EvolDir

June 1, 2017

Month in Review

Foreword

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

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

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

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Conferences

Austin Texas SMBE 2017 Jul2-6

SMBE 2017 Official Accommodation Options and Registration Deadline

View this email in your browser

Accommodation: Make the Most out of Austin

Choosing the right accommodation can make all the difference in how you experience a meeting - how you work, how you learn, how you network, and how you relax. SMBE has secured exclusive discounted rates at the J.W. Marriott - the official meeting hotel - and the rooms are going fast! Once they've gone, we can't guarantee the rate, so please do book your accommodation today and rest easy. You can book your room directly through our registration system, even if you completed your registration at an earlier date. Just log back in to the registration system to add accommodation to your booking.

Book Accommodation

Attention: Oral and Poster Presenters

For all those Oral and Poster presenters who have not registered, please do so before midnight, Wednesday, 31st May. If you do not register before that date, we will not be able to include you in the program. So, join the over 1,000 delegates already coming to Austin and register today!

SMBE 2017 <SMBE2017@mci-group.com>

Austin TX SMBE2017 Jul2-6 LateBreakingPosters

SMBE 2017 Late Breaking Posters and Accommodation View this email in your browser (http://mailchi.mp/mci-group/smbe-2017-late-breaking-posters?e=21532bf94c) http://mci-group.us14.list-manage1.com/-

track/click?u=8f41f38197339eb69a8a6daa2&id=-4878f642cb&e=21532bf94c ** SMBE 2017 | Accommodation

We would like to remind you to book your SMBE 2017 (http://mci-group.us14.list-manage.com/-track/click?u=8f41f38197339eb69a8a6daa2&id=-32582c3979&e=21532bf94c) accommodation. Rooms in the J.W. Marriott are going fast. You can book a room directly through our registration system, even if you completed your registration at an earlier date. Just log back in to the registration system to add accommodation to your booking.

In addition to rooms in the conference hotel, we have also secured low rates on student accommodation. These accommodations are available through the registration system as well. Book Accommodation (http://mci-group.us14.list-manage.com/-track/click?u=8f41f38197339eb69a8a6daa2&id=-c34e629b4d&e=21532bf94c) If you still need to submit an abstract, be advised that the late-breaking poster deadline is Thursday, May 18th 2017. Be sure to submit before then! Submit Late Breaking Poster (http://mci-group.us14.list-manage1.com/-track/click?u=8f41f38197339eb69a8a6daa2&id=-497dbfeecb&e=21532bf94c)

SMBE 2017 <SMBE2017@mci-group.com>

Barcelona RECOMB-CG Oct4-6 2ndCallForPapers

RECOMB Comparative Genomics 2017

SCOPE The annual RECOMB Comparative Genomics Satellite Conference (RECOMB-CG) brings together leading researchers in the mathematical, computational and life sciences to discuss cutting edge research in comparative genomics, with an emphasis on computational approaches and the analysis of novel experimental results. The program will include keynote talks, contributed talks, and a poster session.

The 15th RECOMB-CG conference will be held in the Centre for Genomic Regulation (CRG), Barcelona, Spain, on October 04-06 2017. With this Call for Papers we invite high-quality original full papers on topics related to the conference theme. The conference will also have a poster session. A detailed call for posters will be published later on the conference web page:

http://www.crg.eu/en/event/15th-recomb-comparative-genomics-satellite-workshop TOPICS Papers are solicited on, but not limited to, the following topics: - genome evolution - genome rearrangements - genome variation, diversity and dynamics - phylogenomics - comparative tools for genome assembly - population genomics - comparison of functional networks - comparative epigenomics - paleogenomics - cancer evolution genomics - epidemiology - gene identification and/or annotation

IMPORTANT DATES - Paper Submission Deadline: June 11, 2017 - Author Notification: July 07, 2017 - Final Version Due: July 21, 2017 - Conference: October 04-06, 2017

DETAILS ON SUBMITTING MANUSCRIPTS Submitted papers must have not been published or be currently under consideration for publication in any other journal or conference with formal proceedings. Each accepted paper has to be presented by one of the authors at the conference. Accepted papers will be published in the conference proceedings, a volume in the Lecture Notes in Bioinformatics (LNBI) series. In addition, arrangements are being sought for providing extended publication with additional refereeing in a prestigious journal in the area. These arrangements may involve Open Access journals, in which case there will be an author fee in the event that an article is accepted. Authors are encouraged to submit their manuscripts in PDF format according to the LNBI series guidelines:

http://www.springer.com/us/computer-science/lncs/-conference-proceedings-guidelines Submitted papers must be within 15 pages, with optionally a clearly marked appendix containing supplementary material made available to the reviewers.

All submissions must be made online, through the EasyChair submission system, at the following address:

https://easychair.org/conferences/?conf=recombcg17 Authors need to register on that web site before submitting. A standard PDF file must be received by midnight on June 11, 2017 (any time zone) in order for a submission to be considered. Re-submission of already submitted papers will be possible until midnight June 11, 2017 (any time zone).

CONFIRMED KEYNOTE SPEAKERS - Iria Fernández Silva (Department of Biochemistry, Genetics and Immunology, School of Biology, University of Vigo ES) - Toni Gabaldón (Centre for Genomic Regulation, Barcelona ES) - Iñaki Ruiz-Trillo (ICREA Research Professor at Institut de Biologia Evolutiva [CSIC-IBE], Barcelona ES) - Wes Warren (McDonnell Genomics Institute, Washington University School of Medicine USA)

ORGANIZING COMMITTEE Tomàs Marquès-Bonet (UPF) tomas.marques@upf.edu Roderic Guigó Serra (CRG) roderic.guigo@crg.eu Laura Prat Busquets (CRG Conference Officer) laura.prat@crg.eu

PROGRAM COMMITTEE Max Alekseyev (George Washington University) Lars Arvestad (Stockholm University) Anne Bergeron (UQAM) Marilia Braga (Bielefeld University) Cedric Chauve (Simon Fraser University) Leonid Chindelevitch (Simon Fraser University) Miklós CsÅ±rös (University of Montréal) Ingo Ebersberger (Goethe University Frankfurt) Nadia El-Mabrouk (University of Montréal) Guillaume Fertin (UniversitWarning: base64 decoder saw premature EOF! y of Nantes) Katharina Jahn (ETH Zurich) Asif Javed (Genome Institute of Singapore) Kevin Liu (Michigan State University) Ketil Malde (Institute of Marine Research, Norway) Joao Meidanis (UNICAMP, co-chair) István Miklós (Rényi Institute, Hungarian Academy of Sciences) Siavash Mirarab (UCSD) Luay Nakhleh (Rice University, co-chair) Aïda Ouangraoua (University of Sherbrooke) Marie-France Sagot (INRIA, LBBE, Lyon) Michael Sammeth (Federal University of Rio de Janeiro) Jens Stoye (Bielefeld University) Krister Swenson (CNRS, University of Montpellier) Eric Tannier (INRIA, LBBE, Lyon) Glenn Tesler (UCSD) Tamir

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Bialowieza Poland ProgrammingForEvolBiol Sep16-20

Registration is now open for 3rd Programming for Evolutionary Biology Conference 16-20 Sept 2017, BiaÂ³owieÂ¿a, Poland

Closing date for registration is 15 July Fee, including accommodation and meals, is 250 euro.

The Programming for Evolutionary Biology (PEB) conference brings together biologists broadly interested in applying bioinformatic tools to answer evolutionary and ecological questions.

It aims to serve as a platform for discussing the ongoing projects and related bioinformatic pitfalls. The meeting consists of plenary talks by renowned specialists in the field, contributed talks by the participants (works in progress are more than welcome!) and workshops.

This year, we are fortunate to be joined by an outstanding list of Plenary Speakers: Mark Blaxter from University of Edinburgh, Stuart Baird from Czech Academy of Sciences, Katja Nowick from University of Leipzig. The workshops will be provided by PrzemysÂ³aw Biecek, a data scientist and R enthusiast from University of Warsaw.

More info: pebconference.info

Look forward seeing you in Bialowieza!

On behalf the organising committee, Agnieszka Kloch

– dr Agnieszka Kloch ZakÂ³ad Ekologii WydziaÂ³ Biologii, Uniwersytet Warszawski ul. Âwirki i Wigury 101, 02-089 Warszawa budynek CNBCh (Cent3), pok. 4.47 tel. (22) 55 26 603 http://perlism.org/akloch/ –

"akloch@biol.uw.edu.pl" <akloch@biol.uw.edu.pl>

Bogor ID BiodiversityHealth Aug28-Sep01 EarlyBird

Biodiversity & Health Symposium Conference on Southeast Asian Gateway Evolution (sage2017.org) 28 August - 1 September 2017 Bogor, Indonesia

We invite contributions to the symposium "Biodiversity & Health" (abstract below), which will be held at the "3rd International conference on Southeast Asian Gateway Evolution" (sage2017.org) in Bogor, Indonesia, 28 August - 1 September 2017.

The deadline for the submission of abstracts (and early-bird registration) is on Monday, May 15th.

Looking forward to seeing you in Indonesia, Jan Schnitzler Alexandra Muellner-Riehl Ludger Wessjohann

Symposium: Biodiversity and Health Organizers: Alexandra Muellner-Riehl, Jan Schnitzler, Ludger Wessjohann Keynote speaker: Nina Rønsted

Plants and fungi play an important role in healthcare worldwide, with about 25% of modern prescription drugs containing at least one compound derived or patterned after substances derived from flowering plants. With an estimated 350,000 species, angiosperms provide a rich potential for finding new lead compounds for drug development. However, research so far has largely focused on single species, on only a few metabolites of medicinal importance, and/or on specific commercial applications only, e.g. drugs, colours, aromas, or cosmetics. The aim of this symposium is to bring together researchers who are working on plants (and/or fungi), microrganisms and animals, and are interested in a broader picture of chemo-biodiversity, phylogenetic relatedness, and a biogeographic perspective. We will welcome contributions shedding light on the distribution of chemodiversity both across taxonomic and biogeographic scales and on the predictive power of phylogenies.

"jan.schnitzler@uni-leipzig.de" <jan.schnitzler@uni-leipzig.de>

Calgary EvoDevo Aug19-23 Deadline2

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

Register Today! - Extended Abstract Registration closes this Friday, May 26

http://www.evodevopanam.org/2nd-biennial-meeting.html Don't miss the opportunity to share your research with the evo-devo community, as a part of the The Second Biennial Meeting of the Pan-American Society for Evolutionary Developmental Biology. We will meet August 19-23, 2017, on the campus of the University of Calgary in Alberta, Canada. Please join us this summer by the beautiful Canadian Rockies!

Excursions to the Burgess Shale at the historic Walcott Quarry and Mt. Stephen fossil beds are also available to meeting participants on the days immediately preceding and following the conference. A limited number of openings are available on both dates, so act now!

To register for the meeting or to find more information on invited speakers, meeting events, accommodations, transportation, support for child care, and other topics, please visit our website.

http://www.evodevopanam.org/2nd-biennial-meeting.html If you had trouble registering on our website earlier, technical problems have been resolved!

We look forward to seeing you in Calgary! - The PASEDB Executive Council

"drangeli@colby.edu" <drangeli@colby.edu>

Calgary EvoDevo Aug19-23 ExtendedDeadline

EvoDevoPanAm The Pan-American Society for Evolutionary Developmental Biology

2nd Biennial Meeting, August 19-23, 2017 University of Calgary, Alberta, Canada

Abstract and early-bird registration EXTENDED to MAY 26

http://www.evodevopanam.org/2nd-biennial-meeting.html Don't miss the opportunity to share your research with the evo-devo community, as a part of the The Second Biennial Meeting of the Pan-American Society for Evolutionary Developmental Biology. We will meet August 19-23, 2017, on the campus of the University of Calgary in Alberta, Canada. Please join us this summer by the Canadian Rockies!

*** If you had trouble registering on our website recently, technical problems have now been resolved!

*** Discounted excursions to the famous Walcott Quarry and Mt. Stephen Burgess Shale sites are available for attendees, but filling up fast!

To register for the meeting or to find more information on invited speakers, meeting events, accommodations, transportation, support for child care, and other topics, please visit our website

http://www.evodevopanam.org/2nd-biennial-meeting.html We look forward to seeing you in Calgary! - The PASEDB Executive Council

"drangeli@colby.edu" <drangeli@colby.edu>

Frankfurt ClimateAdaptation Jan17-18

GENOMIC BASIS OF CLIMATE ADAPTATION A symposium hosted by Senckenberg Biodiversity and Climate Research Centre, Frankfurt, Germany January 17th to 18th 2018 Senckenberg Museum of Natural History in Frankfurt am Main Senckenberganlage 25 60325 Frankfurt am Main Germany

Global warming and changing climatic conditions will require organisms to either track their climatic niche or rapidly adapt to new conditions. Our understanding of the genomic basis underlying climate adaptation across various taxa is currently growing fast. We have so far learned about adaptive inversion clines, polygenic traits, the interplay of standing genetic variation and newly arising mutations, adaptation in symbiotic systems, and the role of adaptive introgression between species. These species-specific responses now raise more general scientific questions: I) Which processes and genomic features further or hinder adaptation? II) Are common patterns arising in terms of genes or pathways responding to climate stress selection? What are the relative roles of transcription changes versus structural changes? III) Which directions of research are promising for the future? IV) Which next generation sequencing techniques, and other methods, are most appropriate in the near future? This symposium aims at bringing together leading scientists in the field to discuss recent results in genomic climate adaptation. Particularly, we want to integrate knowledge across disciplines (e.g. population genetics, molecular ecology/evolution, bioinformatics), and across taxa (e.g. plants, animals, fungi). Together, we want to identify open questions and promising methodology, and conceptually advance this scientifically and societally important field.

Confirmed keynote lecturers: Outi Savolainen (University of Oulu, Finland) Alan O. Bergland (University of Virginia, USA)

Confirmed plenary speakers: Thomas Flatt (University Lausanne, Switzerland) Robert Kofler (VetMedUni, Vienna, Austria) Christian Rellstab (WSL, Zürich, Switzerland) Thomas Bataillon (Aarhus University, Denmark) Karl Schmid (University of Hohenheim, Germany) Victoria Sork (University of California, USA)

Registration is now open: http://www.bik-f.de/root/-index.php?page_id=362&cms_veranstaltung_id=234 The organizers and scientific committee cordially invite you!

Markus Pfenninger (markus.pfenninger(q)senckenberg.de) Imke Schmitt (imke.schmitt(q)senckenberg.de) Barbara Feldmeyer (Barbara.Feldmeyer(q)senckenberg.de) Ann-Marie Oppold (Ann-Marie.Oppold(q)senckenberg.de)

pfenninger@bio.uni-frankfurt.de

Galway Ireland EvoDevo 2018 CallForSymposia

Join us at the 7th meeting of the European Society for Evolutionary Developmental Biology (EED) that will be held from June 26-29, 2018 in the National University of Ireland, Galway, Ireland.

CALL FOR SYMPOSIA

The Scientific Committee of the EED invites proposals for symposia for the Galway Conference. It is the aim of our conferences to stimulate the communication between sub-disciplines and researchers from different countries.

The Deadline for Symposia is 1 September 2017. All submission inquiries and submissions should be sent to: eed.soc@gmail.com. For further details regarding submissions please click here < http://www.evodevo2018.eu/ehome/evodevo2018/-Callforsymposia/ >

SAVE the DATE Ensure you have EURO EVO DEVO in your diary for 2018! Please have a look at the event Dates & Deadlines < http://www.evodevo2018.eu/-ehome/evodevo2018/Dates&Deadlines/ >

Make sure that you take time to explore Ireland when visiting in 2018. We look forward to welcoming you to Galway in 2018!

The EED Scientific Committee and Programme Committee

tvdooren@gmail.com

Gothenburg BioSystEU Aug15-18

Welcome to the third BioSyst.EU meeting held 15-18 August 2017 in Gothenburg, Sweden

The BioSyst.EU meeting of 2017, organised by the Swedish Systematics Association in corporation with the University of Gothenburg, is held 15-18 August at the Wallenberg Conference Centre, Gothenburg, Sweden.

The meeting will feature one whole-day and eleven half-day symposia held by member societies of BioSyst.EU and external organisations. There are also three open sessions with mixed presentations.

Abstract submission as soon as possible but no later than May 31, 2017 Early Bird Registration open until June 1, 2017

For more information, go to: http://www.conferencemanager.se/BiosystEU2017/ "Catarina.Rydin@su.se" <Catarina.Rydin@su.se>

Marseilles EBM21 Sep26-29

Dear all ,the 21st evolutionary biology meeting at Marseilles will take place from September 26-29, 2017

dead line June 30

The following subjects will be discussed:

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

more info : http://aeeb.fr/?page_id=524 note that as for the former meetings, the best presentations will be published in a collective opus edited by Nature Springer http://aeeb.fr/?page_id=376 best regards

Pierre

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

MichiganState MidwestPopGen Aug4-5

Dear Colleagues,

The field of population genetics has a remarkable tradition of being a tight-knit and nurturing community. In order to continue to foster that sense of community for popgen groups in the Midwest, *we are organizing the fourth annual Midwest PopGen conference*.

The location and date this year will be Michigan State University on August 4th-5th. The meeting will begin Friday at noon and continue to Saturday evening with a BBQ on Friday evening.

Approximately fifteen 25-minute talks will be selected from submitted abstracts, and there will be a poster session. The meeting will again be trainee-oriented, so students and postdocs are especially encouraged to present their work. There will be prizes awarded for best poster and best talk by a student and postdoc.

Please RSVP by July 21st by adding your name and information to the registration list (https://goo.gl/wm0dDu). If you would like to give an oral presentation, submit your abstracts by July 21st to Anna Di Rienzo <dirienzo at bsd dot uchicago dot edu>. Submitters will be notified if their abstract is chosen for a talk by July 1st. Accommodation advice is also provided in a tab on the registration GoogleSheet (https://goo.gl/wm0dDu). We hope you can make it and that we can continue this meeting for the population geneticists in our region!

All the best,

Gideon Bradburd, MSU Yaniv Brandvain, UMinnesota Anna Di Rienzo, UChicago Boris Igic, UIC John Novembre, UChicago Sebastian Zoellner, UMichigan

"bradburd@msu.edu" <bradburd@msu.edu>

Montpellier PlantConservation Jul16-20

Chers collègues,

J'ai plaisir à vous envoyer l'appel à communication du 1er Congrès International de Protection des Plantes dans les Agroécosystèmes Méditerranéens (Montpellier, France, 16-20 juillet 2018) qui portera sur les Invasions biologiques dans les agroécosystèmes méditerranéens, ainsi que la liste des Comités d'organisation et scientifique. Je vous invite à en faire la diffusion la plus large possible.

Bien cordialement Thierry MATEILLE

I'm pleased to send you the call for the 1st International Congress for Plant Protection in Mediterranean Agroecosystems (Montpellier, France, 16-20 July 2018) that will deal with Biological Invasions in Mediterranean Agroecosystems, with the list of the organizing and scientific committees. I invite you to disseminate it as widely as possible.

Best regards Thierry MATEILLE

Thierry MATEILLE IRD - UMR CBGP 755 Avenue du Campus Agropolis - CS 30016 34988 Montferrier-sur-Lez Cedex - France Tel. +33 (0)499623313 Fax: +33 (0)499623345 GSM : +33 (0)642547669

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Philadelphia Sept16-17

We invite you to a two-day symposium at Temple University in Philadelphia (September 16-17, 2017)

On the first day (Saturday, September 16th, 2017), we will have the Molecular Evolution informs Medicine event, where we will highlight the impact of molecular evolutionary studies on the understanding, diagnosis, and treatment of disease. There will be sessions on Mendelian (rare) diseases, Complex diseases, Cancers, and Infectious diseases. Invited and contributed presentations will be showcased.

On the second day (Sunday, September 17th, 2017), we will have the Molecular Evolutionary Genetics event, where we will celebrate the contributions of Dr. Masatoshi Nei, his students, and long-time associates. There will be invited and contributed presentations, which will be organized in scientifically coherent sessions based on individual contributions, including evolutionary genomics, phenotype evolution, molecular phylogenetics, and evolutionary resources.

Confirmed speakers include: Wen-Hsiung Li, Aravinda Chakravarti, George Zhang, Partha Majumder, Takashi Gojobori, Joel Dudley, Jeff Townsend, Sarah Tishkoff, Josh Akey, Randy Nesse, and Yana Bromberg.

Program information is listed at http://igem.temple.edu/mem/program To register, click on http://igem.temple.edu/mem/registration To present a contributed talk or poster, visit http://igem.temple.edu/mem/abstracts For all inquiries, please contact igemevents@temple.edu

“s.kumar@temple.edu” <s.kumar@temple.edu>

Poland EMPSEB23 Sep10-15 ExtendedDeadlineMay23

23 European Meeting of PhD Students in Evolutionary Biology - we extended the registration to 23th of April!

This year, EMPSEB23 will be held in Krasiczyn castle in Poland. We invite all PhD students to present their research, discuss other projects and to take part in plenary talks of our guests!

The deadline for abstract submission is on May 23. For more details, check our webpage: http://empseb23.com/ and facebook for more information https://www.facebook.com/empseb23/ If you have any question, feel free to e-mail us: contact@empseb23.com

EMPSEB provides a platform for PhD students studying Evolutionary Biology to present their work and to meet their peers from across Europe. Joining the participants are 8-10 senior scientists who are invited to give plenary talks, run discussion groups, and to provide guidance about starting your scientific career. The meeting provides the unique opportunity for students to hear the latest research being conducted in Europe, meet future international collaborators, and to present their own work to peers.

empseb23@gmail.com

Prague CichlidScience Sep04-07 DeadlineJun15

Cichlid Science 2017 - research meeting focused on cichlid fishes.

We would like to invite scientists to the upcoming Cichlid Science meeting held in Prague (Czech Republic) on 4th - 7th September. The main goal of the meeting is to bring together scientists from various research fields studying cichlid fishes.

The previous meetings in Basel (2010), Leuven (2012), Bangor (2013) and Graz (2015) covered wide range of aspects of cichlid biology including (but not only) contributions on speciation, adaptive evolution, behavioural or parasitology research, and we hope to continue the tradition.

More info here: http://web.natur.cuni.cz/zoologie/-CichlidScience2017/ We look forward to meeting you in Prague.

cichlid.science@natur.cuni.cz

Roscoff HostParasite Oct30-Nov3 2

Second Announcement, Jacques Monod Conference Open Questions in Disease Ecology and Evolution: from Basic Research to Evolutionary Medicine 30 October -3 November 2017.

Please note that participant slots are allocated on a first come first served basis and that we will stop handling applications once all slots are filled.

Dear all,

Registration is still open for the next Jacques Monod Conference on the ecology and evolution of host-parasite interactions. The conference, entitled Open Questions in Disease Ecology and Evolution: from Basic Research to Evolutionary Medicine, will take place in Roscoff (Brittany, France) from the 30th of October to the 3rd of November 2017.

Please see below for the full list of invited speakers. There are 85 other slots available. Some will be selected for a short oral presentation.

Please use this URL for instructions on how to apply: http://www.cnrs.fr/insb/cjm/2017/Rivero_e.html Looking forward to seeing you in Roscoff!

Best wishes, Andrea Graham & Ana Rivero

algraham@princeton.edu ana.rivero@cnrs.fr

INVITED SPEAKERS (and provisional titles)

ANTONOVICS Janis (Charlottesville, Virginia, USA) Blinded by vectorial capacity: rethinking transmission by pollinators and mosquitoes

BLANC Stéphane (Montpellier, France) A pluricellular way of life for multipartite viruses

de BOER Rob (Utrecht, The Netherlands) Are viruses immunologically pre-adapted to their hosts?

BORER Elisabeth (St Paul, Minnesota, USA) Experimental insights into the structuring and functional role of the host microbiome across sites, regions, and continents

BOULINIER Thierry (Montpellier, France) The transfer of maternal antibodies: from evolutionary immunology to albatross conservation

BUCKLING Angus (Exeter, United Kingdom) Consequences of polymicrobial infections for pathogen evolution

CORDAUX Richard (Poitiers, France) Wolbachia reproductive parasites and the evolution of sex determination in the isopod Armadillidium vulgare

DAY Troy (Kingston, Ontario, Canada) Can we design evolution-proof antimicrobial drugs?

EBERT Dieter (Basel, Switzerland) Getting at the mechanistic core of host-parasite coevolution

EZENWA Vanessa (Athens, Georgia, USA) Helminth-microbe coinfection: insights from natural systems

FERGUSON Heather (Glasgow, United Kingdom) Ecology and evolutionary responses of malaria vectors to control measures: implications for elimination

GRAHAM Andrea (Princeton, USA) Evolutionary causes of susceptibility to inflammatory disease

KALTZ Oliver (Montpellier, France) Environmental heterogeneity and epidemiological dynamics in Paramecium

KREMER Natacha (Lyon, France) Specificity and stability of the squid-Vibrio symbiosis

LAMBRECHTS Louis (Paris, France) Integrative genomics of host-pathogen interactions

LIVELY Curt (Bloomington, Indiana, USA) Genetic diversity, disease spread, and sex

MILINSKI Manfred (Plön, Germany) Do eggs prefer sperm with complementary MHC immunogenes?

NAVARRO Arcadi (Barcelona, Spain) Genome diversity and susceptibility to infection in humans

PARKER Jane (Köln, Germany) Plant host-pathogen evolution and tracing local adaptation of a plant resistance gene locus

PEDERSEN Amy (Edinburgh, United Kingdom) A systems ecology approach to infection and immunity in the wild

PRUGNOLLE Franck (Montpellier, France) Origin and evolutionary adaptation of human malaria agents

REECE Sarah (Edinburgh, United Kingdom) Once upon a time: the ecology of rhythms in malaria infection

REGOES Roland (Zurich, Switzerland) Are viruses immunologically pre-adapted to their hosts?

RIGAUD Thierry (Dijon, France) A host/parasite biological invasion in European rivers: Why, how and how to reduce the risk of an emerging disease

RIVERO Ana (Montpellier, France) Heterogeneity of infection outcomes in malaria-infected mosquitoes

de ROODE Jaap (Atlanta, Georgia, USA) Competitive suppression of drug resistance in human malaria infections

SORCI Gabriele (Dijon, France) Plastic and microevolutionary responses of a nematode to the immune environment

VAVRE Fabrice (Lyon, France) Evolution of addiction in host-symbiont(s) interactions

WILFERT Lena (Exeter, United Kingdom) Evolutionary ecology of multi-host pathogens in pollinators

ZUK Marlene (Minneapolis, Minnesota, USA) Medicine, evolution and the model male

– Andrea L. Graham Associate Professor Department of Ecology and Evolutionary Biology Princeton University Princeton, NJ 08544 USA

Tel: (+1) 609-258-6703 E-mail: algraham@princeton.edu

Graham Group: http://algraham.princeton.edu/ ISI Researcher ID: http://www.researcherid.com/rid/A-8808-2010 ORCID ID: http://orcid.org/0000-0002-6580-2755

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UCalgary EvoDevo Aug19-23 Deadline

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

Submit Abstracts by MAY 15

Abstract and early-bird registration close May 15! Don't miss the opportunity to share your research with the evo-devo community, as a part of the The Second Biennial Meeting of the Pan-American Society for Evolutionary Developmental Biology. We will meet August 19-23, 2017, on the campus of the University of Calgary in Alberta, Canada. Please join us this summer by the Canadian Rockies!

Remember, you must renew your membership to register. If you joined the PASEDB at or before our 2015 conference, you must update your society membership before registering for the 2017 meeting. Memberships starting in 2017 will remain current through December 31, 2018.

To register for the meeting or to find more information on invited speakers, meeting events, accommodations, transportation, support for child care, and other topics, please visit our website

http://www.evodevopanam.org/ We look forward to seeing you in Calgary!

- The PASEDB Executive Council

Dave Angelini <drangeli@colby.edu>

UEssex GenomicsEpigeneticsAndGeneRegulation Sep14

REGISTRATION OPEN!

Dear colleague,

The registration for the 'Genomics, Epigenetics and Gene Regulation Symposium' is now OPEN. The meeting is being primarily sponsored by the Genetics Society (UK) and co-sponsored by Wellcome Open Research and Chromatrap. Thanks to our generous sponsors, registration is free in a first come first served basis. Abstract submission is also welcomed until the 2nd of June.

The 'Genomics, Epigenetics and Gene Regulation Symposium' at the University of Essex aims to gather researchers to present their work on this fast growing field. This one-day symposium on the 14th of September will cover DNA-based regulation (chromatin and methylation) and RNA-based gene regulation (regulatory RNAs). We strongly encourage submissions of abstracts from PhD students and postdocs, as we aim to host contributed talks from scientists at different levels in their careers.

We will also have a keynote talk by Prof. Anne Ferguson-Smith (U. Cambridge) and three invited speakers: Prof. Tamas Dalmay (UEA), Dr. Alessia Buscaino (Kent) and Prof. Boris Lenhard (Imperial)

Our campus is located at Wivenhoe Park, close to Colchester (Essex), which is less than one hour away from Stansted Airport. If you require accommodation, there are plenty of options on campus or in town.

For more information and registration please visit our webpage:

http://gate.essex.ac.uk/ Please share this email with your colleagues and/or anyone that may be interested.

Best regards from the organizing committee,

Antonio Marco Pradeepa Madapura Radu Zabet Andrea Hatlen

– Antonio Marco School of Biological Sciences University of Essex

Web: http://amarco.net Blog: http://eblogution.wordpress.com Twitter: http://twitter.com/amarcobio amarco.bio@gmail.com

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UGothenburg PhylogenyErrors Aug15-18

Hi,

As part of the Third BioSyst.EU meeting in Gothenburg, Sweden (http://www.conferencemanager.se/BiosystEU2017/start.html) from August 15th to 18th 2017 we organise a symposium on the "Identification and avoidance of sources of error in phylogeny inference" (http://www.conferencemanager.se/BiosystEU2017/identification-and-avoidance-of-sources-of-error-in-phylogeny-inference-gfbs.html). The symposium is hosted by the German Society for Biological Systematics.

DEADLINE FOR ABSTRACT SUBMISSION AND EARLY BIRD REGISTRATION: MAY 31, 2017

Phylogenetic tree reconstruction is a central task of modern evolutionary biology, in which the assessment of phylogenetic relationships provides the foundation for the interpretation of comparative and evolutionary biological data. Molecular data for phylogenetic tree inference has increased from single gene analyses of few taxa to phylogenomic analyses comprising hundreds of genes and taxa. Due to the exponential growth of molecular data along with reduced stochastic sampling errors, the goal of approximating the "Tree of Life" seems to be more attainable today than ever. However, although substantial progress has already been achieved in respect of certain relationships within the "Tree of Life", several phylogenetic questions still remain unresolved. Therefore, the phylogenomic era appears also to be the beginning of an era of strong incongruence due to the further accumulation of data affected by systematic biases. These biases might arise from rate or compositional heterogeneity, missing data or model misspecifications. In such cases, phylogenetic methods may be inconsistent due to their inability to sufficiently account for the evolutionary complexity of genomic data. The consequence is strongly supported, but incorrectly resolved phylogenetic trees.

In this symposium we want to discuss various reasons of systematic bias and introduce new algorithms, which enable more reliable reconstructions of large-scale phylogenetic trees or, equally important, will indicate when reliable inferences are not possible given the currently available data (e.g. the effect of incomplete lineage sorting and recombination to phylogenetic reconstruction). Topics are discussed. Thereby, we put a special emphasis on the potential and possible pitfalls of recent supertree, coalescence, and supermatrix approaches. The two invited and renowned keynote speakers, John Gatesy and Mark Wilkinson, address their points of view concerning these methodologies. The titles of their talks are:

John Gatesy (Institute for Comparative Genomics & University of California Riverside): A single outlier gene tree can overturn hundreds of perfectly congruent gene trees in phylogenetic coalescence analyses Mark Wilkinson (Natural History Museum London): Supertrees, supermatrices and pluralism in phylogenenetics (Coauthor will be Peter G. Foster)

However, we are also very interested in contribution by others. Therefore, if you have a topic fitting this venue in a general sense and not only concerning supertree, coalescence, and supermatrix debate you are invited to come to the conference and present your work as a talk or a poster. We especially invite students at this conference is a good opportunity to get in contact with your fellows working on the same subject and showcast your work to a diverse and interested international audience. Presentations from a purely theoretical perspective, which can initiate new research in known or yet unrecognized biases, are also welcome.

