckling, Prof. David Hosken and Dr Bram Kuijper. You will also have the opportunity to present data at international conferences.

We particularly encourage women and minority candidates to apply.

Applications close on February 3rd.

For informal enquiries please contact Edze Westra: E.R.Westra@exeter.ac.uk

Prof DJ Hosken Dean Strategic Development, Cornwall University of Exeter, Cornwall Tremough, Penryn TR10 9FE UK

01326 371843 D.J.Hosken@exeter.ac.uk

http://biosciences.exeter.ac.uk/staff/-index.php?web_idÚvid_hosken “Hosken, David” <D.J.Hosken@exeter.ac.uk>

UExeter InsectVirusEvolution

Dear all

I am advertising a postdoc position to look at mechanisms underlying differences in susceptibility across species of Drosophila. The project will examine why viruses can successfully infect some hosts and not others by examining the cellular and immune factors underlying these differences in susceptibility - specifically looking at viral suppression of antiviral RNAi immunity. We plan to examine the ability of the DCV-1A suppressor of RNAi to prevent processing of dsRNA into siRNAs by Dicer-2 in different host species. Some background to the project can be found here https://journals.plos.org/plospathogens/-article?id.1371/journal.ppat.1004728 and here http://-

genesdev.cshlp.org/content/20/21/2985.long The position will be based at the University of Exeters Cornwall Campus but will collaborate with and spend time in the lab of Prof Ronald Van Rij (Radboud Institute for Molecular Life Sciences, Nijmegen, the Netherlands) and also collaborate with Dr Darren Obbard (University of Edinburgh, UK).

Full info and application here https://-jobs.exeter.ac.uk/hrpr_webrecruitment/wrd/run/-ETREC107GF.open?VACANCY_ID“5666Nfzg&WVID817591jNg&LANG=USA Best wishes,

Ben Longdon

– Dr Ben Longdon Sir Henry Dale Wellcome Trust/Royal Society Senior Research Fellow University of Exeter Penryn Campus Cornwall TR10 9FE +44 (0) 1326 259460 https://benlongdon.com/ ”Longdon, Ben“ <B.Longdon2@exeter.ac.uk>

UFlorida 2 StatGen

There are openings for two postdoctoral research associates with Dr. Lauren McIntyre at the University of Florida Department of Molecular Genetics and Microbiology. The positions will be affiliated with the UF Genetics Institute. Dr. McIntyre's research is in the area of quantitative genetics, and statistical genetics. The successful applicants will be working on projects projects focused on the analysis of regulatory variation in Drosophila and/or Elegans populations. Skills expected include: knowledge and interest in Genetics, particularly Evolutionary/Population Genetics, as well as substantial quantitative skill and interest/experience in programming. Candidates with PhD's in either Genetics/Biology or Statistics/Biostatistics/Computer Science will be considered for these positions. The work will be highly interdisciplinary and require interaction among a diverse group of scientists. The most important qualities are analytic thinking and problem solving, highly developed writing skills, and a genuine interest in working in a successful team. The initial term of the position is one year, with renewal for up to three years, pending successful analytic and writing endeavors. Email: mcintyre@ufl.edu with a CV or for questions about the job(s).

“McIntyre, Lauren M” <mcintyre@ufl.edu>

UFribourg 2 BehaviourDiseaseDynamics

A 2-year post-doc —position is available in the research group of Professor Nathalie Stroeymeyt in —the Department of Biology, University —of Fribourg, to study the effect of social network properties on disease transmission dynamics in ant colonies.*//*BACKGROUND*/. /*Group living offers favourable conditions for the spread of infectious diseases, because high population densities and frequent social contacts facilitate pathogen transmission. To mitigate that risk, social animals have evolved a variety of defence mechanisms to prevent the entry and propagation of pathogens within the group, ranging from a raised investment in personal immunity to highly coordinated collective sanitary actions ('social immunity'). Recent studies have shown that social groups can also adopt organizational features, such as the subdivision into well-separated subgroups, which reduce epidemic risk through transmission bottleneck effects. However, the importance of organizational immunity features in disease risk management by real animal groups is still poorly understood. Our research adopts an empirical approach based on the experimental manipulations of garden ant colonies (/Lasius niger/) to (i) quantify the effect of social organization on disease transmission and test key predictions from network epidemiology, and (ii) evaluate the relative of importance of personal immunity, collective sanitary actions and organizational features under different environmental conditions and at different stages of development (for more detail see https://stroeymeyt-lab.ch/research).PROJECT. The goal of this post-doc project will be to experimentally manipulate the social network topology of ant colonies (e.g. by manipulating nest architecture) to quantify the effect of network properties on disease transmission and test key predictions from network epidemiology. The candidate will use a combination of automated behavioural tracking, social network analysis, simulation of disease transmission, monitoring of the transmission of pathogenic and non-pathogenic agents, and fitness measurements to produce an integrative understanding of the effect of social organization and network structure on epidemic risk/. /The project will be embedded within an overall project team consisting of two PhD students and two post-doctoral researchers (https://stroeymeyt-lab.ch/open-positions/) and will be fully funded for two years by an ERC Starting

Grant. The salary will be set according to the guidelines of the University of Fribourg (c. 75'000 CHF per year).//PROFILE. We are looking for candidates with a strong quantitative background and solid experience in programming, exploratory analysis of large biological datasets, social network analysis and/or epidemiological simulations. As the project will involve an important experimental component, the candidates would ideally have a good working knowledge of statistics and experimental design and prior experience with social insects. Experience with laser-cutting or 3D-printing software and tools would be a plus. Candidates must be creative, motivated and passionate about science, have excellent oral and written communication skills, and be at ease working both independently and as part of a team. A PhD will be required prior to taking up the position. LOCATION. The Department of Biology at the University of Fribourg is a highly dynamic, —international and interdisciplinary —environment, spanning a wide range of —research in evolution and ecology, behaviour, population genomics, and bioinformatics, —developmental genetics, neurobiology, biochemistry and proteomics, across 27 —groups (_https://www3.unifr.ch/bio/en/_). STARTING DATE. The starting date is flexible; the earliest possible start will be May 1^st , 2019. HOW TO APPLY. Please send your application by email to Nathalie.Stroeymeyt@gmail.com. Your application should consist of a single merged pdf file including a letter of motivation, a full CV and publication list, the names and contact details of at least two referees, and copies of your publications and/or your PhD thesis (if available). Evaluation of candidates will begin on February 15th, 2019, and continue until the position is filled.

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A 3-year post-doc position is available in the research group of Professor Nathalie Stroeymeyt in the Department of Biology, University of Fribourg, to study the role of caste-specific microbiota in the disease defences of ant colonies.*//*BACKGROUND*/. /*Group living offers favourable conditions for the spread of infectious diseases, because high population densities and frequent social contacts facilitate pathogen transmission. To mitigate that risk, social animals have

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UGothenburg Speciations

Postdoc position in evolutionary genetics of speciation.

Department of Marine Science, University of Gothenburg.

Working with Roger Butlin, Kerstin Johannesson, Rui Faria and Marina Rafajlovic

At the Marine Science department there is a long tradition in working with marine snails of the genus Littorina as models for studies of local adaptation, hybrid zones and speciation. This study focuses on ecotype formation and the subsequent evolution of barriers to gene exchange in L. saxatilis. This species forms multiple ecotypes but we concentrate on contrasting adaptations to crab predation and wave action that occur in many parts of its North Atlantic distribution, particularly comparing Spanish and Swedish contact zones. We have extensive phenotypic and genomic data sets (targeted capture sequencing, whole genome re-sequencing and SNPs). This postdoc project will contribute to bioinformatic processing of data and analyses aimed at detecting selection and its phenotypic correlates, including contributions to reproductive isolation. An L. saxatilis reference genome and a genetic map is available. The postdoc may also contribute to efforts to improve these resources.

For more information and to apply, see:

https://www.gu.se/english/about_the_university/job-opportunities Postdoc (24 months): ref. PAR 2019/50

Or email Roger Butlin on r.k.butlin@shef.ac.uk

– Roger Butlin

Professor of Evolutionary Biology Animal and Plant Sciences The University of Sheffield

Guest Professor Marine Sciences University of Gothenburg

r.k.butlin@shef.ac.uk

Roger Butlin <r.k.butlin@sheffield.ac.uk>

UGothenburg Sweden BirdsMacroecolMacroevol

Apply by: February 1st 2019

Anthropogenic biases in macroecological and macroevolutionary patterns in birds

Carl Tryggers Postdoctoral Fellow in macro ecology and macro evolution of birds at the Department of Biological and Environmental Sciences Zoology, Gothenburg University

Project description

Birds are one of the most charismatic and well-studied group of animals, yet we know very little about how humans have affected their global patterns of diversity and evolutionary history. This project is part of a larger initiative on the effects of humans on macroecological and macroevolutionary patterns in birds. The project has Søren Faurby (https://tinyurl.com/Faurby) as a PI and Tim Blackburn (https://tinyurl.com/Tim-Blackburn; a bird macro-ecologist at University College London) and Manuel Steinbauer (https://tinyurl.com/-Steinbauer; an island biologist at Friedrich-Alexander University Erlangen-Nürnberg) as major cooperation partners. The postdoc will work in very close collaboration with Ferran Sayol (https://tinyurl.com/Ferran-Sayol) who is working in the same project. The postdoc will also have the opportunity to collaborate with a wide group of scientists at the Gothenburg Global Biodiversity Centre, which the wider working environment where the post doc will be based (ggbc.gu.se).

Earlier work by the PI has discovered substantial biases in macro-scale analyses of mammals, when conclusions are drawn based only on present-day distributions (example manuscripts below). The goal of this project is to investigate whether those biases are restricted to mammals (which are expected to be particularly sensitive to anthropogenic impacts), or are more general and affect other organisms, like birds.

Ferran Sayol is currently leading the creation a complete database of birds that have gone extinct in the Late Pleistocene and Holocene, and this work is expected to be finished when the incoming postdoc is starring. Part of the work for the incoming postdoc is to expand on this and build a model of the approximate number and plausible taxonomic assignment of the of undescribed bird species that would have gone extinct in the period and to gather the needed data for this model to work.

Related manuscript from previous work:

onlinelibrary.wiley.com/doi/10.1111/ddi.12369/full

nature.com/articles/s41558-018-0089-x

onlinelibrary.wiley.com/doi/10.1111/ecog.02287/abstract

Eligibility The applicant must hold a PhD in an area relevant for the tasks at hand (macroecology, ornithology, spatial analysis, macroevolution, palaeontology, or related fields). Note that the thesis must be awarded prior to the starting date of this position.

Other required qualifications:

Documented capacity to work both in groups and independently

Advanced skills in R or potentially another analytical platform

Excellent written and spoken communication skills in English

Assessment (other desirable qualifications)

A strong publication record (relative to the applicants' scientific age)

Experience with handling and ideally generating large databases

Experience with spatial and macro-evolutionary analyses

Knowledge of the study group (birds)

Experience in palaeontology and or taxonomy

Application is by email (to soren.faurby@bioenv.gu.se), must be written in English and must include (all combined into a single PDF file):

A cover letter with the applicant's justification for the application which describes how the applicant meets the selection criteria and potentially her / his plans for this project (max. two A4 pages)

A list of qualifications (full CV)

Certificate of PhD exam and other relevant education

Complete list of publications, including submitted and accepted manuscripts highlighting the up to five most important papers related to the application

Contact information for at least two referees that are familiar with the applicant's work

The top ranked candidates will be selected for an interview, which will be held in English and may be performed by phone /skype. Postdoctoral positions are appointed primarily for purposes of research. Applicants are expected to hold a doctoral (PhD) degree. The position is funded by a tax-free 2-year Carl-Tryggers postdoctoral scholarship. Start date: as per agreement (but expected to start during spring 2019) Gothenburg University strives to be a workplace free from discrimination and with equal opportunities for all. Please do not hesitate to contact me (Soren.Faurby@bioenv.gu.se) with any questions related to the position.

Søren Faurby http://antonelli-lab.net Sören Faurby <soren.faurby@bioenv.gu.se>

UHelsinki SalmonSexConflictModelling

A postdoctoral researcher position is available for up to 3.5 years in Professor Craig Primmer's research group at the University of Helsinki, Finland. The position is available immediately, until 8/2022. The position is funded by an ERC Advanced Grant entitled "Age at maturity in Atlantic salmon: molecular and ecological dissection of an adaptive trait".

The postdoctoral researcher will conduct and co-supervise research to extend and expand our earlier research reporting sex-specific selection responses and resolution of a sexual conflict in Atlantic salmon via means of sex-dependent dominance leading to sex-specific patterns of maturation timing and size (see Barson et al. 2015; Czorlich et al. 2018). More specifically, the aim is to use evolutionary genetic modelling approaches to better quantify sex-specific selection, sexual conflict and to understand the population genetic consequences of its resolution. This work is complemented by ecological and quantitative and molecular genetic research being conducted within the same project by others in the group.

An appointee to the position shall hold a doctoral degree and have the ability to conduct independent scholarly work. Suitable applicants will have a strong background in evolutionary genetics as demonstrated by publications in relevant fields. Previous research experience in statistical and/or evolutionary modeling and knowledge of empirical population genetics is an advantage. Enthusiasm and ability to work as a part of a larger research team addressing related questions is also important.

The salary will be based on level 5 of the demands level chart for teaching and research personnel in the salary system of Finnish universities. In addition, the appointee will be paid a salary component based on personal performance with the overall starting salary amounting to c. 3100-3500 EUR per month, depending on the previous relevant research experience of the candidate. A six-month trial period will be applied.

Formal applications should include as a single pdf file: - a CV including a list of publications and with names and contact details of at least two referees - a max. 2 page letter of motivation

Please submit your application using the University of Helsinki Recruitment System via the link Apply for the position. https://www.helsinki.fi/en/open-positions/postdoctoral-researcher-evolutionary-genetics-of-sex-specific-selection-and-sexual-conflict-resolution-in-salmon The deadline for applications is Wednesday 13 February 2019, with the preferred starting date being April 2019 (the position is available immediately).

Informal inquiries can be directed to Professor Craig Primmer (craig.primmer(at)helsinki.fi).

Finland is a member of the EU, has high quality free schooling (also in English), very affordable childcare, generous family benefits and healthcare, and was recently ranked as the best country in the world for expat families and in the world's top ten most livable cities. The University of Helsinki is a top 100 ranked university in most ranking lists, and is currently investing heavily in life sciences research (see https://www.helsinki.fi/en/helsinki-institute-of-life-science).

Relevant articles: Barson et al. (2015) Sex-dependent dominance at a single locus maintains variation in age at maturity in salmon. Nature 528:405-408.

Czorlich Y, Aykanat T, Erkinaro J, Orell P, Primmer CR (2018). Rapid sex-specific evolution of age at maturity is shaped by genetic architecture in Atlantic salmon. Nature Ecology and Evolution, 2: 1800-1807.