The BioSyst website above has detailed information on registration, submission procedures, symposia and their speaker as well as travelling and accommodation.

We hope to see you in Gothenburg,

Patrick & Torsten.

- NEW CONTACT INFORMATION - Torsten Hugo Struck Department of Research and Collections Natural History Museum phone: +47-228-51740 e-mail:

t.h.struck@nhm.uio.no

Torsten Hugo Struck <t.h.struck@nhm.uio.no>

UNotreDame ArthropodGenomics Jun7-11

The 10th Arthropod Genomics Symposium < http://globalhealth.nd.edu/10th-annual-arthropod-genomics-symposium/ > and Arthropod Bioinformatics Workshop < http://globalhealth.nd.edu/10th-annual-arthropod-genomics-symposium/vectorbase-workshop/ > will be held from June 7 - June 11, 2017 and is hosted by the Eck Institute for Global Health at the University of Notre Dame.

*May 26, 2017: Poster Abstracts Due** & **Registration Deadline*

http://globalhealth.nd.edu/10th-annual-arthropod-genomics-symposium/ The website above has information on registration, speakers, abstract submissions, the accompanying bioinformatics workshop, and accommodations. Feel free to contact me (ascott12@nd.edu, 574-631-9227) with questions.

– Ashley Scott Program Director Eck Institute for Global Health University of Notre Dame Notre Dame, IN 46556 574-631-9227

ascott12@nd.edu

UNotreDame ArthropodGenomics Jun7-11 deadline

The 10th Arthropod Genomics Symposium < http://globalhealth.nd.edu/10th-annual-arthropod-genomics-symposium/ > and Arthropod Bioinformatics Workshop < http://globalhealth.nd.edu/10th-annual-arthropod-genomics-symposium/vectorbase-workshop/ > will be held from June 7 - June 11, 2017 and is hosted by the Eck Institute for Global Health at the University of Notre Dame.

*May 26, 2017: Poster Abstracts Due** & **Registration Deadline*

http://globalhealth.nd.edu/10th-annual-arthropod-genomics-symposium/ The website above has information on registration, speakers, abstract submissions, the accompanying bioinformatics workshop, and accommodations. Feel free to contact me (ascott12@nd.edu, 574-631-9227 <(574)%20631-9227>) with questions.

– Ashley Scott Program Director Eck Institute for Global Health University of Notre Dame Notre Dame, IN 46556 574-631-9227

ascott12@nd.edu

Zurich PolygenicAdaptation

SYMPOSIUM

Aug 31 - Sept 1, 2017, Zurich, Switzerland

POLYGENIC ADAPTATION Detecting Genomic Signals of Polygenic Adaptation and the Role of Epistasis in Evolution

Registration fees: 80CHF + 70CHF for dinner on Aug 31 (100 persons max)

Extended deadline for ABSTRACT SUBMISSION: June 1st

registration and abstract submission: http://conf.wsl.ch/polygenic2017/ more information here: http://www.evolution.uzh.ch/en/events/symposium.html INVITED SPEAKERS and tentative titles:

Nick BARTON (Vienna, Austria) Epistasis and the limits to selection

Jeremy BERG (Columbia, New York) The problem of population structure: dealing with structured GWAS panels in tests of polygenic adaptation

Ã rjan CARLBORG (Uppsala, Sweden) Complex trait genetics beyond additivity

Josephine DAUB (Barcelona, Spain) Detecting polygenic selection at different time scales in human evolution

Thomas HANSEN (Oslo, Norway) Epistasis: The ugly duckling of evolutionary genetics

Joachim HERMISSON (Vienna, Austria) >From soft sweeps to polygenic adaptation

Sergey KRYAZHIMSKYI (San Diego, California) Epistasis and genetic variation in adaptability in yeast

John McKAY (Fort Collins, Colorado) Are alleles underlying local adaptation rare and/or conditionally dependent?

Josh PAYNE (Zurich, Switzerland) A thousand empirical adaptive landscape and their navigability

Peter VISSHER (Brisbane, Australia) Evidence of polygenic selection and adaptation in human populations

Sam YEAMAN (Calgary, Canada) Detecting and interpreting the genomic basis of convergent local adaptation

– There are only about 10 slots for contributed talks, so register quickly!

We are looking forward to seeing many of you in Zurich this summer!

Greetings on behalf of the organizers, Frédéric Guillaume

<frederic.guillaume@ieu.uzh.ch>

Organizers: Dr Katalin Csilléry (ETH Zurich & WSL Birmensdorf) Prof Dr Frédéric Guillaume (University of Zurich - IEU) Dr Alejandra Rodriguez-Verdugo (ETH Zurich) Dr Felix Gugerli (WSL Birmensdorf) Dr Christian Rellstab (WSL Birmensdorf) Prof Dr Alex Widmer (ETH Zurich)

Funding: Adaptation to a Changing Environment, ETH Zurich URPP "Evolution in action", University of Zurich Gentree EU

"frederic.guillaume@ieu.uzh.ch"
<frederic.guillaume@ieu.uzh.ch>

GradStudentPositions

Amiens France PhylogeographyLandscapeGenetics

3-yr PhD position in ecology, phylogeography and landscape genetics

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/Title/

Incorporating Phylogeographic infOrmation into niche moDels to improve species re-distribution projections under climAte waRming and habitat fragmentation: the Case of forest-dwelling specIes across European agricultural landscapeS[PODARCIS]

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/Aim/

Climate warming and habitat fragmentation are two key components of global change that push species to redistribute or evolve to adapt to the new conditions (Lenoir & Svenning 2015; Pecl et al. 2017). To hindcast and forecast species redistribution under past and future environmental conditions, respectively, the state-of-the-art is to use species distribution models (SDMs) (Guisan & Zimmermann 2000). However, traditional SDMs assume that individuals from all populations of a given species respond equally to environmental changes although genetic differences among populations interact with environmental factors such that fitness can vary among populations (Savoleinen et al. 2007; Leimu & Fischer 2008; Valladares et al. 2014). The most recent scientific literature on SDMs suggests that incorporating intraspecific variation into SDMs leads to less pessimistic redistribution projections (Pearman et al. 2010; Oney et al. 2013). Both phylogeography (Guiller & Madec, 2010; Guiller et al. 2012) and landscape genetics can provide spatially and temporaly explicit information on the genetic structure and differences among populations of the same species that could be used to incorporate intraspecific variation into SDMs and thus improve redistribution projections under climate change.This PhD project entitled PODARCIS specifically aims at incorporating intraspecific variationdata obtained from a union of phylogeography and landscape genetics (Rissler 2016) into SDMs. PODARCISis part of the EU (BiodivERsA) project Woodnet and the regional (Hauts-de-France) project Pegase. Three model species of European temperate forests will be studied throughout the PhD prject: the plants /Geum urbanum/ and /Oxalis //acetosella/characterized by different dispersal capacities as well as the tick /Idoxes ricinus/ considered as the main vector of the Lyme Borreliosis in Western Europe and thus implying potential public health hazards. PODARCIS rests on three basic pillars:

i.Phylogeography and historical demography to determine the phylogeographic structure of each species and to disentangle the relative impacts of past /versus/ current climatic changes in shaping the geographic distributions of genealogical lineages ;

ii.Fundamental ecology to develop SDMs adapted to each genealogical lineage and to compare these lineage-specific SDMs to classical SDMs at different periods (Quaternary and Anthropocene);

iii.Landscape genetics to identify landscape and environmental features that constrain genetic connectivity and thus to account for dispersal and gene flow across the landscape.

/Keywords/

/Climate/change, ecoepidemiology, forest ecosystems, landscape genetics, phylogeography, population genetics, spatial statistics,species distribution modelling

/Qualifications/

The candidate is expected to have good training in statistics or mathematical modelling and have a strong background in evolutionary biology (population genetics and phylogeography). Good PhD candidates will have a master degree in evolutionary biology. Basic knowledge and interest in ecology and landscape genetics is required.Experience in molecular genetics and GIS knowledge will be further appreciated. /Programming skills in Free and Open Source Software (FOSS) such as in the R and GRASS environments will be a clear advantage//. /Teamwork skills, curiosity, autonomy at work as well as good oral and written communication skills in English will also be valued.

/Supervision/

The student will be hosted within the research unit EDYSAN (/Ecologie et Dynamique des Systèmes Anthropisés/, FRE 3498 CNRS - UPJV, head Prof. Guillaume Decocq),33 rue Saint Leu, 80000 Amiens, France. EDYSAN is a young, diverse, vibrant and international research community with strong collaborative interdisciplinary ties within and beyond Amiens. More information about the people and research activities of the group can be found at:

http://www.u-picardie.fr/edysan/?lang=en Main supervisor: Annie GUILLER (Professor), annie.guiller@u-picardie.fr <mailto:annie.guiller@u-picardie.fr>, +33 3 22 82 75 76

Co-supervisor: Jonathan LENOIR (Lecturer), jonathan.lenoir@u-picardie.fr <mailto:jonathan.lenoir@u-picardie.fr>+33 3 22 82 54 67

/Application/

Applications (letter, CV and 2 contacts for references) should be sent to Annie Guiller, Jonathan Lenoir and Guillaume Decocq no later than May 31. The selected candidate will have an audition with the Doctoral Department at UPJV (Université de Picardie Jules Verne, Amiens)in the

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

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ANU Australia Pylogenetics

Dear colleagues

I have funds to support two graduate students for following projects:

1. Phylogenetics and next-generation sequencing. The student will work with next-generation sequencing data, both real and simulated, to develop phylogenetic methods for mixtures of DNA samples. 2. Models of microbiomes. This project builds on work that we have done on the evolution of microbiomes (see Zeng et al, PLoS Comput Biol 11: e1004365). There are many ways to build on this framework, and the student will have the freedom to propose his/her own research.

These projects will suit students who have a strong background in computational biology or equivalent. Students will enrol at the Research School of Biology of The Australian National University, ranked top in Australia and 22 in the world (QS Rankings 2016-17). Doctoral degree programs in Australia typically last for 3.5 - 4 years. In addition to excellent colleagues, researchers at the ANU have access to significant computational resources – the University is a partner institution of the National Computational Infrastructure, Australia's high-performance computing provider.

Please contact me with a brief CV if you are interested. Thanks in advance.

Allen Rodrigo

Prof Allen Rodrigo PhD DSc FRSNZ Director, Research School of Biology The Australian National University Acton —ACT —2601 —Australia

E: allen.rodrigo@anu.edu.au

allen.rodrigo@anu.edu.au

BangorU PollenBiodiversity

Exploring the ecology of airborne pollen biodiversity using environmental DA analysis and identifying links to hay fever

We are advertising for a PhD opportunity to be hosted in the Molecular Ecology & Fisheries Genetics Laboratory (MEFGL), at Bangor University (http://mefgl.bangor.ac.uk/) to commence in October 2017. The PhD has been made possible via the availability of the ERC Industrial Strategy CASE Studentship scheme and strong links with project partner, the ational Botanic Garden of Wales. The studentship will form part of the ERC EVISIO Doctoral Training Programme (http://www.envision-dtp.org/), a PhD consortium partnership between Bangor, ottingham and Lancaster Universities, alongside numerous environmental bodies, aimed at equipping the next generation of Environmental Biologists with advanced skills.

Project rationale: In addition to providing benefits to society, biodiversityâ€also brings costs. The aerial biosphere includes ecologically complexâ€mixtures of pollens that negatively affect human health. Almost a quarterâ€of people display allergic reactions to tree and grass pollen, causingâ€symptoms ranging from hay fever to asthma, with associated socio-â€economic costs. Identifying tree pollens can be achieved using microscopy,â€but the process is challenging. evertheless, since most grass pollens lookâ€the same, we need to devise novel ways to identify different species toâ€understand which species of grass contribute to allergies. This studentshipâ€has three components. The first aims to use an environmental DA (eDA) approach to enhance the way that we assess aerial tree pollen mixtures. Secondly, to use modelling approaches to compare and contrast the aerial transit of tree and grass pollens in relation to biology/ecology and finally, to identify which species of grass pollen are linked with hay fever. The PhD will form a distinct component within a larger ERC funded study "PollerGE" (http://pollergen.bangor.ac.uk/) and provide an opportunity to work with an interdisciplinary team of scientists from a range of UK Universities, the UK Met Office and the CASE Partner, ational Botanic Garden of Wales (BGW - home of the Wales Plant DA Barcode library). The successful candidate will become a highly skilled, interdisciplinary graduate working at the interface between molecular ecology and environmental epidemiology with the potential to make substantial advances to our understanding of UK flora pollination dynamics and interactions with the allergic response. Co-supervision will be provided by atasha De-Vere/Gareth Griffith/Mat Hegarty (BGW and Aberystwyth), Carsten Skjøth (Worcester), Ben Wheeler/ick Osborne (Exeter/Sydney) and the UK Met Office. Training will be provided in the main areas of molecular ecology, genomics, taxonomy, bioinformatics, modelling; multidisciplinarity skills and epidemiology, complemented by a host of additional opportunities for postgraduate development. Fieldwork will occur within the UK, with opportunities for travel/collaborations in Europe and Australia.

Applicants should hold a minimum of a UK Honours Degree at 2:1 level or equivalent in subjects such as Biology, Environmental or atural Sciences, with a strong motivation to study eDA biodiversity- environment interactions. Eligibility requirements and application portal can be found at http://www.envision-dtp.org . If you are interested in applying, we would strongly recommend contacting Prof. Simon Creer in the first instance (http://-mefgl.bangor.ac.uk/staff/si.php; s.creer@bangor.ac.uk; Twitter @spideycreer) and he will be on hand to assist with any questions related to the project, important information on the application process and life in the group.

Closing date for applications: 2nd of July 2017 with interviews predicted to take place between 13th-14th July and look forward to hearing from you!

Rhif Elusen Gofrestredig 1141565 - Registered Charity o. 1141565

Georgina Brennan <g.l.brennan@bangor.ac.uk> Georgina Brennan <g.l.brennan@bangor.ac.uk>

Bolzano Italy AncientDNA

Job Announcement

PhD position in the field of ancient DNA research

Institute for Mummy Studies, Eurac Research, Bolzano, Italy

We are looking for a scientist with strong expertise in advanced molecular techniques and an interest in applying innovative methods to the field of ancient DNA research. Our Institute is internationally renowned for its research on the Iceman and other mummified and skeletal human remains of different periods from all over the world. Our research aim is to answer fundamental questions in the field of human history, pathogen evolution and conservation.

We offer a three years doctoral position at the Eurac Research - Institute for Mummy Studies. The PhD project will focus on the evolution of pathogens. The position is available as early as September 2017.

What we seek We are looking for a highly motivated and independently working scientist with a strong conceptual and practical background in the application of molecular techniques on ancient human remains. Experience in one or more of the following areas/techniques will be of advantage: genomics, microbiology, bioinformatics, and population genetics. The successful candidate should show interest in applying advanced molecular methods, in the field of ancient DNA research. Proficiency in spoken and written English is mandatory.

What we offer We offer up to 3 years of appointment as a PhD student according to the salary scheme of the EURAC. The candidate will work in a young and international team with a highly stimulation research environment. The EURAC is an equal opportunity employer.

How to apply Please send an E-mail before 20.06.2017 to mummy.studies@eurac.edu containing a pdf-file with a short cover letter and a detailed CV (including a brief description of research interests and of the educational background). Please mention in your E-mail the subject: PhD ancient DNA research.

Please attach, after reading the privacy policy, the following consent to your personal record, in accordance to the data security decree 196/2003 about personal data handling: 'I have read the privacy policy under http://www.eurac.edu/en/aboutus/Jobs/Pages/-default.aspx and hereby authorize Eurac Research to use my personal data in accordance to decree 196/2003.' We inform you that we can not consider any application without this compliancy declaration. Candidates, who might be interested in future vacancies, should add the following consent: "I hereby explicitly authorize Eurac Research to store my personal data for the purpose of being contacted for potential future job openings".

Maixner Frank <frank.maixner@eurac.edu> Maixner Frank <frank.maixner@eurac.edu>

BotanicalGarden Geneva MadagascarPlants

PhD position at the Botanical Garden of Geneva, Switzerland

Systematics, species delimitation and conservation in a Madagascar endemic genus of Sapotaceae

We are seeking a highly motivated candidate for a PhD project at the Plant Systematics and Biodiversity Laboratory, Conservatoire & Jardin botaniques de Genève and University of Geneva, Switzerland. The project is supported by the Swiss National Science Foundation and includes species delimitation, phylogenomic diversity and species distribution modelling and their application to the conservation of *Capurodendron*, a Malagasy endemic genus of ca. 30 valuable tree species in the family Sapotaceae.

The ideal candidates should be a botanist who enjoys working in the laboratory (targeted gene capture) with field experience in the Tropics (with understanding of conservation issues; possibly one trip scheduled to Madagascar), and should have good basic knowledge of taxonomy, phylogenetics, population genetics and bioinformatics. We are particularly interested in students who already have experience with Next Generation Sequencing techniques. Good writing skills in English are a must and familiarity with French is a plus.

Applications (motivation letter, CV, email address of 2/3 reference persons) should be sent before *June 15th**,* *2017* to: Yamama Naciri (yamama.naciri@ville-ge.ch / yamama.naciri@unige.ch).

Project starting *October 2017*.

Prof Jean Mariaux Curator, Dpt of Invertebrates T. +41 22 418 6343 F. +41 22 418 6301 jean.mariaux@ville-ge.ch mariauxj@gmail.com Muséum d'histoire naturelle (MHN) Département de la culture et du sport route de Malagnou 1 1208 Genève - Switzerland www. < http://www.ville-ge.ch/mhng >museum-geneve.ch orcid.org/0000-0002-9601-855X Notre environnement est fragile, merci de n'imprimer ce message qu'en cas de nécessité. Do you really need to print this message ?

Jean Mariaux <mariauxj@gmail.com>

Colombia GenomeEnvironmentAssociationsBeans

La Selva (Colombia) is seeking a MSc student to study Genome Environment Associations in Beans.

The project combines field work, environmental modelling and bioinformatics (using genomic data already generated) in order to identify adaptive variation through genome-environment associations.

The selected student must have a minimum GPA of 3.6 and must be willing to move to La Selva for 18 months.

Apply by sending a document with a short cover letter, a CV, transcripts and a certificate of student status to nvelez@corpoica.org.co.

Start date is anticipated to be in the Fall of 2017. Monthly compensation is 1,475,434 COP, which is equivalent to 2,200 USD after correcting for PPP.

The deadline for applying is Friday 19th of May (ECT)

Any enquiry should be forwarded to nvelez@corpoica.org.co

La Selva <laselvacol@gmail.com>

DurhamU EvolutionaryGenetics

A competitive PhD studentship opportunity is available in evolutionary genetics at Durham University, UK. This 3.5 to 4-year fellowship provides a full tuition fee waiver, a competitive living stipend, and a considerable research allowance. The starting date is October 2017 (no delays are possible).

Please note the short deadline: Applications must be received by *20 June 2017.*

Using ancient DNA to uncover historical disease dynamics in North American and British deer

Diseases can have dramatic impacts by limiting population growth rates, producing strong selection pressures, and potentially leading to adaptive responses. While not infective to humans, chronic wasting disease (CWD) is a fatal disease in cervids (deer, elk, and moose). Analyses of the underlying *Prnp* gene suggest that particular alleles may influence susceptibility through decreased infection rates and/or slower disease progression. We will use ancient DNA techniques to examine changes in the frequencies of *Prnp* alleles through time in two deer species, European red deer (Cervus elaphus) and closely related North American elk (Cervus canadensis). For work on elk, the student will travel to the US and be hosted in the lab of our collaborator for three moths to study both infected and non-infected populations. While CWD is not currently present in the UK, evidence suggests that similar diseases may have influenced populations of red deer in the past, and investigation of contemporary populations will provide insights into current susceptibility, should CWD spread to the UK. Thus the student will have multiple opportunities to interface with UK governmental agencies working to prevent the spread of CWD to Britain. This project is in association with the British Deer Society.

Eligibility: UK citizens and EU citizens who have resided in the UK >3 years

For more information see https://sites.google.com/site/andreannajwelch/andreanna-j-welch or contact Dr. Andreanna Welch by email at a.j.welch@durham.ac.uk.

To apply, email Dr. Welch: 1) a covering letter explaining why you are interested in the project, 2) your CV, 3) your university transcripts, and 4) arrange to have two letters of reference sent by the deadline of 20 June 2017.

Andreanna J Welch <andreanna05@gmail.com>

DurhamU Phylogeography

Competitive CASE PhD studentship available in the Department of Biosciences, Durham University

Title: Phylogeography of European ungulates from the last interglacial period and their subsequent evolution.

Outline: This project will involve ancient DNA and next generation sequencing to explore the genetic diversity of deer and other ungulates from the Eemian interglacial period, ~120,000 years ago. A key aspect of the study will be the integration of environmental data (including stable isotope analyses in collaboration with the British Geological Survey), so that changes in demography (quantified based on the genetic data), distribution and diversity can be interpreted in the context of changing environments, providing predictive inference on the future impact of climate change. Ancient DNA together with coalescent methods provides a window into the historical demographics of species during periods of environmental change, and the integration of stable isotope data permits the more specific tracking of environmental transitions and the behavioural responses of herbivore species. Further support provided by the British Deer Society and British Geological Survey

Note the short deadline - applications must be received (to a.r.hoelzel@dur.ac.uk) by June 20th 2017, for a start date in October 2017. Please include your c.v., course records and a cover letter, and have two letters of recommendation sent independently in advance of the deadline.

The studentship competition is through the NERC IAPETUS DTP (full scholarships available to UK citizens only). A detailed flyer describing the project is available at http://www.iapetus.ac.uk/, and please email with any further questions.

"HOELZEL, RUS A.R." <a.r.hoelzel@durham.ac.uk>

EDYSAN Amiens PlantPhylogeography

Title: Integrating the Phylogeographic infOrmation into niche moDels to improve re-distribution projections of species facing climAte waRming: the Case of plant specIes in temperate European forestS [PODARCIS]

Abstract

Climate change and habitat fragmentation are two key components of global change causing the redistribution and the evolution of species globally. In response to anthropogenic pressures and climate warming, various animal, plant or microbial species show spatial and temporal variation of their range, change in dispersal capacity, phenology, abundance and biotic/abiotic interactions. However, predictions of changes in potential distribution are difficult as vulnerability to climate change is species-specific.

The PhD project is part of the BiodivERsA project Woodnet and the regional project Pegase. The aim is to develop, within the framework of global climate warming, an innovative multiscale approach based on empirical data sets to (i) describe patterns of diversity, (ii) identify the evolutionary forces acting on genetic variation, (iii) predict species distribution for conservation (threatened species) or prevention (invasive species) decisions. Three model species of European temperate forest will be studied: the plants Geum urbanum and Oxalis acetosella that exhibit contrasted dispersal capacities and niche width, and the tick Idoxes ricinus which is the main vector of the Lyme Borreliosis in Western Europe. Three fields structure this integrative study:

i. a phylogeography and historical demography approach to determine the phylogeographic structure of each species and disentangle impacts of past versus current climatic changes in shaping their genetic distribution;

ii. a fundamental ecological approach to estimate potential distribution areas of species and to model environments favorable to species populations' persistence. The aim is to develop Species Distribution Models (SDMs) adapted to each genetic lineage. These specific lineage SDMs will be compared to classical SDMs at different periods (Pleistocene and Anthropocene);

iii. a landscape genetic approach for modeling the permeability of landscapes to species individuals' movement. From each lineage-specific SDM obtained at step ii., a predicted friction map will be modeled to identify landscape and environmental features that constrain genetic connectivity. Locating genetic corridors across landscapes will be crucial for the maintenance (plants) or the removal (tick) of metapopulations. From spatial and temporal configurations of landscapes obtained, structural connectivity metrics derived from graph and percolation theory will be compared to functional connectivity measured as gene flows among populations.

Keywords

Eco-epidemiology, temperate forest, species distribution models (SDM), climate change, phylogeography, population genetics, landscape genetics.

Profile of the PhD candidate

Applicants should have a master degree in ecology and evolutionary biology. The candidate should be trained in mathematical modelling and have a strong background on evolutionary biology (population genetics, phylogeography). Applicants are expected to have strong skills in R programming, molecular genetics, GIS, communication and teamwork. . Curiosity and autonomy at work will be appreciated.

Supervision

The student will be hosted at the research unit EDYSAN (Ecologie et Dynamique des Systemes Anthropises, FRE 3498 CNRS - UPJV, head Prof. Guillaume Decocq), 33 rue Saint Leu, 80000 Amiens, France, https://www.u-picardie.fr/edysan/ Main supervisor: Annie GUILLER (Professor), annie.guiller@u-picardie.fr, +33 3 22 82 75 76

Co-supervisor: Jonathan LENOIR (Lecturer), jonathan.lenoir@u-picardie.fr +33 3 22 82 54 67

Application

Applications (letter, CV and 2 contacts for references) should be sent to Annie Guiller, Jonathan Lenoir and Guillaume Decocq before the 15th of June 2017. The final selection of projects/candidates will be made by the Doctoral Department of the UPJV (Universite de Picardie Jules Verne, Amiens) at the beginning of July. The PhD would start on September 2017. -

annie <annie.guiller@u-picardie.fr>

LavalU HumanMicrobiota

PhD: ZEBRIGHT micro: Developing an instant, high throughput and integrative vertebrate model to decipher the interplay of factors controlling host-microbiota interactions at the interface of health/disease. Supervisors: Dr Nicolas Derome, Dr Grant VandenBerg, Dr Arnaud Droit (Laval University, Quebec, Canada).

This PhD projet is connected to projects focusing on optogenetics control and monitoring of gut microbiota, optogenetics monitoring of neural function, leaded by Dr Paul De Koninck and Dr Sylvain Moineau.

The intestinal microorganisms hosted by humans and other vertebrates play a central role in maintaining their hosts in healthy conditions. However, when the host encounters a physiological stress, the microbiota ecosystem equilibrium is broken, allowing opportunistic microbial strains to induce negative effects on the host, including physiological disturbances on neuroendocrine functions and epigenetics modifications. During host development, a stressed microbiota might induce irreversible consequences on its brain development and neural functions, affecting mental health. The Northern ecosystem is undergoing unprecedented assaults from human activities, leading to severe environmental changes that are modifying the microbiota, eventually impacting on their host vertebrates. The relationship between these complex systems are poorly understood. To learn more about host-microbiota interactions and their impact on mental health, we must develop models and tools with which we can accurately control the variables, relevant to the environment, in a laboratory setting.

This PhD project objective is to develop a fish experimental model in which we can control factors (nutrition, contaminants/toxins, xenobiotics, bacterial strain, phages, viruses) that modulate host-microbiota functional interactions and measure the impact on the microbiota evolution, on brain function, and on host gene expression. Basically, the student will investigate the impact of these factors on the gut microbiota, on neuronal development and brain circuit function and on epigenetics. To reach this goal, two specific aims are needed: to develop i) a protocol to produce routinely axenic larvae of zebrafish (Danio rerio), ii) synthetic microbiota (5 to 10 strains) to conventionalize axenic zebrafish larvae. This PhD project will involve a transdisciplinary approach combining physiology, genomics and transcriptomics analyses of horizontal gene transfer in bacterial strains, and epigenetics analyses on developing host. Also, the PhD candidate will have the invaluable opportunity to closely interact with sister projects focusing on optogenetics control and monitoring of gut microbiota, optogenetics monitoring of neural function. The project will lay the bases of an experimental setting in which several variables critically important for the Northern ecosystems will be investigated.

Qualifications and Requirements * Relevant background in Molecular Evolution, Ecology, Molecular Biology, Biochemistry or Cell Biology with related laboratory experience. * Basic molecular techniques such as bacterial culture, PCR, sequencing library preparation. * Background in bioinformatics (phylogeny, population genetics, genomics, metagenomics), fish and bacteria manipulation will be considered an asset. * Excellent written/verbal communication skills and organizational skills. * Demonstrated ability to work in a team environment.

Salary

18 000$/year, 3 years

Application Procedures

To apply for this position, please forward a current CV, a covering letter and two support letters via e-mail to Nicolas DEROME nicolas.derome@bio.ulaval.ca by May 31, 2017.

Nicolas Derome, PhD Professeur titulaire Departement de Biologie Chaire de recherche du Canada en Genomique et Conservation des Ressources Aquatiques Institut de Biologie Integrative et des Systemes (IBIS) Pavillon Charles-Eugene Marchand, bureau 1255 1030, avenue de la Medecine Universite Laval, Quebec QC G1V 0A6 Canada Telephone : 1 (418) 656-7726 Telecopie : 1 (418) 656-2043 Courriel : nicolas.derome@bio.ulaval.ca Internet : http://www.deromelab.org Nicolas Derome <Nicolas.Derome@bio.ulaval.ca>

MasseyU WGD PathwayEvolution

Position: A three year PhD scholarship is available to study genetic pathway evolution following whole genome duplication (polyploidy)

Project description: The majority of eukaryotic lineages show evidence of ancestral whole genome duplication. Although the theoretical fates of individual genes following duplication were identified long ago, how integrated genetic pathways evolve following duplication requires further examination. The PhD candidate will be part of a project analyzing a well-characterized genetic pathway in a group of plant species that diverged following an ancient allopolyploidy event. The fates (retention/loss/expression change) of homeologs in the pathway will be determined to investigate how integrated genetic systems respond to the common phenomenon of duplication. The project will involve both wet lab and field work.

This position will be funded by a Massey University Doctoral Scholarship (http://www.massey.ac.nz/massey/-admission/scholarships-bursaries-awards /doctorate-scholarships/doctorate-scholarships_home.cfm). Successul applicants will have a BSc Honors, MSc or equivalent in Botany, Genetics, Molecular Biology or a similar field.

The position is available in the lab of Dr Vaughan Symonds (http://vvsymonds.massey.ac.nz) at Massey University in Palmerston North, New Zealand. The lab group has diverse interests that include population genetics, molecular evolution, and conservation. To apply for the position, please send the following to v.v.symonds@massey.ac.nz with “PhD Scholarship” as the subject:

(1) letter of interest

(2) CV

(3) academic transcripts

(4) the names and contact details for three references

The deadline for applications is May 26, 2017. Applications will be considered on a rolling basis until the position is filled. International applicants are welcomed. Starting date is flexible but should be no later than 1 November 2017. Please feel free to email any questions about the scholarship or project.

Vaughan Symonds, PhD

Senior Lecturer in Plant Molecular Genetics

Massey University

Palmerston North, New Zealand

"Symonds, Vaughan" <V.V.Symonds@massey.ac.nz>

NicolausCopernicusU PlantEvolBiology

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

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

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

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

The stipend for position is 3 000 PLN net monthly (app. 700 EURO) for three years. The living cost in Torun is low. For example, a room in a student house (inc. Wi-Fi, kitchen, heating, hot water) is app. 100-150 EURO monthly, loaf of bread 0.5 EURO, beer 0.5-0.7 EURO, beer in pub 1-2 EURO, dinner in restaurant 5-8 EURO.

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

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

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

Marcin Piwczynski, PhD

Personal website: http://piwczynski.prac.umk.pl/ Departmental website: www.keib.umk.pl e-mail: piwczyn@umk.pl

Nicolaus Copernicus University Faculty of Biology and Environment Protection Chair of Ecology and Biogeography Lwowska Street 1, PL-87-100 Torun Poland

"Marcin.Piwczynski@umk.pl"
<Marcin.Piwczynski@umk.pl>

StAndrewsU EvolutionaryTheory

PhD in Evolutionary Theory (Phylogenomics)

The PhD project is part of a larger project entitled “Genome-wide molecular dating” between the groups of Carolin Kosiol (University of St. Andrews / Vetmeduni Vienna, http://biology.st-andrews.ac.uk/contact/-staffProfile.aspx?sunid=ck202), Gergely Szöllösi (Etvös University Budapest, http://ssolo.web.elte.hu/), Asger Hobolth (Aarhus University, http://www.daimi.au.dk/-~asger/). The recent sequencing of genomes of closely related species and of many individuals from the same species enables the study of speciation and the inference of the history of populations. Standard phylogenetic methods reduce entire populations to single points in genotypic space by modelling evolution as a process in which a single gene mutates along the branches of a phylogeny. In this project, we envisage developing new theory and software to tackle the problem of species tree estimation and molecular dating genome-wide. The PhD student will be based with Dr. Carolin Kosiol at the Centre of Biological Diversity of the University of St. Andrews/Scotland. Visits to Vienna, Budapest and Aarhus for close collaboration are planned. Starting date is September 2017 or shortly thereafter. The position will be funded for 3.5 years.

Candidates will be expected to have a strong interest in applying quantitative methods and modelling to Biology. They will have a degree in Bioinformatics, Mathematics, Physics, Statistics, Computer Science or a related field. Prior experience with either population genetics or comparative genomics is a benefit. Preferably the candidate will have experience in programming language such as C, C++, Java and a scripting language such as Python or Perl.

Please send informal inquires to Carolin Kosiol ck202@st-andrews.ac.at

Carolin Kosiol Lecturer in Bioinformatics Centre for Biological Diversity School of Biology University of St Andrews St Andrews Fife KY16 9TH United Kingdom

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

TrentU MScWildlifeGenomics

Krystal Dixon (BC Gov’t) and Aaron Shafer (TrentU) are seeking a MSc student to study mountain goats in mountains of northwestern British Columbia.

The project: Based out of TrentU the project combines field work in BC and genomic data to better delineate management units and understand individual behaviour.

Qualifications: The selected student must meet the minimum requirements of the Environmental and Life Sciences Graduate Program at TrentU. Previous field or lab experience is an asset, domestic applicants are preferred.

How to apply: Send an email to aaronshafer@trentu.ca complete with a cover letter, CV, transcripts, and contact information for two referees. Start date is anticipated to be either Jan or May 2018.

shaferab@gmail.com

UCCork Ireland EvolutionaryEcolFish

Ph.D.opportunity in fish evolutionary ecology

Applicationsare invited for a motivated and enthusiastic PhD candidate who will join the BEYOND 2020 multi-institute research cluster project (Burrishoole Ecosystem Observatory Network 2020). The Burrishoole research station (managed by the Marine Institute) is an international index site for diadromous fish and a world leader in the use of in-situ automated monitoring systems to track changes in freshwater systems. The BEYOND 2020 research team builds on the existing biological and sensor monitoring programmes at the Burrishoole research station by using next generation science and technology to further inform species and ecosystem response to both natural and human mediated environmental change.

Weseek a highly-motivated graduate who wants to gain a PhD in the area of evolutionary ecology and population biology with particular focus on the genetic architecture of phenotypic variation. The successful applicant will investigate genetic architecture of ecological divergence in three-spined sticklebacks in the Burrishoole system. This system comprises mountain and lowland streams and lakes tidal lakes, estuaries and access into the ocean providing a unique opportunity to study evolutionary change genetic architecture under different ecological pressures and investigate adaptive changes in response to climate change in complex environments. Following assessment of the biology and the ecology of the stickleback within several habitat types the student will have the opportunity to apply quantitative methods to determine phenotypic divergence in a range of ecologically relevant traits (e.g. presence of armour plate body morphology, behaviour, micro- and macro-parasite infection feeding strategies, respiratory metabolism). The use of genomics metagenomics and transcriptomic tools on wild-caught and experimental fish (in collaboration with research collaborators at Queen's University Belfast and University of Glasgow) will allow genotype-phenotype mapping of phenotypes in complex and variable environments.

Theposition is based at the Marine Institute's research facility in Newport Co. Mayo Ireland. The student will be joining a multidisciplinary team of researchers and other Ph.D. students and will be will working closely with project collaborators in University College Cork Queen's University Belfast University of Glasgow and the Marine Institute.

Theposition is funded for 3 and a half years. Funding is through a Marine Institute project-based award (Marine Research Programme 2014-2020) and provides a 3.5-year stipend of €16000 per annum plus fees (with possibility of an extension). The successful candidate will be registered as a full time research student in the School of Biological Earth & Environmental Sciences at UCC (Cork) under the supervision of Drs Phil McGinnity and Joshka Kaufmann (UCC) and Prof. Paulo Prodöhl (QUB). The PhD degree will be awarded by University College Cork.

Applicantsshould have a First or Upper Second Class Honours BSc or MSc. in an appropriate discipline (e.g. Ecology Evolution, Zoology, Biology, Genetics). A strong background and interest in quantitative genetics is essential as well as a solid training in evolutionary, ecological and/or population genetics theory. Applicants must be selfâwith good communication organisational and writing skills. Experience working with fish handling in field or aquaria settings would be advantageous but not essential; as would molecular laboratory skills. Experience in using R is a plus.

InformalEnquiries: Please contact Dr P. McGinnity (Email: p.mcginnity@ucc.ie <mailto:joshka.kaufmann@ucc.ie>)

Toapply please send by email a CV details of 2 referees, and an accompanying letter of application outlining your relevant experience to Dr P. McGinnity School of Biological, Earth & Environmental Sciences, University College Cork Cork, Ireland. Eâp.mcginnity@ucc.ie

Dates:Application deadline is 15 June 2017. Start date Summer 2017.

joshka.kaufmann@ucc.ie

UGlasgow 2 MarineMicrobialEvolution

1) BBSRC-SFI PhD opportunity: Exploring the microbial ecology and energetics of wild and domesticated Atlantic Salmon.

Background: Energy economy underpins the success and survival of all living organisms. Atlantic Salmon must run numerous energetic gauntlets throughout their lifecycle: seasonal anorexia in freshwater phases; outward migrations as smolts; gorging and fat deposition in marine feeding grounds; fasting as returning spawners. The timing of such events in the wild is likely to be highly adaptive. Farmed fish, by contrast, may have lost many key traits that guarantee survival in this respect. An ambitious new research program is underway at the University of Glasgow and University College Cork (Ireland) to define the contribution of intestinal microbes to the energetic plasticity in salmon. Using a unique experimental river system based at the Burrishoole Catchement, County Mayo, wild and domesticated salmon are being reared in a common garden experiment prior to transfer to experimental marine sea cages to explore adaptive and maladaptive phenotypes in the context of wild fish, farmed fish and farm escapes.

Aims and Objectives: The aim of this PhD program is to evaluate the impact of the gut microbiome and fermentation on the energetics (adiposity, SMR, growth, nutritional energy harvest etc) of wild and domesticated Atlantic Salmon in both freshwater and marine life cycle phases. There is also an opportunity to study the energetic profiles of gut microbial communities isolate in the field in a novel ex-vivo system based at the University of Glasgow.

Personal Specification: We are looking for an exceptionally motivated and talented student to fill this generously funded position. The student should have a 2.1 undergraduate degree (or equivalent) in a biological field and a demonstrable interest and aptitude in one or more aspects of this project. A master's degree is preferable but not essential. Funding is provided through University College Cork, but the student will be based at the University of Glasgow with considerable time at the Burrishoole Field site.

Funding and Eligibility: This PhD carries a full stipend for 4 years as well as some consumables and travel funds. Fees are limited to EU nationals only.

2) Burrishoole Ecosystem Observatory Network (Beyond 2020): Microbial ecology of anadromous and catadromous teloests.

Background: The Newport catchement system at Burrishoole on the West Coast of Ireland (Co Mayo) is among the most exenstively monitored aquatic ecosystems in the world. Full records of anadromous and catadromous fish movements and assciated environemntal data have been gathered since 1970 with the eariest records dating back to 1955. The catchement system is comprised of a series of freshwater loughs and water courses, as well as brackish water loughs that stretching from Bunaveela Lough on the far north of the system to the brackish water Lough Furnace, adjacent to neighbouring Clew Bay. A new project BEYOND 2020 will use the unique Burrishoole ecosystem as a living laboratory to understand aquatic ecology in an era of unprecedented environmental change, via the exploitation of past data and current sample collection facilities.

Aims and Activities: The aim of this PhD program will be to explore the role of tissue-specific microbial communities of stickleback and European eel collected from contrasting saltwater and freshwater environments in the Burrishoole ecosystem in influencing adaptation and environmental tolerance. We expect this PhD program to take a holistic approach, potentially incorporating host genetics, host-microbiome interactions, pathogen exposure and resistance, to understand the potential constraints involved with exploiting novel and/or changing environments. The project will also have access to common garden experiment facilities, both in the lab, as well in nature via the Burrishoole experimental stream system.

Personal Specification: We are looking for an exceptionally motivated and talented student to fill this generously funded position. The student should have a 2.1 undergraduate degree (or equivalent) in a biological field and a demonstrable interest and aptitude in one or more aspects of this project. A master's degree is preferable but not essential.

Funding and Eligibility: This PhD carries a full stipend for 3.5 years as well as generous consumables and travel funds. Fees are limited to EU nationals only.

Many thanks Martin

Dr. Martin Llewellyn IBAHCM Room 207 Graham Kerr Building University of Glasgow G12 8QQ Phone - 00441413305571 Mob - 447968587547 Skype - martin_llewellyn https://llewellynlab.wordpress.com/ http://www.gla.ac.uk/schools/lifesciences/staff/martinllewellyn/ Martin Llewellyn <Martin.Llewellyn@glasgow.ac.uk>

UGreifswald ButterflyEvolution

University of Greifswald (Germany),

Institute of Medical Biochemistry and Molecular Biology & Zoological Institute and Museum

Master project: Population differences in redox status in response to variable temperature regimes in a European butterfly.

The Institute of Medical Biochemistry and Molecular Biology and the Zoological Institute & Museum at the University of Greifswald jointly offer a Master project at the interface between biochemistry and ecology. In the context of climate change, the general aim of the project is to examine whether animal populations naturally subject to different temperature regimes differ physiologically when exposed to new stressful thermal conditions. More specifically, the project will focus on the effects of variable temperature regimes on the redox status of different populations of green-veined white butterflies (Pieris napi). Butterflies have already been collected across a latitudinal gradient in different European countries, exposed to different temperature regimes, and prepared for further laboratory analyses. The project can therefore start as soon as possible.

The candidate should have a strong background in biochemistry and laboratory techniques as well as a clear interest for ecological questions (e.g. student in biochemistry, biology, veterinary medicine). The candidate should also be willing to spend much time in the lab and to analyze large datasets. If desired, following this Master project, the selected candidate will have the opportunity to apply to a PhD position within the framework of the Graduate School RESPONSE (https://biologie.uni-greifswald.de/en/research-activities/research-traninig-groups-german-research-council-dfg/research-training-group-2010/).

Successfully conducting the proposed Master project will obviously be a clear advantage to enter this PhD program (although with no guarantee).

Research Training Group 2010 - Faculty - University of ... < https://biologie.uni-greifswald.de/en/-research-activities/research-traninig-groups-german-research-council-dfg/research-training-group-2010/ > biologie.uni-greifswald.de The Research Training Group (RTG 2010) "Biological RESPONSEs to Novel and Changing Environments" is funded by the Deutsche Forschungsgemeinschaft (DFG) and runs for ...

Applications should include: (1) a cover letter with a short statement of motivation, (2) a CV, and (3) the contact details of one or two academic referees. Applications should be submitted electronically as a single PDF file to: Dr. Michaël Beaulieu e-mail: beaulieum@uni-greifswald.de

For further information, please visit http://-www.lillig.de/index.html and https://zoologie.uni-greifswald.de/en/organization/departments/animal-ecology/ or directly contact Michaël Beaulieu.

Animal Ecology - Faculty - University of Greifswald < https://zoologie.uni-greifswald.de/en/-organization/departments/animal-ecology/ > zoologie.uni-greifswald.de On these sites you will find information on staff, research and teaching of the Department of Animal Ecology. Our expertise includes lab-based experimental approaches ...

group lillig < http://www.lillig.de/index.html > www.lillig.de group lillig ... Â© 1998-2017

Dr. Michaël Beaulieu Zoological Institute & Museum Greifswald University J.-S.-Bach-Str. 11/12 D-17489 Greifswald Phone: +49-3834-864268 Fax: +49-3834-864252 "Dr. Michaël Beaulieu" <beaulieum@uni-greifswald.de>

Michael Beaulieu <MiKLvet@hotmail.fr>

UGroningen TheoreticalBirdBehaviour

PhD position on computational models of collective escape of bird flocks 1.0 fte (217006H)

- Back to the overview

Organisation

Founded in 1614, the University of Groningen enjoys an international reputation as a dynamic and innovative center 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 center of knowledge.

The Groningen Institute for Evolutionary Life Sciences (GELIFES - http://www.rug.nl/research/gelifes/) GELIFES, the largest institute of the Faculty of Mathematics and Natural Sciences (FMNS) fills a special niche in the life sciences by covering and integrating mechanistic, evolutionary and ecological approaches, aiming to understand adaptation on all levels of biological organisation. Researchers pursue fundamental questions while collaborating with partners from industry, medicine and other realms of society. Our research fields include behavioural biology, chronobiology, ecology, evolutionary biology, genetics and genomics, neurobiology, physiology and theoretical modelling, using a wide array of research tools. Research levels range from molecular and organismal to population and community, performed under laboratory, semi-natural and field conditions.

Job description

One of the advantages of group life, such as in birds, is increased protection against predation. Increased protection is, for instance, assured by the complex patterns of collective escape by bird flocks under attack. These patterns may confuse the predator. Collective behaviour of flocks is, however, difficult to investigate empirically. As a solution, the proposed project concerns the computational modelling of collective escapes. This is done with the help of empirical data collected by another PhD candidate using robot-falcons (RoboFalcons) for controlled attacks on flocks. The empirical study is aimed at driving flocks away in a specific direction for preventing collisions between flocks and airplanes. The PhD candidates will closely exchange data and results. The modelling project aims to gain understanding on what causes different patterns of collective escape under different conditions. For this, the PhD candidate will extend our computational model, StarDisplay, and may develop new models. The model will be informed by two empirical sources, namely, the experiments with RoboFalcons and the movies of huge starling flocks under attack by Peregrine falcons above Rome. The student will experiment with different escape strategies and attack strategies in the model to improve both understanding of the observations of patterns of collective escape and methods of driving flocks away. Daily supervision will come from Prof. Charlotte Hemelrijk and Dr Hanno Hildenbrandt; Dr Colin Torney (Glasgow, UK) will co-supervise the project.

Qualifications

The successful candidate will have previous research experience in theoretical modelling, be in good command of the English language (oral and written) and possess excellent communication skills (indicated by the ability to write scientific papers and deliver presentations). Since studies on self-organisation are highly interdisciplinary, successful candidates are expected to demonstrate an active and supportive approach to interdisciplinary research and collaborate with other group members. Suitable candidates can be either individuals with a background in the computational (life) sciences, with interest in evolutionary and biological questions, or evolutionary biologists with experience in computational modelling.

Candidates for the PhD position should have: - MSc in theoretical biology, a MSc in computational science with focus on biology or an MSc in computational physics with specialization in biology, MSc in Artificial Intelligence with a specialization in an area of computational or mathematical biology or a MSc in Biology, with a specialization in an area of computational or mathematical biology - experience with developing computer simulation code and a sufficient background in mathematics - a strong interest in collective, swarming behaviour, biomechanics of flight, attack and escape. Candidates with research experience in these areas are particularly encouraged to apply.

Conditions of employment

The University of Groningen offers a salary of euro 2,191 gross per month in the first year, up to a maximum of euro 2,801 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 must result in a PhD thesis within

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UHuddersfield ProtistGenomics

Evolutionary Biology of Transposable Elements In Protists

Supervisors: Dr Martin Carr, Dr Christopher Cooper (University of Huddersfield), Dr Roy Chaudhuri (University of Sheffield)

The research programme for this studentship, part of our Huddersfieldâ euro s Leverhulme Trust funded Postdoctoral Training Centre, will focus on the evolution of transposable elements (TEs) within the genomes of unicellular eukaryotes (protists). Past research on TEs has centred upon the multicellular eukaryotes, with an emphasis on animals, fungi and plants; however, most of life's diversity is found within protists. Protist species have very different population dynamics to multicellular organisms and this is likely to have a resulting impact on the evolution of their TEs. The choanoflagellates are the protistan sister-group to animals and preliminary work has shown major differences between their TE families and the families present in animal genomes. This project aims to expand upon this work. The full TE compliments of 19 species of choanoflagellate will be sequenced and subject to phylogenetic and population genetic analyses. Phylogenetics will be used to determine the con tribution of horizontal transfer, as well gene loss, to TE evolution. Population genetic analyses will determine the role of natural selection on TE family evolution, with an emphasis on the codon usage of TE genes. Bioinformatics approaches will be used to study TEs in additional protist groups to identify any general trends in their evolution.

The proposed research will cover transcriptomics, high-throughput sequencing, phylogenetics and population genetics. The successful applicant will also be encouraged to devise their own research projects during the course of the PhD.

The students will work in new molecular biology facilities alongside existing students in protist research, who will provide day to day guidance, along with the supervisor. There will be a strong emphasis on data analysis and interpretation, as well cutting-edge laboratory work, and on producing world-class research papers.

Applicants should hold, or be expected to gain, a good bachelor's degree in Genetics, Molecular Biology, Statistics, Computing, or other relevant subject, and ideally have experience of computer programming, as well as generic biological lab techniques. Although training and hands-on supervision will be provided, it is essential that the candidates can operate independently and take the initiative to direct their research.

The studentship will cover the full cost of tuition fees for UK/EU students, and will pay an annual tax-free bursary of 14,553 for three years (RCUK rates). There are additional funds available for laboratory consumables and travel for conferences, visits to collaborating laboratories and sample procurement.

To apply, please go to: http://halo.hud.ac.uk/-pgr_onlineapps/ and complete the on-line application, ensuring you select full-time PhD Biology. Please type 'Leverhulme Trust' in the 'Personal Statement' field. Please also email your CV, transcripts and two letters of recommendation in support of your application to Leverhulme PTC co-ordinator Professor Richards (email m.b.richards@hud.ac.uk) andcopy to PGR Administrator Fiona Cross (email sasresearchadmin@hud.ac.uk)

Please indicate in your email why you believe you are well-qualified for the project.

For informal enquiries please contact:

Dr Carr on +44 (0)1484 471608 (email m.carr@hud.ac.uk)

Related web links:

http://www.hud.ac.uk/research/researchcentres/-egrg/eeg/ https://hud.academia.edu/MartinCarr Martin Carr http://www.protistology.org.uk martcarr74@gmail.com

ULausanne ComputEvolGenomics

SNSF PhD student position in computational evolutionary biology

Job information Expected start date in position : 01.09.2017 or to be discussed Contract length : 1 year, This contract can be renewed for two years Activity rate : 100% Workplace : Lausanne Dorigny

Job description The incredible diversity of insects makes them fascinating to study, with important applications in the characterisation of animal biology, the control of disease vectors and pests, and the conservation of threatened insects. Falling sequencing costs are improving genomic species sampling and enriching sources of functional data, challenging researchers to find innovative approaches to best exploit these data to bring new levels of depth and detail to our understanding of biology. Overcoming these challenges requires substantial methodological advances in data integration and interrogation, supported by robust computational infrastructures. With an initial focus on disease-vector mosquitoes, this SNSF-funded research project aims to exploit genomic evolutionary signatures to enhance the understanding of putative functions of thousands of currently uncharacterised genes from hundreds of organisms.

The successful candidate will be based at the Department of Ecology and Evolution of the University of Lausanne, under the supervision of Prof. Robert Waterhouse (www.rmwaterhouse.org). S/he will work very closely with a postdoctoral student to implement the core research project goals in line with the aims of the doctoral thesis. In particular, designing and developing cross-species comparisons to quantify patterns of evolutionary change and exploring strengths and interdependencies of correlations amongst evolutionary metrics and global functional properties to confirm and refine our understanding evolutionary-functional correspondences. Confidence with statistics will help with the detailed resolution of the complex relations amongst evolutionarily defined modules and the different hierarchies of biological functions, and is thus desirable. 100% of the rate of employment is devoted to the realization of the doctoral thesis. The University of Lausanne offers a world-class international research environment with state-of-the-art facilities.

Your qualifications In order to complete our team, we are looking for someone with the following skills : Essential: Master's degree in computer science (with life sciences experience) or bioinformatics / computational biology Demonstrable programming skills and experience (e.g. Python, Perl, C/C++, R) Scientific research motivation in genomics Strong teamwork and interdisciplinary skills Good spoken and written English proficiency Desirable: Experience with web technologies (e.g. Javascript, HTML, CSS) Confidence in large-scale statistical analyses Scientific research experience in genomics Interest in evolutionary genomics of arthropods Knowledge of arthropod biology

What the post offers you We offer a nice working place in a multicultural, diversified and dynamic academic environment, opportunities for professional training. Possibilities of continuous training, a lot of activities and other benefits to discover. Contact for further information For further information please contact Prof. Robert Waterhouse (robert.waterhouse@gmail.com)

Your application by 16.06.2017 Please, send your full application in Word or PDF. Your complete application should contain : Motivation letter (max. one page) Curriculum vitae including lists of publications, conferences, and awards (where relevant), and a detailed description of programming skills and experience Master's thesis summary (max. one page) The names and contact details of 2-3 referees Applications should be made exclusively online.

Robert Waterhouse <robert.waterhouse@gmail.com>

ULaval ArmsRaceStickleback

PhD position: Genomics basis of the arms race between a parasite and its host, the threespine stickleback

A fully-funded 4-year PhD position is available in the Aubin-Horth and Landry Laboratories at Universite Laval in Quebec City, Canada. The PhD student will work on a project aimed at dissecting the genomic bases of the co-evolution between the threespine stickleback and its worm parasite, Schistocephalus solidus.

The candidate is expected to have a Master degree in biology or a related discipline, and a background in bioinformatics (R, Python or Perl), statistics and genomics. The candidate should have strong leadership skills, motivation and creativity and be able to work in a team of collaborators.

The Aubin-Horth and Landry Laboratories are located at the Institut de Biologie Intégrative et des Systèmes (IBIS) at Université Laval. IBIS offers a very stimulating training environment and cutting edge on-site platforms in genomics, proteomics and microscopy. The Aubin-Horth Lab members are evolutionary biologists, neuroendocrinologists and behaviour biologists working together using an integrative approach to uncover the mechanisms underlying the alteration of stickleback behaviour by its endoparasite, by studying both the host and its parasite at the molecular, cellular and hormonal level, as well as how they interact. The Landry lab is an international team of 15 students, PDFs and research associates from different backgrounds (microbiology, biology, bioinformatics, biochemistry) addressing questions in evolutionary cell and systems biology.

The application package (1 single PDF file) should include a motivation letter demonstrating the interest of the candidate for the field and his/her ability to perform this type of research, a CV and the contact information of three people who can provide letters of reference. The file should be sent to Nadia.Aubin-Horth@bio.ulaval.ca

Starting date could be as early as September 2017. The competition will remain open until a candidate is selected.

-For more information on research ongoing in the Aubin-Horth and Landry laboratories, please visit:

http://wikiaubinhorth.ibis.ulaval.ca/Main_Page http://landrylab.ibis.ulaval.ca/ -Recent publications from the two laboratories on this subject:

Hébert FO, Grambauer S, Barber I, Landry CR, Aubin-Horth N. Major host transitions are modulated through transcriptome-wide reprogramming events in Schistocephalus solidus, a threespine stickleback parasite. 2-17. Molecular Ecology. 26:1118-1130.

Grécias L, Hébert FO, Berger CS, Barber I, Aubin-Horth N. 2017. Can the behaviour of threespine stickleback parasitized with Schistocephalus solidus be replicated by manipulating host physiology? J Experimental Biology. 15: 237-246. doi: 10.1242/jeb.151456. Epub 2016 Nov 3. PubMed PMID: 27811294.

Hébert FO, Grambauer S, Barber I, Landry CR, Aubin-Horth N. 2016. Transcriptome sequences spanning key developmental states as a resource for the study of the cestode Schistocephalus solidus, a threespine stickleback parasite. Gigascience. 5:24.

Hebert FO, Phelps L, Samonte I, Panchal M, Grambauer S, Barber I, Kalbe M, Landry CR, Aubin-Horth N. 2015. Identification of candidate mimicry proteins involved in parasite-driven phenotypic changes. Parasites and Vectors. 15 :225.

Hébert FO, Aubin-Horth N. 2014. Ecological genomics of host behavior manipulation by parasites. Adv Exp Med Biol. 781:169-90. d

Landry CR, Aubin-Horth N. 2014. Recent advances in ecological genomics: from phenotypic plasticity to convergent and adaptive evolution and speciation. Adv Exp Med Biol. 781:1-5.

Pavey SA, Bernatchez L, Aubin-Horth N, Landry CR. 2012. What is needed for next-generation ecological and evolutionary genomics? Trends in Ecology and Evolution. 27:673-8.

Christian Landry, PhD Professeur agrégé

Chaire de Recherche du Canada en Biologie évolutive des systèmes cellulaires // Canada Research Chair in Evolutionary Cell and Systems Biology

Département de Biologie Institut de Biologie Intégrative et des Systèmes PROTEO Centre de recherche en données massives (CRDM)

Local 3106, Pavillon Charles-Eugène-Marchand 1030, Avenue de la Médecine Université Laval Québec (Québec) G1V 0A6 Canada

http://landrylab.ibis.ulaval.ca/ http://journalclub.ibis.ulaval.ca/ Téléphone: 418-656-3954 Télécopieur: 418-656-7176

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

UManchester ConservationGenetics

A NERC funded PhD studentship starting in September 2017 is available at the University of Manchester, UK. This is a CASE studentship with Chester Zoo. Please note the deadline for application is 31 May 2017.

Please contact Cathy Walton at Catherine.walton@manchester.ac.uk or +44 161 275 1533 for further information on the project and how to apply. Applications can be initiated from the findaphd weblink given below.

Title: Using genetics of captive and wild metapopulations of mega-herbivores (elephants and rhinos) to inform conservation planning initiatives

Project Outline

Wild populations of large herbivores play a vital role to the functioning of African ecosystems but are increasingly endangered as a result of poaching and loss and fragmentation of their habitat (Ripple et al. 2015). The International Union for Conservation of Nature (IUCN) Conservation Breeding Specialist Group(CGSG) highlights that to achieve viable populations of species thriving in healthy ecosystems conservation planning initiatives must involve integrated species conservation planning that considers all populations of the species (inside and outside the natural range) under all conditions of management. Therefore, prior to implementing gene flow between in situ and ex situ populations, it is key that we characterise genetic diversity and understand the likely consequences of gene flow within and among captive and wild populations. It is essential to avoid: inbreeding depression due to the breeding of closely related animals; loss of genetic distinctiveness and loss of local adaptation due to the interbreeding of genetically distinct subspecies; and adaptation to captivity that results in individuals poorly adapted to natural conditions. Any of these can result in reducing the fitness of managed populations, making matters worse rather than better. However, knowledge of the genetic composition of potential donor and recipient populations can ensure that introduced individuals enhance and complement local genetic variation boosting the success of that population and so the whole species. This project will focus on the population genetics of two African large herbivores; the eastern black rhino and the African elephant with the aim to integrate genetic information into population management and improve overall viability of endangered species.

https://www.findaphd.com/search/ProjectDetails.aspx?PJID=86268&LID=1024 Catherine Walton <Catherine.Walton@manchester.ac.uk>

UMelbourne LeafminerGeneticsBiocontrol

Masters(or PhD) opportunity at the University of Melbourne

Helpcontrol the vegetable leafminer, a major quarantine threat for our food production systems

Supervisors:Prof Ary Hoffmann (Bio21 Institute, the University of Melbourne), Dr Peter Ridland (Honorary Fellow, the University of Melbourne) and Dr Paul Umina (Bio21 Institute, the University of Melbourne and cesar)

Thegreater project: The vegetable leaf miner (VLM) is a polyphagous species of agromyzid fly capable of infesting vegetable and flower crops and driving severe crop losses. In 2015, the first detection of VLM within Australia was made on Cape York Peninsula, and VLM is now considered at high risk of establishing within major production zones across Australia and causing severe detrimental impacts on Australian agriculture. This masters project will form one part of a greater project, funded by Horticulture Innovation Australia, which will combine molecular, morphological, modelling, chemical and biocontrol methods to detect, eradicate and manage VLM.

Thecollaborative team: The greater project, “RD&E program for control, eradication and preparedness for Vegetable leafminer” involves several partners including The University of Melbourne, AUSVEG, cesar pty ltd, Plant Health Australia and the North Australian Quarantine Authority.

Themasters component: Biological control is a potentially significant tool for the management and eradication of VLM. This project will identify candidate parasitoid wasps for the biocontrol of VLM through a combination of literature reviews and field collections of agromyzids and their parasitoids across Australia. The project is expected to include a significant field work component, largely within key agricultural production areas of southern Australia, but with the potential to travel to the Cape York Peninsula. An interest in taxonomy and/or molecular methods would be ideal.

Thisproject includes scholarship support of $7,500 per annum, and also includes ALL funds to support research and fieldwork costs.

Thestudent undertaking this research will play a crucial role in developing sustainable control of a new threat to Australia's agricultural industry.

Eligibilityand application: The successful student will have a strong undergraduate record in a relevant field and an interest in entomology/sustainability.

Furtherinformation: ProfAry Hoffmann (ary@unimelb.edu.au 03 8344 2282) orDr Paul Umina (pumina@unimelb.edu.au 03 9349 4723)

epirtle@cesaraustralia.com

UMontpellier France ArbovirusEvolution

We have a funded PhD position on the population genetics of Bluetongue virus during host alternation. If interested, please contact serafin.gutierrez@cirad.fr and etienne.loire@cirad.fr <mailto:etienne.loire@cirad.fr> with the string "PhD_BTV" in the subject field.

Where: ASTRE lab, Montpellier, France (http://umr-astre.cirad.fr/)

Title: Adaptive mechanisms facilitating host alternation in Bluetongue virus

Starting date: September 2017

Deadline for application: 15th July 2017

Funding: The candidate is funded for 3 years (H2020-funded project)

Context:

Many viruses are transmitted by arthropod vectors, like mosquitoes and biting midges, and cause significant disease in humans and livestock worldwide. The life cycle of such arthropod-borne viruses (arboviruses) is rather complex as it necessitates alternation between largely unrelated hosts: arthropods and vertebrates. This situation suggests that viral mechanisms have evolved to facilitate host switching, thus increasing the likelihood of disease emergence in new hosts. Given the importance of these viruses, it is surprising that the existence of such mechanisms has been largely understudied.

Goals:

The candidate will explore three potential mechanisms facilitating host alternation: (i) rapid adaptation following horizontal transmission1, (ii) cooperation among the genotypes infecting a host (i.e. quasispecies behaviour)2 and (iii) variation in viral gene expression through regulation of gene copy number variation3. To this end, the candidate will analyse the genetics of virus populations in experimental infections in arthropods and vertebrates using, among others, deep sequencing and bioinformatics. The main biological model will be Bluetongue virus (BTV), an arbovirus transmitted by biting midges and causing disease in ruminants worldwide4. The hosting laboratory already possesses samples from experimental infections of sheep and midges that can facilitate rapid result generation. In addition, the candidate will carry out experimental evolution of BTV populations in insect and vertebrate cell cultures to further investigate the existence of the proposed mechanisms. Depending on timing, the conservation of the results in other arbovirus models (for example, mosquito-borne viruses) will be attempted.

Profile: We seek for a candidate interested in virus evolution and willing to use bioinformatics and experimental infections.

Keywords: Arbovirus, evolution, emergence, host alternation, bluetongue, sheep, vector.

Disciplines/Background: Population genetics, evolution, bioinformatics, virology.

serafin.gutierrez@cirad.fr

UNaples PlantPollinator

The Department of Biology of the University of Naples (http://www.dipartimentodibiologia.unina.it/) is seeking a PhD student working on ecological and molecular aspects of plant pollinator interactions. The duration of the PhD is 3 years.