Mobley KB, Granroth-Wilding H, Ellmen M, Vähä J-P, Aykanat T, Johnston SE, Orell P, Erkinaro J, Primmer CR (2019) Home ground advantage: local Atlantic salmon have higher reproductive fitness than dispersers in the wild. Science Advances (in press) (see also preprint on BiorXiv)

Craig Primmer, Academy Professor PO Box 56 Organismal & Evolutionary Biology Research Program | Biotechnology Institute 00014, University of Helsinki, FINLAND Visiting: Room 3404, Biocenter 1C Mobile +358 503116374 craig.primmer@helsinki.fi Twitter @FishConGen http://www.helsinki.fi/evolution-conservation-and-genomics "Primmer, Craig" <craig.primmer@helsinki.fi>

UHongKong EvolutionaryGenomics

*** Postdoctoral Position in Evolutionary Genomics ***

We are looking for a Postdoctoral Researcher to work on genomics projects on birds and other non-model species. The lab has several study systems and active projects addressing population genomics, comparative genomics, genotype-phenotype association, and behavioural genetics. A key focus of the lab is to use genomic, epigenomic and transcriptomic data to understand the genetic basis and evolution of phenotypic traits. Collaborative international projects are already underway, ensuring a quick and productive start. The Postdoctoral Researcher will have extensive opportunities to interact with collaborators and involve in different evolutionary and ecological genomics projects.

Duration: The initial appointment is for one year, with renewal based on performance. Funding is available for two years. This is a full time appointment.

Qualifications: Applicants must have completed a PhD (or will have completed a PhD before the position start) in bioinformatics, genomics, evolutionary biology, population genetics, or a related discipline, with a demonstrated record of research achievement (via publications). They will also be proficient with programming in a scripted language (e.g. Python, Perl, or R). Experience with shell scripting and computing cluster environments and/or experience working with whole genome datasets in population or comparative genomics will be beneficial.

Working Environment: The University of Hong Kong is an English-speaking institute and one of the most international universities in Asia. It has a rank of 36 according to the Times Higher Education World University Rankings 2019.

Start Date: Flexible between early-2019 to mid-2019.

Salary: A highly competitive salary plus annual leave and medical benefits will be offered.

How to apply: Please send a CV (with contact information for three references), cover letter describing research interests and skills, and copies of publications to Simon Sin (sinyw@hku.hk). Review of applications will begin immediately and continue until the position is filled.

Simon Sin

Assistant Professor School of Biological Sciences Kadoorie Biological Sciences Building The University of Hong Kong Pok Fu Lam Road, Hong Kong www.simonywsin.com <sinyw@hku.hk>?

sinyw@hku.hk

UIllinois DiseaseEvolution

Post-doctoral position in Genetic Epidemiology - Chronic Wasting Disease

The Wildlife Veterinary Epidemiology Laboratory at the Illinois Natural History Survey (INHS) (https://wwv.inhs.illinois.edu/directory/show/nohram) is seeking a Postdoctoral Research Associate to study genetic characteristics, gene flow and prion sequence polymorphisms of managed white tailed deer in Illinois. Topics of interest include use of modeling and genetic techniques in the study of CWD in Illinois; genetic evaluation of geographical clusters of CWD infection, the use population genetic analysis to describe patterns of genetic structure, spatial distribution and gene flow that draw insights into the epidemiology and management of CWD. The work entails the use of molecular tool epidemiological modeling, GIS tools, and strong collaborative interactions with biologists, faculty, staff and students across INHS and the U of I campus.

The job announcement and application instructions can be found at: https://blogs.illinois.edu/view/7426/744695 The University of Illinois conducts criminal background checks on all job candidates upon acceptance of a contingent offer.

Illinois is an equal opportunity employer and all qualified applicants will receive consideration for employment without regard to race, religion, color, national origin, sex, sexual orientation, gender identity, age, status as a protected veteran, or status as a qualified individual with a disability. Illinois welcomes individuals with diverse backgrounds, experiences, and ideas who embrace and value diversity and inclusivity. (www.inclusiveillinois.illinois.edu).

Amber Hall Human Resource Associate Prairie Research Institute 1816 S. Oak St. Champaign, IL 61820 P: 217-300-4080 www.prairie.illinois.edu "Hall, Amber Renee" <amberh@illinois.edu>

UIllinois VirusHeterogeneityEvolution

The Brooke Lab (brookelab.org) at the University of Illinois at Urbana-Champaign is looking to a postdoctoral research associates to work on an NIH-funded project aimed at understanding how patterns of viral and host heterogeneity influence infection dynamics.

Influenza viruses are highly heterogeneous at the population level, and the vast majority of virions express variable, incomplete subsets of viral genes. Our lab has pioneered efforts to understand the role of population heterogeneity in shaping patterns of viral replication, evolution, and pathogenesis. We are looking for someone to build on preliminary work from our lab by using single cell RNAseq to understand how changing patterns of viral heterogeneity and co-infection influence infection dynamics, in vitro and in vivo. We are also interested in the broader question of how selection may act on patterns of viral population heterogeneity.

We are multidisciplinary team that bridges molecular virology, immunology, evolutionary biology, and bioinformatics. The successful candidate will also have the opportunity to work with colleagues in microfluidics, mathematical modeling, and evolutionary/ecological theory as part of ongoing collaborations aimed at more broadly understanding the importance of heterogeneity during viral infection.

This position is fully funded for 5 years, and comes with full benefits. Highly motivated, creative individuals with experience in molecular virology, population sequencing, and/or single cell approaches are encouraged to apply. Ideal candidates will be highly motivated and creative, with strong interpersonal skills and command of written and spoken English. Applicants must have published in high quality peer-reviewed journals, and must have a PhD or have successfully defended their thesis prior to starting the position. Bioinformatics experience is highly desirable but not essential.

Applications will be reviewed until the position is filled. Interested candidates should contact Chris Brooke (cbrooke@illinois.edu) with a cover letter and CV.

The University of Illinois at Urbana-Champaign is a world class public research institution located in idyllic Urbana, Illinois. We have all of the amenities of a thriving college town, paired with a low cost of living and relaxed, family-friendly atmosphere. Urbana is a 2 hour drive from Chicago, and a 3 hour drive from St. Louis.

“Brooke, Christopher Byron” <cbrooke@illinois.edu>

UKentucky EvolutionRegeneration

Postdoctoral Positions in the Evolution of Regenerative Ability

The Seifert lab in the Department of Biology at the University of Kentucky (UK) is seeking exceptionally creative postdoctoral researchers. We utilize a diverse array of species to understand the cellular and molecular basis for complex tissue regeneration in mammals. In addition to maintaining an active breeding colony of spiny mice (Acomys cahirinus) at UK, we continue to work with wild-trapped rodent species in Kenya (regenerating and non-regenerating). Successful applicants will initially join an NIH funded project investigating how macrophages regulate the regenerative response to injury. Specifically, the project looks to define the interaction of macrophage subpopulations and how specific phenotypes induce behavioral changes in local fibroblasts. Ideal candidates will have a strong background in developmental and evolutionary biology, experience working with model or non-model organisms, expertise in microscopy and comfortability with bioinformatics. Field experience is a plus as opportunities exist for integrating field based research in Kenya. While this is a funded position, postdocs in the Seifert lab are strongly encouraged to develop their own projects and external funding portfolios as a pathway toward independence. Salary follows NIH guidelines for postdoctoral researchers. Informal inquiries are strongly encouraged. For additional information visit: http://www.ashleyseifert.com/opportunities.html Review of applications will begin January 30th and will continue until the position has been filled. Candidates will have completed their Ph.D. prior to starting the position but need not have defended their dissertation prior to applying. Applicants should send a single pdf document to Ashley Seifert (awseifert@uky.edu) that includes their CV, names of three references, and a 1-2-page synopsis of their current research interests and how these complement our overall research program.

The Department of Biology houses a strong group of research labs interested in regenerative, developmental and evolutionary biology using a diverse array of animal models (e.g., spiny mice, salamanders, planarians, lampreys, zebrafish) and in vitro systems. Together, these labs create a vibrant atmosphere to pursue interdisciplinary projects across comparative genomics, developmental, regenerative and evolutionary biology.

Ashley W. Seifert, PhD Department of Biology | Univ. of Kentucky 211 THM Bldg | Lexington, KY 40506 859-218-2668 | www.ashleyseifert.com "Seifert, Ashley" <awseifert@uky.edu>

ULiverpool 2 EvolutionaryGenetics

The Betancourt lab in at the University Liverpool, UK, is seeking TWO postdoctoral researchers for 5-year appointments each. These positions are funded by the ERC, and are to investigate transposable element invasions using Drosophila as a model. Informal enquires to A.Betancourt@liverpool.ac.uk very welcome.

Both applicants should have a PhD in a relevant field. As the project encompasses molecular work, genomic analysis, and fly work, ideally one postdoc will be trained in molecular methods and one in bioinformatics or population genetics. They will work as part of a team that includes the PI and a full-time research technician, and will be encouraged to develop their own research interests.

Dr. Betancourt's group has tackled a wide variety of questions in evolutionary genetics, addressing the role of recombination and sex-linkage in evolution, and the spread of selfish elements in Drosophila (more information here: http://www.flyevolution.net/).

The Institute of Integrative Biology (IIB) at the University of Liverpool houses a large and active research faculty (see: https://www.liverpool.ac.uk/integrative-biology/about/), and includes several active groups in evolutionary biology (see https://www.liverpool.ac.uk/integrative-biology/staff/evolution-ecology-and-behaviour/). IIB also houses several excellent core facilities, including a genomics and proteomics centres (more here: https://www.liverpool.ac.uk/integrative-biology/facilities-and-services/).

The posts are available for 5 years from the time of appointment.

Apply at the links below (or search for the appropriate job reference at https://recruit.liverpool.ac.uk). Please include a cover letter, CV, and details for three references.

Bioinformatics/Population genetics Postdoctoral Research Associate Grade 7 Department: : Evolution, Ecology And Behaviour Job Reference: : 010756 Salary : £33,518 - £38,833 pa Closing Date : 03-Feb-2019 23:30 https://bit.ly/2MaNnQw Molecular work Postdoctoral Research Associate Grade 7 Apply Department: : Evolution, Ecology And Behaviour Job Reference: : 010753 Salary : £34,188 - £39,610 pa Closing Date : 05-Feb-2019 23:30 https://bit.ly/2FtAM9J Cheers, Andrea

Andrea Betancourt | Senior Lecturer Department of Evolution, Ecology, and Behaviour (DEEB) | Institute for Integrative Biology (IIB) University of Liverpool Biosciences Building Rm 238 / Crown St. / L69 7ZB Liverpool / United Kingdom http://www.flyevolution.net | +44 (0) 151 795 4516 | aabt@liverpool.ac.uk

"Betancourt, Andrea" <A.Betancourt@liverpool.ac.uk>

ULiverpool EvolutionRodentMicrobiome

Postdoctoral Research Associate Grade 7

Evolution, Ecology And Behaviour

010948

34,188 - 39,610 pa

20-Feb-2019 23:30

We are seeking an enthusiastic and able researcher to work on an interdisciplinary project investigating the control of the composition of the microbiome community of wild rodents, specifically studying the interaction between the effects of individual's diet, behaviour and immunological state. This work builds on previous work by Mark Viney investigating the eco-immunology of wild mouse populations and of Jane Hurst investigating the role of scent communication in rodent behaviour. You will join the research group of Mark Viney, and further information about the research interests of this group can be found at: www.MarkViney.com The post is available for 3 years.

Closing date: 20 February 2019

https://recruit.liverpool.ac.uk/pls/corehrrecruit/erq_jobspec_version_4.display_form?p_company=1&p_internal_external=E&p_display_in_irish=N&p_process_type=&p_applicant_no=&p_form_profile_detail=&p_display_apply_ind=Y&p_refresh_search=Y&p_recruitment_id0948 Best wishes,

Bernie

Bernie King On behalf of

IIB Staffing Administration Account Institute of Integrative Biology University of Liverpool Biosciences Building Liverpool L69 7ZB iib@liv.ac.uk http://www.liverpool.ac.uk/integrative-biology "King, Bernadette" <B.King@liverpool.ac.uk>

UMainz PhD PDF InsectSymbiosis

PhD and postdoc positions available at the University of Mainz, Germany, within the ERC-funded project SYMBeetle: 'Symbiont-assisted cuticle biosynthesis as a key innovation contributing to the evolutionary success of beetles'

Recent evidence indicates that beetles across multiple different families associate with microbial symbionts that provision their host with tyrosine, an aromatic amino acid necessary for cuticle biosynthesis, hardening, and tanning. SYMBeetle addresses the hypothesis that the acquisition of tyrosine-supplementing microbes constituted a key innovation across phylogenetically distinct beetles that allowed them to expand into novel ecological niches. To test this, SYMBeetle will combine experimental manipulation of symbiotic associations to assess the symbionts' contribution to cuticle biosynthesis and its fitness consequences as well as the molecular basis of host-symbiont interactions with large-scale comparative approaches aimed at elucidating the taxonomic distribution, ecological contexts, and evolutionary origins of cuticle-supplementing symbioses. The results are expected to broaden our understanding of microbes as important facilitators for the evolution of herbivory and the colonization of dry habitats in beetles, two factors of major relevance for the emergence of economically relevant insect pests of agricultural crops and stored products.

Within the context of SYMBeetle, the group of Dr. Martin Kaltenpoth (Evolutionary Ecology Department of the Johannes Gutenberg University in Mainz, Germany) offers several PhD (65% TV-L EG13) and postdoc positions (up to 100% TV-L EG13). We are looking for highly motivated candidates with an MSc or PhD degree in biology, molecular biology or bioinformatics (or equivalent), excellent English speaking and writing skills and a deep interest in the evolutionary ecology of insect-microbe interactions. Previous experience with insect rearing, microbiology, molecular biology (qPCR, RNAi, FISH), phylogenetic analyses, and/or bioinformatics techniques (genomic and transcriptomic datasets) are of advantage, but not a prerequisite.

We offer a dynamic, international working group with broad expertise and state-of-the-art equipment in entomology, microbiology, molecular biology, and chemical analytics at the new Biocenter I of the Johannes Gutenberg-University in Mainz. The research group is integrated into the recently established Institute for Organismic and Molecular Evolution. Mainz is a charming, medium-sized, historic city situated at the river Rhine, in close vicinity to the Frankfurt metropolitan area.

Applications should include a cover letter (1-2 pages) describing the motivation, previous research activities and current research interests of the applicant; the CV of the applicant (with copies of BSc/MSc/PhD certificates, list of publications if applicable); and one (PhD applicants) or two (postdoc applicants) reference letters. Please send all documents as a single PDF file (except for the references, which should be sent directly by the referees) before February 15th, 2019 to Dr. Martin Kaltenpoth (mkaltenpoth@uni-mainz.de). Candidates that are in the finishing stages of their MSc or PhD theses but do not have their certificates yet are also explicitly encouraged to apply. Pre-selected candidates will be invited to participate in a recruitment symposium at the University of Mainz on March 22nd, 2019. The positions are available at the earliest convenience.