We are looking for:

- highly qualified and motivated scientists with expertise in Plant pollinator interactions - Candidates should be able to communicate effectively in English and should enjoy working in an interdisciplinary context

How to apply:

Please send your complete application as a single PDF file to Dr Giovanni Scopece (giovanni.scopece@unina.it), including:

1. detailed CV (with list of publications or poster presentations) 2. contact details of references

"giovanni.scopece@unina.it"
<giovanni.scopece@unina.it>

UNewSouthWales PhylogeneticComparativeAnalysis

A PhD position: Climate Change: phylogenetic comparative analysis, meta-analysis and computational modelling UNSW has announced another round of prestigious PhD scholarship (http://www.2025.unsw.edu.au/apply). We have been lucky enough to have been awarded one of these.

This project comes with $40,000 per year stipend and $10,000 of research funding per year (for full 4 years). It is open to both Australian and international applicants.

The topic is broad intentionally to attract an outstanding student: Climate change is impacting ecosystems worldwide. Many plant and animal species will not survive unless their distributions shift. However, not all species are moving and we don't systematically understand why.

This is a key challenge for understanding climate impact. In this project students will tackle important knowledge gaps: Can we use functional traits to predict species' ability to shift distributions? Which biotic and abiotic factors are important in determining species range? Do different processes act at northern vs southern limits? And, are distributions shaped by extreme climate events, or by the average conditions at a site? We will tackle a range of questions relating to climate change using phylogenetic comparative methods, meta-analysis and computational modelling (our supervisor team members are experts in these areas).

Given the generous stipend and project funding, an applicant is expected to be very competitive. We expect an applicant to have at least one peer-reviewed publication or an equivalent publication or experience which demonstrate their outstanding abilities.

Supervisory team: A/Prof Shinichi Nakagawa (http://www.i-deel.org/) A/Prof Will Cornwell (http://willcornwell.org/) Dr Daniel Falster (http://danielfalster.com/) If you would like to be considered, send your CV, cover letter, and contact information to three references to Vera Banschikoff – v.banschikoff@unsw.edu.au – by 18 June 2017. For more information on the scholarship program, see https://research.unsw.edu.au/unsw-scientia-phd-scholarship-scheme . Dr Shinichi Nakagawa (Associate Professor / ARC Future Fellow) Deputy Director of Research, Evolution & Ecology Research Centre, EERC (Visiting Scientist at Garvan Institute of Medical Research) Room 5102, Biological Sciences Building (E26) School of Biological, Earth and Environmental Sciences, BEES The University of New South Wales Randwick NSW 2052, Sydney, Australia Mobile: 0422 655 854 Office : 0293 859 138 Website: http://www.i-deel.org/ Shinichi Nakagawa <s.nakagawa@unsw.edu.au>

UOttawa FungalMetagenomics

The Corradi Lab is currently seeking motivated graduate students (MSc or PhD level).

Students will be supervised by Dr. Nicolas Corradi within a CIFAR (Canadian Institute for Advanced Research) - affiliated laboratory located in the Department of Biology of the University of Ottawa, Canada.

Lab Website: http://corradilab.weebly.com/ The selected candidates will pursue and expand work in one of several new exciting research areas in the lab:

1) Environmental genomics of Arbuscular Mycorrhizal Fungi

2) Metagenomics of eukaryotic intracellular pathogens (Microsporidia, Rozellomycota)

3) Genome and mating-type organization in the Arbuscular Mycorrhizal Fungi

Enquiries about specific projects can be sent to ncorradiATuottawa.ca.

Applicants are expected to have good background in one (or more) of the following areas:

Mycology, Arbuscular Mycorrhizal Fungi, Plant-microbe interaction, Amplicon-sequencing analysis, Population

Genetics/omics, Comparative genomics.

For international applicants, Fluency in French is desired (but not required).

A complete application package includes 1) a CV, 2) a short description of past research accomplishments and future goals, and 3) the names and e-mail addresses of at least 2 references. Evaluation of applications starts immediately until suitable candidates are found.

The University of Ottawa is a large, research-intensive university, hosting over 40.000 students and located in the downtown core area of Canada's capital city (http://www.science.uottawa.ca/fac/welcome.html). Ottawa is a vibrant, multicultural city with a very high quality of life (http://www.ottawatourism.ca/fr/)

Complete applications can be sent to Dr. Nicolas Corradi (ncorradiATuottawa.ca).

Representative Publications:

1. Corradi N. and A. Brachmann. Fungal mating in the most widespread plant symbionts? Trends in Plant Sciences 2017, 22 (2), 175-183

2. Ropars J., Kinga SÃdzielewska Toro K. Noel J., Pelin A., Charron P., Farinelli L., Marton T., KrÃÂ¼ger M., Fuchs J., Brachmann A., and N. Corradi. Evidence for the sexual origin of heterokaryosis in Arbuscular Mycorrhizal Fungi. Nature Microbiology 1(6): 16033, 2016.

3. Corradi N. Microsporidia: Intracellular Parasites Shaped by Gene Loss and Horizontal Gene Transfer. Annual Review of Microbiology 69 (1): 167-183. 2015

4. Pelin A., Selman M., Laurent Farinelli, Aris-Brosou S. and N. Corradi. Genome analyses suggest the presence of polyploidy and recent human-driven expansions in eight global populations of the honeybee pathogen Nosema ceranae. Environmental Microbiology 17 (11): 4443-4458, 2015.

5. Riley R., Charron P., Idnurm A., Farinelli L., Dalpe Y., Martin F. and N. Corradi. Extreme Diversification of the MATA-HMG Gene Family in the Plant - Associated Arbuscular Mycorrhizal Fungi. New Phytologist 201(1): 254-268, 2014.

Nicolas Corradi <ncorradi@uottawa.ca>

UQueensland MicrobialEvolution

The Engelstaedter Lab at The University of Queensland, Brisbane, Australia, invites applications for a PhD position in microbial evolutionary biology. The successful candidate will work on projects investigating the evolution of recombination and antibiotic resistance in bacteria. Specific projects are fairly flexible and will be arrived at in discussion with the candidate. Our previous research includes work on the evolution of natural transformation, integron evolution and fitness landscapes underlying drug resistance evolution. For details about our research and recent publications, see our website at http://engelstaedterlab.org/ . We are looking for a highly motivated student with a strong background in evolutionary biology, population genetics and/or microbiology. Applicants should possess a Bachelor's degree with Honours, Master of Science, MPhil or equivalent. Good communication skills, scientific curiosity and enthusiasm for research in evolutionary biology are essential.

Whilst the research to be conducted as part of the PhD will be fully funded, acceptance for this PhD is contingent on successful application for a PhD scholarship. Several PhD scholarships for international students are available at the University of Queensland Graduate School and the School of Biological Sciences. Students within Australia can apply for an Research Training Program award (RTP, this has replaced the previous APA scheme). For further information on scholarships, please visit http://www.biology.uq.edu.au/scholarships or contact our Postgraduate Administration Officer Gail Walter (gj.walter@uq.edu.au).

The School of Biological Sciences is a large and research-intensive unit at the University of Queensland, one of Australia's most prestigious universities. Brisbane is the third-largest city in Australia and offers mild subtropical climate, vibrant cultural life, plenty of outdoor activities and native wildlife.

Interested applicants should send a cover letter, CV, academic transcript, and a brief outline of their research interests to j.engelstaedter@uq.edu.au. Informal inquiries are also welcome.

— Dr Jan Engelstädter ARC Future Fellow & Senior Lecturer School of Biological Sciences The University of Queensland Brisbane QLD 4072 Australia phone: +61 7 336 57959 fax: +61 7 336 51655 http://-engelstaedterlab.org/ j.engelstaedter@uq.edu.au

URhodeIsland MarineMicrobialEvolution

PhD positions in plankton eco-evolutionary dynamics and global change biology

The Rynearson lab has two open positions for PhD students to focus on the broad themes of understanding eco-evolutionary dynamics in marine phytoplankton.Both projects include aspects of global change biology.One position includes opportunities to examine phytoplankton gene flow, connectivity and diversity using population genetics and experimental evolution approaches.A second position includes opportunities to use genomics and transcriptomics to examine the metabolic responses of phytoplankton to their changing environment.

Applicants should have MSc and/or undergraduate degrees, with backgrounds in population genetics, physiology, ecology microbiology and/or evolutionary biology. Both positions include funding for tuition and salary. More information on research in the Rynearson lab can be found here: (http://www.gso.uri.edu/rynearson-lab/).If interested, please send a short research interest statement and CV to Tatiana Rynearson with the subject line “Fall 2017 graduate position”.

Time line:

Start date for the position is late August 2017.

Initial queries should be sent by June 15 2017.

“T. Rynearson” <rynearson@uri.edu>

USherbrooke Evolution Treeswallows

We are seeking to recruit a student at the MSc and/or PhD level to join our research team at the Département de biologie, Université de Sherbrooke, starting in September 2017 or January 2018.

Our research aims at assessing the effects of environmental heterogeneity on a population of Tree swallows (Tachycineta bicolor) living in an agricultural landscape. The research project of the candidate will thus be developed within this framework. The candidate will participate to a long-term study conducted in southern Québec since 2004 and will benefit from biological data collected on more than 13000 individuals. The candidate will contribute to field work (2-3 months each year) and should ideally have skills in handling birds and a good knowledge of statistical analyses and ecology. The Université de Sherbrooke is a French-speaking institution, therefore either some knowledge of French or an interest in learning it is essential.

Interested candidates should send a CV and a cover letter, as well as the contact information of two references before 23 July 2017 to:

Marc Bélisle : Marc.M.Belisle@USherbrooke.ca Dany Garant : Dany.Garant@Usherbrooke.ca Fanie Pelletier : Fanie.Pelletier@Usherbrooke.ca

See also cret-recherche.weebly.com for more details on our research group.

“Dany.Garant@USherbrooke.ca” <Dany.Garant@USherbrooke.ca>

UVienna CephalopodGenomeEvolution

PhD position available at the Department of Molecular Evolution and Development, University of Vienna (https://molevodevo.univie.ac.at/).

Cephalopods (octopus, squids, cuttlefish, and nautilus) are fascinating animals to both the general public and science. The evolution of the molecular cascades specifying their complex nervous system and development remains elusive. With the recent decoding of the octopus genome, cephalopods are becoming increasingly important for molecular studies of the underlying genomic innovation. We are looking for an enthusiastic student with interdisciplinary background or interest to explore approaches in bioinformatics and experimental areas to investigate the ancient transitions in the genome architecture and function in cephalopods. The student will take part in several ongoing and future cephalopod genome-related projects, with a major aim of reconstructing the molecular basis of the ancient transitions and early diversification within the clade. Utilizing the emerging small cephalopod model species Euprymna scolopes (Hawaiian bobtail squid), the functional aspects of those known conserved and novel regulators can be studied during development.—

The work will be integrated and highly collaborative with several groups at the University of Vienna and the Center for Organismal Systems Biology (http://www.univie.ac.at/Lebenswissenschaften/-OrgSysBiol/osbiol.html), in particular the Departments of Molecular Evolution and Development, Integrative Zoology, and Neurobiology, as well as other research institutes. Additionally, the student can be associated with either of the two Vienna Doctoral Schools "Molecules of Life" and "Cognition, Behavior and Neuroscience".

Description and application procedures at the University website:— https://goo.gl/igy8gt . (Reference number: 7549)

Contact for questions: Oleg Simakov (oleg.simakov (at) univie.ac.at)—

oleg.simakov@univie.ac.at

UWyoming WildlifePopGenetics

PhD Student Opening (Univ of Wyoming): WILDLIFE POPULATION GENOMICS

See details at website: http://-www.wildlifegenetichealth.org/phd-wildlife-genomics/ A PhD student position is available to work on wildlife population genomics and health at the University of Wyoming (UW) in Laramie. The position will be primarily lab-based within the Ernest Wildlife Genomics and Disease Ecology Laboratory in the Department of Veterinary Sciences with course work and degree granted in the UW Graduate Program in Ecology (PiE; http://www.uwyo.edu/pie/). Research will use genomic and other genetic tools to study wildlife populations in the Rocky Mountain West and/or California, especially large mammal species, and with intersections with disease ecology.

The Ernest Wildlife Genomics and Disease Ecology Laboratory is a dynamic and highly collaborative lab at UW with University of California affiliation and works with other academic institutions, as well as state, federal, and non-governmental agencies. check out our work at http://www.wildlifegenetichealth.org There are many opportunities to work with recognized leaders who apply excellence in science toward wildlife conservation and management. Quality mentorship of trainees of all educational levels, including this PhD student position, is a priority for the laboratory. University of Wyoming hosts excellent wildlife and ecology science and a collegial academic atmosphere. Laramie offers easy access to the Rocky Mountains and outdoor activities including skiing, hiking, climbing, birding, and sport-hunting.

To apply for this position first review the qualifications desired here:

http://www.wildlifegenetichealth.org/phd-wildlife-genomics/ Next, please submit an electronic application via email in PDF format (preferably as a single pdf file) by email to holly.ernest@uwyo.edu with subject line including "Wildlife Genomics PhD student application" and include a cover letter stating research and education interests, C.V., transcripts and GPA for undergrad and MS grad program, GRE scores (exam taken within 5 years) including both percentiles and specifically list how the "required" and any of the "preferred" qualifications are met, and the contact information (name, position, email, phone, institutional affiliation, and research area) for at least three research/academic-related references including MS adviser(s) to Dr. Holly Ernest, Professor of Wildlife Genomics and Disease Ecology and Wyoming Excellence Chair.

Preferred start date is for Fall 2017 semester (considerations also might be made for Spring 2018 (January 2018). Applications reviews will begin as soon as received after June 1, 2017, and the position may remain open until filled.

—

Holly Ernest DVM PhD

Professor, Wildlife genomics and disease ecology

Wyoming Excellence Chair in Disease Ecology

Department of Veterinary Sciences

Program in Ecology

University of Wyoming, Laramie

http://www.wildlifegenetichealth.org/ | Holly.Ernest@uwyo.edu | 307-766-6605

Facebook: http://www.facebook.com/-wildlifegenetichealth Twitter: http://twitter.com/-hollyernest Linked In: http://www.linkedin.com/in/-hollyernest holly-logo-final-02-crop3

"Holly B. Ernest" <Holly.Ernest@uwyo.edu>

UZH Switzerland PlantAdaptation

Two PhD positions funded by the Swiss National Science Foundation are available from June 2017 in the group of Prof. Schiestl at the Department of Systematic and Evolutionary Botany, University of Zürich, for a period of four years. The positions are to study the ecological and molecular bases of plant adaptation to biotic and abiotic habitat parameters. In one project, reciprocal transplants in natural populations will be conducted to study local adaptation to pollinators, herbivores, and soil in a wild species of Brassica in Southern Italy. In the second project, experimental evolution using fast cycling Brassica plants will be used to investigate real-time adaptation to these habitat parameters. In both projects, the traits modulating adaptations as well as their molecular bases will be studied using selection analysis, phenotyping (including floral volatiles), as well as molecular and bioinformatics tools. You should have a Master degree in any field of biology and a thorough interest in evolutionary biology. Prior experience with plants and/or insects is an advantage. Proficiency in English both orally and written is a must; for the project including field work in Italy, knowledge of Italian and a drivers licence is desirable. The successful candidates will work in an exciting research environment focussing on patterns and process of plant evolution. Our department is located in the botanical gardens and house modern molecular and ecological labs, including greenhouses and climate chambers for plant cultivation. The University of Zürich has a very broad coverage of organismal and molecular biology, and several research groups work on evolutionary topics (www.lifescience-zurich.ch). The city also offers excellent quality of life through cultural programs and infrastructure, as well as an attractive surrounding.

If you are interested in the job, please send me by e-mail (florian.schiestl@systbot.uzh.ch) a letter describing your motivation, C.V., copy of degrees, publications (manuscripts), and e-mail addresses of two academic referees, by 25st of June 2017. If you have any further questions, don‘t hesitate to contact me.

Florian Schiestl <florian.schiestl@systbot.uzh.ch>

UZurich PlantInteractions

PhD position: Ecology of plant-mycorrhizal interactions

We are seeking a PhD student with a background (MSc degree) in ecology, biology, or a closely related discipline. The successful applicant will be based at the Department of Evolutionary Biology and Environmental Studies of the University of Zurich, Switzerland.

The mutualism between plants and arbuscular mycorrhizal fungi (AMF) is widespread and has persisted for over 400 million years. The stability of this mutualism depends on a “fair trade” between plants and fungi, and on mechanisms that protect this system from exploitation by “cheaters”. Indeed, plants and AMF are able to discriminate symbiotic partners through a range of mechanisms and invest selectively into different partners, depending on the relative quality of their service.

The successful applicant will analyze the trade of carbon and nutrients among plants and AMF in a series of experiments, using methods that include isotope labeling and molecular tools. The overall objective of the project is to characterize the strategies of both partners in the light of game-theoretical and network-based model predictions. A particularly interesting question will be how strategies of plants and fungi scale from pairwise interactions to systems with multiple species involved.

We are looking for a highly motivated, enthusiastic, and independent PhD candidate who has a strong interest in ecological and evolutionary questions. An accurate and clean laboratory working style is absolutely essential. Experience with standard molecular biological techniques is beneficial. A high standard of written and spoken English is essential.

The successful applicant will be supported and supervised by Pascal Niklaus and Jordi Bascompte (University of Zurich), Ansgar Kahmen (University of Basel), and Marcel van der Heijden (Agroscope Reckenholz).

http://www.ieu.uzh.ch/en/staff/member/niklaus_pascal.html http://www.ieu.uzh.ch/en/staff/member/bascompte_jordi.html http://botanik.unibas.ch/forschungsgruppen-der-botanik http://www.agroscope.admin.ch The PhD candidate will benefit from training offered within the PhD program in ecology (http://www.ieu.uzh.ch/en/teaching/phd/graduate.html) and the Zurich-Basel Plant Science

Center (http://www.plantsciences.uzh.ch/en.html), through which this project is funded. The appointment is for three years, starting no later than October 1, 2017. Salaries will follow University of Zurich regulations. The University of Zurich is the largest University of Switzerland and offers outstanding work conditions, a high quality of life in Zurich, and an excellent support environment.

To apply, please send a single pdf containing motivation letter, complete CV, and the names of two references to pascal.niklaus@ieu.uzh.ch, with subject PSC-PLANT-AMF. Application deadline is June 15, 2017.

"Pascal A. Niklaus" <Pascal.Niklaus@ieu.uzh.ch>

Vienna PopulationGenetics ApplyByMay21

Call for PhD students at the Vienna Graduate School of Population Genetics

Over the past years, Vienna has developed into one of the leading centres of population genetics. The Vienna Graduate School of Population Genetics has been founded to provide a training opportunity for PhD students to build on this excellent on site expertise.

We invite applications from highly motivated and outstanding students with a background in one of the following disciplines: bioinformatics, statistics, evolutionary genetics, functional genetics, theoretical and experimental population genetics. Students from related disciplines, such as physics or mathematics are also welcome to apply.

Topics include: - Evolution of gene expression - Understanding thermal adaptation - The impact of new transposable element insertions on adaptation to a new environment - Wolbachia infection dynamics in evolving Drosophila populations - The adaptive value of diversity produced by recurrent whole genome doubling - Epigenetic variation in Arabidopsis - Genetic footprints of adaptive introgression - Statistical inference concerning population genetic parameters from repeated genomic measurement data - New methods for modelling and analysis of data from experimental evolution - Maximum likelihood inference of population genetic parameters using genome-wide data - Macroevolutionary dynamics of selfish DNA unravelled by third generation sequencing - Dynamics of a selfish DNA invasion - Population trees and polymorphism-aware phylogenetic models - Evolution of bird sex chromosomes

Only complete applications (application form, CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by May 21, 2017 will be considered. Two letters of recommendation need to be sent directly by the referees. Accepted PhD students will receive a monthly salary based on currently EUR 2071 before tax according to the regulations of the Austrian Science Fund (FWF).

All information about the about available topics, the training program and the application procedure can be found at www.popgen-vienna.at We're on Twitter: https://twitter.com/PopGenViennaPhD – Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator www.popgen-vienna.at https://twitter.com/PopGenViennaPhD c/o Institut für Populationsgenetik Veterinärmedizinische Universität Wien (Vetmeduni Vienna) Veterinärplatz 1, 1210 Wien

T +43 1 25077 4338 F +43 1 25077 4390

http://www.vetmeduni.ac.at/en/population-genetics/ https://twitter.com/PopGenVienna julia.hosp@gmail.com

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Jobs

ArizonaStateU 6 CenterForMechanismsOfEvolution

CENTER FOR MECHANISMS OF EVOLUTION

We wish to announce the establishment of a novel center, focused on the mechanistic processes underlying evolutionary change. To a large extent, the research focus will be at the cellular level. The group will be populated with scientists from the areas of cell biology, biophysics, biochemistry, and population genetics, bound together with a common interest in evolution and a dedication to integrating theory with empirical work. The center will be housed at Arizona State University in a new building in the Biodesign Institute (https://biodesign.asu.edu/), which itself supports a diversity of other interdisciplinary centers and is well-endowed with state-of-the-art facilities. The CME is just part of a growing community of evolutionary biologists at ASU (https://sols.asu.edu/evolutionary-biology-faculty and http://asupopgen.org/), which itself is not far from the University of Arizona.

Over the next few years, we will be adding six new faculty into open-rank positions, with the first search for two biologists being initiated in fall 2017. Support is available for postdoctoral fellows and graduate students. Inquiries are welcome, and can be addressed to Michael Lynch (mlynch11@asu.edu).

Michael Lynch, Distinguished Professor, Class of 1954 Professor

NOTE: MOVING IN FALL 2017 TO ARIZONA STATE UNIVERSITY, TO START A NEW CENTER FOR MECHANISMS OF EVOLUTION WITHIN THE BIODESIGN INSTITUTE (https://biodesign.asu.edu/).

FOCUS IS ON EVOLUTIONARY ISSUES AT THE CELLULAR LEVEL: CELL BIOLOGICAL, BIOPHYSICAL, BIOCHEMICAL, POPULATION GENETICS; COMPUTATIONAL, THEORETICAL, EMPIRICAL.

WE WILL BE HIRING SIX OPEN-RANK FACULTY INTO A NEW BUILDING, RECRUITING POSTDOCS AND GRADUATE STUDENTS, ETC.

INQUIRIES ARE WELCOME.

Department of Biology 1001 East Third Street Indiana University Bloomington, IN 47405 Phone: 812-855-7384 Fax: 812-855-6705

http://www.indiana.edu/~lynchlab/

CambridgeU HerbariumCurator

The Cambridge University Herbarium is seeking a full-time Curator.

The successful candidate will be responsible for maintaining, organising and developing the Herbarium, its collections, services and profile. The Herbarium holds a scientifically and historically important collection of 1.1 million specimens of vascular plants, bryophytes, algae and fungi, together with an 8,000 photographic slide collection, 6,000+ book collection and other archives.

Fixed-term: The funds for this post are available for 3 years in the first instance.

For further information contact Professor Beverley Glover (bjg26@cam.ac.uk).

For more information and to apply go to:

http://www.jobs.cam.ac.uk/job/13776/ "B.J. Glover" <bjg26@cam.ac.uk>

ClaremontColleges 2 ConservationAndOrganismalBiol

Two Visiting Positions in Biology at the Claremont Colleges

The W.M. Keck Science Department (www.kecksci.claremont.edu) of Claremont McKenna, Pitzer, and Scripps Colleges (three of the five undergraduate Claremont Colleges) in Southern California, seeks to hire two visiting assistant professors in biology. One is for the full academic year 2017-2018 and the other is for spring 2018 only. Teaching responsibilities include teaching in an introductory biology class and lab focused on ecology and evolution, an upper division organismal/ecology class with lab and a class for non-science majors on conservation ecology. Participation in research, particularly directing undergraduate research projects may be possible. A Ph.D. in biology or related subject is required and prior teaching experience is preferred.

Apply online at https://webapps.cmc.edu/jobs/faculty/faculty_opening_detail.php?PostingID=16018 Please upload (i) a cover letter that includes a succinct description of your background, teaching experience, and research experience, (ii) a c.v., (iii) a diversity statement (of no more than 1 page) outlining the applicant's philosophy for fostering an educational environment that is inclusive of all students and (iv) the names and e-mail addresses of three or more references (at least two of whom can address teaching). All named references will be automatically contacted and sent instructions for uploading their reference letters. Review of applications will begin immediately, and the positions will remain open until filled. Further inquiries may be directed to Dr. Melissa Coleman at mcoleman@kecksci.claremont.edu.

Sarah Gilman Associate Professor Biology

W.M. Keck Science Department, of Claremont McKenna, Pitzer, and Scripps Colleges 925 N. Mills Avenue Claremont, CA 91711

http://faculty.jsd.claremont.edu/sgilman
sgilman@kecksci.claremont.edu 909-607-0715

"Gilman, Sarah" <SGilman@kecksci.claremont.edu>

CSIRO Australia PopulationGenetics

CSIRO is currently seeking to recruit a research scientist to advance our understanding of the use of CRISPR/Cas9 gene drives to manage agricultural pests (i.e. insects, pathogens and weeds). The Research Scientist will be responsible for leading the development of a modelling platform to consider how pest biology, spatial and temporal deployment strategies and management scenarios influence the short-term spread of gene drives and longer-term durability within pest populations. We would particularly welcome candidates with a research interest in mathematical modelling of population and genetic dynamics of pest organisms, and in the application of ecological and evolutionary principles to solving applied problems in agricultural landscapes.

Based in Canberra, Australia, this 3 year, fixed term position offers the opportunity to take a lead role in shaping the science around the use of gene drives to develop sustainable and efficient pest control solutions. Interested candidates are encouraged to contact Luke Barrett (luke.barrett@csiro.au) with any queries.

Location: Canberra, ACT Salary: $92K - $100K plus up to 15.4% superannuation Tenure: Specified term until June 2020 Reference: 38344 Applications are due May 28. For more details, and to apply, please visit https://jobs.csiro.au/job/Canberra%2C-ACT-FSP-Research-Scientist-Synthetic-Biology-Gene-Drive-Modeller/404245800/ Luke.Barrett@csiro.au"

EndowedChair MathBio UPenn

The Departments of Mathematics and Biology invite applications at the level of Associate or Full Professor for the Calabi-Simons Chair in Mathematics and Biology. This is a permanent endowed chair for which we are seeking an exceptionally accomplished mathematical biologist, particularly in the fields of Probability Theory and Evolution. Responsibilities include teaching undergraduate and graduate courses in Mathematics and Biology and conducting research in the field. The chairholder will help build excellence in this field at Penn and strengthen links between the Mathematics and Biology departments. The Simons Foundation provides generous programmatic funds, which could support graduate students and postdoctoral fellows as well as seminars and conferences.

Applications should be submitted online through mathjobs.org and include the following items: a cover letter, curriculum vitae, research statement, and a publication list.

Review of applications will begin July 1, 2017 and will continue until the position is filled. It is anticipated that the position will start July 1, 2018.

The Departments of Mathematics and Biology are strongly committed to Penn's Action Plan for Faculty Diversity and Excellence and to creating a more diverse faculty (for more information see: http://www.upenn.edu/almanac/volumes/v58/n02/diversityplan.html). The University of Pennsylvania is an EOE. Minorities/Women/Individuals with disabilities/Protected Veterans are encouraged to apply.

Joshua B. Plotkin Professor of Biology & Mathematics University of Pennsylvania http://mathbio.sas.upenn.edu/ "jplotkin@sas.upenn.edu" <jplotkin@sas.upenn.edu>

MelbourneU FieldAssist FairyWrens

Volunteer field assistants We are looking for field assistants to help monitor a colour-banded population of superb fairy-wrens near Melbourne, Australia for a study on animal personalities.

Time periods: Four-month minimum, commencing early September, or early January.

Duties include catching birds for personality testing before and after the breeding season (Oct-Jan), and regular censusing of colour-banded birds during the breeding season, searching for and monitoring nests, behavioural observations, video analysis, and data proofing. Working days are long, with early starts six days a week. Enthusiasm, self-motivation, and a strong work ethic are a must.

The study is based at Serendip Sanctuary, a small reserve with abundant birdlife on the outskirts of Melbourne.

Qualifications: experience monitoring colour-banded birds, nest-searching, and mist-netting. Must also be early riser, physically fit, able to work in extreme weather conditions, and enjoy basic shared living conditions.

Onsite accommodation in a house with shared dorm-style room is provided, but assistants cover travel to the site and their own food costs. The project will reimburse up to AU$750/mo towards receipted food and travel expenses.

For more information contact: Timon van Asten (t.van@unimelb.edu.au). To apply, please email a letter outlining previous relevant field research experience, and a resume including names and contact information for 3 referees that are familiar with your mist-netting and/or nest-searching experience.

"t.van@unimelb.edu.au" <t.van@unimelb.edu.au>

METU-IMS Turkey MarineEvolution

We are looking for excellent applicants from any areas involving aquatic sciences. Therefore, evolutionary scientists with relevant background would seriously be considered. Therefore, although our announcement does not directly aiming at evolutionary biologists, we hope to reach qualified candidates among evolutionary biologists.

METU-IMS is searching for new faculty members

Application deadline: July 05, 2017

Applications from all nationalities are invited for full-time tenure-track faculty positions in Middle East Technical University, Institute of Marine Sciences (METU-IMS). METU-IMS is the leading international marine science institute in Turkey with a 100% English education and research. All METU-IMS faculty engage in teaching, research and service towards the overall goal of sustainable of management of aquatic ecosystems based on excellent science. Faculty search involves all areas of marine and aquatic sciences, but in particular on four thematic areas:

. Physical oceanography with a strong emphasis on an empirical, seagoing field program that uses state of the art observational tools

. Aquatic microbial ecology to ecosystem ecology, including benthic and pelagic marine biology

. Marine renewable energy (offshore wind, wave), focusing on quantitative approaches

. Paleoceanography; focusing on marine and aquatic sediment archives

For the selected applicants a hiring procedure within the University and Turkish Higher Education Council will be initiated. During this period, the successful applicants are highly encouraged to apply to mobility funds such as TUBITAK 2232 Reintegration Grants (for Turkish citizens), Marie Sklodowska-Curie fellowships, and European Research Council Starting Grants. For consideration, the applicants have to satisfy the minimum requirements for recruitment at METU:

- A PhD degree, preferably obtained in USA or Europe
- If the PhD is from Turkey, at least one year of postdoctoral stay in a leading research institution abroad
- Proven ability of teaching in English

If interested, please forward a CV, contact information of three references and a two-page statement of research and teaching interest as a single pdf file to *faculty-search@ims.metu.edu.tr*.

For more information, please visit www.ims.metu.edu.tr – Korhan O:zkan Middle East Technical University - Orta Dod-u Teknik U:niversitesi Institute of Marine Sciences - Deniz Bilimleri Enstitu:su: Mersin, Turkey Tel: 0090 324 521 2406 (ext 1401) Fax: 0090 324 521 2327 (attn: K Ozkan) www.korhanozkan.org Korhan Ãzkan <korhan@ims.metu.edu.tr>

MuseumAKoenig 3 Biodiversity

The Zoological Research Museum A. Koenig, Germany, is looking for three scientists in Ecological Statistics, Metabarcoding and Comparative Morphology, respectively. All three positions are tenure -track positions. Please, see details below:

Position 1:

Vacant position for ecological statistics

The Zoologisches Forschungsmuseum Alexander Koenig, Leibniz-Institut für Biodiversität der Tiere (ZFMK) in Bonn, Germany, seeks to fill the position of a researcher (100%) for the statistical analysis of biodiversity data. The position is available immediately.

Potential candidates will hold a PhD in zoology or related areas, have their research focus on ecological biodiversity research, and present a substantial publication record. He/she should be able to design sampling campaigns, establish workflows for data analysis of species diversity in terrestrial habitats and supervise young researchers. We are especially interested in the development of biodiversity monitoring schemes. The candidate is also expected to integrate into ongoing research projects at the ZFMK and teaching programmes at the University of Bonn and to be successful in raising external funds. The successful candidate will be active in research projects relevant for nature and species conservation and will cooperate with the institute's team. He/she will also be involved in administrative duties for the institute. The candidate is also expected to demonstrate commitment to community engagement in his/her field of research.

We expect excellent communication skills with fluency in English and a working knowledge of German for the tenure.

The ZFMK is a Leibniz Institute in close cooperation with the University of Bonn and funded by the Federal State of NRW and the German Federal Government. We offer a highly motivating environment. Salary and benefits are according to a public service position in Germany (TV-L E 13). The ZFMK advocates gender equality. Women are therefore strongly encouraged to apply. Equally qualified severely handicapped candidates will be given preference. The contract will initially be restricted to three years. A tenured position will be subject to personal performance reviewed by a commission. An upgrade of salary and benefits to TV-L E 14 is possible and will be subject of the tenure evaluation. Please send your application by e-mail, including a detailed CV, a complete publication record, a statement of teaching experience, research funding, visions for future research, copies of certificates of university degrees and a maximum of 5 selected publications until 23 June 2017 to Mrs. Heike Lenz, (e-mail: h.lenz@leibniz-zfmk.de). For more information about the museum see http://www.zfmk.de . Position 2:

Vacant position for Metabarcoding

The Zoological Research Museum Alexander Koenig (ZFMK) is seeking a researcher for the analysis of metabarcoding data to work in the Metabarcoding Section headed by Dr. Vera Fonseca for a tenure-track position (100%). The position is available immediately.

Potential candidates will hold a PhD in Biology or related areas, have their research focus on metabarcoding research using Next Generation Sequencing tools, and present a substantial publication record in this field. He/she should be able to establish workflows for metadata analysis (assembly, binning, analysis) and should be proficient in processing amplicon high-throughput sequencing data (e.g. via QIIME, MICCA). The candidate should also be experienced in using programs for data visualization and manipulation of community ecology and taxonomic diversity (e.g. VeganR, MetacodeR and EstimateS). It would be desirable if the candidate could help design campaigns for the analysis of species diversity in environmental samples and supervise young researchers. The candidate is also expected to integrate into ongoing research projects at the ZFMK and teaching programs at the University of Bonn and to be successful in raising external funds. The successful candidate will be active in research projects relevant for nature and species conservation. He/she will also be involved in administrative duties for the institute. The candidate is also expected to be involved in outreach activities.

We expect excellent communication skills with fluency in English and a working knowledge of German for the tenure.

The ZFMK is a Leibniz Institute in close cooperation with the University of Bonn and funded by the Federal State of NRW and the German Federal Government. We offer a highly motivating environment. Salary and benefits are according to a public service position in Germany (TV-L E 13). The ZFMK advocates gender equality. Women are therefore strongly encouraged to apply. Equally qualified severely handicapped applicants will be given preference. The contract will initially be restricted to three years. A tenured position will be subject to personal performance reviewed by a commission. An upgrade

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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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NewMexicoStateU LabManager MosquitoPopGenet

The Hanley lab at New Mexico State University is searching for a Lab Manager for a lab and field-based study of mosquito abundance, distribution and population genetics in New Mexico. The person in this position will be responsible for: Oversee laboratory day-to-day operations; coordinate the setup, operation, maintenance, and troubleshooting of the program's equipment, instrumentation, and facilities; ensures compliance with environmental, safety, and infection control regulations and standards. Collect, analyze, and interpret data; prepare statistical and narrative reports and/or graphs; prepare manuscripts for publication; present research results to scientific conferences and other professional groups to include seminar presentations. Provide supervision, and leadership to undergraduate and graduate researchers engaged in the execution of research protocol and in the operations of scientific research equipment and technology.

Required qualifications include: Bachelor's degree in related field and five (5) years of professional experience related to duties as outlined. Preferred qualifications include: Master's degree in related field. Experience working with BSL2 laboratory. Experience conducting research under field conditions. Familiarity with the biology of arthropod-borne viruses. Experience in data stewardship and analysis. Experience with in oral and written scientific communication.

New Mexico State University is a land-grant, Hispanic-serving institution classified as Research University with High Research Activity by the Carnegie Foundation. It is located in the stunning high desert of New Mexico and offers a wealth of cultural events and outdoor adventures. It has an active and collegial group of researchers working in vector biology and disease evolution and ecology. Candidates from groups underrepresented in the sciences are strongly encouraged to apply.

Interested candidates should visit the position posting via the online application process at: http://jobs.nmsu.edu/postings/28094 Review of applications will begin on 05/05/2017 and will continue until the closing of the position posting 05/19/2017.

Dr. Kathryn A. Hanley Professor Department of Biology New Mexico State University Telephone: 575 646 4583 email: khanley@nmsu.edu website:http://biology-web.nmsu.edu/ ˜ hanley/ Kathy Hanley <khanley@nmsu.edu>

NHM London AvianCurator

The Natural History Museum is one of the world's leading museums, internationally recognised for its dual role as a centre of excellence in scientific research and as a leader in the presentation of natural history through exhibitions, public programmes, publications and the web.

Embedded within the Vertebrates Division of the Department of Life Sciences, the Senior Curator in Charge (SCiC) of Birds will lead and manage a curatorial team (currently three full-time and two half-time collections managers) ensuring best practice in collections care and providing a world-class collection of natural history specimens in ornithology. Bird specimens are to be acquired, curated and used and made available to facilitate research, teaching, training, reference and exhibitions. An expert in their field of collections-based science, the SCiC of Birds will demonstrate a high level of scientific scholarship (e.g. taxonomy, systematics, organismal biology). The SCiC of Birds will work with other SCiCs across the Vertebrates Division, and will line manage other Curators and Senior Curators within the Division. The SCiC of Birds is in turn line managed by and is expected to support the Principal Curator in Charge of Vertebrates. [A Band 3 appointment would be expected to lead strategic development of, and engagement with, the collections].

The NHM Bird collection is based at Tring, though the SCiC of Birds will be expected to work closely also with NHM staff at South Kensington. This is an exciting opportunity to lead and integrate ornithological curation and collections-based research in one of the World's largest and most important bird collections.

Salary: ????35,164 - ????42,420 (plus a 5% responsibility allowance). We may consider a higher salary for exceptional candidates

Contract: Permanent

Application Close Date: 9am on Friday 16 June 2017

Interviews expected: Week commencing 24 July 2017

For a full job description and to submit an application, please visit the Natural History Museum website.

Regards

Jan

Mr Jan Manthey

Resourcing Officer

The Natural History Museum, Cromwell Road, London, SW7 5BD

logo

Advancing the science of nature

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Jan Manthey <J.Manthey@nhm.ac.uk>

NHM London BioinformaticsManager

Job: Bioinformatics Manager Salary: 35,164 per annum plus benefits Contract: Fixed term, 23 months Closing date: 9am on Monday 5 June 2017

The Natural History Museum is one of the world's leading museums, internationally recognised for its dual role as a centre of excellence in scientific research and as a leader in the presentation of natural history through exhibitions, public programmes, publications and the web.

The Bioinformatics Manager will build and maintain the bioinformatics infrastructure to facilitate NHM research in molecular evolution and genomics, by curating sequencing data, by assessing, improving, and using bioinformatics processes, and by curating and communicating current best practice.

Additionally the post holder will work with external partners (e.g. Sanger Institute, EBI) in strengthening existing and emerging links.

The successful candidate will have a good knowledge of current bioinformatics procedures relevant to genome assembly, metagenomics, metabarcoding, and gene expression profiling, and familiarity with different sequencing platforms such as Illumina and MinION. A good understanding of Python, R and bash is a key requirement as well as having experience with Linux system administration With the ability to operate on multiple concurrent projects, with multiple concurrent collaborations, you will have experience of successful delivery of informatics projects.

Please complete your application online in our recruitment portal:

https://careers.nhm.ac.uk You should upload the following documents:

- A comprehensive curriculum vitae giving details of relevant achievements in recent posts as well as your education and professional qualifications. - A covering letter that summarises your interest in this post, providing evidence of your ability to match the criteria outlined in the Person Specification. Please ensure your letter includes details of your latest salary and notice period.

Mr Jan Manthey Resourcing Officer The Natural History Museum, Cromwell Road, London, SW7 5BD

Advancing the science of nature

Jan Manthey <J.Manthey@nhm.ac.uk>

NMFS US MuseumSpecialist

Hi All, Below is information about a great job opening (unfortunately only US citizens are eligible as it is a federal position) for someone interested in marine animals and research. You should be highly organized and hopefully have some experience with either invertebrates or fishes, preferably with collecting and museum experience.

Contact Allen with any questions, Good luck, Karen

Begin forwarded message:

From: "Collins, Allen" <COLLINSA@si.edu> Subject: Museum Specialist position opening Date: May 12, 2017 at 1:27:38 PM EDT To: NMNH-IZ-ALL <NMNH-IZ-ALL@si.edu

The NMFS National Systematics Lab is looking to fill a Museum Specialist position. Please share with anyone who might be interested. Thank you. –Allen

https://www.usajobs.gov/GetJob/ViewDetails/-469767700 https://www.usajobs.gov/GetJob/-ViewDetails/469767200 Dr. Allen G. Collins < http://invertebrates.si.edu/staff/collins.cfm > Zoologist & Director, NOAA's National Systematics Lab < http://www.nefsc.noaa.gov/nefsc/systematics > Allen.Collins@NOAA.gov

SMITHSONIAN INSTITUTION NATIONAL MUSEUM OF NATURAL HISTORY Dept of Invertebrate Zoology < http://invertebrates.si.edu/index.htm >, MRC-163 10th & Constitution Aves. NW Washington DC 20560 w 202.633.0645

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

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

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

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

PrincetonU LabTech Genomics

Research Specialist I Position Andolfatto Laboratory—Lewis-Sigler Institute for Integrative Genomics - Princeton University

The Andolfatto laboratory—at the—Lewis-Sigler Institute for Integrative Genomics seeks applicants for a research specialist position. Our group uses computational and experimental approaches to learn about genome evolution and elucidate the genetic mechanisms underlying evolutionary adaptations. Historically the lab has focused on Drosophila as a model system, but more recent work explores evolutionary/ecological genetics questions using a broad range of non-model organisms (e.g. butterflies and moths, freshwater fish, Milkweed-feeding insects, fireflies, amphibians and reptiles). We are looking for a highly motivated individual to carry out large-scale genomics projects and to support various lab activities. In addition to research, this—technician—will assist in training undergraduate students and be responsible for the day-to-day management of the lab, including maintaining equipment and the inventory of laboratory materials and supplies. The research—technician—may be responsible for the development and execution of research projects (which can lead to authorship on scientific publications).

The ideal candidate is one who seeks professional development as a scientist and is therefore interested in reading the current scientific literature and conducting an independent research project. The candidate will take ownership of their project. The position is open and review of applications will begin immediately. The position will start as soon as possible. Salary will be commensurate with experience and will include the full Princeton benefits package.— This is a one-year term position, with the possibility of renewal based on available funding and satisfactory performance.

Responsibilities will include: - Drosophila—maintenance, crossing, and screening. - Molecular biology including DNA/RNA preparation, PCR, qRT-PCR, next generation sequencing, plasmid vector construction, design of CRISPR- cas9 genome editing experiments. - Lab organization, maintenance, and purchasing. - Participation in group meetings.

Essential qualifications: - Bachelor's degree in biology or related field. - One to three years of experience in a research laboratory working with a (broadly-defined) "model" genetic system such as—Drosophila,—C. elegans, mouse,—Arabidopsis. - Experience with executing molecular biology protocols. - Capacity to work both independently and collaboratively. - Strong attention to detail and meticulous lab notebook keeping. - Excellent communication skills. - Enthusiasm for evolutionary biology and/or genetics. - The final candidate will be required to complete a background check successfully.

To apply, please submit an application online at Princeton University's Careers Website (Requisition No. 2017-7387) at: https://research-princeton.icims.com/jobs/-7387/research-specialist-i/job Princeton University is an—Equal Opportunity/Affirmative Action Employer and all qualified applicants will receive consideration for employment without regard to age, race, color, religion, sex, sexual orientation, gender identity or expression, national origin, disability status, protected veteran status, or any other characteristic protected by law.—EEO IS THE LAW

Laura Gallagher-Katz <lgallagh@Princeton.EDU>

RZSSWildGenesEdinburgh AppliedConservationGenetics

Research Scientist (Conservation Genetics) - (3 years Fixed Term)

Location: Edinburgh Zoo

About Us

The charity that owns both RZSS Edinburgh Zoo and RZSS Highland Wildlife Park - are looking for committed, compassionate and conservation-minded individuals to join our expert staff team.

RZSS aims to connect people with nature and safeguard species from extinction, a mission that sees us work both here in Scotland and in over 20 countries around the world. From inspiring the next generation about wildlife in our parks to protecting chimpanzees in the Ugandan rainforest; looking after some of the world's most endangered species to saving the Scottish wildcat, RZSS is making a huge difference and we need your help to continue to grow.

The role

Due to the expansion of our team, an opportunity has arisen for a committed researcher to join the Royal Zoological Society of Scotland WildGenes lab. Reporting to the Conservation Programme Manager - Wildgenes in our Conservation team, the successful candidate will initiate, implement and disseminate conservation genetics projects in the WildGenes laboratory. Duties include assisting with the project management and analysis of genetic data for a diverse portfolio of conservation genetic projects.

Who we are looking for

The successful candidate will have a PhD in Conservation Genetics or Population Genetics/Genomics, a proven track record of scientific publication, and a commitment to conservation. You will enjoy working at multiple levels, from complex data analysis to presenting results to a wide range of audiences. Since our projects are based across the globe, the role will involve international travel and willingness to travel to attend meetings is therefore essential.

Applicants with additional background in any of the following disciplines will be welcomed: Quantitative Genetics, Population Modelling, Bioinformatics, Project

Management within the conservation sector.

Closing date: Sunday 28 May 2017

Invitation to interview will be by email/phone and interviews will take place on the week commencing 19th June 2017. Due to the level of interest in these positions, we are not able to contact each unsuccessful applicant individually. Therefore, if you have not been contacted by the 12 June, please assume that you have been unsuccessful this time.

For any questions and queries, please email Dr Helen Senn at hsenn@rzss.org.uk quoting "Research Scientist" as the subject, or call 0131 314 0317.

How to apply

To apply for this role, please download the Research Scientist Role Profile < http://www.rzss.org.uk/-media/5375/cons-1709-research-scientist.pdf > (467kb pdf) and complete an Application Form < http://www.rzss.org.uk/media/5124/rzss-employment-application-form.docx > (1.89 MB Word Doc) and a Recruitment Monitoring Form < http://www.rzss.org.uk/-media/5139/rzss-recruitment-monitoring-form.docx > (1.91Mb Word Doc)

CV's are welcomed and should be submitted along with the Application Form.

Once completed you should email it to recruitment@rzss.org.uk

Applications may also be sent in the mail to:

The Royal Zoological Society of Scotland Edinburgh Zoo - HR Team 134 Corstorphine Road Edinburgh EH12 6TS

Dr Helen Senn WildGenes Programme Manager 0131 314 0317 hsenn@rzss.org.uk THE ROYAL ZOOLOGICAL SOCIETY OF SCOTLAND RZSS Edinburgh Zoo, Edinburgh EH12 6TS 0131 314 0300 rzss.org.uk < http:/-/www.rzss.org.uk/ > @RZSS < https://twitter.com/-rzss > /RZSSofficial < https://www.facebook.com/-RZSSofficial?ref=hl > REGISTERED CHARITY NUMBER: SC004064 [http://www.rzss.org.uk/downloads/-RZSS_brand_email_sig.jpg] < http://www.rzss.org.uk/ >

Helen Senn <HSenn@rzss.org.uk>

SGN Frankfurt Biodiversity

Job offer ref. #11-17015

The Senckenberg Gesellschaft für Naturforschung (SGN) is a member of the Leibniz Association and is based in Frankfurt am Main, Germany. SGN conducts natural history research with almost 800 employees and research institutions in six federal states. Within SGN, the Senckenberg Biodiversity and Climate Research Centre (BiK-F) explores the interactions between biodiversity, climate, and society. Senckenberg BiK-F invites applications for a

PhD position in Evolutionary Genomics of Mammals (50 %)

There is an exciting opportunity for a talented and motivated applicant to join the working group of Prof. Dr. Axel Janke. The applicant is expected to be closely involved in evolutionary, population or phylo-genetics to study speciation in mammals (bears, giraffe, kangaroos or allies) at the genomic level.

Your profile: - Master degree in Biology, Genetics, Bioinformatics or a related field - Strong interest and proven skills in evolutionary, population or phylo-genetics - Experience in analyzing genomic data - Very good written and oral communication skills in English - Interest to be involved in an international and interdisciplinary group to expand the work to species distribution modeling, paternal inference and conservation genetics

Salary and benefits are according to a full time public service position in Germany (TV-H E 13, 50%). The contract should start on October 1st, 2017 and will initially be limited until September 30th, 2020. The Senckenberg Biodiversity and Climate Research Centre supports equal opportunity of men and women and therefore strongly invites women to apply. Equally qualified handicapped applicants will be given preference. The place of employment is in Frankfurt am Main, Germany. The employer is the Senckenberg Gesellschaft für Naturforschung.

Please send your application, mentioning the reference of this job offer (ref. #11-17015) before June, 08th 2017 by e-mail (attachment in a single pdf document) and including a cover letter detailing research interests and experience, a detailed CV and a copy of your Master degree to:

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

For scientific enquiries please get in contact with Prof. Dr. Axel Janke, axel.janke@senckenberg.de

Mit freundlichen Grüßen /Best Regards

Jessica Helm Personalsachbearbeiterin

SENCKENBERG Gesellschaft für Naturforschung (Rechtsfähiger Verein gemäß Â§22 BGB) Senckenberganlage 25 60325 Frankfurt am Main

Besucheradresse: Voltastraße 1, 60486 Frankfurt am Main (5. Obergeschoss)

Telefon/Phone: 0049 (0)69 / 7542 -

Leiterin Personal & Soziales - 1458 Loke, Uta

Stellv. Leiterin Gruppe Personal & Soziales - 1319 Elsen, Carina

Mitarbeiter/in Personalbeschaffung (Recruiting) - 1313 di Biase, Maria - 1313 Helm, Jessica - 1478 Gajcevic, Isabel

Fax: 0049 (0)69 / 7542-1467 Mail: recruiting@senckenberg.de

Direktorium: Prof. Dr. Dr. h.c. Volker Mosbrugger, Prof. Dr. Andreas Mulch, Stephanie Schwedhelm, Prof. Dr. Katrin Böhning-Gaese, Prof. Dr. Uwe Fritz, Prof. Dr. Ingrid Kröncke Präsidentin: Dr. h. c. Beate Heraeus Aufsichtsbehörde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

Senckenberg forscht für Ihr Leben gern! www.200jahresenckenberg.de recruiting <recruiting@senckenberg.de>

SLU Sweden MolecularEcolEvol

JOB: Associate senior lecturer position in Molecular Ecology

The Department of Wildlife, Fish, and Environmental Studies at SLU, Sweden, is seeking to recruit an excellent molecular ecologist on a four year contract to further strengthen our competence in this expanding research area. We are seeking a motivated candidate with a broad background in the ecology of wild populations and established experience of genetic analyses in silico. The potential of the candidate to develop an independent research profile with the subject area will be evaluated, as well as the likelihood of attaining the requirements for promotion to senior lecturer within the allocated four years. More information about our department can be found at www.slu.se/wfe For more details about the position please go here.

For additional questions contact: Goran Spong Molecular Ecology Group Dept. of Fish, Wildlife, and Environmental Science SLU, 901 83 Umea, Sweden +46 730-350641 goran.spong@slu.se

Göran Spong <Goran.Spong@slu.se>

SouthAfrica StationManager StripedMouseProject

1 position as station manager at the striped mouse project in South Africa,

starting September 2017 for 1.5 - 3 years

We are looking for an extremely motivated and independent biology student with a master's degree to join the striped mouse project in August/September 2017 at least until November 2018 and for a maximum of 3 years as station manager. Somebody who would like to gain experience in field work and scientific management. Managers get free accommodation at the station and a compensation of R4500/month to cover their daily costs. Travel costs can be refunded by up to an additional R 12 000 / year. As such, the position compensates for all arising costs but does not represent a legal employment.

The station manager will work closely together with the research manager and both managers will share responsibilities. Each will have specific main duties, but should also be able to deal with all other duties (for example when the other manager is on leave, or when a new manager has to be trained).

We have an acting research manager while our present station manager will leave the project in November 2017 after 3 years. The new station manager will be instructed by the present station manager and both will overlap for 3 months.

Great opportunity: This is a great opportunity to spend 1-3 years in Africa, acquiring important skills in field biology and project management, while improving your CV. These skills will become valuable whether you later continue with a PhD or other jobs. It will be very hard and demanding, but also a once in a life time experience!

You must be hard-working, highly motivated, able to work independently, good in communicating with people, able to supervise others, and not afraid of snakes. You should love to live at a remote place in nature, without regular internet and cell-phone reception. Most importantly, you are fascinated by nature and science! The station manager must also have technical skills (respirometry laboratory) and be able to do some maintenance work at the research station (handy man skills).

Shared duties

We want to know at all time all striped mice present at the field site and their social tactic!

. Trapping

. Observing

. Radio-tracking, putting radio-collars on

. Blood sampling

. Collect data for specific research projects (to be determined. Examples would be collecting urine samples, data on basking, cognitive testing .)

Primary duties station manager / secondary duties research manager

. Technical support research station:

o Water system incl. sewage system

o Solar system

o Gas bottles replacement

o House and furniture

o Running of the respirometry laboratory

o Management of the captive colony

o Management of the research station car

o Management of bank account and cash box

o Management of research station supplies

Primary duties research manager / secondary duties station manager

. Data:

o Weekly data entry

o Weekly data check

o Monthly data backup

o Monthly data report

o Training and supervision of field assistants

o Training of students and postdocs

o Support for students and postdocs

o Management of transmitters

o Management of field and laboratory supplies

Job description: Five working days a week (Mo, Tue, Thu, Fr, Sat), with Wednesday being used for a shopping trip to town (not counted as working day) and Sundays being free. Included are four weeks of holiday for 12 months, which has to be taken outside the main breeding season (August to November) during periods when other students are present at the research station.

Compensation:

. Free accommodation.

* A monthly compensation of R 4 500, which is sufficient to pay all costs of living (approx. 3500/month). * For travel costs, R12 000 per year can be refunded, but proof (receipts) must be presented for this. This refund is only payable after 12 months. * You can become a honorary researcher at the University of the Witwatersrand in the group of Prof. N. Pillay. * Scientific co-authorship will be possible if the manager contributes to the success of projects by not only collecting the majority of data, but also by data analysis and writing of the manuscript.

Responsibilities:

. The manager has to cover the costs to get to the station, including travel costs and visa fees. For this, a refund can be paid (see above).

* The manager needs to arrange for a health insurance covering him / her during the stay. A copy must be sent to C. Schradin before travelling to the stations.

Place and project: Succulent Karoo Research Station in the Goegap Nature Reserve near Springbok in the Northern Cape of South Africa. The research projects are on the socio-ecology of small mammals, studying ecological and physiological reasons of social behaviour, behavioural flexibility, and physiological adaptation.

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Stockholm SeniorCuratorZoology

The Swedish Museum of Natural History is hiring a researcher for a position as Senior Curator at the Department of Zoology

The Department of Zoology was formed in spring 2013 after merging of the former departments of entomology, invertebrate zoology, and vertebrate zoology. At the department we curate large research collections of non-fossil animals which are continuously expanded and used by researchers at the museum as well as international researchers. Research at the Department of Zoology is focused on phylogenetics, evolution, biodiversity, morphology, taxonomy and biogeography in a range of animal groups.

We seek an excellent researcher with an independent research program in systematic zoology to strengthen research and collections at the Department, and contribute to outreach and higher education activities. The research must be collection-based, or otherwise beneficial for collection enrichment and enhancement.

Tasks: Conducting research at a high international level in systematic zoology; acquiring external research funding; publishing in high ranked international journals; presenting results of research at national and international conferences. Participating in enrichment and revising of the scientific collections. The position includes curatorial responsibilities for part of the collections. Supervising students at MSc and PhD level. Teaching at graduate (including doctoral) and undergraduate levels. Conveying scientific results to the public. Participating in other activities at the department and the museum.

Qualifications: A doctoral degree (PhD) in biology with a specialty in systematic zoology. Well-documented scientific outcome with papers in international journals. A proven record of external funding is highly desirable. Experience of teaching and supervision, as well as building and managing a research group, is qualifying. Experience from museum-based collection management and fieldwork is qualifying. Preference may be given to a qualified candidate specialized in an organism group in which we are currently lacking taxonomic expertise.

Proficiency in English, social skills, and excellent ability to cooperate are requirements.

The application (in English) should consist of a single PDF with the following items 1. Cover letter explaining your interest in the position. 2. Curriculum vitae, including all past and present academic career steps and employments. 3. Publication list including all published scientific papers 4. The five most important papers. 5. Description of experience in research and collection management. 6. Research plan within the announced position. 7. Name, affiliation and e-mail address of two references. 8. Other qualifications or information the applicant finds relevant for the present position.

The position is a full time permanent appointment with a six month probationary period.The Swedish Museum of Natural History can promote an employee to professor. Non-Swedish speaking employees are expected to learn Swedish. The Swedish museum of Natural History strives for gender balance and ethic and cultural diversity among its staff.

For more information (no applications), please contact Kjell Arne Johanson Head of the Department of Zoology (kjell.arne.johanson@nrm.se). Union representative is Emily Dock Ãkerman, SACO-S phone + 46 8 519 540 00.

The complete application must be submitted to rekrytering@nrm.se or the Swedish Museum of Natural History, P. O. Box 50007, SE-104 05 Stockholm, Sweden, no later than June 9, 2017. Mark your application dnr 2.3.1-270-2017.

Ulf Jondelius, PhD Professor of Invertebrate Zoology, Swedish Museum of Natural History ulf.jondelius@nrm.se

Ulf.Jondelius@nrm.se

TempleU DataAnalyst

Genomics and Evolutionary Data Analyst

Multiple positions are available for individuals with skills to assist in the application of standard research practices and bioinformatics techniques in genomics and evolution. Responsibilities include analysis of various types of sequence and related data, including high throughput data for empirical research. We require proficiency in (a) statistical or computational tools for molecular evolutionary analysis using genome scale sequence datasets AND (b) conducting data analysis, including the building of pipelines for data retrieval and analysis. Knowledge of principles of molecular evolution, population genetics, biomedical data, or next generation sequencing will be considered a plus. Successful candidates will solve variable problems, make complex decisions under general policies and specialized standards, and consider suggestions of project team members. Ultimately, they will serve as a technical resource and work in highly skilled team. Required qualifications include a Master's degree or Bachelor's degree with at least two years of experience in relevant data analysis and/or computer programming. Postdoctoral candidates will also be considered. Interested applicants should send a CV and cover letter detailing related experience to igem@temple.edu

Application will be reviewed on June 15, 2017 and July

30, 2017, and every month after that until the positions are filled. For any scientific or other questions, please write to s.kumar@temple.edu

Sudhir Kumar

www.kumarlab.net igem.temple.edu

"s.kumar@temple.edu" <s.kumar@temple.edu>

TempleU Phylogenomics

Research Faculty Positions (iGEM@Temple)

A multi-year research faculty position (non-tenure-track) is available in the Institute for Genomics and Evolutionary Medicine (iGEM) at Temple University in Philadelphia, USA. We are interested in early and mid-career scientists who integrate concepts, methods, and tools from evolutionary biology to address significant questions in Phylogenomics. Successful candidates will have a primary focus on one or more of the following: large scale analytics of sequences, big data phylogenetics, and development of methods and computational tools. They will be core faculty of iGEM @ Temple. They will work closely with and benefit from our expertise in molecular evolution, population genetics, phylogenomics, phylomedicine, and computational biology.

Applicants should submit their detailed curriculum vitae and a summary of current and future research interests by an e-mail to igem@temple.edu (send a single PDF file). Successful candidates will be provided salary support for an initial period and they will work closely with one or more of the current or future tenured faculty in iGEM (http://igem.temple.edu/people/core). They will be expected to develop a strong, extramurally funded, and collaborative research program. [Applicants interested in postdoctoral fellowships are also encouraged to apply.] For all questions, please contact Sudhir Kumar by email (s.kumar@temple.edu). Application will be reviewed on June 15, 2017 and July 30, 2017, and every month after that until the positions are filled.

Temple University located is in the heart of historic Philadelphia, and is the sixth largest provider of graduate school education in the USA. Situated in close proximity to New York City and Washington DC, Philadelphia is home to a large biotech industry and has many outstanding academic and research institutions.

Sudhir Kumar

s.kumar@temple.edu

Director, iGEM@Temple

Institute for Genomics and

Evolutionary Medicine

Carnell Professor, Biology

Temple University

1925 N. 12th Street

Philadelphia, PA 19122

"s.kumar@temple.edu" <s.kumar@temple.edu>

Toulouse CNRS ResAssit PlantEvol

JOB OFFER

Research Assistant

Plant experiments and survey in nature

*General informations *Lab: UMR5174 EDB Evolution and Biological Diversity

http://www.edb.ups-tlse.fr/Pujol-Benoit Place: Toulouse (31)

Publication: 19/05/2017 Type of contract: short term contract Duration of contract: 2 years Date of hiring wanted: 1st September 2017 Workload: Full-time Desired level of education: Bachelor's degree or higher Experience: 3 to 5 years Salary: approximately 2000 euro gross rate / 1700 euro net rate monthly (for experience of at least 3-5 years)

*Mission *The research assistant will be part of the EDB lab (Pujol's research group) and the ANGI ERC project. The objective of this project is to investigate the impact of non-genetic inheritance on the ability to adapt to environmental constraints of /Antirrhinum majus/ (Muflier), both in natural populations and through experiments in controlled conditions.

*activities *- Organization and realization of plant experiments in controlled conditions: Preparation, management, implementation and monitoring of the experiment, cultivation, controled crosses, morpho-physiological measurements and tissue sampling. - Organization and realization of population surveys in the wild: measuring phenotypic (vegetative and reproductive) traits and sampling tissues. Use of GPS equipment for localization. - Molecular biology work: DNA extraction, microsatellite markers PCR and genotyping. - Management and analysis of the data collected and preparation of reports and oral presentations of the activities and results, participation in the writing of scientific articles.

*skills *- General knowledge in evolutionary ecology and population genetics. - To master the tools for studying the biology of plant populations, the evolutionary ecology of natural plant populations and population genetics. - Knowledge of several techniques for collecting and analyzing data related to the study (statistics, morphometry, tissue sampling, molecular biology, GIS, computer tool, etc.). - adapt his/her activity to the project and manage the experiments (adapt the protocols according to the problems, operational knowledge of the rules and practices, draw up dashboards and files to follow-up the funding allocated, manage a team of students and specify the roles and objectives of each student).

*Context *The Lab Evolution & Diversité Biologique is a joint CNRS / ENSFEAE / IRD / Université Toulouse III Paul Sabatier research unit. A part of the work will be done outside the site of Paul Sabatier University on the experimental platforms available for the cultivation of plants under controlled conditions (CNRS experimental station at Moulis) and outdoors (monitoring populations near Peyriac de mer / Bages, in the region "Occitanie" and possibly North East of Spain), possibly in rough conditions. The recruited research assistant will be potentially associated with the devellopment and the management of the project as well as with the publication of the results obtained (under condition of involvement).

Please contact Benoit Pujol (benoit.pujol@univ-tlse3.fr) by sending a CV, a letter of motivation and contact details (email and phone) of two contacts for references. Deadline for application: 15/06/2017. An interview will be scheduled soon after this date for the selected applicants.