The Johannes Gutenberg University of Mainz is seeking to increase the number of women in science. Applications from women are therefore strongly encouraged. Qualified candidates with disabilities will be preferred.

— Prof. Dr. Martin Kaltenpoth Department for Evolutionary Ecology Institute of Organismic and Molecular Evolution Johannes Gutenberg University Mainz Hanns-Dieter-Husch-Weg 15 55128 Mainz Phone: +49-6131-3924411 Fax: +49-6131-3923731 Email: mkaltenpoth@uni-mainz.de

"Kaltenpoth, Dr. Martin" <mkaltenpoth@uni-mainz.de>

UManchester ExperimentalEvolution

Research Associate in Experimental Evolution School of Biological Sciences Faculty of Biology, Medicine, & Health The University of Manchester

Applications are invited for a two-year Research Associate position in experimental evolution of antibiotic-resistant clinical strains of E. coli. The position is based in the School of Biological Sciences at The University of Manchester.

The project is funded is through a Wellcome Trust ISSF interdisciplinary award involving experimental, theoretical, and clinical researchers working in the Faculty of Biology Medicine and Health and the Faculty of Science and Engineering.

Please note that we anticipate a second theoretical/computational focused postdoc will also be advertised shortly.

Start date is ASAP and before July 2019 at the latest.

Project description:

The increasing prevalence of anti-microbial resistance (AMR) is one of the key health challenges of the 21 st century. An important but neglected part of this problem is the interaction between the microbes and the aspects of their environment aside from antibiotics. Understanding of these interactions in relation to AMR offers the possibility of developing novel approaches that have the potential to produce not only better or more 'evolution-proof' antibiotics but also allow us to harness evolutionary processes themselves to allow antibiotic sensitive microbes to outcompete resistant ones. However, the evolutionary and environmental interactions and trade-offs are not well understood.

This project will ask a range of fundamental questions directly:

1. Does genomic background determine the genes involved in antibiotic and post-antibiotic adaptation?

2. Are the genes that evolve in the absence of antibiotics the same or different following more or less adaptation to antibiotics?

3. How do resistance and competitive fitness evolve in the absence of antibiotics: does the rate differ for strains longer to adapted to antibiotics?

Critically, the answers will allow us to detect signatures of antibiotic adaptation in the genomes of bacteria found in a hospital setting as well as those used experimentally. This work will allow us to shape antibiotic prescription regimes (e.g. altering usage periods of particular antibiotics, tailoring treatments to specific infections) in novel, evidence-based ways, founded in a molecular, genomic and population understanding of AMR evolution.

Please send informal enquiries to Danna Gifford (danna.gifford@manchester.ac.uk), Chris Knight (chris.knight@manchester.ac.uk) or Simon Lovell (simon.lovell@manchester.ac.uk)

For application details and further information, please visit https://www.jobs.manchester.ac.uk/displayjob.aspx?jobid542 Sincerely,

Danna Gifford

– Dr Danna Gifford Research Fellow Faculty of Biology, Medicine & Health The University of Manchester A.4034a Michael Smith Building, Oxford Road, Manchester M13 9PT United Kingdom https://dannagifford.com danna.gifford@manchester.ac.uk

UMississippi MicrobiomePhylogenetics

The Jackson lab (www.colinrjackson.com) and Garrick lab (www.rcgarrick.org) in the Department of Biology at the University of Mississippi seek applications for a Postdoctoral Research Associate. This is a 2-3 year position, renewable annually, funded by a collaborative NSF Dimensions in Biodiversity grant. The project is focused on understanding geographic scaling of diversity and interactions between microbiomes and their mussel hosts, mussel communities, and the freshwater environments in which they perform critical ecosystem services.

The Postdoc will focus on generating and interpreting DNA sequence data that can be used to characterize microbiomes, and contribute to phylogenetic analysis of large data sets. Other duties will include leading authorship of publications, presenting research at conferences, and mentoring graduate and undergraduate researchers in the PIs' labs.

Minimum qualifications are a PhD in Biology or related field, and strong publication record relative to opportunity. Preferred qualifications include experience in microbiome analysis, familiarity with microbial ecology and phylogenetics, strong interests in host-microbe interactions and connecting field-based research with genetic analyses, and a willingness to contribute to biodiversity-related public outreach.

Applicants should contact Dr. Colin Jackson via email (cjackson@olemiss.edu) to express interest in the position and for further information.

The start date is anticipated to be late Spring / early summer 2019, but is flexible.

Ryan Garrick Department of Biology 508 Shoemaker Hall University of Mississippi University, MS 38677-1848, USA

webpage: http://www.rcgarrick.org rgarrick@olemiss.edu

UMontana UNebraska EvolutionaryGenomics

Postdoctoral positions: Genome-to-phenome connections in wild populations

THE UNIVERSITY OF MONTANA and THE UNIVERSITY OF NEBRASKA are seeking applications for two 2-year postdoctoral fellowship positions. The positions are funded by a recent NSF award aimed at establishing a collaborative research and training network to advance the science of genome-to-phenome connections in wild populations (www.unveilnetwork.org). One fellow will be placed at each institution. Research activities will center around three core projects, which are united by their conceptual focus on adaptation to spatiotemporal environmental variation: 1.) high altitude adaptation and hypoxia resistance in deer mice, 2.) adaptation to climate change in snowshoe hares and other species that undergo seasonal phenotypic change and 3.) thermal adaptation in yellow monkeyflowers. Successful applicants may extend these core projects in novel directions or propose to work on complementary questions and/or systems with active mentorship from one or members of the UNVEIL network (https://www.unveilnetwork.org/our-team/).

The expected salary is approximately $50,000 and the fellows will be provided generous research funds to support their work.

To apply, please visit http://umjobs.silkroad.com and click the job title for this position (Tracking Code 2152-254) under All Openings. Candidates must apply online and will be asked to upload the following application materials: a CV, a 2-3 page research statement that outlines previous and current research, and as well as a brief statement about future directions. In the statement of future directions, applicants should also identify potential mentors from the set of PIs listed below. In addition, the applicants must provide contact information for 3 references.

Review of applications will begin on March 15, 2019 and the position will remain open until filled. The appointment is a 12-month Letter of Appointment. The start date is flexible. The position renewable for up to two years.

Applicants are strongly encouraged to contact one or more the following project PIs to further refine their application materials:

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

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

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

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

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

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

Jay Storz (Evolutionary genetics and physiology, http://storzlab.unl.edu/)

General inquires can be addressed to Zac Cheviron (zac.cheviron@mso.umt.edu)

Zac Cheviron <zcheviron@gmail.com>

UNamur Belgium RotiferGenomics

Post-doctoral researcher in extreme resistance RNAseq/Genomic analysis UNamur Belgium

Description:

The postdoctoral researcher would integrate, asap, the Laboratory of Evolutionary Genetics and Ecology of Karine Van Doninck at UNamur (Belgium) and will join the group RISE (Rotifer In Space) supported by Dr B.

Hespeels.

RISE is a project started in 2016 that aims to send rotifer bdelloids to the International Space Station. Experiments on the rotifer bdelloid A.vaga, with its unique characteristics and a draft genome available, may contribute significantly to our understanding of living in extreme environments. RISE was designed with the intention to use bdelloids as a new model organism for space research. Research group addresses the following questions: 1) How microgravity and space flight are affecting biological processes of A. vaga? 2) What are the limits of bdelloids extreme resistance to radiation? 3) What are the molecular mechanisms involved in protection and repair of damage induced by different radiation sources? 4) Are microgravity and space flight affecting protection and repair mechanisms of A. vaga?

The postdoctoral researcher will be involved in RNAseq and genomic data analysis in order to document question described before. Specific aims are: -find pathways and genes and transcriptomic peculiarities involved in desiccation, x-ray tolerance and adaptation to μG using available RNAseq data; Evaluate how genome structure is evolving after massive exposure to DNA DSB under 1G and μG environment.

For this project our laboratory would like to hire a postdoctoral researcher with strong expertise in bioinformatics and genome assemblies and with a strong interest in questions related to extreme resistance and genomic evolution induced by radiation. Applications from women and international researcher are encouraged.

Send CV and motivation letter to boris.hespeels@unamur.be and karine.vandoninck@unamur.be before 31th January 2019

Skills/Qualification

Strong background in RNAseq data analysis are required. Skills in comparative genomics are also appreciated : management, trimming and analysis of NGS data; de novo genome assemblies; read mapping; genome annotation; SNP calling; creation of bio-informatic pipelines.

Boris Hespeels <boris.hespeels@unamur.be>

UOxford MolMicroSymbiosis

Postdoctoral Researcher position in Molecular Microbiology and Symbiosis

Salary: Grade 7.1 pounds 32,236

The King Lab is offering a Postdoctoral Researcher position in the Department of Zoology for a fixed-term of 3 years (with the possibility of extension). This position is part of an ERC Starting Grant (COEVOPRO) to investigate the impact of microbe-mediated protection on host-parasite interactions using a tripartite system ' Caenorhabditis elegans, Enterococcus faecalis, and Staphylococcus aureus.

We are seeking a molecular microbiologist (who might also have experience with bioinformatics) to empirically elucidate the patterns and processes of coevolving protective symbioses, and assess impacts on parasite infection outcomes. This post is part of a dynamic and interdisciplinary research group ' the lab of Dr Kayla King ' working on the ecology and evolution of good and bad host-microbe symbioses.

This post is ideally suited for applicants with a PhD/DPhil with a strong molecular microbiology component, particularly involving gram-positive bacteria. Previous experience or intense interest in ecology and evolution is an asset.

Only applications made online before 12.00 midday (UK time) on 15 February 2018 will be considered. You will be required to upload your CV and supporting statement. See https://www.zoo.ox.ac.uk/job-vacancies#vacancy_138955 Please send inquiries to kayla.king@zoo.ox.ac.uk

Dr. Kayla King Associate Professor, Department of Zoology Tutorial Fellow, Christ Church University of Oxford

https://www.zoo.ox.ac.uk/people/dr-kayla-king https://sites.google.com/site/kckingevolution/ Kayla King <kayla.king@zoo.ox.ac.uk>

UPannonia AvianBehaviouralEvolution

POST-DOC POSITION IN BEHAVIORAL ECOLOGY AND EVOLUTION OF SHOREBIRDS UNIVERSITY OF PANNONIA, Veszprém, Hungary

Social interactions are among the most fascinating aspects of animal behaviour. This project will focus on the demographic drivers of sex role reversal in shorebirds (plovers, sandpipers and allies), when females compete for mates and males provide parental care. Results from cutting edge research carried out by our team (see references below & on our websites)suggest that role reversal occur in species where males are the more common sex. However, solid field data on sex ratios are scarce and the processes generating skewed sex ratios are largely unknown.

The successful candidate will join an international team of scientists working on shorebird ecology, behaviour and conservation, and will carry out a field study on a sex role reversed, polyandrous species. Most likely target species include the Bronze-winged and/or Pheasant-tailed Jacana, with potential field sites in India or Taiwan. This exciting project will collect data on breeding behaviour, offspring sex ratio, and survival of males and females in a closely monitored population. We will use demographic modelling to estimate adult sex ratio and to identify its most important determinants. The project will also contribute to our largescale comparative studies in shorebirds worldwide (see https://elvonalshorebirds.com/).

The project is led by Prof András Liker (Univiversity of Pannonia, Veszprém, Hungary, see http://-ornithology.limnologia.hu/), and is part of a collaboration with Dr VojtÄch Kubelka (Univiversity of Debrecen, Hungary), Prof Tamás Székely (University of Bath, UK), and Dr András Kosztolanyi (University of Veterinary Science, Budapest, Hungary) to understand breeding system evolution using shorebirds as model organisms. The research group uses English as the communication language.

This job offers an opportunity for an early-stage post-doc who wants to combine fieldwork with cutting-edge evolutionary and behavioural science. The main tasks of the post-doc are to organize, carry out and supervise field studies. We seek candidates with experience in behavioural ecology and field biology preferable with birds/shorebirds. Publications in high-quality peer-reviewed journals, excellent communication skills, and solid skills in data handling are essential. See further specifications below.

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 Western Europe and in the US. The current position is for 22 months (subject to probation period), with possibility of extension (pending on the availability of further funding).

Application deadline is 31 January 2019, although the screening of candidates may start earlier. The application should include (1) a max two pages cover letter, (2) a CV with list of publications, and (3) the name and contact details of four referees preferably from research, academia or conservation. The applications should be emailed to Prof András Liker (andras.liker@gmail.com).

The position is available from 1st March 2019.

Selected publications:

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

Pipoly, I., Bókony, V., Kirkpatrick, M., Donald, P. F. Székely, T. & Liker, A. 2015. The genetic sex determination system predicts the adult sex ratio in tetrapods. Nature 527: 91'94.

Schacht, R., Kramer, K.L., Székely, T. & Kappeler, P.M. 2017. Adult sex ratios and reproductive strategies: a critical re-examination of sex differences in human and animal societies. Phil. Trans. R. Soc. B 372: 20160309.

Eberhart-Phillips, L. J. et al. 2018. Demographic causes of adult sex ratio variation and their consequences for parental cooperation. Nature Communications 9: 1651

Kubelka V., Åálek M., Tomkovich P., Végvári Z., Freckleton R. P. & Székely T. 2018: Global pattern of nest predation is disrupted by climate change in shorebirds. Science 362: 680'683.

Job description:

The post-doc will organize and carry out field work in a foreign country,

Supervise PhD students and research assistants, coordinate research with external collaborators,

Coordinate data collection and analyses, and preparation of publications,

Present and promote the results at conferences and research seminars,

Assist administration associated with the project, Carry out other scientific and/or academic activities that are deemed necessary for the success of the project.

Requirements:

PhD in evolutionary biology, behavioural ecology, zoology, or relevant field of life sciences,

Solid knowledge of evolutionary biology, behavioural ecology, and/or

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UppsalaU EvolutionaryGenetics

POST DOC POSITION IN EVOLUTIONARY GENETICS - Sexual Selection and Mutation Rate The Department of Ecology and Genetics at Uppsala University are looking to hire a post doc on a 2-year contract.

PROJECT DESCRIPTION: Mutations form the raw material for evolution and do not only affect rates of adaptation and extinction but also cause fundamental human health problems. New evidence has demonstrated that mutation rates can vary systematically both across the genome and with the health of individuals. In many species, including humans, there are also systematic differences between the two biological sexes, with frequently observed male-bias in mutation rate. These findings have broad implications for a wide range of evolutionary and demographic processes but the ultimate causes for the observed variation remain a matter of considerable debate. The successful applicant will take an approach combining experimental evolution and genome sequencing to understand the role of sexual selection in shaping within- and between-population variation in mutation rate.

The first aim is to explore the molecular basis for a link between investment in sexually selected traits and germline DNA repair by comparing gene expression in experimental evolution lines of seed beetles stored from a previous experiment.

The second aim is to use DNA sequencing to explore the type and location of mutations left unchecked by the DNA repair system in individuals challenged to engage in sexual competition. This will explore heterogeneity in DNA repair across the genome and link this variation to trade-offs with investment in sexual reproduction.

The candidate will work in close association with the host Dr. David Berger and PhD student Julian Baur, and share lab space and interact with members of the groups of Prof. GÃÂArnqvist and Dr. Elina Immonen. Currently, the beetle lab consists of 8 members and occasional project students.

WORKING ENVIRONMENT: The Evolutionary Biology Centre hosts one of the world's largest aggregations of evolutionary biologists and Uppsala University was recently ranked 7th in the world in evolutionary biology (CWUR 2017). The Department of Ecology and Genetics is an international environment with staff from all over the world. Our research spans from evolutionary ecology and genetics to studies of ecosystems. A number of high-profile projects address natural and sexual selection, local adaptation, speciation, molecular evolution, microbial diversity, and ecosystem processes. For more information, see: ieg.uu.se. 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.

QUALIFICATIONS: A Phd degree in evolutionary, quantitative, population or molecular genetics, or equivalent. We seek highly motivated candidates with a broad interest in evolutionary biology. Experience with sequence data is a merit, including familiarity with laboratory molecular methods and experimental design, and/or analytical methods and statistical programming (e.g. R, Python, C).

POSITION: The postdoc is funded by a tax-free 2-year scholarship from Carl Tryggers Foundation, amounting to 23,000 SEK per month.

HOW TO APPLY: Application deadline: Application sent in before February 9, 2019 will be given priority. The position will be open until filled.

Send an e-mail to david.berger@ebc.uu.se with the subject heading ÂPOST-DOC APPLICATION', with the following documents combined into ONE pdf file:

- A cover letter describing your research interests and suitability (1 page) - A CV detailing your education, previous positions and other achievements (max 3 pages) - A list of your publications (submitted manuscripts can be included) - Contact details of 2-3 references who can be contacted by telephone or e-mail before or after the interview.

Prospective candidates will be invited for interviews in person or over Skype in February 2019.

Informal inquiries can be directed to: david.berger@ebc.uu.se Lab home page: http://www.ieg.uu.se/animal-ecology/Research+groups/berger-lab/ Publications: https://scholar.google.se/citations?hl=sv&user'ko_8EAAAAJ We are looking forward to receiving your application

– David Berger Animal Ecology Department of Ecology and Genetics Evolutionary Biology Centre Uppsala University david.berger@ebc.uu.se

E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here: http://www.uu.se/en/about-uu/data-protection-policy David Berger <david.berger@ebc.uu.se>

UppsalaU PlantEcoEvolutionaryDynamics

Postdoctoral researcher position in Plant Eco-Evolutionary Dynamics at Uppsala University, Sweden

We seek a Postdoc to join a project examining how adaptive genetic variation and demographic processes influence evolutionary response and population dynamics in a changing environment. The research uses the short-lived, perennial herb Primula farinosa as a model system, and focuses on the importance of variation in floral traits and life history in relation to differences in the intensity of biotic interactions and climate along a latitudinal gradient.

Tasks of the postdoc include the establishment and monitoring of experiments in the field, modelling of eco-evolutionary processes based on available demographic data collected in the field for seven years, statistical analysis and manuscript preparation. Three overarching questions will be addressed: (1) How is population viability influenced by variation in mutualistic and antagonistic biotic interactions and climate?, (2) How does variation in biotic interactions and climate influence the genetic structure of plant populations?, and (3) How does the presence of genetic variation in traits of adaptive significance and evolutionary responses influence population viability in a changing environment? Specific subprojects can be tailored to the skills and interests of the successful candidate.

The project is a collaboration between the labs of prof Jon Ågren at the Department of Ecology and Genetics, Evolutionary Biology Centre, Uppsala University, and prof Johan Ehrlén at the Department of Ecology, Environment and Plant Sciences, Stockholm University.

We are looking for a candidate with a keen interest in population biology and eco-evolutionary dynamics. Previous experience of modelling, and field or experimental work is desirable. Proficiency in English is a requirement.

The successful postdoc candidate should have a PhD completed within 3 years of the application deadline (reasons such as prolonged periods of illness and parental leave can motivate a longer period). The postdoc position lasts for two years.

Deadline for application is 28 February 2019.

Please find the announcement, with all information about how to apply, at:

http://www.uu.se/en/about-uu/join-us/details/
For informal enquiries, please contact Jon Ågren, jon.agren@ebc.uu.se, +46-18-471 2860

Some publications from the project:

Thomann, M., J. Ehrlén, and J. Ågren. 2018. Grazers affect selection on inflorescence height both directly and indirectly and effects change over time. Ecology 99:2167-2175.

von Euler, T., J. Ågren, and J. Ehrlén. 2014. Environmental context influences both the intensity of seed predation and plant demographic sensitivity to attack. Ecology 95:495-504.

Ågren, J., F. Hellstrom, P. Toräng, and J. Ehrlén. 2013. Mutualists and antagonists drive among-population variation in selection and evolution of floral display in a perennial herb. Proceedings of the National Academy of Sciences USA 110:18202-18207.

Vanhoenacker, D., J. Ågren, and J. Ehrlén. 2013. Nonlinear relationship between intensity of plant-animal interactions and selection strength. Ecology Letters 16:198-205.

Jon Ågren Plant Ecology and Evolution Department of Ecology and Genetics Evolutionary Biology Centre Uppsala University Norbyvägen 18 D SE-753 36 Uppsala Sweden

När du har kontakt med oss på Uppsala universitet med e-post så innebär det att vi behandlar dina personuppgifter. För att läsa mer om hur vi gor det kan du läsa här: http://www.uu.se/om-uu/dataskydd-personuppgifter/ E-mailing Uppsala University means that we will process your personal data. For more information on how this is performed, please read here: http://www.uu.se/en/about-uu/data-protection-policy Jon Ågren <jon.agren@ebc.uu.se>

UTuebingen InvasivePlantEpigenomics

Christina Richards and Oliver Bossdorf at the University of T'bingen are seeking a motivated POSTDOC IN ECOLOGICAL (EPI-)GENOMICS OF INVASIVE PLANTS to develop genomic and epigenomic resources for invasive knotweeds (Reynoutria ssp aka Fallopia ssp). The postdoc will work in the project °Genomics and Epigenomics of Plant Invasion± which attempts to understand large-scale variation and adaptation, and their underlying (epi)genomic mechanisms, in native vs. introduced populations of invasive knotweeds. S/he will develop approaches to full-genome sequencing for these complex polyploid species, and will be responsible for analysing RNA-Seq and reduced-representation bisulfite sequencing (epiGBS) data together with phenotypic and environmental data, as well as for writing manuscripts.

The project is funded through the °Make Our Planet Great Again± initiative (www.daad.de/mopga-gri/). It entails a collaboration between the University of T'bingen (Christina Richards, Oliver Bossdorf, University of Rennes (Malika Ainouche, Armel Salmon) and various groups in Eastern Asia, in particular the Institute of Biodiversity Science (Bo Li, Ji Yang) at Fudan University, China.

Applicants should have a PhD in ecology, evolution, genetics, bioinformatics, or a related field. Expertise in statistics, genomics and bioinformatics is required. Previous experience with bisulfite sequencing, reduced-representation approaches and/or polyploidy will be ideal. Strong candidates will also possess the following attributes: (1) creativity, independence, and a desire to learn new things, (2) excellent oral/written communication skills, and (3) a proficiency in bash, python and R. The position is full-time and for 2 years, with a possible 1-year extension. It will be based at University of T'bingen, but the postdoc will also spend a significant amount of time in Rennes, France. The payment will be at German payscale level TV-L E13.

The University of T'bingen is one of the oldest universities in Germany, with a particular strength in Plant Sciences. T'bingen is a beautiful university town with a high quality of life. The Plant Evolutionary Ecology group (uni-tuebingen.de/plantevoeco) at T'bingen, which will soon welcome Christina Richards (ecologicalepigenetics.com) as MOPGA group leader, studies a broad range of questions on plant variation and adaptation in changing environments. The Ainouche group (ecobio.univ-rennes1.fr/evolution-genome-adaptation-ega-thematiques.php) in Rennes has expertise in genomics of polyploids, and an excellent NGS/bioinformatics environment. Application review will begin January 20, 2019 and will continue until the position is filled. The starting date is flexible, but ideally in spring 2019. To apply, please email a cover letter, CV and the names and contact details of three references to Christina Richards (clr@usf.edu).

The University of T'bingen is committed to increase the proportion of women in science, and qualified women are therefore particularly encouraged to apply. Equally qualified applicants with disabilities will be given preference.

Prof. Dr. Oliver Bossdorf University of T'bingen Plant Evolutionary Ecology Auf der Morgenstelle 5 D-72076 T'bingen, Germany oliver.bossdorf@uni-tuebingen.de www.uni-tuebingen.de/PlantEvoEco Oliver Bossdorf <oliver.bossdorf@uni-tuebingen.de>

UVermont EpigeneticsThermalPlasticity

A post-doctoral position is available in the Helms Cahan lab at the University of Vermont to join a new NSF/EPSCoR-funded project on epigenetic regulation of thermal plasticity in Drosophila. The overarching goals of the project are to characterize and test molecular mechanisms driving plastic adjustment of upper and lower thermal limits occurring across a range of timescales, from developmental acclimation to rapid hardening, and role of shifts in epigenetic drivers in the process of thermal adaptation within and among species across the genus. The post-doctoral associate will use cutting-edge approaches in high-throughput sequencing and bioinformatic network analysis to identify putative epigenetic regulators in D. melanogaster and experimentally test their roles using functional genetic techniques. The successful candidate will join a multi-investigator collaborative team with complementary expertise in epigenomics and systems biology (Seth Frietze, UVM), biochemical adaptation and thermal physiology (Nick Teets, UKY and Brent Lockwood, UVM), insect respiratory physiology (James Waters, Providence College) and phylogeography (Heather Axen, Salve Regina Univ.). There will be plenty of opportunities for additional selfdesigned projects in the candidate's area of interest.

The Biology Department at the University of Vermont is a research-intensive integrative department, with internationally-recognized faculty conducting both theoretical and empirical research in disciplines from cells to ecosystems. The department has a vibrant PhD program and is dedicated to a teacher-scholar model of engaging undergraduates in the research enterprise. Founded in 1791, UVM is consistently ranked as one of the top public universities in the United States. The University is located in Burlington, Vermont, a vibrant and environmentally-minded small city rich in cultural and recreational activities for graduate students and their families.

Applicants for the position should have a strong interest in evolutionary genetics and a PhD in a relevant discipline. Familiarity with high-throughput genomics benchwork and/or bioinformatics, and prior experience working with Drosophila or other insects, are desirable. The position is available beginning January 1 for two years, with the possibility of renewal. Our team is dedicated to promoting diversity of experience and perspective in the scientific enterprise; we encourage applicants from under-represented groups to apply. To apply, please send a cover letter detailing your interest and qualifications for the position, a current CV, and the names and e-mail addresses of three potential references to Sara Helms Cahan (scahan@uvm.edu). Although the position is available immediately, I am happy to consider applicants on schedule to finish their degree in May or over the summer.

To find out more about research in the Helms Cahan lab, go to: http://shelmscahan.github.io/index.html# < http://shelmscahan.github.io/index.html >

To find out more about the Biology Department, go to: https://www.uvm.edu/cas/biology Sara Helms Cahan Associate Professor and Chair Department of Biology University of Vermont Burlington, Vermont 05405 (802)656-2962 scahan@uvm.edu

Sara Cahan <scahan@uvm.edu>

VirginiaInstMarineScience 2 EvolutionAlgalBlooms

The Research Laboratory of Dr. Juliette Smith at William & Mary's Virginia Institute of Marine Science (VIMS) is seeking 2 Postdoctoral Research Associates focused in Harmful Algal Blooms and/or their associated toxins. The Postdoctoral Research Associate will join the interdisciplinary team in their investigations into environmental and biological controls over harmful algal blooms and toxin production, and/or the persistence, fate, and effects of their associated toxins. Apply at https://jobs.wm.edu/postings/34500. Application materials are due on March 15, 2019 for full consideration, but will continue to be accepted until November 30, 2019, or until both positions have been filled.

The university is an EO/AA employer and encourages applications from women, minorities, protected veterans, and individuals with disabilities. The university conducts background checks on applicants for employment.

William & Mary's Virginia Institute of Marine Science/School of Marine Science (VIMS/SMS) invites applications for two postdoctoral research associates to join in their study of the environmental and biological controls over harmful algal blooms (HABs) and/or the persistence, fate, and effects of their associated toxins along the salinity gradient. Start date is negotiable, but ideally the positions will begin in spring/summer 2019 (but no later than December 2019). The positions are for one year, but funding for additional years is possible.

Qualifications: At the time of appointment, the successful candidates will hold an earned doctorate (Ph.D.) or equivalent in chemistry, biological sciences, environmental science, or a related field. Demonstrated experience in conducting and publishing research (at least one manuscript submitted) focused on toxins/natural products, harmful algal bloom dynamics, or phytoplankton cultures is required. Preference will be given to those candidates whose research experience (or interests) align with recent publications and/or grants led by the Smith research group.

Responsibilities: The postdoctoral research associates will work with Dr. Juliette Smith, and join an interdisciplinary team in their investigations into one or both of the current research areas: 1) environmental and biological controls over harmful algal blooms and toxin production, and/or 2) the persistence, fate, and effects of their associated toxins in the ecosystem. Depending upon the successful candidates' expertise and interests, the postdocs will utilize analytical techniques, conduct culturing studies, and/or lead large-scale field studies. The postdoctoral research associates will have opportunities to be involved in projects utilizing the Imaging FlowCytobot. Additional responsibilities may include, but are not limited to, proposal and manuscript preparation, management and analysis of large environmental datasets, and statistical analysis.

About the Virginia Institute of Marine Science: Chartered in 1940, the Virginia Institute of Marine Science < http://www.vims.edu/ > is currently among the largest marine research and education centers in the United States. VIMS has a three-part mission to conduct interdisciplinary research in coastal ocean and estuarine science, educate students and citizens, and provide advisory service to policy makers, industry, and the public. The School of Marine Science at VIMS is the graduate school in marine science for William & Mary < http://www.wm.edu/ >. VIMS currently employs 52 full-time faculty members and 256 staff, and has 80 graduate students in master's and doctoral programs.

Application materials for the positions should include: 1) a 2-page statement summarizing relevant experience and how this experience will support one (or both) of the 2 current research areas above; 2) a cover letter identifying availability for this position; 3) a full curriculum vitae; and 4) the names, addresses (including titles and institutions), e-mail addresses and telephone numbers of 3 professional references.

Application materials should be addressed to: Search Committee Chair, HAB Postdoctoral Associates, and will be accepted through our On-Line Application System at https://jobs.wm.edu < http://jobs.wm.edu/postings/34069 >. Application materials are due on March 15, 2019 for full consideration, but application materials will continue to be accepted until November 30, 2019.