– *Benoit PUJOL* Researcher in evolutionary ecology at CNRS, France Quantitative genetics in the wild and non genetic inheritance

Lab. Evolution & Diversité Biologique (EDB) Office 104, Bat. 4R1, Université de Toulouse Paul Sabatier, 118 Route de Narbonne 31062 Toulouse Cedex 09 Mail: benoit.pujol@univ-tlse3.fr Follow me on twitter: @BenoitPujol

Benoit PUJOL <benoit.pujol@univ-tlse3.fr>

TulaneU ChairDeptEcolEvolBiol

Tulane University, School of Science and Engineering, Department of Ecology and Evolutionary Biology: Professor and Department Chair

The Dept. of Ecology & Evolutionary Biology at Tulane University invites applications and nominations for Professor and Department Chair. The ideal candidate must have a Ph.D., qualify for appointment as full professor, and possess outstanding interpersonal, leadership, entrepreneurial, and administrative skills and experience; and also have an internationally recognized research program supported by extramural funding, and be committed to mentoring department faculty and fostering effective research and education. Area of research expertise open within organismal biology (Ecology and/or Evolution), but ability to strengthen or compliment existing expertise and opportunities within the department is desirable. Term for chair is five years. Position includes competitive package of research and administrative support, and the opportunity to participate in at least one new tenured/tenure-track faculty hire. Consult following address for more information about the position and department:http://www2.tulane.edu/sse/eebio/about/positions/ To apply please submit the following tohttps://apply.interfolio.com/42158: (1) cover letter, (2) Curriculum Vitae, (3) statement of research accomplishments and future directions, (4) teaching statement, (5) statement of administrative experience and accomplishments, and (6) name and contact information (address, e-mail, phone) of four professional references. Review of applications will begin July 1, 2017 and search will remain open until the position is filled, with a start date of July 1, 2018. Tulane University is an Affirmative Action/Equal Employment Opportunity Employer.

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

ederrybe@tulane.edu

UArizona LabManager HostParasite

New Lab Manager position in the Schlenke Lab at the University of Arizona

Position summary: The Schlenke Lab studies host-parasite coevolution using Drosophila (fruit flies) as model hosts. We are developing parasitoid wasps, which lay their eggs in fly larvae and consume their hosts from the inside out, as model parasites. Flies mount cellular and behavioral defense responses against wasps, but wasps have adaptations for finding host fly larvae, suppressing host cellular immunity, and manipulating host behavior. We use a variety of "omics" tools to understand the molecular genetics of fly cellular immunity and wasp virulence, as well as patterns of host immunity and pathogen virulence coevolution across fly and wasp phylogenies. For more information, visit our lab website at: https://cals.arizona.edu/research/schlenke/ We are looking to hire a motivated, creative, and collaborative lab manager to keep the lab running smoothly. Our lab attempts to understand the fly-wasp interaction at multiple biological levels, and thus we are searching for a candidate with expertise (or the willingness to gain expertise) in multiple aspects of biology, such as in evolutionary ecology, genetics, molecular and cell biology, immunology, neurobiology, and/or bioinformatics. Our lab is based at the University of Arizona in the Department of Entomology and the position is available immediately. Feel free to contact Todd (schlenke@email.arizona.edu) with questions.

Duties and Responsibilities: The lab manager will oversee the day-to-day operations of the lab, including the inventorying and ordering of supplies, insect husbandry, and maintaining lab compliance with safety regulations. The lab manager will also be involved in multiple aspects of the lab's research program, from experimental design to data analysis. In coordination with Todd, the lab manager will assist and/or train other lab members including postdocs, graduate students, and undergraduates. The lab manager will regularly consult with Todd on a plan to enhance their professional growth and meet their future career goals.

Minimum qualifications: B.S. in a biological field. Good communication and critical thinking skills. Hands-on laboratory experience.

Preferred qualifications: M.S. or Ph.D. in a biological field. Lab management experience. Experience studying: Drosophila or other insects, host-parasite interactions, behavior, cell biology, cell culture, molecular biology techniques, microscopy, genetic mapping, genomics, statistics;

Salary: $36,000 - $39,000 annually (depending on experience)

Instructions: See the official ad at https://uacareers.com/postings/19063. To apply please submit (1) a cover letter with a brief description of how this position would match your background and your career goals, (2) a CV, and (3) a list of three people that we can contact as professional references. Todd Schlenke University of Arizona Entomology Department (520) 621-7167

Todd Schlenke <schlenke@email.arizona.edu>

UCalifornia Berkeley 2 LabManagerTech

https://hhmi-openhire.silkroad.com/epostings/index .cfm?fuseaction=app.jobInfo&version=2&jobid‘3

Job Summary

The Howard Hughes Medical Institute has an exciting opportunity for a career level Lab Manager to join the laboratory of Dr. Nicole King at the University of California, Berkeley.

The King laboratory studies choanoflagellates, the closest living relatives of animals, to reconstruct animal origins and investigate molecular mechanisms underlying host-microbe interactions. The job will consist of both laboratory management responsibilities and performing/assisting with experiments. We seek a highly motivated and exceptionally organized Lab Manager to assist in day-to-day lab operations, including budget management, lab facilities planning, overseeing equipment maintenance, ensuring adequate supplies for experimental needs, recommending improvements for lab processes, assisting Prof. King in personnel management, and managing lab safety programs to ensure compliance with all applicable regulations. The Lab Manager will also work at the bench, collaborating with current lab members on high priority scientific projects and exploring new, high-risk research topics.

Principal Responsibilities

- Provide a high level of lab support to Prof. King and research staff. - Manage day-to-day lab activities including the maintenance of essential equipment and software, ordering and maintaining adequate supply levels for routine experimental procedures - Monitor and maintain operational budgets.

- Develop supplier relations for contract negotiation. - Recruitment, hiring, and training of new employees. - Maintain databases for chemical, supply, and equipment inventories and other lab organization tools to maintain a highly organized, functioning lab. - Oversee management of laboratory collections of protocols, lab organisms, and reagents.

- Serve as a liaison between the lab, HHMI, and UC Berkeley administrative offices on issues as budget management, fixed asset inventories, purchasing, etc. - Enforce laboratory compliance with safety regulations and act as the main contact between campus safety and regulatory offices. - Perform other laboratory management duties as requested, including scheduling of lab events and organizing lab meetings. - Identify and implement improvements to lab organization, communication and general lab processes. - Perform experiments using cell culture, microscopy, genetics, and molecular biology techniques. - Assist in the development of new techniques. - Collaborate with lab members on research projects in the lab.

Knowledge/Understanding/Skills & Abilities

- Prior experience with choanoflagellates is not expected. Candidates with prior experience in cell culture and using sterile technique will likely have the necessary skills. - Candidate must be self-motivated, energetic, able to solve problems and work in a diverse laboratory environment. - Ability to supervise others. Excellent communication and interpersonal skills. Ability to work both independently and collaboratively on a team, build trust and lead teams as necessary. - In-depth knowledge in the biological sciences and general knowledge in the sciences. - Ability to review goals, analyze processes necessary to achieve those goals, and develop techniques and systems required to meet those goals. Initiative in exploring emerging technical and laboratory science and tools, and seeking opportunities to apply new knowledge. Ability to develop and troubleshoot new techniques. - Knowledge of safety and laboratory procedures. - Excellent organizational, time management, and decision-making skills. Ability to maintain a high level of accuracy. Excellent computer and record-keeping skills. Ability to handle multiple tasks or projects with competing deadlines. - Ability to initiate and compose communications for various purposes in an appropriate style. - The ideal candidate should be able to manage his or her own research project(s), plan and schedule short-to-intermediate term goals and schedule work to meet all goals. The appointed lab manager will review work with Prof. King at key stages, but will largely be self-directed.

Preferred Qualifications, Education and Experience

- Bachelor's degree in biology, chemistry, or a related field.

- Five or more years of lab experience, including at least one year of supervisory experience.

Please upload the following items when you apply:

- Cover letter - Resumé, emphasizing prior research experience - Contact information for three references

HHMI is an Equal Opportunity Employer Job Location Berkeley, California, United States Position Type Full-Time/Regular

Nicole King Investigator, Howard Hughes Medical Institute

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UCambridge Evolution

The Department of Zoology at the University of Cambridge, together with Sidney Sussex College, is seeking to recruit an outstanding evolutionary biologist to complement and extend our strengths in research and teaching. The successful candidate will have an excellent research record in evolutionary biology, and its interface with medicine, and will have a strong commitment to teaching.

We seek a candidate with the ambition and ability to develop a world-class research group. We shall be looking for an innovative research agenda that is well placed to benefit from the diverse interactions that are possible within our broadly interdisciplinary department, and from interactions with the wider University community. As well as giving lectures in the Department, the appointee will become a Fellow of Sidney Sussex College, with responsibility for Direction of Studies in Natural Sciences and providing small-group teaching in evolutionary biology to undergraduates.

For more details follow this link http://www.jobs.cam.ac.uk/job/13493/ Please get in contact if you have any questions

Chris Jiggins Professor of Evolutionary Biology (2014) Department of Zoology University of Cambridge Tel: (+44)(0)1223 769021 http://www.heliconius.org/ http://heliconius.zoo.cam.ac.uk/ @mel_rosina

Fellow of St John's College, Cambridge, UK. CB2 1TP

The Ecology and Evolution of Heliconius Butterflies Available through all good bookshops, or direct from Oxford University Press

Chris Jiggins <c.jiggins@zoo.cam.ac.uk>

UConnecticut Stamford EvolutionaryBiol

https://academicjobsonline.org/ajo/jobs/9162 The Department of Ecology and Evolutionary Biology at the University of Connecticut invites applications for an Assistant Professor in Residence appointment at the Stamford Campus, to begin August 2017. The Stamford campus's transition from a commuter to residential institution will be accompanied by a significant increase in enrollment. We seek a biology instructor whose teaching responsibilities will include introductory biology lecture and lab courses for majors and non-majors. Additional teaching may be assigned in other undergraduate courses that complement existing course offerings, e.g., General Ecology, Evolutionary Biology, and scientific writing. Faculty will also advise biology students. Service and pedagogy-related activities are highly encouraged.

The University of Connecticut is a top 20 public university whose Stamford campus is located in a vibrant downtown area, with proximity to restaurants, shopping, entertainment, and public transportation to destinations such as New York City. The small size of the campus (ca. 2,300 students) makes it attractive to students and instructors who want one-on-one interaction, small class sizes, and personalized attention. UConn-Stamford takes pride in its collegial environment, interdisciplinary collaboration, and small college atmosphere.

The University of Connecticut (UConn) is in the midst of a transformational period of growth supported by the $1.7B Next Generation Connecticut (http://nextgenct.uconn.edu/) and the $1B Bioscience Connecticut (http://biosciencect.uchc.edu/) investments and a bold new Academic Plan: Path to Excellence (http://issuu.com/uconnprovost/docs/academic-plan-single-hi-optimized_1).We are pleased to continue these investments by inviting applications for faculty positions in the Department of Ecology and Evolutionary Biology at the rank of Assistant Professor in Residence.

Minimum Qualifications PhD in Biology or a related discipline by the start date of employment. The candidate should demonstrate a strong commitment to high quality undergraduate education.

Preferred Qualifications Prior experience teaching Biology lecture/laboratory courses; background in ecology or evolution.

Appointment Terms This is a full-time, nine-month, non-tenure track position that will report to both the Head of the Ecology and Evolutionary Biology Department and the Director of the Stamford campus. This one-year contract may be renewed or lead to a multi-year contract in the future. This position does not lead to permanent academic tenure. The teaching load for these positions is seven 3-credit courses per year, or the equivalent. Salary will be commensurate with background, qualifications, and experience.

To Apply Select "Apply Now" to be redirected to Academic Jobs Online to complete your application. Please submit the following: a cover letter, curriculum vitae, teaching statement, teaching evaluation, and the names and contact information for three references. Letters of reference will be sought for interviewed applicants. Review of applications will begin immediately. For full consideration, online applications should be received no later than June 7, 2017. Employment of the successful candidate will be contingent upon the successful completion of a pre-employment criminal background check. (Search # 2017525)

All employees are subject to adherence to the State Code of Ethics which may be found at http://www.ct.gov/ethics/site/default.asp . Carl Schlichting Professor & Head Ecology & Evolutionary Biology University of Connecticut (860) 486-4056 http://eeb.uconn.edu/ "Schlichting, Carl" <schlicht@uconn.edu>

UGuam LabManager

We are looking for a lab manager to work with us at the Marine Lab at the University of Guam (see attached job description). We are a diverse team of researchers, using ecological, genomic and oceanographic approaches to study the coral reefs around Guam and across Micronesia. We are looking for someone with excellent organizational skills who will support us in running our molecular and chemistry labs smoothly and in compliance with safety regulations. Ideally, the future lab manager would also be able work with us in the field (i.e. snorkel and dive) and provide support for our flow-through seawater systems.

Please forward to anyone who might be interested and share generously. I would be happy to discuss further details with anybody interested in the position at combosch-AT-triton.uog.edu or alternatively contact the University of Guam Human Resources Office at (671)735-2350 or email at uoghro@triton.uog.edu.

The deadline for applications is Monday May 15th Guam time, i.e. Sunday 14th most everywhere else.

Cheers, David

https://uog.peopleadmin.com/postings/987 David J. Combosch, Ph.D Assistant Professor University of Guam Marine Laboratory UOG Station, Mangilao, Guam 96923 USA https://www.researchgate.net/-profile/David_Combosch "comboschd@triton.uog.edu" <comboschd@triton.uog.edu>

Uliverpool Fieldtech FrenchPolynesia

We are looking for a research field technician to assist on a project that is investigating a recent evolutionary event - the rescue of male Hypolimnas bolina butterfly embryos from Wolbachia-induced male-killer activity. Normally, female butterflies infected with a male-killing strain of Wolbachia are only able to produce female offspring. H. bolina has evolved the ability to rescue male embryos, so that infected females are able to produce both male and female offspring. This project aims to understand the genetic basis of this suppressor trait and to assess the impact that Wolbachia infection and suppression have on the fitness of butterflies.

The position is tenable for 5 months, commencing in June 2017 and will primarily be based in French Polynesia. The main responsibilities of the role will be to assist a post-doctoral research associate with breeding large butterfly pedigrees. You will assist with all aspects of maintaining butterfly stocks e.g. collecting caterpillar food, feeding and cleaning out caterpillars, feeding butterflies. You will also assist with performing a series of behavioural and fitness assays, storage of biological samples, data recording, molecular biology work e.g. DNA extraction, PCR, and other duties that may also arise.

We are looking for someone who is experienced at insect handling, and with previous experience of rearing insects and performing experiments involving insects. The nature of the work will mean that you must be happy to work outdoors in different weather conditions, and be prepared to work flexible hours, depending upon the stage of the experiment. The candidate will need to hold at least a BTEC National level qualification or its equivalent and be in possession of a full drivers licence. Previous experience of overseas fieldwork is desirable as are French language skills.

This position requires the right to the work in the UK, and is not eligible for a visa.

For a full job description and to apply for this post please visit: 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_id=007128# The deadline for applications is Tuesday 9th May. Interviews will take place the week beginning the 15th May.

Louise Reynolds Post-Doctoral Research Associate Department of Evolution, Ecology and Behaviour Institute of Integrative Biology University of Liverpool Crown Street Liverpool L69 7ZB

"Reynolds, Louise" <Louise.Reynolds@liverpool.ac.uk>

UManchester EvolutionaryBiology

The University of Manchester is seeking applicants for the Dame Kathleen Ollerenshaw Research Fellowship. The fellowship will last for 5 years with the opportunity to achieve full academic tenure upon completion. The fellowship are aimed at early career researchers. Apponited fellows will normally have no more than 5 years of post-PhD research experience, but exceptions are detailed in the full announcement at:

http://www.jobs.ac.uk/job/AYQ109/dame-kathleen-ollerenshaw-research-fellowships/ Fellowships are available to researchers in any field of Science and Engineering, but members of the new Evolution and Ecology group in the School of Earth and Environmental Science are eager to see an appointment in our field. We strongly encourage applicants who have identified substantial and significant research challenges in any area of evolutionary biology, ecology, or conservation science.

Formal applications should be made according to the instructions in the full announcement. The deadline for the initial phase of the application process is 22 May 2017.

Tucker Gilman tucker.gilman@manchester.ac.uk

UmeU EvolutionaryEcologicalGenetics

The Department of Ecology and Environmental Science at UmeÃ¥ University, Sweden, invites applicants for a research fellow (assistant professor) position in Evolutionary and Ecological Genetics funded by the Faculty of Science and Technology. The start date is September 1st, 2017 or upon agreement. Apply before June 30, 2017.

We seek a biologist with strong theoretical and practical research experience in evolutionary or ecological genetics. The successful candidate is expected to establish a competitive independent line of research within population genetics or evolutionary genomics. The research may focus on how patterns of genetic diversity in space and time are shaped by selective and neutral processes, and how these in turn influence long-term ecosystem dynamics.

The position is primarily research-oriented, with the possibility of teaching (10-15 %) in undergraduate and Master's level courses involving genetics and evolution. Therefore, interest for, and experience with, university-level teaching and supervision is a merit.

To be eligible for a position as Assistant professor you must have a doctoral degree or equivalent research expertise. Priority shall be given to applicants who have obtained their doctoral degree or achieved equivalent competence at most seven years prior to the end of the application period. Area of expertise should be in ecology with a focus on evolutionary and ecological genetics. Postdoctoral experience is a merit, and the candidate should preferably have: -A strong background in population genetics and evolutionary genomics, and experience with theoretical, computational and empirical approaches. -Demonstrated competence in bioinformatics and genomic analyses. -The ability, or potential, to establish a competitive research program, as documented by external funding, publications, and plans for future research. -Experience with teaching and supervision.

The application should include: -A short cover letter (max 2 pages) describing why you are interested in the position -CV, including information about external funding and of teaching activities -List of publications -Research plan, describing current and future research concepts (max 3 pages) -Copy of PhD degree -Digital copies of PhD thesis and up to five selected publications -Contact information to three reference persons. Your application must be registered in UmeÃ¥ University's e-recruitment system MyNetworkPro/Varbi no later than June 30, 2017.

Assessment of applicants will primarily consider their documented scientific production and other research achievements, as well as their teaching experience. Collaboration and outreach qualifications of applicants will also be considered.

The successful applicant of this call will be placed at the Department of Ecology and Environment Science at the level of Assistant Professor, full-time and time limited for 4 years. Starting date is September 1st, 2017 or as otherwise agreed.

Questions about this employment are answered by: Tom Korsman, Head of Department: tom.korsman@umu.se Jon Moen, deputy Head of Department: jon.moen@umu.se

URL to the e-recruitment system: http://www.umu.se/-english/about-umu/open-positions?languageId=1 "folmer.bokma@umu.se" <folmer.bokma@umu.se>

UNAM Mexico EvolutionaryEcol

... we mentioned that we want a chemical ecologist that uses -omic approaches (metabolomics, proteomics and genomics). I hope this broken the scope to included chemical ecologist with evolutionary interests as potential candidates.

Best regards, Juan

Instituto de EcologÃa

2017

The Universidad Nacional Autonoma de Mexico (UNAM) invites applications to fill a tenure-track Assistant Professor position at the Departamento de EcologÃa Funcional, Instituto de EcologÃa.

Located in the main campus of UNAM to the South of Mexico City, the Institute of Ecology (http://web.ecologia.unam.mx/) harbours 40 researchers grouped in four Departments: Evolutionary Ecology, Functional Ecology, Ecology of Biodiversity, and the National Laboratory for Sustainability Sciences. It is a leading Ecology Institute in Mexico, and has strong links with similar Institutes both within Mexico and abroad.

We are searching for an independent researcher in Chemical Ecology with expertise in "omic" approaches, willing to join the Department of Functional Ecology and to collaborate with the members of the Institute in general (Departments of Evolutionary, Functional and Biodiversity Ecology, and of Sustainability) on Chemical Ecology sensu lato.

The successful candidate will be required to develop an independent research program in Chemical Ecology. It will be expected that she/he develops collaborations, primarily but not exclusively with members of the Departamento de EcologÃa Funcional. Lecturing regularly at undergraduate and graduate programmes is compulsory.

Candidates should hold a PhD degree, or equivalent, on Chemistry, Biology or Ecology, and be competent in the use of -omics approaches for the study of chemical ecology in plants. A strong publication record (> 20 high-impact peer-reviewed papers in the relevant area), a track record of securing competitive funds, and demonstrable experience teaching and supervising students. Ability to teach in Spanish is expected.

Selection will be based 1) on the strength of the candidate's CV, 2) on a written research proposal (only the outline is needed) combining the study of chemical ecology with -omics tools to help understanding the responses of organisms to interactions with the biotic and abiotic environment, and 3) on the merits of a work program specifying the research (including collaborations with local colleagues), teaching and supervision activities to be conducted in the following three years.

The application should include a letter addressed to the director of the Institute, Dr. Constantino MacÃas Garcia stating the candidate's reasons to apply, Curriculum vitae, a brief description of current and future research interests, the proposal and work plan specified above, a copy of the PhD title, 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 theses supervision).

All documents should be sent electronically as a single PDF file to secacad@iecologia.unam.mx and avargas@ecologia.unam.mx. The closing date is May 19^th, 2017. Shortlisted candidates will be required to send the documents by post to: Instituto de EcologÃa, UNAM, Ap. Postal 70-275, Ciudad Universitaria, Ciudad de Mexico, CP 04510, Mexico.

Dr. Juan Fornoni

Secretario Academico

Instituto de EcologÃa, UNAM

Juan Enrique Fornoni Agnelli <jfornoni@iecologia.unam.mx>

Uppsala AdvancedNatlBioinformaticsSupport

1-2 positions providing advanced bioinformatics support, located at the SciLifeLab Bioinformatics Platform, Uppsala, Sweden.

Science for Life Laboratory (SciLifeLab, www.scilifelab.se) in Sweden serves as a national infrastructure to support advanced high-throughput life science research, and is currently one of the fastest-growing life science research establishments in Europe. The SciLifeLab bioinformatics platform (www.nbis.se) is a national infrastructure in rapid development, now looking for a 1-2 staff members to join the Bioinformatics Long-term Support team (WABI), placed in Uppsala. The Bioinformatics Long-term Support team provides advanced bioinformatics analyses to some of the most scientifically exciting projects across Sweden, and with 24 full-time senior bioinformaticians, the team is one of the strongest units for analysis of large-scale genomics and integrative omics in Sweden.

Please note the short application time, we are looking forward to your application at the latest May 10, 2017 http://www.uu.se/en/about-uu/join-us/details/?positionId=3D149000 Björn Nystedt, bjorn.nystedt@scilifelab.se Pär Engström, par.engstrom@scilifelab.se Joint Heads of SciLifeLab Bioinformatics Long-term Support

http://www.nbis.se/support/longtermsupport.html http://www.scilifelab.se/platforms/bioinformatics/ Bjorn Nystedt, PhD Manager, SciLifeLab Bioinformatics Long-term Support (WABI) www.scilifelab.se/-facilities/wabi/ BMC E10:3206, entrance C11 Husargatan 3, SE-752 37 Uppsala

Phone: 018 - 471 4413 E-mail: bjorn.nystedt@scilifelab.se

bjorn.nystedt@scilifelab.se

UppsalaU EvolutionaryFunctionalGenomics

Tenure track position as Assistant Professor in Plant Evolutionary Functional Genomics at Uppsala University

Department of Ecology and Genetics, program in plant ecology and evolution, Evolutionary Biology Centre.

Description of Subject Area: Evolutionary Functional Genomics with specialization in plants involve molecular analyses to understand evolutionary and ecological processes underlying the generation and maintenance of biological diversity among plants. The subject area includes functional studies of variation at the molecular level as well as analysis and interpretation of large-scale omics-data to understand biological function, evolution of diversity, and adaptation of plants to the abiotic and biotic environment.

The position is for four years and can then be tenured - an associate senior lecturer (the Swedish term for Assistant Professor) has the right to apply for promotion to senior lecturer. If the associate senior lecturer is deemed suitable and fulfills the criteria for promotion established by the Faculty Board he/she shall be promoted to and employed permanently as senior lecturer. At a subsequent step, an application for promotion to full professor can be made.

According to the Swedish Higher Education Ordinance those qualified for appointment as associate senior lecturer are persons who have obtained a doctoral degree or achieved the equivalent competence. Priority is given to those how obtained their degree no more than seven years prior to the end of the application period.

Uppsala University is an international research university focused on the development of science and education, and the Evolutionary Biology Centre is an internationally very strong environment within the evolutionary biology field.

The position is part of the SciLifeLab Fellow program 2017-2021 and comes with a core funding of three million SEK per year for four years. SciLifeLab (www.scilifelab.se) is a national centre for large-scale hypothesis driven research within molecular bioscience.

You are welcome to submit your application no later than 2017-05-29, UFV-PA 2017/1353.â euro Â Further information is available through this link: http://www.uu.se/en/about-uu/join-us/details/-?positionId=147856# Ulf.Lagercrantz@ebc.uu.se

UppsalaU Sex-specSelec

The Department of Ecology and Genetics is seeking to appoint an assistant professor in sex-specific selection. The employment is for four years and is intended to qualify the holder (a promising early-career scientist) for a teaching position with higher qualification requirements.

Description of Subject Area: World-leading research in the interface of ecology, evolution and genomics is conducted in the Department of Ecology and Genetics at Uppsala University. One area of strength is genomic research geared towards evolutionary processes such as speciation, local adaptation and evolution of fitness traits. In this context, the understanding of evolutionary processes behind phenotypic differences between sexes, and the molecular genetic basis to such differences, are important aspects. Combining genetic and genomic techniques, such as the use of line crosses and RNA sequencing, in an experimental setting provides a unique opportunity to examine the phenotypic and molecular targets of sex-specific selection.

Applicants who have obtained a doctoral degree or achieved the equivalent competence in seven years or less prior to the end of the application period will be given priority.

The ranking of eligible applicants will be based primarily on research expertise. Research expertise comprises research merits as well as the applicantÂs potential to contribute to the future development of both research and teaching. In assessing research expertise special weight will be given to candidates with merits that combine experimental work with genetic and genomic analyses (including RNA seq and other molecular techniques) to address causes and consequences of sex differences.

Appointment period: The position can be held for a maximum of four years.

For further information about the position, please contact Professor Hans Ellegren, e-mail: Hans.Ellegren@ebc.uu.se

You are welcome to submit your application no later than 28 May, 2017, UFV-PA 2017/1555. Applications are only accepted through the University job application system at http://uu.se/en/about-uu/join-us/details/?positionId=150990 Hans Ellegren <hans.ellegren@ebc.uu.se>

UStockholm FunctionalAnimalMorphology

Associate Professor in Functional Animal Morphology

at the Department of Zoology, Stockholm University. Closing date: 8 June 2017.

The advertised position in Functional animal morphology will be affiliated to the Division of Functional morphology that has a long tradition of research in neuroscience, endocrinology, reproductive biology, and also more recently insect sensory physiology and behavior, as well as genomics and evolution of life history traits of insects. Research in Evodevo also falls under this division.

At present the organisms under study are insects, including Drosophila, the water flea Daphnia, several butterfly species and fish, for all of which rearing facilities are available. Access to state of the art imaging equipment, as well as genomics and bioinformatics resources are provided by affiliated core facilities. Researchers at the division actively collaborate with scientists at several of the other divisions in the Department in projects such as "Insect life cycle genomics and adaptations in the wild" and "Insect - host plant interactions".

The Department of Zoology has a long history of basic and applied research on animals ranging from insects to large mammals, at five divisions: Ecology, Ethology, Population genetics, Functional morphology and Systematics and evolution. The Department holds a staff of around 100 employees, of which 16 are permanent Lecturers/Professors and 40 PhD students. The Department keeps a research station (Tovetorp) south of Stockholm with facilities for various field- and laboratory experiments.

Subject/subject description Experimental zoological organism biology with focus on physiology and morphology.

Main responsibilities Research, supervision and teaching. The teaching is primarily in animal diversity, comparative anatomy and physiology.

Qualification requirements In order to qualify for employment as associate professor, the applicant must have demonstrated good teaching skills and have a doctoral degree, or equivalent research expertise, of relevance to the subject area and the main responsibilities of the position.

All teaching positions at Stockholm University require the ability to collaborate and the general ability and suitability to perform one's duties.

Assessment criteria In the appointment process, special attention will be given to research and teaching skills. The assessment of research skills will focus primarily on merits within the subject area of the position.

In the case of otherwise similar qualifications, the following criteria will be used to distinguish between candidates:

§Documented teaching proficiency regarding teaching in Animal diversity, comparative anatomy and physiology.

Teaching and learning in higher education Completed training in teaching and learning in higher education, or equivalent knowledge, is an advantage. An applicant who has not completed at least 15 credits of teaching and learning in higher education and is not considered to have otherwise acquired equivalent knowledge should undergo such training within the first two years of employment.

Additional information Female applicants are particularly welcome, as most associate professors at the department are men. The Faculty's criteria for assessment of research and teaching skills: www.science.su.se The language of instruction in first-year courses and programmes is Swedish. If the successful candidate does not speak Swedish at the time of appointment, he/she is expected to acquire the necessary language skills during the first two years of employment.

Stockholm University strives to be a workplace free from discrimination and with equal opportunities for all.

Ref. No. SU FV-0806-17

Contact Further information about the position can be obtained from the Head of the Department, Professor Birgitta Tullberg, telephone: +46 8 16 40 36, birgitta.tullberg@zoologi.su.se or professor Dick Nässel, telephone: +46 8 16 40 77, dick.nassel@zoologi.su.se.

For questions regarding the application process, please contact administrator Mikael Stenberg, telephone: +46 8 16 20 86, mikael.stenberg@su.se.

Union representatives Anqi Lindblom-Ahlm (Saco-S) and Lisbeth Häggberg (Fackförbundet ST and Lärarförbundet), telephone: +46 8 16 20 00 (operator), and seko@seko.su.se (SEKO).

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

We would appreciate it if your application is written in English. Since it will be examined by international experts, English is the working language.

The University's rules of employment and instructions for applicants are available at: Instructions - Applicants.

You are welcome to apply!

Closing date: 08/06/2017

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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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WSL Birmensdorf Head ForestBioticInteractions

See job posting online and find link for uploading your application: https://apply.refline.ch/273855/0704/pub/2/index.html The Swiss Federal Institute for Forest, Snow and Landscape Research WSL is a part of the ETH domain. Approximately 500 people work on the sustainable use and protection of the environment and on the handling of natural hazards.

The newly established research unit Forest Health and Biotic Interactions focuses on research in forest entomology and pathology and provides diagnostic and advisory services on forest pests and diseases. As a core infrastructure, the unit operates the plant protection laboratory of WSL, which harbours state-of-the-art biosafety class 2 and 3 laboratories including a corresponding green house. The directorate of WSL wishes to fill in the new position of a

HEAD OF RESEARCH UNIT FOREST HEALTH AND BIOTIC INTERACTION

As a researcher with an international reputation, you will manage the research unit in cooperation with the group leaders. You will run your own research projects, but also support and coordinate research activities within the unit. You are expected to successfully apply for third party funding and promote research cooperation within WSL and at national and international levels. You are motivated not only to foster research in the unique plant protection and biosafety laboratory of WSL, but to also support ecological studies on biotic interactions in forest ecosystems. Likewise, you promote the important consulting and outreach activities of this unit.

You are at an advanced stage of your scientific career with several years of independent research in entomology or plant pathology, preferentially in the field of forest health or biological invasions. You have experience in managing research groups and/or in leading interdisciplinary research projects. Furthermore, you possess a proven record in successful grant applications, an excellent publication list and an established international network in your field of excellence. You have an integrative personality with negotiating skills and, preferentially, a good command of one of the Swiss national languages.

Please send your detailed application online to Stefania Pe, Human Resources WSL. Prof. Dr. Konrad Steffen, Director WSL, Tel. +41 (044) 739 24 55, will be happy to answer any questions or to offer further information. The WSL strives to increase the proportion of women in its employment, which is why qualified women are particularly called upon to apply for this position.

"felix.gugerli@wsl.ch" <felix.gugerli@wsl.ch>

Other

Apply For PhylotasticHackathon Aug8-11

Dear evoldir communityâ euro “

We invite interested scientists, programmers and educators to apply for a 4-day hackathon centered on leveraging resources of the Phylotastic project, including its graphical web portal, its suite of web services, and its toolbox code.