William & Mary values diversity and invites applications from underrepresented groups who will enrich the research, teaching and service missions of the university. The University is an Equal Opportunity/Affirmative Action employer and encourages applications from women, minorities, protected veterans, and individuals with disabilities. William & Mary conducts background checks on applicants for employment.

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YaleU GlobalBiodiversity

Postdocs in Global Biodiversity Science and Conservation Focal groups: mammals, butterflies, dragonflies, bees, epiphytes

Several positions are available associated with the Yale Center for Biodiversity and Global Change (BGC Center; https://bgc.yale.edu), the Max Planck - Yale Center for Biodiversity Movement and Global Change (MPYC, https://mpyc.yale.edu), Map of Life (https://mol.org), and the Jetz Lab (https://jetzlab.yale.edu). Target start date is spring/summer 2019.

We are seeking innovative thinkers with a strong quantitative background who are interested in addressing ecological questions at large spatial scales. Qualifications for the position include a PhD in ecology, conservation, (bio-)geography, or biological informatics, combined with experience in spatial biodiversity analysis and inference. The preferred candidates will have a strong interest in the model-based integration of large, disparate biodiversity and environmental data, a dedication toward conscientious work in a team, attention to detail, and strong communication skills. An ability to traverse ecological, evolutionary, and conservation perspectives and to address processes at different spatial and temporal scales are particularly welcome. We expect strong analysis and scientific writing skills. Experience in several scripting languages, database management, taxonomic name management, remote sensing, and/or biodiversity informatics are highly welcome.

The positions offer broad thematic flexibility, and focal research questions may be macroecological, macroevolutionary, biogeographical, or conservation-focused. There is also openness regarding the preferred taxonomic study systems. Our current funding has a particular emphasis on mammals, butterflies, dragonflies, bees, and epiphytes, and we are especially (but not exclusively) interested in applicants who have experience in one of these groups. We ask candidates to briefly describe their preferred area of activity in the cover letter. Several junior or senior positions are available, with a typical contract length of 2-3 years.

The positions will be based at Yale University, with close collaborative links to our partners worldwide. The Yale BGC Center connects biodiversity scientists from across campus and hosts a range of speaker and workshop events. It supports research and training around the use of new technologies and data flows for model-based inference and prediction of biodiversity distributions and changes at large spatial and taxonomic scales. Flagship Center projects include Map of Life and associated activities supporting the Half-Earth Map and the development of the GEO BON Species Population Essential Biodiversity Variables. For animal movement data we are partnered with the Icarus initiative, a space station-based near-global GPS animal movement observation system, and Movebank, which supports the management and integration of movement data. For camera trapping data we are members of the Wildlife Insights initiative. Other Center initiatives include the integration of phylogenetic information with spatial distributions (e.g., VertLife), and the NASA-supported development and application of remote sensing-informed layers for biodiversity modelling (EarthEnv).

Yale University offers researchers and staff competitive salaries and a generous package of benefits. Yale has a thriving and growing community of young scholars in ecology, evolution and global change science in the EEB Department, the Yale Institute for Biospheric Studies, the Peabody Museum, and the Yale School of Forestry and Environmental Studies. The town is renowned for its classic Ivy League setting, 75 miles north of New York City. To apply please send, in one pdf, a short motivation (i.e. cover) letter, CV and names and contact information for three referees to michelle.duong@yale.edu, subject "BGC Postdoc" For questions contact walter.jetz@yale.edu. The final selection process will begin on 20 January 2018. We passionately believe that a diverse team will enable a broader perspective and enhance creativity, and we strongly encourage applications from women and minorities.

"Jetz, Walter" <walter.jetz@yale.edu>

WorkshopsCourses

Arizona UltraLargePhylogenies Apr12-14

Trees in the Desert 2019 (http://treesinthedesert.org)

** Grad student travel funds still available **

A workshop on ultra-large phylogenetic trees April 12-14, 2019 Tucson, Arizona

Phylogenetic trees with thousands of species, genes or individuals are now being published regularly, and numerous efforts around the globe are aimed at scaling this up even further. The algorithmic challenges for assembling, evaluating, and applying these large trees remain formidable, however, with plenty of room for novel approaches. We invite graduate students in phylogenetic biology, bioinformatics, mathematics and computer science to join us in a three-day workshop on this topic, supported by a grant from the U.S. National Science Foundation. The goal is to communicate aspects of known approaches to the problem, brainstorm collectively about new ideas, and get our hands dirty with exemplar data sets. The ideal student for this will be a mid- to-late Ph.D. student in one of these fields, with some experience in phylogenetic toolkits, programming and bioinformatics infrastructure (e.g., scripting languages, UNIX shell, etc.). Funds are available to support travel, lodging and meals for students.

Topics will likely include constructing large trees, evaluating their robustness and reliability, and integrating them with various post-phylogenetic analyses. Specific topics will be driven by interests and experience of the participants but may include scalability of conventional tree building methods, alignment-free tree construction, model-selection in large trees, coalescent and gene-tree approaches, missing data and terraces, assembling confidence sets of trees for subsequent study, and scalable inference of tree annotations such as divergence times, ancestral states, etc. Aside from short talks the first day, the format will be almost entirely "hands-on", focusing on developing and testing new ideas and pushing existing ones to their feasibility limits.

The workshop will be held at the University of Arizona's Biosphere 2 (http://biosphere2.org) facility, located in the foothills of the Santa Catalina Mountains about 30 miles north of Tucson. Tucson proper is flanked on its east and west sides by Saguaro National Park, founded as a reserve for the saguaro cactus that is so emblematic of the Sonoran Desert. April is an exceptional time to visit southern Arizona, with the spring desert bloom well underway, sunny warm days and cool nights. Biosphere 2 is located in mesquite grassland not far from trailheads for the Arizona Trail and other hikes into the Catalina Mountains.

Confirmed instructors:

Mukul Bansal, University of Connecticut Mark Holder, University of Kansas Michelle McMahon, University of Arizona Emily Jane McTavish, University of California, Merced Jeff Oliver, University of Arizona Dan Portik, University of Arizona Mike Sanderson, University of Arizona (Organizer) Mike Steel, University of Canterbury John Wiens, University of Arizona Derrick Zwickl, University of Arizona

Application and financial aid

Class size will be kept small, and funds are available to support graduate student travel, meals and lodging. Please copy and paste the questions below and your answers into an email to Mike Sanderson (sanderm@email.arizona.edu) by January 25, 2019, together with a copy of your C.V. Also arrange to have one letter of recommendation from your advisor sent to the same email by the deadline.

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1. Name and email address:

2. University, degree program, years in program, name of advisor:

3. Briefly describe your knowledge of phylogenetic methods and experience with phylogenetic software tools:

4. Briefly describe your programming experience, if any

5. How is the question of constructing large phylogenetic trees relevant to your research interests?

6. What specific topics would you like to see discussed at this workshop?

Michael J. Sanderson, Professor Department of Ecology and Evolutionary Biology University of Arizona Tucson, AZ 85721

Office: BSW 412 Phone:520-626-6848 email:sanderm@email.arizona.edu

lab web site: http://ceiba.biosci.arizona.edu Ceiba phylogenetic tree visualization: http://sourceforge.net/projects/ceiba r8s software: https://sourceforge.net/projects/r8s Mike Sanderson <sanderm00@gmail.com>

Barcelona PopulationGeneticAnalyses Jun17-20

Dear colleagues,

This course might be of interest for the members of this list: MANIPULATION OF NGS DATA FOR GENOMIC AND POPULATION GENETICS ANALYSES.

Date: June 17th-20th, 2019, Barcelona (Spain).

PLACE: Capellades, Barcelona.

INSTRUCTORS: Dr. FranÃÂSabot (Institute of Research for Development, France) and Dr. Christine Tranchant-Dubreuil (Institute of Research for Development, France).

PROGRAM: - Monday: Introduction to NGS sequencing platforms. Introduction to basic command lines. Basic raw data manipulations (counting sequences, listing files). - Tuesday: Raw data QC & Cleaning. Introduction to TOGGLe, a NGS pipeline framework. Mapping: principle, tools, execution. Mapping: cleaning, data control, realigning, duplicates marking. - Wednesday: SNP calling: raw calling, cleaning calling, filtering. VCF manipulations: filtering on MAF, heterozygosityÂ Impact of SNPs on genes. Population genomics using sNMF. - Thursday: Context-based analyses. Piping large scale analyses for multiple samples using TOGGLe. Testing new tools and different conditions to answer different biological questions.

Questions.

More information and registration: https://www.transmittingscience.org/courses/genetics-and-genomics/manipulation-ngs-data-genomic-population-genetics-analyses/ Other Transmitting Science's upcoming courses that can be of interest:

* An introduction to Metagenomics and Metabarcoding (https://www.transmittingscience.org/courses/genetics-and- genomics/introduction-metagenomics-metabarcoding/) * Introduction to Evolutionary Quantitative Genetics (https://www.transmittingscience.org/courses/genetics-and- genomics/introduction-evolutionary-quantitative-genetics/) * Introduction to Bayesian Inference in Practice (https://www.transmittingscience.org/courses/statistics-and- bioinformatics/introduction-bayesian-inference-practice/) * Mapping Trait Evolution (https://www.transmittingscience.org/courses/evolution/mapping-trait- evolution/)

With best regards

Sole

Soledad De Esteban-Trivigno, PhD Scientific Director Transmitting Science www.transmittingscience.org Soledad De Esteban Trvigno <soledad.esteban@transmittingscience.org>

Barcelona QuantGenetics Apr8-12 EarlyBirdExtended

Dear colleagues,

Early bird fee has been extended to January 31st for the course ^{o}Introduction to Evolutionary Quantitative Genetics±

Instructors: Dr. Erik Postma (University of Exeter, UK) and Dr. Jes^{2}s Martnez-Padilla (Universidad de Oviedo, Spain).

Dates and place: April 8th-12th, 2019. Capellades, Barcelona (Spain).

Check if you can benefit of 20 % discount: https://www.transmittingscience.org/funding/organizations-with-discount/ Course Overview:

By simultaneously using the resemblance among all individuals in the pedigree, these methods provide more precise and accurate estimates of genetic and non-genetic variance components (heritabilities and genetic correlations). Furthermore, they allow for the estimation of individual-level genetic effects (breeding values), and thereby the inference of evolution.

In this course, we will cover everything from basic quantitative genetic theory and statistics to advanced mixed model-based approaches. You will learn how to estimate genetic variances and covariances in wild and captive populations, and how to test for evolutionary change.

Along the way, you will be exposed to the main software packages, and the R packages MCMCglmm and ASReml-R in particular, and you will learn about their strengths and weaknesses.

You are strongly encouraged to bring your own data (if you have it), which you will be able to work on during the course and which will allow you to put the theory into practice.

More information and registrations: http://bit.ly/transmitting-science-course-quantitative-genetics or writing to courses@transmittingscience.org

Other courses that can be of interest for people in this list: https://www.transmittingscience.org/courses/evolution/ With best regards Sole

Soledad De Esteban-Trivigno, PhD Scientific Director Transmitting Science www.transmittingscience.org

Berlin 16SMetabarcoding Apr1-5

Dear all,

we still have a few places left for our course “16 S/ITS Metabarcoding of microbial communities”

(https://www.physalia-courses.org/courses-workshops/course30/)

When: 1-5 April 2019

Where: Free University of Berlin (Germany)

Instructors:

Dr. Antti Karkman (University of Gothenburg, Sweden)

Dr. Anna Sandionigi (University of Milan Bicocca, Italy)

Dr. Bruno Fosso (Institute of Biomembrane,Bioenergetics and Molecular Biotechnologies, CNR, Italy)

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. All the hands-on exercises will be carried out using QIIME2 platform ((https://qiime2.org/)).

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/)

Should you have any questions, please feel free to contact us: info@physalia-courses.org

Best regards,

Carlo

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR info@physalia-courses.org http://www.physalia-courses.org/ Twitter: @physacourses mobile: +49 17645230846 https://groups.google.com/forum/#!forum/physalia-courses “info@physalia-courses.org” <info@physalia-courses.org>

Berlin aDNAPaleogenomics Jun17-21

Course: aDNA Paleogenomics

Berlin , 17th -21st of June 2018

Instructors:

Dr. Claudio Ottoni (Sapienza University of Rome (Italy))

Dr. Amine Namouchi (University of Oslo (Norway))

Overview

This course will introduce biologists to the main bioinformatic tools for the analysis of Next Generation Sequencing (NGS) data from ancient samples. Through a series of theoretical and practical hands-on sessions, the main goal of this course is to provide a clear understanding of the most common bioinformatic methods adopted in a wide range of paleogenomics projects (from metagenomic screening of ancient samples, to NGS reads mapping and phylogenetic tree reconstruction). Particular attention will be given to quality control, DNA damage assessment and variants calling. A basic introduction to NGS platforms and the main file formats used in most common bioinformatics pipelines will be provided. Each day will consist of a mix of introductory lectures on the theoretical background of the programs that will be used, followed by hands-on exercises using command line tools performed by the participants under guided supervision.

Target Audience & ASSUMED BACKGROUND

The course is aimed primarily at researchers (MSc and PhD students, postdoctoral fellows, engineers) interested in learning the different steps from NGS raw data analysis to phylogenetic tree reconstruction in archaeological samples. The hands-on sessions are targeted to beginners and more advanced users alike. The practical sessions will cover the most common pipelines adopted in paleogenomics, and can be applied to a wide range of projects, from metagenomics to genome resequencing. Attendees should have a background in biology and some familiarity with genomic data.

STRUCTURE

The course material will be delivered over 5 days, in 10 half-day sessions. These lessons will build off of one another, and feature a mix of lecture and in-class exercises.

For more information about the course program, please visit our website: (https://www.physalia-courses.org/-courses-workshops/course27/)

Here is the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

All the best, Carlo

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR info@physalia-courses.org http://www.physalia-courses.org/ Twitter: @physacourses mobile: +49 15771084054 https://groups.google.com/forum/#!forum/physalia-courses "info@physalia-courses.org" <info@physalia-courses.org>

Berlin EukaryoticMetabarcoding Mar4-8

Dear all, we still have a few places left for our course: "Eukaryotic Metabarcoding", that will be held in Berlin (Free University of Berlin) from the 4th to the 8th of March.

Application deadline is: February 4th, 2019.

Instructors:

Dr. Owen S. Wangensteen (University of Tromsø, Norway; https://www.physalia-courses.org/instructors/t2/)

Dr. Vasco Elbrecht (University of Guelph, Canada; https://www.physalia-courses.org/instructors/t7/)

This workshop gives an overview of metabarcoding procedures with an emphasis on practical problem-solving and hands-on work using analysis pipelines on real datasets. After completing the workshop, students should be in a position to (1) understand the potential and capabilities of metabarcoding, (2) run complete analyses of metabarcoding pipelines and obtain diversity inventories and ecologically interpretable data from raw next-generation sequence data and (3) design their own metabarcoding projects, including bioinformatic data analysis and planning of laboratory work. 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.

For more information about the course, please visit our website: (https://www.physalia-courses.org/courses-workshops/course4/)

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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mobile: +49 17645230846

(https://groups.google.com/forum/#!forum/physalia-courses)

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Berlin EukaryoticMetabarcoding Mar4-8 LastCall

Dear all,

we would like to inform you that we have the last 5 places left for our Eukaryotic Metabarcoding Workshop, that will be held in Berlin (Free University) from the 4th to the 8th of March.

Registration deadline: 10th February

Instructors:

1) Dr. Owen S. Wangensteen (University of Tromsø, Norway)

2) Dr. Dr. Vasco Elbrecht (University of Guelph,

Canada)

This workshop gives an overview of metabarcoding procedures with an emphasis on practical problem-solving and hands-on work using analysis pipelines on real datasets. After completing the workshop, students should be in a position to (1) understand the potential and capabilities of metabarcoding, (2) run complete analyses of metabarcoding pipelines and obtain diversity inventories and ecologically interpretable data from raw next-generation sequence data and (3) design their own metabarcoding projects, including bioinformatic data analysis and planning of laboratory work. 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.

For more information, please visit our website: https://www.physalia-courses.org/courses-workshops/course4/ Here is the full list of our courses and Workshops: https://www.physalia-courses.org/courses-workshops/ All the best, Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org http://www.physalia-courses.org/ Twitter: @physacourses mobile: +49 17645230846 https://groups.google.com/forum/#!forum/physalia-courses "info@physalia-courses.org" <info@physalia-courses.org>

Berlin GenomeAssemblyAnnotation Feb11-15

Dear all, we would like to inform you that we have the last 4 places left for our course: "Assembly and Annotation of genomes", that will be held in Berlin (Free Uuniversity) from the 11th to the 15th of February.

Application deadline is: January 11th, 2019.

Instructor: Dr. Thomas D. Otto (University of Glasgow, UK; (https://www.physalia-courses.org/instructors/t28/))

Assistant instructor: Mr. Maximilian Driller (Begendiv, Germany; (http://bit.ly/2zcwmQT))

The course is aimed at researchers interested in learning more about genome assembly and annotation. It will include information useful for both the beginner and the more advanced user. We will start by introducing general concepts and then continue to step-by-step describe all major components of a genome assembly and annotation workflow, from raw data all the way to a final assembled and annotated genome. There will be a mix of lectures and hands-on practical exercises using command line Linux.

Attendees should have a background in biology. We will dedicate one session to some basic and advanced Linux concepts. Attendees should have also some familiarity with genomic data such as that arising from NGS sequencers.

For more information about the course, please visit our website: (https://www.physalia-courses.org/courses-workshops/course20/)

Here is the full list of our courses and Workshops: (https://www.physalia-courses.org/courses-workshops/)

Best regards and happy 2019,

Carlo

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR info@physalia-courses.org (http://www.physalia-courses.org/) Twitter: @physacourses mobile: +49 17645230846 (https://groups.google.com/forum/#!forum/physalia-courses)

"info@physalia-courses.org" <info@physalia-courses.org>

Berlin PathwayAnalysisInR Mar11-15

Workshop "Squeezing biology out of statistics: Gene set and pathway analysis in HT data"

Where: Free University of Berlin When: 11-15 March.

Our instructor for this course is Dr. January Weiner (Staff Scientist at the Max Planck Institute for Infection Biology, Germany).

Registration deadline: 10th February. We have a limited number of places available for this course.

This course offers computational techniques that go beyond a simple technical or statistical analysis. It covers techniques for the analysis of gene set enrichments, pathway analysis, gene ontologies, functional analysis of metabolomic profiling and making use of correlations and coexpression networks. A prominent part of the course will be devoted to data visualization and visual data exploration.

The students will gain the ability to independently process and analyse HT data sets, select the appropriate tools, functionally interpret the results as well as learn the paradigms of computational biology and statistics which will allow them to efficiently communicate with computational biologists.

As an incentive, each student will receive a set of gene expression profiles for a different organism, and during the course they will use these to generate species-specific gene expression modules and test their utility. If we are successfull, we will attempt a joint publication.

For more information about the course, please visit the course website: (https://www.physalia-courses.org/-courses-workshops/course32/)

Here you can find the complete list of our courses and Workshops:(https://www.physalia-courses.org/courses-workshops/)

Should you have any questions, please feel free to contact us at: info@physalia-courses.org

Best regards, Carlo

Carlo Pecoraro, Ph.D

Physalia-courses DIRECTOR info@physalia-courses.org http://www.physalia-courses.org/ Twitter: @physacourses mobile: +49 17645230846 https://groups.google.com/forum/#!forum/physalia-courses "info@physalia-courses.org" <info@physalia-courses.org>

Berlin RADseq Jun10-14

Dear all, happy to inform you that we will run for our RAD-seq data analysis Workshop based on the last version of the Stacks pipeline this June (10th-14th June) in Berlin, with Dr. Julian Catchen (University of Illinois, Urbana-Champaign; http://catchenlab.life.illinois.edu/-).

In this course, we will introduce the different approaches for obtaining reduced representation genome sequencing data and will specially focus on the data analysis. We will cover all necessary steps to obtain genome variants from short read data that are informative for population genetics, phylogenetic and association studies.

This course is aimed at researchers and technical workers who are generating and/or analyzing reduced representation genome sequencing data (RAD-seq, ddRAD, 2bRAD, GBS,). Examples demonstrated in this course will involve primarily non-model organisms and examples of applications of this data type for different purposes will be covered. Attendees should have a background in biology. We will dedicate one session to some basic and advanced Linux concepts. Attendees should have also some familiarity with genomic data such as that arising from NGS sequencers.

Please visit our website to have more information about the course content: https://www.physalia-courses.org/-courses-workshops/course16/ Here is the full list of our courses and Workshops: https://www.physalia-courses.org/courses-workshops/ Best regards,

Carlo

Carlo Pecoraro, Ph.D Physalia-courses DIRECTOR info@physalia-courses.org http://www.physalia-courses.org/ Twitter: @physacourses mobile: +49 15771084054 https://groups.google.com/forum/-#!forum/physalia-courses "info@physalia-courses.org" <info@physalia-courses.org>

Bogor Indonesia ConservationResearch Jul15-18

This is a call for applications to participate in a Workshop to Enhance Collaboration Between US and Indonesia in Biodiversity and Conservation Research. Participant travel and accommodation costs will be covered. A brief overview is below, but more information and the application can be found here: https://-/sites.northwestern.edu/workshopinfo/ What: NSF-funded workshop co-sponsored with Bogor Agricultural University, in Bogor, Indonesia. The goal of the workshop is to bring together a broad range of scientists who share an interest in biodiversity and conservation research in one of the worlds biodiversity hotspots.

Where/When: The workshop will run from July 15-18, 2019 in Bogor, Indonesia. Participants will be expected to arrive in Jakarta, Indonesia by July 14, and can fly out of Jakarta by the evening of July 19.

Who: We aim to have a diverse group of participants, who span career stages (from graduate students to later career professionals) and underrepresented groups in science. Participants will have expertise in organisms across the evolutionary tree of life and employ a wide range of methodological approaches. To be eligible you must be studying or working at a US institution (e.g. university, museum, zoo, botanical garden, etc.).

How to apply: We are now accepting applications to participate in this workshop. Participants travel and accommodation costs will be covered. For more information about the workshop and the brief application process, please visit our website https://sites.northwestern.edu/-workshopinfo/. The deadline for an application is Feb. 20. We will aim to get back to applicants by early March.

Questions V contact Nyree Zerega (n-zerega@northwestern.edu)

Sincerely, Nyree Zerega, Ph.D, Professor of Instruction and Herbarium Curator Jeremie Fant, PhD, Conservation Scientist Plant Biology & Conservation Chicago Botanic Garden & Northwestern University

Nyree J C Zerega <n-zerega@northwestern.edu>

ColoradoStateU WildlifeGenomics Jun2-8

Where: Colorado State University

What: The 3nd Genomics of Disease in Wildlife Workshop

When: June 2-8, 2019

Website for more information and application instructions: https://www.gdwworkshop.colostate.edu/ Application Deadline: February 9, 2019

Email inquiries: CSU_gdw@colostate.edu

Overview:

Title: Genomics of Disease in Wildlife: A Workshop

Location: Lory Conference Student Center, Colorado State University, Fort Collins, CO

Dates: June 2-8, 2019

Website: https://www.gdwworkshop.colostate.edu/ Application deadline: February 9, 2019.

Wildlife biodiversity can be drastically affected by the outbreak and transmission of disease pathogens in both natural habitats and ex situ populations. Recent technological advances in genomic sciences and increasingly affordable Next Generation Sequencing (NGS) assay costs have coalesced to result in powerful tools to monitor, detect, and reconstruct the past, present and future role of pathogens within wildlife biodiversity. This 3rd annual ¥Genomics of Disease in Wildlife workshop will provide hands-on training for researchers seeking to incorporate genomic data into their wildlife disease related projects. The course will be taught by a core group of experts in genome data analyses along with invited preeminent scientists researching host-pathogen genomics in wildlife.

Why is the workshop needed?

Advances in genomic technology now provide an extraordinary opportunity to rapidly assess the impact of disease in wildlife biodiversity, management, and conservation. Wildlife and animal health researchers are uniquely positioned to merge ecological, biological, and evolutionary studies with genomic technologies to generate unprecedented ¥Big Data tools in disease research. The workshop will provide a venue to accomplish this goal, will provide networking opportunities for colleagues from intersecting interests, and will advance genomic tools in wildlife and animal health disease investigations.

How will the workshop address the need?

GDW2019 will provide essential training to those with skills and interest in some or all of the following: genome sciences & bioinformatics, animal health & veterinary sciences, wildlife biology & conservation, disease ecology of host & pathogen.

Attendees will conduct hands-on analyses of ¥real world genomic data of both host and pathogen. The course will provide: (1) an overview of current bioinformatics developments and approaches; (2) guidance to implement genomic tools in study design; (3) NGS data analysis and interpretation; and, (4) opportunities for interaction with peers, core faculty, and invited experts.

Workshop Syllabus

The workshop will cover a typical workflow commonly used in NGS analyses starting with the initial raw sequence through the final stages of identifying host:pathogen variants linked with disease. Each day of the workshop will cover an essential component of the NGS workflow in succession.

Morning sessions will be a series of instructional lectures and demonstrations that will concisely present the purpose, justification and implementation of the specific workflow unit. Short and exciting ¥flash talks presented by CSU faculty will present some of their ongoing investigations using genomic tools in both host and pathogen. The afternoon sessions will be computer-intensive labs in which attendees will perform ¥hands-on analyses with real-world genomic data for each workflow topic. Evening plenary lectures from invited speakers will conclude each days activities.

Teaching tools will include exercises using ¥real-world NGS data from a range of pathogens and host species. Participants will learn the importance of integrating NGS data from both host and pathogen in order to better understand current epidemics in wildlife.

For the duration of the course, each attendee will be provided with a MacBook Pro computer and peripheral equipment, and prepared genome datasets from several host species and associated pathogens. These datasets will be organized into various files and formats prior to the course, demonstrate key concepts, and be the foundation for computer exercises and teaching tools.

Summary of Workshop Schedule:

Optional Pre-Workshop UNIX Command Line and Coding Clinic. Sunday June 2, 2019 9AM-3PM

Day 1 V Sunday June 2, 2019* Official Opening of Workshop 6 PM

Arrival, Registration and Opening Reception

The workshop begins in the evening of Sunday June 2, 2019 at the Lory Conference Center. A welcome session will introduce faculty and an overview of the workshop. NGS workflow projects for teams will be introduced. An informal welcome reception follows with faculty, staff and participants.

*Participants will prepare a short 3-4 minute introduction of their

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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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FridayHarborLabs EvolQuantGenetics Jun10-14

Evolutionary Quantitative Genetics Workshop Friday Harbor Laboratories, University of Washington, 9-15 June 2019

Credits: 0 Instructor(s): Dr. Stevan J. Arnold, Dr. Joe Felsenstein Dates: Arrive Sunday, June 9th; depart Saturday, June 15th Max students: 30 Dates of instruction: Monday, June 10th - Friday, June 14th Application deadline: March 15, 2019

The application form will be found here: https://tinyurl.com/EQG2019Application The blog web pages for the workshop will be found at https://blogs.uw.edu/fhleqg/ They currently include a 2018 workshop schedule which has links to the materials for that year's workshop. The web page for the workshop at Friday Harbor Laboratories will be found at https://tinyurl.com/EQG2019 Instructors: Dr. Stevan J. Arnold, Department of Integrative Biology, Oregon State University Dr. Joe Felsenstein, Dept. of Genome Sciences and Dept. of Biology, University of Washington

This workshop has been given yearly since 2011. Since 2017 it has been given at the Friday Harbor Laboratories of the University of Washington, on San Juan Island.

The workshop will review the basics of theory in the field of evolutionary quantitative genetics and its connections to evolution observed at various time scales. One aim of the workshop is to build a bridge between the traditionally separate disciplines of quantitative genetics and comparative methods.

Quantitative genetic theory for natural populations was developed considerably in the period from 1970 to 1990 and up to the present, and it has been applied to a wide range of phenomena including the evolution of differences between the sexes, sexual preferences, life history traits, plasticity of traits, as well as the evolution of body size and other morphological measurements.

Phylogenetic approaches to comparative biology were developed in the 1980s and 1990s, including inferring how traits covary in evolution and how optimum values of traits vary between species.

Textbooks have not kept pace with these developments, and currently few universities offer courses on these subjects aimed at evolutionary biologists.

Evolutionary biologists need to understand this field because of the ability to collect large amounts of data by computer, the development of statistical methods for changes of traits on evolutionary trees and for changes in a single species through time, and the realization that quantitative characters will not soon be fully explained by genomics. This workshop aims to fill this need by reviewing basic aspects of theory and illustrating how that theory can be tested with data, both from single species and fro multiple-species phylogenies. Participants will use R, an open-source statistical programming language, to build and test evolutionary models.

The workshop involves lectures and in-class computer exercises. You can consult the 2018 workshop website for examples, using the links found at the 2018 schedule mentioned above.

The intended participants for this workshop are graduate students, postdoctoral fellows, and junior faculty members in evolutionary biology. The workshop can accommodate up to 30 participants. Guest instructors are:

* Marguerite Butler, Biology, Univ. Hawai'i, Manoa * Patrick Carter, Evolutionary Physiology, Washington State University, Pullman * Adam Jones, Biology, Texas A&M University, College Station * Brian O'Meara, Ecology & Evolutionary Biology, Univ. of Tennessee, Knoxville * Patrick Phillips, Biology, University of Oregon * Samantha Price, Biological Sciences, Clemson University * Josef Uyeda, Biological Sciences, Virginia Tech, Blacksburg

Cost: $1000, to be paid to Friday Harbor Laboratories. This fee will cover housing and meals at FHL and all other workshop expenses, except travel. Participants who have been admitted to attend will make their payment prior to arrival at FHL. Details of payment by credit card or check will be provided once the applicant has been admitted to attend.