An implicit promise of the Tree of Life project is that, ultimately, expert knowledge of species phylogeny will be accessible and usable by everyone. The Phylotastic project (http://www.phylotastic.org) aims to meet this challenge with a sustainable ecosystem of open web services providing access to dispersed resources covering the tree of life and related knowledge of taxonomy, characters, and biodiversity. The system includes over 20 web services for operations such as reconciling names, managing lists of taxa, getting trees, finding images, and so on. Workflows based on these services can be invoked with toolbox code in various programming languages. The Phylotastic web portal (access via http://www.phylotastic.org) illustrates on-the-fly delivery of species trees based on web services that extract taxon names from electronic sources, find topologies from available supertrees, scale them by time, harvest images and other data, and render the results graphically. This tool is suitable for use in developing lesson plans about phylogeny for students in both K-12 and in universities.

The purpose of the hackathon, which will take place August 8 to 11, 2017 at NIMBioS (Knoxville, TN), is to stimulate further developments that add to this system or leverage it to support research, education, or public appreciation of science. The targets of the hackathon are not determined in advance: projects and teams will emerge in a bottom-up participatory process. Examples of suitable projects would be to embed Phylotastic functionality into existing tools (e.g., tree-viewers, apps of any kind that generate or use taxon lists), to build new clients (e.g., phylogeny-learning games, tools to populate EOL taxon pages with trees), to develop classroom exercises, and so on. We welcome big-picture ideas like developing a system to gather, cross-map and disseminate phyloreferences, or using available tools to evaluate robustness and coverage of OpenTree's resources.

Whether you are a researcher, a curator, an educator, or something else, we encourage you to apply for participation: our goal is a collaborative environment welcoming the contributions of all. Support for airfare, lodging and meals will be provided. To apply, use the online form at http://bit.ly/2qAXuDk to provide brief descriptions of your ideas, your skills and your domain knowledge. Members of underrepresented groups are especially encouraged to apply. Further information is available at http://bit.ly/2qMyMSc. Applications are due June 16, 2017.

We encourage pre-application questions, which may be directed to Arlin Stoltzfus (arlin@umd.edu), Enrico Pontelli (epontell@cs.nmsu.edu), Brian O'Meara (bomeara@utk.edu) or Dmitry Mozzherin (dmozzherin@gmail.com).

Arlin Stoltzfus (arlin@umd.edu) Research Biologist, NIST; Fellow, IBBR; Adj. Assoc. Prof., UMCP IBBR, 9600 Gudelsky Drive, Rockville, MD, 20850 tel: 240 314 6208; web: www.molevol.org Arlin Stoltzfus <arlin@ibbr.umd.edu>

EquatorialGuinea VolResAssist Biodiversity

Job Title: Monkey & Sea Turtle Research Assistant

Job Type: Volunteer Position

Opportunity location: Bioko Island, Equatorial Guinea, Africa

Start date: November 2017; 5 months commitment.

Closing date: 31 August 2017

Opportunity Description:

The Bioko Biodiversity Protection Program (BBPP) is seeking volunteers to assist with data collection primarily on the ecology of primates and nesting sea turtles in our two research camps on the southern beaches of Bioko Island, Equatorial Guinea. BBPP will engage field assistants for a period of 5 months during the upcoming dry season, beginning in November and lasting through March. Field assistants are expected to devote at least 40 hrs/week to the project, but due to the nature of the project and living conditions, hours will likely be considerably more.

Field assistants work under the supervision of BBPP Research Camp Managers, Drexel & UNGE Researchers, the BBPP In-Country Manager, and Dr. Mary Katherine Gonder (BBPP Director). They are encouraged to participate in all aspects of field research during their stay on Bioko Island and may explore additional opportunities to participate in educational outreach projects with local school children as well as training exercises with local wildlife patrols.

Primary research activities include tagging nesting sea turtles, gathering reproductive output data on leatherback and green turtles, conducting large mammal biomonitoring surveys, and fecal collection for microbiome analyses. Turtle surveys are conducted every night until 5 am. Assistants will walk an average of 10 km/night while patrolling the beaches. Primate surveys will be conducted during the day for 2 weeks each month along established BBPP transects together with a trained team of local survey workers. Sampling of primate and other mammal feces will also be conducted during the day, but will occur off-trail with the use of a handheld GPS unit. Participation in other research projects are possible and encouraged.

Due to accessibility, tourism, hunting and other factors, the dynamics differ between the two field camps. Volunteers working at Moaba, located 5km from the nearest road, will participate mostly in the following activities: aiding in the facilitation of short-term ecotourism visits to research camps as part of a small-scale, locally lead ecotourism initiative; monitoring nesting beaches nightly as part of BBPP's marine turtle research program; and aiding park management authorities in conservation activities and monitoring. Conversely, Moraka is located 13km from the nearest road and is visited less frequently. Volunteers at Moraka will focus their efforts on marine turtle monitoring research, primate surveys, and sample collections. However, assisting in all aspects of the project is possible throughout the season.

Our field sites are in remote areas with no road access. Researchers and field assistants must hike in and out of the field site(s) when necessary along extremely rough terrain. Researchers and field assistants will be living in tents, cooking over fire, and using water from nearby streams. Field assistants are also required to participate in daily upkeep and maintenance of the camp, including preparation of meals. The diet is very limited due to lack of electricity/refrigerators. There is no internet connection, but cell service is available yet unreliable. A satellite phone will be available in case of an emergency. The camp does have generators to charge research equipment, which may be used for occasional personal items.

This is an unpaid (volunteer) position. However, BBPP will provide housing (tents), food and local transportation. You are expected to provide international transportation to and from Malabo, Equatorial Guinea (Â± $2000 for a round trip flight from US), medical and evacuation insurance, appropriate immunizations (yellow fever) and medications (anti-malarial medications). Non-US citizens will need to apply for a visa to enter Equatorial Guinea. We will try to obtain a letter of invitation through the local university in Malabo but cannot guarantee a visa.

Qualifications:

- Field assistants are expected to be at least 21 years old.

- Field assistants are REQUIRED to have:

- B.A. or B.S. in biology, ecology, environmental science, or related disciplines

- Spanish language proficiency

o Spanish is the national language of Equatorial Guinea.

- Prior field experience in biology, ecology, environmental science, or related disciplines.

- Physical fitness and a positive attitude towards physically exhausting work in a hot and humid climate. All assistants should be prepared for very demanding and time consuming work.

- Preference will be given to applicants who have experience in remote locations in developing countries and experience camping and hiking in wilderness areas.

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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

Evolution VideoContest Deadline 2

DEADLINE ALMOST HERE!!! 2017 Evolution Film Festival/Video Contest

This is it folks; the final push! You have just over a week to submit your video to the Seventh Annual Evolution Video Competition, sponsored by the Duke Initiative for Science & Society, the Howard Hughes Medical Institute (HHMI), the Society for the Study of Evolution (SSE) and the BEACON Center for the Study of Evolution in Action.

To enter, please submit a video that explains a fun fact, key concept, compelling question, or exciting area of evolution research in THREE MINUTES OR LESS.

Entries may be related or unrelated to your own research, and should be suitable for use in a classroom (K-12, undergraduate, graduate?? your choice). Videos should be both informative and entertaining. (In other words, no taped lectures or narrated Powerpoint presentations!) Animations, music videos, and mini documentaries are all fair game.

The finalists will be screened at the 2017 Evolution meeting in Portland, OR. (You do not need to attend the conference in order to enter a video.)

First- and second-place winners will receive up to $1,000 and $500, respectively.

The deadline to submit your video(s) is FRIDAY, JUNE 2^nd (11:59 PM, EST). There's still time to work on your video, but start soon if you haven't started yet!

For more information (and to see entries from previous years) please visit evolutionfilmfestival.org or contact Jory Weintraub (jory@duke.edu)

Jory P. Weintraub, Ph.D. Science Communication Director, Duke Initiative for Science & Society Director, Duke Broader Impacts Resource Center (BIRC) Senior Lecturing Fellow, Duke University 304 Research Drive, Box 90222, Durham, NC 27708-0222 Phone: (919) 668-0792 | Email: jory@duke.edu | Skype: jory.weintraub

Jory Weintraub <jory@duke.edu>

Nemours France SummerStudent Killifish

France Summer students comparative analysis Austrolebias annual killifish, July & August 2017

We are looking for a summer student to participate during the summer months in the project COMPAY, funded by PSL-Pépinière Evo-Devo and PLANAQUA. The student will assist in data collection and experiments on Austrolebias annual killifish, small fish that live in temporary ponds and of which the embryos diapause. In the project, we will investigate rates of development and survival of embryos and their size at birth in controlled conditions. We want to understand selection pressures on egg sizes and the evolution of species differences in reaction norms for egg size. We have a preference for students who are almost starting their graduate projects.

The project is carried out at the CEREEP ECOTRON IledeFrance station in Nemours, about 100 km South of Paris. (http://foljuif.ens.fr/) Lodging and a small allowance is provided by the project.

Fore more information, please contact Tom Van Dooren tvdooren@gmail.com You can apply with a short cv and a letter of motivation.

Best regards, Tom Van Dooren, Hélène Morlon

tomvandooren.eu

greenkillies.org/blog

Tom Van Dooren <tvdooren@gmail.com>

Nepal VolunteerTeaching

Dear Sir-

Could you please spread this message to those that are interested?

We are looking a short/long term volunteers to serve in rural areas of Nepal to teach lower secondary level students in one of the Government school. The volunteer teacher may choose to teach science (including evolution), English, Math or their subject of interest with flexible date of start.

The school does not have any other source of funding to support the teacher at the moment. The upcoming teacher may come with their own support (some philantrophic or organization). Living cost here is expected to be around 150 U$$/Month. The volunteer position may also suite to anyone who has free time.

You may choose to live in Tamang community (learn their ethnic language or Nepalese language), do some treks in world famous mountain in this small tiny country located between India and China during holidays. Those who are looking to work in stress free environment and interested in doing something new, it will be a great opportunity as well as challenge. Please keep in mind that earthquake has severely damage many infrastructures and it will take a years to gain original shape. You must be very sensitive/flexible regarding situation. However, your contribution in these timing will be great for the school.

Furthermore, enthusiasts can often do research in their own time, write their scholar activities like books, papers etc.Some of the great question could be asked such as what is DNA lineage and SNPs in these community , if one has facility (lab test, or analysis) to do research besides teaching for their thesis or publications.

Please contact me for further arrangements.

dpathak@uthsc.edu Or, pathakdhruba@gmail.com

Thanking you,

Sincerely,

Dhruba

Dhruba Pathak <pathakdhruba@gmail.com>

NewCaledonia VolFieldAssist AvianCoevolution

Volunteer field assistants

We are looking for 2 field assistants for a study on the co-evolutionary arms race between Fan-tailed Gerygone and Shining Bronze-cuckoo in New Caledonia. This is part of a long-term study conducted by the Behavioural Ecology Unit at the Museum and Institute of Zoology of the Polish Academy of Sciences.

Periods: 3-4 months, from September to December.

Location: fieldwork will be conducted at several field sites in Grande Terre, New Caledonia. These include lush tropical forests and savannah areas with abundant birdlife. There will be plenty of opportunities for birdwatching and for exploring New Caledonia.

Duties: searching for and monitoring nests during the breeding season, behavioural observations, video analysis. Field activities will require 6-8 working hours a day (5-6 days a week) and an early morning start.

Experience: experience with monitoring and banding birds, nest searching, mist-netting and fieldwork in tropical environments is highly desirable, but training will be provided. Fieldwork will be physically demanding and conducted in a variety of environments (tropical forest, savannah, dry grassland) sometimes in extreme weather conditions. Physical fitness, enthusiasm, self-motivation, ability to work in a group and shared living are a must. Knowledge of French and driving license are desirable although not necessary.

The project will cover travel expenses, accommodation and food costs.

For more information contact: Alfredo Attisano (attisano@miiz.waw.pl) or J?rn Theuerkauf (jtheuer@miiz.eu) or visit http://corenc.lagoon.nc. To apply, please email a short CV with a brief description of relevant field work/research experience to attisano@miiz.waw.pl.

Alfredo Attisano <attisano@miiz.waw.pl>

Plant micrographs wanted

Hello Plant Biologists of Evoldir,

A few months ago I sent out an email on evoldir to asses interest among the plant biologist community for an automated tool to phenotype stomatal traits. I received a positive response from many of you and it's clear the community needs a tool to make stomatal phenotyping easier. Sven Eberhardt (Brown Uni.) and I have developed a tool to automatically count stomata and we have trained it on several hundred Balsam Poplar epidermal micrographs. The method appears to work very well for

Balsam Poplars (machine v. human annotation has r2 = 0.92), but can't recognize stoma from other taxa .at all.

It's clear that the training set needs to grow, and that's why I'm reaching out to the plant biologists of ecolog. I'm searching for collaborators who can contribute several hundred high quality epidermal micrographs and then annotate them using the website we've developed. Here are the parameters that your images need to abide by:

+ The sample should come from populations within a species that encompasses a wide range of phenotypic variation. + Micrographs must be high quality, i.e. majority of image in focus, stomata clearly visible and unobstructed by epidermal features (e.g. trichomes). + Micrographs should be imaged at 400x + Any preparation method is acceptable as long as it is a good prep.

I am particularly interested in finding contributors for the following groups: Pinus, Oryza, Arabidopsis, Brachypodium, Maize, Populus, Medicago, and Mimulus.

Collaborators will need to contribute and annotate several hundred (~200 - 500) images in the next few weeks. In recognition of that effort you will be invited to join the project as a co-author, or acknowledged if you prefer. In addition to co-authorship/acknowledgement, contributors will have access to a beta version of the tool/website, and the method will perform very well on your particular preparation methodology and set of individuals.

If you are interested in learning more, please email me and include a zip file of a representative sample of images. If you need to transfer large files, you can use UVM's large file transfer service https://filetransfer.uvm.edu/ . Thanks for the interest Evoldir & I can't wait to see what's out there.

Sincerely,

Karl Fetter

Graduate Student & Smithsonian Fellow Keller Lab Department of Plant Biology University of Vermont kf@uvm.edu

Karl Fetter <kf@uvm.edu>

RoyalSociety AnimalColoration

Royal Society Publishing has recently published a special issue of Philosophical Transactions B entitled Animal coloration: production, perception, function and application compiled and edited by Tim Caro, Mary Caswell Stoddard and Devi Stuart-Fox. This content can be accessed at http://bit.ly/PTB1724 and the articles can be accessed directly at http://rstb.royalsocietypublishing.org/content/372/1724 A print version is also available at the special price of -L-35.00. You can order online via the above web page (enter special code TB 1724 when prompted) or, alternatively, you can contact debbie.vaughan@royalsociety.org

Felicity Davie Royal Society Publishing

T +44 20 7451 2647 http://royalsocietypublishing.org The Royal Society 6-9 Carlton House Terrace London SW1Y 5AG Registered Charity No 207043

"Davie, Felicity" <Felicity.Davie@royalsociety.org>
"Davie, Felicity" <Felicity.Davie@royalsociety.org>

RoyalSociety PhotographyCompetition

Following the success of our 2016 Royal Society Publishing photography competition, we are doing it all over again this year! As always, the competition is run in collaboration with our journals and celebrates the power of photography to communicate science and the role images play in making science accessible to a wide audience. This competition is split into 5 categories, including behaviour, and is free to enter. The overall winner will receive a prize of pounds 500 (or currency equivalent) and winners of the categories not chosen as the overall winner will receive pounds 250 (or currency equivalent). The closing date for entries is 31st August. Full details can be found at https://royalsociety.org/journals/publishing-activities/photo-competition Felicity Davie Royal Society Publishing T +44 20 7451 2647 http://royalsocietypublishing.org The Royal Society 6-9 Carlton House Terrace London SW1Y 5AG Registered Charity No 207043

"Davie, Felicity" <Felicity.Davie@royalsociety.org>

SouthAfrica VolResAssist SocialMoleRats

Cooperative breeding in Damaraland mole-rats (Fukomys damarensis).

We are looking for voluntary research assistants to help with our research on the completely subterranean, highly social Damaraland mole-rat (Fukomys damarensis) in the Kalahari. 1 position starting as soon as possible and one position starting later this year; duration: 6 months.

The position entails assisting in several studies on social evolution and hormonal effects on social behaviour of mole-rats. We are interested in the effects of hormonal variation on allo-parental care and the effects of variation in the social environment on behaviour and physiology in mole-rats. The research assistant will be involved in all steps of the experiments and will mainly work in the laboratory with our captive mole-rats which are housed in large semi-natural tunnel systems. The responsibilities include behavioural observations, hormonal measures (blood sampling, urine sampling), obtaining morphological measures by X-Ray, and hormonal manipulations. The laboratory is situated in the Kuruman River Reserve in the southern Kalahari, Northern Cape province of South Africa. Occasionally the research assistant will have the possibility to assist in trapping wild mole-rats in the surrounding nature reserve.

The successful applicant will work in a team of 5-10 persons and will receive extensive training to acquire the skills needed for the above mentioned data collection. The research station is also the home of several other projects studying meerkats (www.kalahari-meerkats.com), cape ground squirrels, pied babblers, forktailed drongos and hornbills resulting in a stimulating scientific environment. Around 20-30 research assistants are based at the station year round. Research assistants will learn a range of skills such as remote sensing of behaviour, endocrine sampling techniques, behavioural observations, data handling and management.

Applicants should be enthusiastic, willing to work hard and keen to get involved in a research project in a remote location.

We provide accommodation, and research assistants are paid a monthly allowance to cover their personal costs and food. Domestic travel to the field site can be covered but we cannot provide an international airfare, travel insurance, or visa fees for applicants from overseas.

Applications received until the 3rd of June 2017 are ensured full consideration for the position with earlier staring date. Later applications will be considered for the position staring towards the end of this year (flexible staring date). Please apply by email including a cover letter and a CV.

Please apply to or contact for further information:

Markus Zottl and Philippe Vullioud, University of Cambridge, mz338@cam.ac.uk or philippe.vullioud@gmail.com

Markus Zoettl <mz338@cam.ac.uk>

StellenboschU VolFieldAssist PlantEvol

A research assistant position is available for durations of one to two months (within the period from August 1st to November 31th 2017) in the Biological Interactions Lab (www.biointeractionslab.com) in the Department of Botany and Zoology at Stellenbosch University, South Africa.

Work will be based in Namaqualand during the annual spring mass-flowering displays. Namaqualand is a semi-desertic area of astonishing plant diversity which is part of the Succulent Karoo Biodiversity hotspot. We will conduct pollinator observations, in Situ experiments, and collect DNA material and plant trait measurements on the unique long-tongued fly pollination systems across a large area (300km long). Long-tongue flies are unique to southern Africa, many are undescribed as yet, but still they are key-stone species as over 250 species of plants rely on them for reproduction. The plant species we focus on are from the Iridaceae and Geraniaceae families.

Candidates need to be hard-working, naturalist-minded, willing to spend long hours in the field and spend most nights camping. A previous experience in pollination biology will be an advantage. Such fieldwork is highly rewarding to the naturalist-minded persons. Namaqualand is a unique ecosystem, and new discoveries are plentiful.

Food, accommodation, and a small stipend will be provided. Travel costs to South-Africa are not included.

Please direct any questions and applications to me: florent.grenier@ens.fr I can also provide email addresses of former fieldwork assistants if you want extra feedback.

Deadline: June 4th 2016 / florent.grenier@ens.fr

Florent Grenier PhD candidate Institut des Sciences de l'Evolution Université de Montpellier FRANCE and Department of Botany and Zoology Stellenbosch University South-Africa http://www.biointeractionslab.com/ florent.grenier@ens.fr cell phone : +33 6 76 48 10 30

Some pictures of Namaqualand plants are on this flickR album : https://flic.kr/s/aHsk58wtjH A few pictures of the fieldwork conducted in 2016 : https://www.flickr.com/gp/89472795@N05/J3125K References on the study systems Manning, J. C., & Goldblatt, P. (1996). The Prosoeca peringueyi (Diptera: Nemestrinidae) pollination guild in southern Africa: long-tongued flies and their tubular flowers.—Annals of the Missouri Botanical Garden, 67-86.

Manning, J. C., & Goldblatt, P. (1997). The Moegistorhynchus longirostris (Diptera: Nemestrinidae) pollination guild: Long-tubed flowers and a specialized long-proboscid fly pollination system in southern Africa.—Plant Systematics and Evolution,—206(1-4), 51-69.

"fgrenier@clipper.ens.fr" <fgrenier@clipper.ens.fr>

UNSW Australia Volunteer Zebrafish

Scientific Internship/Apprenticeship in Evolutionary Biology at UNSW, Australia

Our lab (www.i-deel.org) is offering one scientific internship/apprenticeship (or volunteer position) for 6 months to help conduct behavioural and physiological experiments on zebrafish. We are located at the Evolution & Ecology Research Centre (E&ERC) within the School of Biological, Earth and Environmental Sciences (BEES) at the University of New South Wales (UNSW), Sydney, Australia. The intern will be engaged in variety of scientific work (e.g, running zebrafish behavioural and metabolic experiments, helping in fish breeding and database management as well as molecular work such as DNA extraction, sequencing, PCR and qPCR). We expect that the apprentice will learn essential skills as well as gain experience necessary for conducting their own projects. As such, an ideal candidate would be someone who plans to undertake a PhD in the future, within the fields of Evolutionary Biology, Ecology and Behavioural Sciences (i.e. someone with BSc or MSc). We will provide an allowance to cover accommodation and food (~up to AU$2000 per month). Importantly, the intern needs to be an Australian or New Zealand resident. Please read our webpage to see what kind of research we conduct (www.i-deel.org). If you are passionate about our science and would like to join our team, please contact Daniel Noble (daniel.noble@unsw.edu.au) or Shinichi Nakagawa (s.nakagawa@unsw.edu.au) with your CV and a one page letter of motivation.

Shinichi Nakagawa

Dr Shinichi Nakagawa (Associate Professor / ARC Future Fellow) Deputy Director of Research, Evolution & Ecology Research Centre, EERC (Visiting Scientist at Garvan Institute of Medical Research) Room 568, Biological Sciences Building (D26) School of Biological, Earth and Environmental Sciences, BEES The University of New South Wales Randwick NSW 2052, Sydney, Australia Mobile: 0422 655 854 Office : 0293 859 138 Website: http://www.i-deel.org/ Shinichi Nakagawa <s.nakagawa@unsw.edu.au>

PostDocs

AlexandervonHumboldt FellowshipAppl

Dear All,

the Alexander von Humboldt Foundation announced their call for 5-year group leader fellowships. Open to all fields, including evolution at institution of the applicant's choice. PhD must be less than six years ago, applicants must not currently be resident in Germany. Details below

Regards, Klaus

Sofja Kovalevskaja Award for young research talents Application deadline: 31 July 2017

Valuable seed capital and the best conditions for junior researchers from abroad: with the Sofja Kovalevskaja Award, the Alexander von Humboldt Foundation promotes outstanding talent and creative approaches to research. Award winners receive up to euro 1.65 million each, enabling them to spend five years establishing and heading their own research groups at a research institution in Germany.

Junior academics of all disciplines from abroad with outstanding qualifications, who completed their doctorates within the last six years, are eligible to apply for the Sofja Kovalevskaja Award. Applications may also be submitted on completion of doctoral studies. Six awards are scheduled to be granted.

Visit www.humboldt-foundation.de/skp_en for further information and a link to the online application package.

Advice and contact

If you have any questions about the Sofja Kovalevskaja Award or would like individual guidance, please contact us at info@avh.de.

You will find examples of previous award winners in the humanities, social and natural sciences in the Sofja Kovalevskaja dossier at www.humboldt-foundation.de/web/dossier-kovalevskaja-award.html . Klaus Reinhardt

Professor of Applied Zoology Biology, TU Dresden, Germany http://tudaz.net "klaus.reinhardt@tu-dresden.de" <klaus.reinhardt@tu-dresden.de>

ANU Australia PhylogeneticsNextGenSequencing

Dear colleagues

I have funds to support a Postdoctoral Fellow for up to 1.5 years on an Australian Research Council grant. The project involves the development of computational methods to jointly infer the sequences, phylogenies and evolutionary parameters of next-generation sequencing data obtained from mixtures of DNA from several untagged (i.e., anonymous) individuals. The project will suit someone with a strong background in computational evolutionary biology, including phylogenetic inference.

The successful candidate will be a member of the Computational Biology and Bioinformatics Unit at the Research School of Biology of The Australian National University. The ANU is ranked highest in Australia and 22 in the world (QS Rankings 2016-17). In addition to excellent colleagues, researchers at the ANU have access to significant computational resources – the University is a partner institution of the National Computational Infrastructure, Australia's high-performance computing provider.

Please contact me with a brief CV if you are interested. Thanks in advance.

Allen Rodrigo

Prof Allen Rodrigo PhD DSc FRSNZ Director, Research School of Biology The Australian National University Acton —ACT —2601 —Australia

E: allen.rodrigo@anu.edu.au

allen.rodrigo@anu.edu.au

ArizonaStateU LizardMultimodalCommunication

We are searching for a postdoctoral researcher to join the Martins Lab at Arizona State University (ASU) and study the evolution of lizard motion, color and chemical signals. Specific research topics are open to discussion although we are especially interested in how multimodal signals and interspecific interactions impact territorial behavior. The successful candidate will join a productive collaborative team (with Diana Hews from Indiana State University) studying behavioral evolution in _Sceloporus_ lizards. Individuals who have experience with behavioral observation, fieldwork, remote-sensing tools (e.g., radiotelemetry, rfid), robotics, color and/or chemical analyses are especially encouraged to apply.

If interested, please send a short summary of research interests, CV, and email addresses for two references to emilia.martins@asu.edu by July 1 2017.

The Martins lab (http://www.indiana.edu/~martinsl) is moving to the ASU Tempe campus in August 2017, where we will also continue our research on sensory mechanisms of social behavior in zebrafish and the development of phylogenetic comparative methods.

"emartins@indiana.edu" <emartins@indiana.edu>

ArizonaStateU PhylogeneticComparativeMethods

We are searching for a postdoctoral researcher to join the Martins Lab at Arizona State University (ASU) in developing and applying phylogenetic comparative methods to study phenotypic evolution. Specific research topics are open to discussion and mutual interest, although we are especially wanting to combine phylogenies with geographic, climate, fossil, and species-incidence data to reconstruct ancestral states of complex phenotypes and a rich image of their historical biotic and abiotic contexts. The successful candidate will join a productive collaboration with Michelle Lawing (Texas A&M) and will interact regularly with researchers at the ASU-Natural History Collections. Individuals who have experience using R to manipulate phylogenetic, geographic, phenotypic and climate data are especially encouraged to apply.

If interested, please send a short summary of research interests, CV, and email addresses for two references to emilia.martins@asu.edu by July 1 2017.

The Martins lab (http://www.indiana.edu/~martinsl) is moving to the ASU Tempe campus in August 2017, where we will also continue our research on sensory mechanisms of social behavior in zebrafish and the evolution of multimodal signals in _Sceloporus_ lizards.

"emartins@indiana.edu" <emartins@indiana.edu>

Barcelona HumanEvolutionaryGenomics

Pompeu Fabra University & Institute of Evolutionary Biology are seeking a post-doc to work with human genome data in an evolutionary perspective. The candidate will work in a new project (whole genomes and SNP arrays) with data from hunter-gatherer populations with demographic and natural selection analyses and will collaborate with ongoing projects of detecting selection in sets of genomes from other populations. Other projects proposed by candidates within the same framework can be considered.

The candidate should have strong genome bioinformatics skills to handle DNA sequence data and program in R, python or similar. Expertise in population genomics and NGS is necessary.

The candidate will join the group led by Jaume Bertranpetit and Hafid Laayouni, collaborating with other PIs in the Institute of Evolutionary Biology and Universitat Pompeu Fabra. The lab is located in the PRBB, Barcelona. Our group offers an unusual and highly stimulating research frame, is part of the Barcelona Biomedical Research Park (http://www.prbb.org), a renowned center for Biomedical research that hosts, besides the University, other institutions offering a thrilling and dynamic scientific atmosphere, driven by leading groups in fields such as (among others) bioinformatics, molecular biology and evolution.

More information on the lab can be found http://biologiaevolutiva.org/jbertranpetit/research-lines/ Applicants should have a PhD. degree, with research experience in computational genomics related to evolution. Salary in the line of the official post-doc programs Beatriu de Pinos, Juan de la Cierva o Ramon y Cajal, with a gross year salary of up to 30,000 euros, depending on expertise. The position will be filled as soon as possible (June 2017, no later than September 2017).

Please send a letter of interests and the curriculum vitae to hafid.laayouni@upf.edu

Dr Jordi Lanuza Masdeu Communication manager Institut de Biologia Evolutiva (IBE) (CSIC-UPF) Despatx P85, Edifici CMIMA Passeig MarÃtim de la Barceloneta 37-49 08003 Barcelona comunicacio@ibe.upf-csic.es Tel. 932309645 (Ext. 6050) Web: http://www.ibe.upf-csic.es Follow us on Twitter: @IBE_Barcelona Follow us on Facebook: IBEvolutiva Follow us on LinkedIn

Jordi Lanuza Masdeu <comunicacio@ibe.upf-csic.es>

Beijing 2 StatPopGenetics

Qiaomei Fu's Lab has two post-doctoral positions. If you have a background in history/anthropology, statistical population genetics and/or data science, this might be for you! Here are the listings: 1) Post-doctoral fellow: Learning about history using genetic data We are searching for a highly motivated post-doctoral researcher to join our group.

The successful candidate will have exceedingly strong statistical / mathematical / computational skills, and an interest in history. While a background in population genetics, bioinformatics or experimental biology is advantageous, it is not necessary. Our lab has the resources to not only analyze large public data sets, but also has access to some of the world???s best new genetic data generated in our own laboratory.

Possible projects are: - Studying human history using ancient DNA and present-day populations - Studying the process of speciation and the mechanisms of natural selection and mutation using genetic data Description of projects in our lab, as well as papers we have recently published, is provided here.

The position will be co-supervised by Dr. Qiaomei Fu and Dr. Albert Ko Please write to fuqiaomei at ivpp dot ac dot cn by December 1, 2017, if you are interested.

http://124.16.247.197/web/36962/team 2) Post-doctoral fellow: Ancient DNA Our ancient DNA laboratory has pioneered large-scale studies of human population history with large numbers of samples simultaneously and we are looking for a highly motivated post-doctoral researcher with appropriate experience and interests to work on analysis of these data.

The successful candidate will have previous experience in a world class ancient DNA laboratory, as well as analytical and computer skills that allow exploration of large and complex genetic data sets.

Description of additional projects in our lab, as well as papers we have recently published, is provided here.

The position will be supervised by Dr. Qiaomei Fu.

Please write to fuqiaomei at ivpp dot ac dot cn by December 1, 2017, if you are interested.

http://124.16.247.197/web/36962/home Melinda Yang (?????????) Institute of Vertebrate Paleontology and Paleoanthropology Chinese Academy of Sciences Beijing, China Postdoctoral Fellow melyang@ivpp.ac.cn

Melinda Yang <melyang@ivpp.ac.cn>

Beijing 2 StatPopGenetics 2

Qiaomei Fu's Lab has two post-doctoral positions.

Her lab's present research focuses on using ancient DNA to study gene flow between modern and archaic humans, to determine early modern human migration routes and to explore how agriculture influences the population structure of the Neolithic expansion in Europe and Asia. The research projects have been published in Nature, Science, PNAS, Current Biology and other international high profile journals. In 2016ï¼she was selected as one of ten "Science stars of China" in Nature. In 2017, she was selected for the International Young Scientist Award, organized by the Howard Hughes Medical Institute (HHMI).

If you have a background in history/anthropology, statistical population genetics and/or data science, this might be for you! Here are the listings: 1) Post-doctoral fellow: Learning about history using genetic data We are searching for a highly motivated post-doctoral researcher to join our group.

The successful candidate will have exceedingly strong statistical / mathematical /computational skills, and an interest in history. While a background in population genetics, bioinformatics or experimental biology is advantageous, it is not necessary. Our lab has the resources to not only analyze large public data sets, but also has access to some of the world's best new genetic data generated in our own laboratory.