We have also applied to two scientific societies for additional support which would enable a 20% refund of the cost, if the societies agree to provide this support.

Joe Felsenstein joe@gs.washington.edu Department of Genome Sciences and Department of Biology, University of Washington, Box 355065, Seattle, WA 98195-5065 USA

felsenst@uw.edu

Guarda Switzerland Evolution Jun15-22

Guarda summer school in evolutionary biology 2019

It is my pleasure to announce the 2019 Guarda summer school in Evolutionary Biology for master and PhD students. The main aim of the course is to develop the skills to produce an independent research project in evolutionary biology.

The summer school takes place 15. V 22. June in the Swiss mountain village Guarda. Faculty include Rosemary and Peter Grant (Princeton University, USA), John Krebs (University of Oxford, UK), Sebastian Bonhoeffer (ETH-Zurich, Switzerland) and Dieter Ebert (Basel University, Switzerland; organizer).

The course is intended for master students and early PhD students with a keen interest in evolutionary biology.

The web page with all details can be found here: http://www.evolution.unibas.ch/teaching/guarda/index.htm Application is open now. Deadline is 1. February 2019

Please communicate this information to interested students.

With best wishes,

dieter ebert

Dieter Ebert University of Basel, Zoology, Vesalgasse 1, 4051 Basel, Switzerland Tel. +41 (0)61 267 03 60 Email: dieter.ebert@unibas.ch

Dieter Ebert <dieter.ebert@unibas.ch>

Jyvaskyla Finland MolecularEvol Feb20-22

Registration extended until January 25th, or until the capacity is filled! Be quick!

Workshop: Molecular Evolution: Patterns and Causes

Time: Feb 20-22, 2019

Place: Konnevesi Research Station of the University of JyvÃÂskylÃÂ, Finland

Confirmed invited speakers: Prof. Adam Eyre-Walker (Sussex), Prof. Sylvain Glemin (Montpellier), Prof. Richard Goldstein (University College London), Prof. Ville Mustonen (Helsinki), Prof. Andreas Wagner (Zurich), Dr. Jessica Abbott (Lund), and Dr. Kim Steige (University of Cologne)

This is a great opportunity for researchers and students to hear talks from world top scientists in evolutionary and ecological genetics and molecular science, to network, and to discuss your work in a cosy atmosphere! Please go to https://www.jyu.fi/en/research/summer-and-winter-schools/ecology/workshop/workshop-1 to see more details about the program.

To register, go to https://payments.jyu.fi/events/population_cycles_and_outbreaks (don't mind the misnaming in the title, please). Registration is open until Jan 25th, but please register as soon as possible to secure your place in the workshop. If we get too many registrations, registration will be closed early.

The rate of molecular evolution varies at several levels of biological organization, e.g. among sites, among proteins, among chromosomes, and among lineages. The forces underlying this variation include mutation rate and the strength of natural selection, which are in turn affected by e.g. population size, linkage, generation time, gene function, gene expression, pleiotropy, and biophysical properties of gene products (e.g. proteins). While there is a reasonable understanding of these patterns and forces, many questions remain, and a holistic view of molecular evolution is still somewhat underdeveloped. The aim of the workshop is to bring together students and researchers from all career stages to discuss recent findings in the field of molecular evolution, and to foster new research and collaborations. The estimated number of participants is 50.

The workshop starts on Wednesday, Feb 20th at 12:45, but it is possible to arrive already on Tuesday, Feb 19th. On Tuesday evening, there will be dinner and sauna provided. The workshop ends on Friday, Feb 22nd at 16:00.

Participation fee includes accommodation, meals, beverages, and banquet during workshop.

Â Tuesday evening to Friday: 260 âÂÂ¬

Â Wednesday morning to Friday: 210 âÂÂ¬

Â for students accepted to the course Introduction to Molecular Evolution, and taking the workshop additionally: 80 âÂÂ¬

– Dr. Mikael Puurtinen Dept. of Biological and Environmental Science PO Box 35 40014 University of JyvÃÂskylÃÂ, Finland Tel. +358503758975 mikael.puurtinen@jyu.fi

“Puurtinen, Mikael” <mikael.puurtinen@jyu.fi>

London EvolutionLanguage Aug29-30

Dear Colleagues interested in the biological and cultural evolution of vocal interactions and language,

we are delighted to announce that VIHAR2019 http://vihar-2019.vihar.org/ International workshop on Vocal Interactivity in-and-between Humans Animals and Robots, will be held in London 29-30 August 2019 (immediately preceding the International Bioacoustics Congress). In this discipline-crossing event, we will bring together perspectives on vocal interaction from cognitive science, linguistics, robotics, animal behaviour, language evolution and artificial intelligence. We aim at bridging the gap across different but contiguous fields of research that have a potential for strong resonances and integration. The contribution of evolutionary biologist will be appreciated. Save the date and join us in London, together with our keynote speakers:

- Sonja Vernes, Max Planck Institute for Psycholinguistics - Mohamed Chetouani, Institute for Intelligent Systems and Robotics (CNRS), Sorbonne University - Tecumseh Fitch, University of Vienna - Verena Rieser, Heriot-Watt University

We will soon announce our calls for papers/abstracts.

This workshop follows the success of the 1st International workshop on Vocal Interactivity in-and-between Humans, Animals and Robots (VIHAR-2017 < http://vihar-2017.vihar.org/ >). To join the VIHAR community, read more about us http://www.vihar.org/, subscribe to our mailing list https://www.freelists.org/list/vihara and follow us on Twitter @vihar2019 https://twitter.com/vihar2019 The Organising Committee http://vihar-2019.vihar.org/committees/ Elisabetta Versace, PhD, Alan Turing Fellow SBCS, Department of Biological and Experimental Psychology Queen Mary University of London Email: e.versace@qmul.ac.uk Phone: + 44 (0) 207882 8798

Twitter: @so_evolutionary

Elisabetta Versace <e.versace@qmul.ac.uk>

Portal Arizona Bees Aug18-28

In Partnership with the American Museum of Natural History and the Southwestern Research Station we are proud to announce the 21st installment of The Bee Course. The Bee Course is a ten day workshop held at the Southwestern Research Station in Portal, Arizona from August 18th through the 28th, 2019. The course is designed to provide biologists interested in pollinators with the tools and knowledge necessary to collect, process, and to begin to identify bee specimens. We encourage all interested parties to apply. For more information, including instructions on how to apply, a list of this years instructors, and course testimonials, please visit our new website at www.thebeecourse.org . Bryan N. Danforth, Professor and Chair Department of Entomology 3124 Comstock Hall Cornell University Ithaca, NY 14853-2601 phone: 607-255-3563/FAX: 607-255-0939 email: bnd1@cornell.edu Lab website: http://www.danforthlab.entomology.cornell.edu/ The Solitary Bees (forthcoming): https://press.princeton.edu/titles/13525.html Northeast Pollinator Partnership: http://www.northeastpollinatorpartnership.org Bryan Nicholas Danforth <bnd1@cornell.edu>

Portugal BioinformaticsUsingJava Mar27-29

This course will introduce students to the fundamentals of programming for bioinformatics using the Java programming language. Many of the concepts covered will be readily transferable to other languages. The course will largely focus on the Java language basics including: data types; program control structures; and object-oriented programming features of the language, with an emphasis on usage within areas of bioinformatics, for example file manipulation, package use and calling external software. By the end of the course students will have had a primer on creating programmatic solutions to real world problems within the scope of their research.

Click < https://cibio.up.pt/workshops–courses/details/introduction-to-programming-for-bioinformatics-using-java > here to see the programme for the course.

COURSE INSTRUCTORS < https://cibio.up.pt/people/details/archerj > John Archer - CIBIO-InBIO | BIOINFORMATICS

INTENDED AUDIENCE

The course will be open to a maximum number of 15 participants.

75% of available student slots are reserved for BIODIV students. Priority will be given to: - 1st year and other PhD students attending the BIODIV Doctoral Program; - PhD students attending other courses; - Other postgraduate students and researchers.

REGISTRATION Registration deadline: February 02, 2019

To apply, please fill the form available < https://docs.google.com/forms/d/e/1FAIpQLSfrU1wjeycZsml7sQ7q3UWwmyPux7MdVD93h1iJGmxmLe0s_Q/viewform?usp=pp_url > HERE

Participation is free of charge for BIODIV students | 65 €(students) | 125 €(other participants). CIBIO-InBIO members will have an additional discount of 20%. All applicants will be notified about whether they are accepted until February 4, 2019.

< https://cibio.up.pt/upload/filemanager/rulesadvancedcourses.pdf > Please note that new rules apply for all BIODIV students.

For more information about the course, please contact: post.graduation@cibio.up.pt . CIBIO - Centro de Investigaçao em Biodiversidade e Recursos Geneticos

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CIBIO-InBIO Divulgaçao

Portugal WildlifeConservation Apr8-11

During this 4 days course we will expose students to the scientific basis and practical applications of the study of wildlife population biology. The modern study of wildlife population ecology orchestrates a dance at the interface of reliable fieldwork and the use of mathematical tools and population genetic techniques. Students will learn how to collect the data necessary to study wildlife populations, and how to assess the factors that affect population growth and interactions with other species. This will include descriptors of population dynamics (eg. trends in abundance, cycles), projections of deterministic and stochastic population models with stage structure, mechanisms and modeling of density dependence (positive and negative), targeting specific conservation actions through sensitivity analysis, metapopulation and source-sink dynamics, viability analysis, and the interface between genetic variation and population performance. The focus will be on how to rigorously analyze population dynamics and apply the inferences to better conservation decision-making.

By the end of the course, students should have the confidence to advance both management and research by effectively using data, models, and the ecological concepts to address pressing questions involving the harvest, monitoring, and conservation of wildlife populations.

Click https://cibio.up.pt/workshops–courses/details/advanced-course-archaeogenetics-approaches-to-investigate-domestication-and-evolution#prettyPhoto here to see the programme for the course.

COURSE INSTRUCTORS

http://www.umt.edu/research/millslab/ L. Scott Mills - University of Montana

https://cibio.up.pt/people/details/psmonter Pedro Monterroso - CIBIO-InBIO | CONGEN

INTENDED AUDIENCE

The course will be open to a maximum number of 20 participants.

75% of available student slots are reserved for BIODIV students. Priority will be given to:

- 1st year and other PhD students attending the BIODIV Doctoral Program; - PhD students attending other courses; - Other post-graduate students and researchers.

REGISTRATION Registration deadline: February 07, 2019

To apply, please fill the form available

https://docs.google.com/forms/d/e/1FAIpQLScjwtC0JnsPUg2xXxVOmC31B8hvsap8OVbMGZhdgmeliBp1g/viewform?usp=pp_url HERE

Participation is free of charge for BIODIV students | 95 €(students) | 200 €(other participants). CIBIO-InBIO members will have an additional discount of 20%. All applicants will be notified about whether they are accepted until February 18, 2019.

https://cibio.up.pt/upload/filemanager/rulesadvancedcourses.pdf Please note that new rules apply for all BIODIV students.

For more information about the course, please contact: post.graduation@cibio.up.pt.

CIBIO - Centro de Investigaçao em Biodiversidade e Recursos Geneticos

InBIO Laboratorio Associado, Universidade do Porto

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

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

CIBIO-InBIO Divulgaçao divulgacao@cibio.up.pt

Procida Italy PopulationGenomics Mar30-Apr6

Deadline for registration is approaching soon for the upcoming EMBO Practical Course "Population Genomics: background, tools and programming".

IMPORTANT DATES for this Course:

Deadline for applications: 31/01/2019

Latest notification of acceptance: 13/02/2019

Course date: 30/03-06/04/2019

Venue: Conservatorio delle Orfane, Terra Murata, 80079, Procida, Italy

A maximum of 24 candidates will be selected based on their application.

Notifications of acceptance will be sent shortly after the closing date of registration.

Full details, including the course programme and the application form,

at: http://meetings.embo.org/event/19-population-genomics Instructors:

Anders Albrechtsen (University of Copenhagen, Denmark)

Andrea Manica (University of Cambridge, UK)

Andrew Clark (Cornell University, USA)

Chiara Batini (University of Leicester, UK)

Garrett Hellenthal (University College London, UK)

Margherita Francescatto (Fondazione Bruno Kessler - Trento, IT)

Mathias Currat (Université de Genève, Switzerland)

Vincenza Colonna (National Research Council, IT)

Course description

Study methods in population genomics have been profoundly reshaped in the last few years, fostered by a rapid growth of DNA sequence production and sharing. This unprecedented opportunity guided major steps forward in the field and calls for new approaches and computational skills to become routine in evolutionary genomics laboratories.

The objectives of this EMBO Practical Course are to give an overview of the state of the art methods in population genomics, including programming, and to enable participants to run their project's analyses with high confidence. The course combines lectures from outstanding experienced population geneticists with practice, both at individual and group level. All conceptual innovation will be presented in lectures and applied in practice.

This EMBO Practical Course will cover coalescent, genetic diversity, natural selection, population demography in time and space, admixture, genetic clustering, and genome-wide association studies. Population genetics topics will be complemented by computational ones such as Python programming and machine learning techniques.

This course aims at evolutionary biologists who already have basic bioinformatics skills. Ph.D. students and Postdoc researchers will benefit the most out of this course, but applications from all candidates will be evaluated in their context.

Thank you for your interest,

Chiara Batini (University of Leicester, UK) and Vincenza Colonna (CNR, Napoli, IT)

"Batini, Chiara (Dr.)" <cb334@leicester.ac.uk>

Roscoff EvolutionNetworkBioinformatics Jun23-29

Introduction to the concepts and methods of networks in evolutionary studies (sequence similarity networks, genome networks and multipartite graphs)

This free summer school will be held in Roscoff, France, between June 23rd 2019 (date of arrival) and June 29th (date of departure).

This school is designed in priority for biologists and bioinformaticians (completing a PhD degree or currently post-doctoral fellows, as well as researchers), who wish to learn the bases of network analyses.

The main notions (regarding various types of networks, the relevance of their analyses, and some bases in graph theory) will be introduced by short theoretical classes, followed by practical case-studies, introducing the basics in programming required to run such network analyses as well as to use the existing software/tools. Our goal is that, by the end of this summer school, all applicants will be qualified to perform network analyses of their own datasets.

More precisely, we will focus on the following concepts and methods:

- Introgressive evolution and large-scale diversity studies.
- Construction and analysis of sequence similarity networks (construction and sorting of connected components, definition of gene families, search for composite genes, implementation of centrality measures)
- Construction and analysis of genome networks (construction of weighted genome networks, implementation of their diameter, shortest paths, analyses of labeled nodes, etc.)
- Construction and analysis of gene-genome bipartite graphs (detection of connected components, and their articulation points, and twins)

In addition, 9 conferences on networks and evolution will be delivered by leading European and North American scientists during this school.

Confirmed speakers (complete list):

Pr. JP Gogarten (UConn, USA): Lateral Gene Transfer and Prokaryotic evolution

Pr. Robert Beiko (Dalhousie University, Canada) : Introduction to phylogenetic networks

Dr. Eric Bapteste (UPMC, France): Introduction to sequence similarity networks

Pr. Debashish Bhattacharya (U. Rutgers, USA): Reticulate evolution in eukaryotes

Pr. Eugene Koonin (NCBI, USA) : Viruses and networks

Pr. Michel Habib (LIAFA, France): Networks and centralities

Dr. Damien Eveillard (U. Nantes, France): Co-occurrence networks and the evolution of geochemical cycles in the environment

Pr. Daniel Huson (U Tuebingen, Germany): Network approaches in microbiome analysis

Pr. Marc-André Sélosse (MNHN, France): The living world as a network

This summer school is funded by ERC grant (FP7/2007-2013 Grant Agreement # 615274). Hence, registration is free, housing and food (breakfast, lunch) are also fully covered. Applicants will only need to fund their travel to Roscoff and their evening dinners.

10 places only are available, with a mandatory requirement: applicants must show basic computer skills (i.e. to be familiar with Linux environment and with at least one programming language, preferably Python).

Applications are to be submitted asap, and no later than February 15th 2019, by email to :

eric.bapteste@upmc.fr , and contain a brief letter describing why this class will be of significant interest for the applicant and his/her future studies.

Applicants will be selected based on their motivation, and their resume, including the names of two scientific referees for PhD and postdoctoral fellows.

We are excited to meet you soon in Roscoff.

Eric Bapteste + Philippe Lopez + Eduardo Corel

Bapteste Eric <epbapteste@gmail.com>

Spain DNAmetabarcoding Mar26-29

DNA metabarcoding and introduction to metagenomics March 26-29 2019 (A Coruña, Spain)

In this 22-hour course, participants will be introduced to the most important computational tools used to analyse Illumina DNA metabarcoding and metagenomic datasets. Participants will learn how to carry out the main DNA metabarcoding data analyses, from preprocessing and quality control of the raw data to the construction of OTU/ASV tables and taxon assignment. The course will also have an introductory metagenomics module in which the most relevant points of a metagenomics study will be discussed. The participants will learn how to analyse a dataset to determine the taxonomic and functional composition of metagenomic samples. The course will combine theory with hands-on exercises using real datasets.

More info at https://www.allgenetics.eu/-index.php/services/training/dna-metabarcoding-and-introduction-to-metagenomics.html Joaquín Vierna <jvierna@udc.es>

Spain NGS Mar14-15

I would like to annouce the course “High-throughput sequencing using Illumina, PacBio, and ONT: key concepts and applications” that will take place March 14 - March 15 in A Coruña (Spain).

More info at https://www.allgenetics.eu/index.php/-services/training/high-throughput-sequencing-using-illumina-pacbio-and-ont-key-concepts-and-applications.html .

Thank you very much!

Joaquín

Joaquín Vierna <jvierna@udc.es>

UCalifornia LosAngeles ConservationGenetics Mar23-27

UCLA/La Kretz Workshop in Conservation Genomics, 23 - 27 March, 2019

Conservation biology, genetics, and evolutionary biology have had a long and intimate relationship, and conservation constitutes one of the key applications of evolutionary analysis to real-world biological problems. The impacts of population and landscape genetics and gene expression studies have been particularly striking, and are helping to solve some of the most pressing problems in biological conservation.

As the field of conservation genetics continues to grow and mature, the availability of genome-scale data stand to make profound new contributions to our ability to identify and protect at-risk populations and recover those that are most endangered. However, genomic analyses also carry a computational burden-data sets are enormous, often require diverse skills and approaches for assembly, quality control and analysis.

The La Kretz annual workshop provides a comfortable, rigorous, and informal training environment for a small group of 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 data sets for conservation-relevant problems. One of the highlights of our workshop is active participation from members of several governmental agencies who are at the forefront of endangered species protection and management, providing a forum for exploring the most relevant aspects of conservation genomics to managers.

This year, the Woolsey fire destroyed most of our beloved UCLA/La Kretz Field Station (https://www.ioes.ucla.edu/santa-monica-mountains-research/) where we normally house the workshop. However, through an incredibly generous subsidy, we will house participants this year at the Calamigos Ranch next door (https://www.calamigos.com), with classes at the UCLA Stunt Ranch Reserve (http://stuntranch.ucnrs.org/), both in the heart of the Santa Monica Mountains. Only 30 miles from UCLA and the LAX airport, but nestled in the relatively undeveloped 160,000 acre Santa Monica Mountains National Recreation Area, Calamigos is a gorgeous setting, and Stunt Reserve provides an ideal location to explore new developments in genomic science and pressing needs in conservation and management together in a single setting.

Our current instructor list, drawn from UCLA faculty and several other partner institutions, includes:

Gideon Bradburd (Michigan State University) Ben Fitzpatrick (U. Tennessee Knoxville) Zach Gold/ Emily Curd Ryan Harrigan Kirk Lohmueller Evan McCartney-Melstad Alice Mouton Brad Shaffer Victoria Sork Erin Toffelmier Ian Wang (UC Berkeley, tentative) Bob Wayne

Agency partners represented: US Geological Survey, Bureau of Land Management, US Fish and Wildlife Service, California Department of Fish and Wildlife, The Nature Conservancy.

Topics covered:

Overview of traditional conservation genetics Next generation platforms: the best tool for the job Data management pipelines: Quality Control Data storage Data organization Data types and analyses: SNPs Sequences Exploring very large data sets Functional genomic data RNA-seq RADseq pipelines, from raw reads to analyzing data Genomic data and GIS Visualizing geographic structure and demographic history Admixture, clines, and hybridization Detecting adaptive variation RNAseq in a conservation context eDNA: promise and reality

Prerequisites Available housing limits course enrollment to ~20 students. Preference will be given to masters and doctoral candidates who are in the early to middle stages of their thesis research, and who have some familiarity with using a command line interface or programming languages (i.e. Perl, python etc.). We also welcome applications from postdocs, faculty, and government researchers. We encourage applications from women, minorities, and individuals from under-represented demographics in the sciences.

ADMISSION AND FEES

Applicants will be admitted based on academic qualifications and appropriateness of research interests. The course fee is $475. This includes food and lodging at Calamigos, as well as all incidental fees, for the duration of the course (arriving Saturday March 23, departing Thursday March 28).

UCLA students are encouraged to take the La Kretz Workshop for graduate credit. Other UC students may also be able to take the course for credit. We will provide documentation of the course if needed at your home institution.

Application Forms and Information Visit the UCLA/La Kretz Center for California Conservation Science website for additional information and to download an application form:

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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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UK ComparativeGenomics Apr29-May3

Comparative genomics (CMGN01)

FINAL CALL!

https://www.prinformatics.com/course/comparative-genomics-cmgn01/ PR informatics are excited to announce their new course “Comparative Genomics” which will be delivered by Dr. Fritz Sedlazeck and Dr. Matthias Weissensteiner in Glasgow city centre from the 29 April - 3rd May 2019

Course Overview:

This course will introduce biologists and bioinformaticians to the field of comparative genomics. The course will give a deeper understanding on the advantages and disadvantages of each of approach in general to enabling an informed decision of study design for the participants for future studies and learn the cutting edge approaches to process state of the art data sets. 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.

We will give a broad introduction on how to:

1. Process short and long read data based on multiple NGS data sets including mapping and de novo assembly 2. Detect SNP and Structural Variations using de novo assembly, short or long read mapping 3. Assess the impact of the detected variations 4. Perform population genetic analysis between multiple samples to obtain a deeper insight into these variants.

Furthermore, we will teach on how to install and manage these methods and give an introduction in Cloud computing. This will enable the participants to set up efficient pipelines on their own institutions. The course will conclude with the participants being aware of the state of the art approaches and a deepened knowledge to decide which study design is the optimal for future studies .

Course programme

Monday 29th V Classes from 09:30 to 17:30 Day 1: Intro + Assembly Lecture: Setting up and getting familiar with the system Data types, technology overview De novo assembly Practical: Getting used to the environment Manipulating read data (filtering, trimming, etc.) Short vs. long read assembly Subprocessing: QC, polishing of de novo assemblies

Tuesday 30th V Classes from 09:30 to 17:30 Day 2: Assembly quality + polishing ; RNA-Seq + short read mapping Lecture: How it works behind the scenes Data formats Common methods Practical: Insight in short read mappers Long read mapping SNP calling RNA-Seq expression

Wednesday 1st V Classes from 09:30 to 17.30 Day 3: SNP? + SVs detection (Assembly, Read based, phasing?) Lecture: Structural variation detection Methods to detect SV Current state of the art of technologies. Practical: Short read based SV calling Long read based SV calling Assembly based SV calling Comparing and filtering SVs Annotation of SVs

Thursday 2nd V Classes from 09:30 to 17:30 Day 4: Larger analysis over multiple data set and assessment of mutations over FST Lecture: Evolutionary genetics of structural variation Study design and sampling schemes Limitations Practical: Downstream analysis: Descriptive (SNP & SV density) PopGen (Fst, genetic diversity) Outlier analysis

Friday 3rd V Classes from 09:30 to 16:00 Day 5: Summary and conclusion Group discussions, final questions and overall summary (own data questions if time permits)

Email oliverhooker@prinformatics.com

Check out our sister sites, www.PRstatistics.com (Ecology and Life Sciences) www.PRinformatics.com (Bioinformatics and data science) www.PSstatistics.com (Behaviour and cognition)

– Oliver Hooker PhD.

PR informatics

2017 publications - Ecosystem size predicts ecomorphological variability in post-glacial diversification. Ecology and Evolution. - The physiological costs of prey switching reinforce foraging specialization. Journal of animal ecology.

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+44 (0) 7966500340

Oliver Hooker <oliverhooker@prinformatics.com>

USheffield UK PopulationGenomics Feb26-28

POPULATION GENOMICS WORKSHOP 26-28th February 2019 University of Sheffield, UK. This course will be held at the NERC Biomolecular Analysis Facility at the University of Sheffield and introduce participants to a variety of population genomics analyses for large next generation sequencing (NGS) datasets. It will include discussion on single nucleotide polymorphism (SNP) calling and filtering options, an introduction to population genomics statistics using the PopGenome R package, examining genetic structure, Fst-based analyses such as outlier detection/genomic islands of divergence, and genome-wide association analysis (GWAS). The majority of the course will comprise practical computer sessions, giving participants hands-on experience in these analyses. We will perform these on the high performance computing cluster at Sheffield and computers will be provided. Prior experience with the Linux environment and basic command line tools would be advantageous. There is no charge for the course, and successful applicants will be provided with accommodation for two nights and up to £100 towards travel costs to Sheffield. The application closing deadline is at 5pm on Monday 14th January 2019. Further details and how to apply can be found at: http://bit.ly/2ffk8L5 Katy Maher

Kathryn Maher <kathryn.maher@sheffield.ac.uk>

UTennessee Knoxville Selection Jun3-7

Feb. 1 Deadline Appr//oaching

/The National Institute for Mathematical and Biological Synthesis (NIMBioS) is now accepting applications for its Tutorial, "The Search for Selection," to be held June 3-7, 2019, at NIMBioS. The tutorial was previously held in June 2018.

Objectives: Biologists are obsessed (indeed, seduced) by the search for signatures of selection in organismal features of interest, ranging from specific traits to genome-wide signatures. A vast number of approaches have been suggested in this search for selection, including genomic-based signatures of recent or ongoing selection, tests based on either excessive amounts or nonrandom patterns of divergence (in both fossil sequences and functional genomics data) and the more classical Lande-Arnold fitness estimates (direct association of phenotypic values with fitness estimates) and their modern extensions (such as aster models). Given the breadth of such searches, a large amount of machinery has been developed, but is rarely presented in a unified fashion. This tutorial presents an integrated overview of all these approaches, highlighting common themes and divergent assumptions.

The goal of this tutorial is to expose investigators from all branches of biology to this rich menagerie of tests. It is applicable for population geneticists, genome biologists, evolutionary ecologists, paleontologists, functional morphologists, and just about any biologist who ponders on how to formally demonstrate that a feature (or features) of interest might have been shaped by selection.

The intended audience is advanced graduate students, postdocs, and faculty with an interest in searching for targets of selection, be they particular genomic sequences or particular traits. Given the breadth of this topic, the material would be of interest to individuals from functional genomics, population and evolutionary genetics, ecology, paleobiology, functional morphology, and statistics (as well as other fields). Background required: some basic introduction to population and/or quantitative genetics.

Location: NIMBioS at the University of Tennessee, Knoxville

Organizer: J. Bruce Walsh, Ecology & Evolutionary Biology, Univ. of Arizona

For more information about the tutorial and a link to the online application form, go to http://www.nimbios.org/-tutorials/selection2 Participation in NIMBioS tutorials is by application only. Individuals with a strong interest in the topic are encouraged to apply, and successful applicants will be notified within several weeks after the application deadline. NIMBioS will cover lodging (5 nights) and provide breakfast and lunch each day at NIMBioS. Limited travel support is available for those with a demonstrated need. Applicants should indicate on the online application whether they need travel support. * **Application deadline: February 1, 2019*

The National Institute for Mathematical and Biological Synthesis (NIMBioS) (http://www.nimbios.org) brings together researchers from around the world to collaborate across disciplinary boundaries to investigate solutions to basic and applied problems in the life sciences. NIMBioS is supported by the National Science Foundation, with additional support from The University of Tennessee, Knoxville.

Sergey Gavrilets Distinguished Professor Department of Ecology and Evolutionary Biology Department of Mathematics Associate Director for Scientific Activities National Institute for Mathematical and Biological Synthesis (NIMBioS) Director, Center for the Dynamics of Social Complexity (DySoC) University of Tennessee, Knoxville, TN 37996 Research Affiliate School of Anthropology, University of Oxford 51-53 Banbury Rd, Oxford OX2 6PE

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WoodsHole MolecularEvolution Aug1-11

The 2019 Workshop on Molecular Evolution at the Marine Biological Lab in Woods Hole, MA will be held August 1 - 11.

Founded in 1988, the Workshop on Molecular Evolution is the longest-running workshop of its kind. 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 and software to address questions concerning the origins, maintenance, and function of molecular variation: ASTRAL, 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 computer cluster.

In 2019 the course instructors include Peter Beerli, Joseph Bielawski, Belinda Chang, Scott Edwards, Laure Eme, Tracy Heath, Mark Holder, John Huelsenbeck, Emilia Huerta-Sanchez, Lacey Knowles, Laura Kubatko, Michael Landis, Paul Lewis, Emily Jane McTavish, Bui Quang Minh, Claudia Solís-Lemus, David Swofford, and Anne Yoder.

Deadline for applications is April 12, 2019: 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 from 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:

Mark Holder (mtholder@ku.edu) and/or Paul Lewis (paul.lewis@uconn.edu)

– Mark T. Holder

mtholder@ku.edu http://phylo.bio.ku.edu/mark-holder Associate Professor 6031 Haworth Hall or 507 Dyche Hall Dept. Ecology and Evolutionary Biology and the Biodiversity Institute Univ. Kansas

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Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. ... plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.