Possible projects are: - Studying human history using ancient DNA and present-day populations - Studying the process of speciation and the mechanisms of natural selection and mutation using genetic data Description of projects in our lab, as well as papers we have recently published, is provided here.http://124.16.247.197/web/36962/team The position will be co-supervised by Dr. Qiaomei Fu and Dr. Albert Ko Please write to fuqiaomei at ivpp.ac.cn by December 1, 2017, if you are interested.

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http://124.16.247.197/web/36962/home The position will be supervised by Dr. Qiaomei Fu.

Please write to fuqiaomei at ivpp.ac.cn by December 1, 2017, if you are interested.

Professor Qiaomei Fu

Laboratory on Molecular Paleontology

Chinese Academy of Sciences

Institute of Vertebrate Paleontology and Paleoanthropology (IVPP)

Beijing, China

fuqiaomei@ivpp.ac.cn

http://124.16.247.197/web/36962/home Melinda Yang <melyang@ivpp.ac.cn>

ColoradoStateU WildlifeDisease

QuantitativeEcologist or Population/Disease Modeler

Weare seeking a highly motivated, innovative individual for a Research Associatejoint position with Colorado State University and USDA, Wildlife Services,National Wildlife Research Center. The overall goal of the fellowshipis to develop novel quantitative decision-support tools for mitigatingdisease risks from rabies in wild carnivores. This will involve employingdifferent communication skills to address multiple stakeholders (academic,government, industry). The successful candidate will work directlywith Dr. Zaid Abdo (Computational Biologist in Department of Microbiology,Immunology and Pathology at CSU), Dr. Amy Gilbert (Rabies Biologist,NWRC) and Dr. Kim Pepin (Quantitative Ecologist, NWRC). This candidatewill possess a strong work ethic, excellent organizational andcommunication skills, and the ability to work independently and as amember of a diverse research team. The candidate's record will also demonstratea high level of productivity and ability to lead research projectsfrom start to finish. Applicants must hold a PhD or MS and atleast 2 years demonstrated experience in the area of quantitative populationbiology, quantitative ecology, epidemiology, mathematical biology,computational biology or similar disciplines. Experience with statistical/computational/mathematicalmodeling of populations and/or diseases,and proficiency in at least one programming language (e.g., R,Matlab, C++, etc...) is required. Experience with individual-based modeling,population-level metapopulation models, hierarchical Bayesian modelsand GIS skills is desired.

Forfull position announcement and to apply go to http://jobs.colostate.edu/postings/44697 CSUis an EO/EA/AA employer and conducts background checks on all final candidates.

ZaidAbdo, PhD AssociateProfessor Departmentof Microbiology, Immunology and Pathology Collegeof Veterinary Medicine and Biomedical Sciences ColoradoSate University Tel.:970-492-4455 E-mail:zaid.abdo@colosate.edu

"Abdo,Zaid" <Zaid.Abdo@colostate.edu>

CornellU GenomeEvolution

Postdoctoral Associate position in genome evolution at Cornell University

The Hendry lab in the Department of Microbiology is seeking a Postdoctoral Associate to study bacterial genomic evolution in bioluminescent symbiosis. The main goal of the project is to understand genome evolution of luminous bacterial symbionts associated with a diverse array of deep sea anglerfish species. The project will investigate the evolution of genome size, gene content, and transposable element abundance in the symbionts of these charismatic deep sea fish.

Work in the Hendry lab ranges across diverse systems and focuses on the evolution and ecology of host-microbe interactions. Potential additional projects, dependent on the candidate's interest, could include other evolutionary genomics questions across luminous symbionts or the host species.

This position is full-time (40 hours/week) and will be located in Ithaca, New York. This is a one year appointment with possible extension depending on funding and performance. Starting date is flexible.

Required Qualifications:

Ph.D in Ecology and Evolutionary Biology, Microbiology, Bioinformatics or related field; Demonstrated research experience with genomic or bioinformatics methods is required; Publication record appropriate for career stage; Ability to work and learn new techniques independently is desired.

To apply:

Submit a cover letter describing your research experience and interests, a CV, and the contact information for three references to Dr. Tory Hendry (th572@cornell.edu). Please feel free to contact me by email with any questions.

The Hendry lab is located in the Department of Microbiology in the College of Agriculture and Life Sciences at Cornell University. Cornell has strengths in evolutionary biology and genomics, including the active EvoGroup seminar series, and the Center for Comparative and Population Genomics group. Within the field of microbiology, >40 affiliated faculty members with diverse interests contribute to strengths in host-microbe interactions across departments and in association with the Cornell Institute for Host Microbe Interactions and Disease.

Tory A. Hendry

Research Scientist

Department of Microbiology

Cornell University

260 Wing Hall

Ithaca, NY 14853

(607) 255-1950

College of Agriculture and Life Sciences

Knowledge with Public Purpose

Cornell University is an innovative Ivy League university and a great place to work. Our inclusive community of scholars, students and staff impart an uncommon sense of larger purpose and contribute creative ideas to further the university's mission of teaching, discovery and engagement. Located in Ithaca, NY, Cornell's far-flung global presence includes the medical college's campuses on the Upper East Side of Manhattan and Doha, Qatar, as well as the new Cornell Tech campus to be built on Roosevelt Island in the heart of New York City.

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

Tory Hendry <th572@cornell.edu>

DalhousieU MicrobialCommunities

Postdoctoral fellowship position in modeling and analysis of complex microbial communities

A position is immediately available to work on a collaborative project between researchers at Dalhousie University (Dr. Joseph P. Bielawski & Dr. Hong Gu, Dept. of Mathematics & Statistics) and the University of Montreal (Dr. B. Jesse Shapiro, Dept. of Biological Sciences). The project is part of a large-scale research initiative, ATRAPP, funded by Genome Canada and focused on genomic solutions to the challenge of assessing, predicting and preventing harmful toxic blooms. The successful candidate will develop novel models for analyzing the structure and metabolic interactions of complex aquatic microbial communities.

The research will follow up, and extend, the Bayesian hierarchical modeling frameworks that were developed for microbial amplicon data (BioMiCo: Microbiome. 2015 10;3:8), and for microbial metagenomic data (BiomeNet: PLoS Comput Biol. 2014 10(11):e1003918). The objectives are to develop novel (i) supervised methods that can simultaneously make use of taxonomic and functional data derived from metagenomes, (ii) statistical frameworks for comparing the fit of alternative models for community structure, and (iii) temporal models for predicting community transitions from serially sampled data. Qualified applicants must have a Ph.D. in statistics, applied mathematics, computer science, bioinformatics, or a related field in computational biology. A strong background in statistics, and proficiency with scripting and programming languages (e.g. python, perl, R, C/C++), is expected.

This position is based at Dalhousie University (Halifax, NS). The recipient will join the Centre for Genomics and Evolutionary Bioinformatics (CGEB), which is a vibrant interdisciplinary research environment at Dalhousie University. More information about CGEB is available at http://cgeb.dal.ca. The recipient will also have the opportunity to visit the University of Montreal and interact with a diverse group of biologists and computational biologists working on bloom-forming freshwater cyanobacteria.

Start date: Review of applications will begin immediately and continue until the position is filled. The start date is negotiable. Applications will be reviewed as they are received. We thank all applicants, however, only selected candidates will be contacted. Interested parties should forward a cover letter, cv, statement of research interests, and a sample of recent writing (article, report or other publication) as well as contact information for 3 references to:

Joseph P. Bielawski Department of Biology Department of Mathematics and Statistics Dalhousie University P.O. Box 15000 Halifax, NS, Canada B3H 4R2â euro Â

(or) email to j.bielawski@dal.ca

Joseph Bielawski <J.Bielawski@Dal.Ca>

EdinburghZoo ConservationGenetics

Research Scientist (Conservation Genetics) - (3 years Fixed Term)

Location: Edinburgh Zoo

About Us

The charity that owns both RZSS Edinburgh Zoo and RZSS Highland Wildlife Park - are looking for committed, compassionate and conservation-minded individuals to join our expert staff team.

RZSS aims to connect people with nature and safeguard species from extinction, a mission that sees us work both here in Scotland and in over 20 countries around the world. From inspiring the next generation about wildlife in our parks to protecting chimpanzees in the Ugandan rainforest; looking after some of the world's most endangered species to saving the Scottish wildcat, RZSS is making a huge difference and we need your help to continue to grow.

The role

Due to the expansion of our team, an opportunity has arisen for a committed researcher to join the Royal Zoological Society of Scotland WildGenes lab. Reporting to the Conservation Programme Manager - Wildgenes in our Conservation team, the successful candidate will initiate, implement and disseminate conservation genetics projects in the WildGenes laboratory. Duties include assisting with the project management and analysis of genetic data for a diverse portfolio of conservation genetic projects.

Who we are looking for

The successful candidate will have a PhD in Conservation Genetics or Population Genetics/Genomics, a proven track record of scientific publication, and a commitment to conservation. You will enjoy working at multiple levels, from complex data analysis to presenting results to a wide range of audiences. Since our projects are based across the globe, the role will involve international travel and willingness to travel to attend meetings is therefore essential.

Applicants with additional background in any of the following disciplines will be welcomed: Quantitative Genetics, Population Modelling, Bioinformatics, Project Management within the conservation sector.

Closing date: Sunday 28 May 2017

Invitation to interview will be by email/phone and interviews will take place on the week commencing 19th June 2017. Due to the level of interest in these positions, we are not able to contact each unsuccessful applicant individually. Therefore, if you have not been contacted by the 12 June, please assume that you have been unsuccessful this time.

For any questions and queries, please email Dr Helen Senn at hsenn@rzss.org.uk quoting "Research Scientist" as the subject, or call 0131 314 0317.

How to apply

To apply for this role, please download the Research Scientist Role Profile < http://www.rzss.org.uk/-media/5375/cons-1709-research-scientist.pdf > (467kb pdf) and complete an Application Form < http://www.rzss.org.uk/media/5124/rzss-employment-application-form.docx > (1.89 MB Word Doc) and a Recruitment Monitoring Form < http://www.rzss.org.uk/-media/5139/rzss-recruitment-monitoring-form.docx > (1.91Mb Word Doc)

CV's are welcomed and should be submitted along with the Application Form.

Once completed you should email it to recruitment@rzss.org.uk

Applications may also be sent in the mail to:

The Royal Zoological Society of Scotland Edinburgh Zoo - HR Team 134 Corstorphine Road Edinburgh EH12 6TS

Dr Helen Senn WildGenes Programme Manager 0131 314 0317 hsenn@rzss.org.uk THE ROYAL ZOOLOGICAL SOCIETY OF SCOTLAND RZSS Edinburgh Zoo, Edinburgh EH12 6TS 0131 314 0300 rzss.org.uk < http:/-/www.rzss.org.uk/ > @RZSS < https://twitter.com/-rzss > /RZSSofficial < https://www.facebook.com/-RZSSofficial?ref=hl > REGISTERED CHARITY NUMBER: SC004064 < http://www.rzss.org.uk/ >

Helen Senn <HSenn@rzss.org.uk>

Embark AnimalDisease

We're hoping to recruit from among the many talented graduate students and postdocs in population genetics, ecology, and evolutionary biology that follow EvolDir

Aaron Sams, PhD Research Scientist Embark Veterinary asams@embarkvet.com

Embark Veterinary

Postdoctoral Researcher

The Company Background

Embark is an early-stage, VC-backed startup launched in 2016. The company's long-term vision is to end preventable diseases in pets. With its high-throughput DNA genotyping platform and cutting-edge bioinformatics, Embark looks to discover and develop a new generation of breeding tools, novel genetic tests, clinical practice, and wellness regimens for pet care. The company believes that these revolutionary advancements in pet health may even have powerful applications in human healthcare.

Embark's flagship product is a canine DNA test that provides a comprehensive genetic profile unmatched in scope or accuracy by any other test on the market today. The test is built around proprietary genotyping technology coupled with the world's largest and fastest-growing canine DNA reference database. This allows Embark to use a simple saliva sample to report on an unprecedented range of health diagnostics, color and coat traits, breeding heritage, and wellness predictors. Taken together, these advantages make Embark "different-in-kind" to everything else on the market today and will be a uniquely powerful engine for scientific discovery.

Embark's founders are recognized leaders in the canine genomics research community and bring more than a decade of field and lab work experience to the venture. The genesis of the company traces back to Dr. Adam Boyko's work at Cornell University's College of Veterinary Medicine, one of the premier veterinary colleges in the world and an ongoing research partner of Embark.

Today, Embark is looking for scientists who will help it realize its long term vision; a vision driven by a deep passion and affinity for our canine companions and the intellectual thrill of opening new realms of scientific medical discovery through genetics.

The Position

Reporting to the Chief Science Officer, the Postdoctoral Researcher is expected to contribute to the company's scientific vision and leadership, manage research projects, and help to develop new analytical tools for Embark's bioinformatics pipeline. Near term, the company is focused on its flagship canine DNA test to establish a leadership position in canine genetic testing and research. Longer term, the company looks to achieve clear leadership in pet bioinformatics and -omics generally, expand Embark's footprint in the veterinary testing and pharmaceutical industries, collaborate on human bioinformatics and pharma projects, and generally drive scientific advancements that extend the brand across a broad range of research areas. To achieve these goals a Bioinformatics Scientist at Embark will:

- Improve and expand the bioinformatics driving our canine DNA test and research objectives

- Play a role in developing research strategies, operating plans, and corporate culture

- Conduct research projects in accordance with Embark's priorities

- Assist efforts to obtain funding for R&D efforts

- Participate in scientific collaborations with canine organizations and with other scientific organizations

The Qualifications

- A strong scientific vision and desire to build a team to accomplish that vision

- Ph.D. in genetics or related field

- A demonstrated capacity for conducting research in the form of peer-reviewed research and successful grant applications

- Research experience in population and statistical genetics with large datasets

- A keen interest in dogs

- Postdoctoral research experience helpful

- Previous start-up experience helpful

Compensation

Embark offers a dynamic work environment, filled with passionate entrepreneurs, leading edge science, and a world of exciting growth opportunities (and dogs!). Compensation for the Postdoctoral position includes a competitive base salary and equity under the terms of the company's ESOP. Additional benefits, defined by applicable company policies include: generous vacation and medical/dental insurance programs.

Timing/Location

Embark is looking to fill this position as soon as possible after the close of Series A funding (expected by the end of May 2017). This position will be based at Embark's Ithaca, NY headquarters. The position may require occasional overnight travel as partnerships and events require.

Notice

Embark Veterinary is an equal opportunity employer. We do not discriminate on the basis of sex, disability, ethnicity, race, religion, sexual orientation, or gender identity.

To apply, send a cover letter and resume (or curriculum vitae) to Dr. Aaron Sams (asams {at} embarkvet.com).

Aaron Sams <asams@embarkvet.com>

FUBerlin EnvironmentalChangeGenomics

We are looking for candidates with a Ph.D. in population genetics, genomics, molecular evolution or related field of research that are interested in applying for an Individual Fellowship of the European Commission (submission deadline: September 14, 2017; see https://tinyurl.com/la7q46l for more information on Individual Fellowships). The proposed research project(s) of the selected candidate(s) should fit current research in the lab on the impacts of environmental change on fungal communities funded by the European Research Council (see https://tinyurl.com/kcspdaj for an overview of the project). Bridge funding may be available for select candidates.

Please send your (informal) inquiries or applications (including a cover letter and detailed curriculum vitae) to Prof. Dr. Matthias Rillig, rillig@zedat.fu-berlin.de.

Application deadline: June 15, 2017.

Prof. Dr. Matthias C. Rillig Freie Universitaet Berlin Institut fuer Biologie Plant Ecology Altensteinstr. 6 D-14195 Berlin Germany

ludo_muller@yahoo.com

GEOMAR Kiel MarinePopulationGenomics

GEOMAR Helmholtz Centre for Ocean Research Kiel is a foundation of public law jointly financed by the Federal Republic of Germany (90%) and the state of Schleswig-Holstein (10%) and is one of the internationally leading institutions in the field of marine sciences. Currently GEOMAR disposes over an annual budget of approx. 72 million Euro and has approx. 950 employees.

The research unit "Evolutionary Ecology of Marine Fishes" of the research division "Marine Ecology",) is offering a

2-years postdoctoral position in Marine Population Genomics

starting on September 1st 2017.

Job Description

The appointment is part of a EU BiodivERsA project on the effect of Marine Protected Areas (MPAs) on Mediterranean artisanal fisheries in collaboration with France, Spain and Sweden. This position concerns the population genomics aspects specifically, which constitute a significant part of the whole project. The main tasks will consist in generating large-scale RADseq data from four exploited species and analyzing these data both de novo and mapped to reference draft genomes in the context of export of individuals from MPAs to fishing areas. The genomic data will be integrated with demographic, oceanographic and socio-economic data/models generated in the scope of the project. The appointment will be based in the Puebla group at GEOMAR in Kiel, Germany, and involves collaboration with Prof. Stéphanie Manel at the CEFE (Centre d'Ecologie Fonctionnelle et Evolutive) in Montpellier, France.

Qualifications

- PhD degree (required) - Background in population genetics (required) - Experience generating and analyzing RAD data is a plus (but not required) - Experience with modeling/simulations is a plus (but not required) - Knowledge of German is a plus (but not required)

The position is available for a funding period until August 31st 2019. The salary depends on qualification and could be up to the class E13 St.4 TVöD-Bund of the German tariff for public employees. This is a full-time position. The position can be split.

GEOMAR Helmholtz Centre for Ocean Research Kiel seeks to increase the proportion of female scientists and explicitly encourages qualified female academics to apply.

GEOMAR is an equal opportunity employer and encourages scientists with disabilities to apply. Qualified disabled applicants will receive preference in the application process.

Applications should include a cover letter, curriculum vitae (short format) a statement of research interests (max 3 pages) and contact information of three references. Please mention the keyword 'RESERVEBENEFIT' in the subject line. Please send your application for this post not later than July 1st in a single pdf-file using the keyword "RESERVEBENEFIT" to the following address:

GEOMAR Helmholtz Centre for Ocean Research Kiel Personalabteilung Bewerbermanagement / "RESERVEBENEFIT" Wischhofstr. 1 - 3 D-24148 Kiel GERMANY bewerbung@geomar.de

As soon as the selection procedure has finished, all application papers will be destroyed according to data protection regulation.

For further information regarding the position and research unit please contact Oscar Puebla (opuebla@geomar.de).

Please do not contact us by phone about the present state of procedures. However, we will answer all your questions if you send us an e-mail to bewerbung[at]geomar.de. In doing so, please refer to the keyword RESERVEBENEFIT.

GEOMAR is a member of the Helmholtz Association and the German Marine Research Consortium (KDM). For further information please visit www.geomar.de or www.helmholtz.de.

Oscar Puebla Junior Professor GEOMAR Helmholtz Centre for Ocean Research Kiel Düsternbrooker Weg 20 24105 Kiel, Germany http://www.puebla-lab.org Oscar Puebla <opuebla@geomar.de>

JacksonLab Maine StatisticalGenetics

The Churchill Lab (http://churchill-lab.jax.org) at The Jackson Laboratory is seeking a Postdoctoral Fellow in statistical genetics and computational biology. Our group is developing statistical design and analysis methods for large-scale genomic data including proteomics, gene expression, and whole genome sequencing. Our approach combines statistical modeling with genetic analysis of animal models to address fundamental biological questions about metabolic diseases and aging.

The Jackson Laboratory (http://www.jax.org) in Bar Harbor, Maine, USA, is recognized internationally for its excellence in research, unparalleled mouse resources, outstanding training environment characterized by scientific collaboration and exceptional core services - all within a spectacular setting adjacent to Acadia National Park. The Jackson Laboratory was voted among the top 15 “Best Places to Work in Academia” in the United States in a poll conducted by The Scientist magazine.

Applicants must have a PhD (or equivalent degree) in quantitative biology or another quantitative discipline such as statistics, computer science, physics, or applied mathematics. Experience in statistical genetics and large-scale data analysis is strongly recommended. Applicants must have a commitment to solving biological problems and good communication skills. Expertise in scientific programming languages such as R or Python is recommended.

To apply, please submit a single PDF containing a current CV, a statement of research interests, and the names of three references to: http://www.jax.org/careers/postdoc.html < http://www.jax.org/careers/postdoc.html%20%20 > (select link for Bar Harbor positions, position #6441).

Exceptional postdoctoral candidates will have the opportunity to apply to become a JAX Postdoctoral Scholar, a selective award addressing the national need for research scientists who are accomplished in the broadly defined fields of genetics and genomics. The award includes an independent research budget, travel funds, and a salary above standard postdoctoral scale.

The Jackson Laboratory is an EOE/AA Employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability or protected veteran status.

Gary Churchill <Gary.Churchill@jax.org>

MaxPlanck Tuebingen GenomicsOfSelectionMice

POSTDOC IN GENOMICS OF SELECTION RESPONSE IN MICE

Friedrich Miescher Laboratory, Max Planck Campus, Tübingen, Germany

A postdoctoral researcher position is available in the Chan Lab to work on a unique genomics dataset in mice, with the aim of understanding the molecular basis of phenotypic variation and response to selection in a population genetics and quantitative genetics framework.

We’re looking for a postdoc skilled in population and/or statistical genomics to take on the analysis of a replicated artificial selection experiment in mice. In order to study major morphological changes in a model organism, our collaborator, Dr. Campbell ROLIAN (Univ. of Calgary, Canada), has performed artificial selection for increased tibia length in mice (2 “Longshanks” selection lines & 1 control line, >6000 total individuals; see Marchini et al., 2014). Over 21 generations, the Longshanks selection experiment has produced 15-20% increase in tibia length but unchanged body mass relative to random-bred controls.

Having retained nearly all individuals from the entire selection experiment, we are now nearly finished with complete re-sequencing of all available breeders (~1800 individuals) in both Longshanks and control lines, with the ultimate goal of re-tracing the entire selection experiment in every individual, at every locus, in the entire genome.

You will work with the complete dataset in close coordination with Prof. Nick BARTON (IST Austria) and his team to link theory with empirical genomic data. Candidates must have a strong background in bioinformatics, including experience with genomic data analysis and strong quantitative and programming skills. Further background in population genetics and modelling will be an advantage. The postdoc will work closely with Prof. BARTON’s group, therefore she or he must show independence and ability to drive her/his own research project. You will enjoy excellent computational and sequencing support, as well as the opportunity to design and conduct functional tests in mice together with our wet-bench team members.

Our on-going work has found many loci showing very strong response to selection, with a substantial fraction of parallel response. Further dissection of top loci has identified specific mutations in limb enhancers. Our functional test in mice showed that these mutations modulate enhancer activity in a way consistent with increased tibia length.

Together with the ROLIAN and BARTON groups, we will study the selection response from multiple angles, ranging from trait mapping, population genomics, theory to developmental genetics. The Longshanks selection experiment combines quantitative, developmental and population genetics and offers a unique opportunity to study how the genome responds to strong selection in a model paradigm.

The Max Planck Campus in Tübingen, Germany is one of the leading campuses in evolutionary genomics research. The Chan Lab enjoys generous funding support by the Max Planck Society as well as the European Research Council (ERC). Our campus hosts world-class research groups, including a Nobel laureate and multiple ERC-funded teams (groups active in evolutionary genomics include Felicity Jones, Detlef Weigel, Ralf Sommer and Ruth Ley). We operate state-of-the-art sequencing (Illumina, PacBio and others) and other core facilities. All seminars and communications are in English.

For informal enquiries and applications (cover letter, CV, and two reference contacts), please e-mail frank.chan@tue.mpg.de. Consideration of applications will begin on 14 May, 2017, with a target start date of Sept 2017. The actual start is flexible.

Frank Chan Max Planck Research Group Leader Friedrich Miescher Laboratory of the Max Planck Society Spemannstrasse 39 72076 Tübingen Germany http://www.fml.tuebingen.mpg.de/chan-group.html [1] Marchini M., Sparrow, L.M., ... Rolian C., BMC Evolutionary Biology 2014 14:258, doi: 10.1186/s12862-014-0258-0 [2] Cosman M.N., Sparrow, L.M., Rolian, C., Journal of Anatomy, 2016 228:6, doi: 10.1111/joa.12459

Frank Chan Max Planck Research Group Leader Friedrich Miescher Laboratory of the Max Planck Society Spemannstrasse 39 72076 Tübingen Germany

T: +49 (0)7071 601 888 F: +49 (0)7071 601 801 @: frank.chan@tue.mpg.de http://www.fml.tuebingen.mpg.de/chan-group.html fraank@gmail.com

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OklahomaStateU Macroevolution-FunctionalMorphology

Postdoctoral researcher in Comparative Biology: Department of Integrative Biology, Oklahoma State University, Stillwater, OK, U.S.A.

The Moen lab at the Department of Integrative Biology at Oklahoma State University is seeking a postdoctoral researcher for an NSF-funded project examining the drivers of macroevolutionary transition rates between different anuran (frog and toad) ecomorphs (e.g. aquatic, arboreal, fossorial, terrestrial). Key duties will focus on collecting morphological data from museum specimens of anurans, conducting large-scale phylogenetic comparative analyses, presenting the results at conferences, and leading publication of the research. Additional research opportunities are available, particularly those that focus on functional morphology in anurans, evolutionary biomechanics, and macroevolution. While data collection for this position will primarily focus on museum specimens, it will involve some travel to U.S. museum collections and the potential for international fieldwork (e.g. Spain). In addition to research, the post-doc will be responsible for mentoring undergraduate and graduate students during the academic year and mentoring undergraduates as part of an eight-week summer Research Experience for Undergraduates program. Initial appointment will be for one year with competitive salary and benefits. Renewal for a second year is possible pending successful performance. The position has an anticipated start date of 1 August 2017, although this is negotiable.

The minimum qualification for this position is a Ph.D. in a relevant field. Competitive candidates will have a strong background in phylogenetic comparative biology (specifically analyses of phenotypic evolution) and data analysis in R. In addition, experience collecting data on frog morphology and knowledge of frog biology and evolution will be beneficial for working on this project.

To apply please email a single PDF of (a) a cover letter summarizing research experience and interests, (b) a curriculum vitae (CV), and (c) contact information (email and phone) for three references, preferably including your Ph.D. advisor and most recent postdoctoral advisor. Please send in an email with the subject line as “Postdoctoral application <your name>” to Daniel Moen at daniel.moen@okstate.edu. For full consideration, apply by 6 June 2017. However, applications will be accepted until the position is filled.

Please direct any questions about the position to Daniel Moen (daniel.moen@okstate.edu; 405-744-6815).

Oklahoma State University is an Affirmative Action/Equal Opportunity/E-verify employer committed to diversity and all qualified applicants will receive consideration for employment and will not be discriminated against based on age, race, color, religion, sex, sexual orientation, genetic information, gender identity, national origin, disability, protected veteran status, or other protected category. OSU is a VEVRAA Federal Contractor and desires priority referrals of protected veterans for its openings. OSU will not discharge or in any other manner discriminate against employees or applicants because they have inquired about, discussed, or disclosed their own pay or the pay of another employee or applicant. However, employees who have access to the compensation information of other employees or applicants as a part of their essential job functions cannot disclose the pay of other employees or applicants to individuals who do not otherwise have access to compensation information, unless the disclosure is (a) in response to a formal complaint or charge, (b) in furtherance of an investigation, proceeding, hearing, or action, including an investigation conducted by the employer, or (c) consistent with the contractor's legal duty to furnish information. 41 CFR 60-1.35(c).

DANIEL S. MOEN Assistant Professor Dept. Integrative Biology, Oklahoma State University 517 Life Sciences West Stillwater, OK 74078, USA Tel: (+1) 405-744-6815 Email: daniel.moen@okstate.edu Website: moenlab.okstate.edu

Daniel Moen <daniel.moen@okstate.edu>

Rockville Maryland Phylotastic

subject: post-doc position with Phylotastic project (Rockville, MD)

Applications are invited for a Postdoctoral Associate position with the Stoltzfus group at the University of Maryland Institute for Bioscience and Biotechnology Research (IBBR) in Rockville, MD.

While experts continue improving the Tree of Life, the focus of the Phylotastic project (www.phylotastic.org) is on getting this knowledge into the hands of scientists, educators, and the general public, so that they can get online species trees as easily as they get online driving directions. Based on a design initially prototyped at a NESCent hackathon, NSF has funded this project to develop an open, distributed system of web services to provide convenient, computable access to ToL knowledge. The successful applicant will join a distributed virtual team with key personnel from IBBR, NMSU, UTK, OpenTree and GlobalNames. Responsibilities will include software design, development, and evaluation, with opportunities for research on topics such as the quality and coverage of available phylogenetic and taxonomic resources.

For the job requirements and application instructions, please see https://ejobs.umd.edu/postings/51494 . The position is available now: applications will be considered immediately, until a suitable candidate if found. Pre-submission inquiries to arlin@umd.edu are encouraged.

Please feel free to redirect this message to anyone who might be interested. Thanks,

Arlin Stoltzfus

Arlin Stoltzfus (arlin@umd.edu) Research Biologist, NIST; Fellow, IBBR; Adj. Assoc. Prof., UMCP IBBR, 9600 Gudelsky Drive, Rockville, MD, 20850 tel: 240 314 6208; web: www.molevol.org Arlin Stoltzfus <arlin@ibbr.umd.edu>

RZSSWildGenesEdinburgh AppliedConservationGenetics

Research Scientist (Conservation Genetics) - (3 years Fixed Term)

Location: Edinburgh Zoo

About Us

The charity that owns both RZSS Edinburgh Zoo and RZSS Highland Wildlife Park - are looking for committed, compassionate and conservation-minded individuals to join our expert staff team.

RZSS aims to connect people with nature and safeguard species from extinction, a mission that sees us work both here in Scotland and in over 20 countries around the world. From inspiring the next generation about wildlife in our parks to protecting chimpanzees in the Ugandan rainforest; looking after some of the world's most endangered species to saving the Scottish wildcat, RZSS is making a huge difference and we need your help to continue to grow.

The role

Due to the expansion of our team, an opportunity has arisen for a committed researcher to join the Royal Zoological Society of Scotland WildGenes lab. Reporting to the Conservation Programme Manager - Wildgenes in our Conservation team, the successful candidate will initiate, implement and disseminate conservation genetics projects in the WildGenes laboratory. Duties include assisting with the project management and analysis of genetic data for a diverse portfolio of conservation genetic projects.

Who we are looking for

The successful candidate will have a PhD in Conservation Genetics or Population Genetics/Genomics, a proven track record of scientific publication, and a commitment to conservation. You will enjoy working at multiple levels, from complex data analysis to presenting results to a wide range of audiences. Since our projects are based across the globe, the role will involve international travel and willingness to travel to attend meetings is therefore essential.

Applicants with additional background in any of the following disciplines will be welcomed: Quantitative Genetics, Population Modelling, Bioinformatics, Project Management within the conservation sector.

Closing date: Sunday 28 May 2017

Invitation to interview will be by email/phone and interviews will take place on the week commencing 19th June 2017. Due to the level of interest in these positions, we are not able to contact each unsuccessful applicant individually. Therefore, if you have not been contacted by the 12 June, please assume that you have been unsuccessful this time.

For any questions and queries, please email Dr Helen Senn at hsenn@rzss.org.uk quoting “Research Scientist” as the subject, or call 0131 314 0317.

How to apply

To apply for this role, please download the Research Scientist Role Profile < http://www.rzss.org.uk/-media/5375/cons-1709-research-scientist.pdf > (467kb pdf) and complete an Application Form < http://www.rzss.org.uk/media/5124/rzss-employment-application-form.docx > (1.89 MB Word Doc) and a Recruitment Monitoring Form < http://www.rzss.org.uk/-media/5139/rzss-recruitment-monitoring-form.docx > (1.91Mb Word Doc)

CV’s are welcomed and should be submitted along with the Application Form.

Once completed you should email it to recruitment@rzss.org.uk

Applications may also be sent in the mail to:

The Royal Zoological Society of Scotland Edinburgh Zoo - HR Team 134 Corstorphine Road Edinburgh EH12 6TS

Dr Helen Senn WildGenes Programme Manager 0131 314 0317 hsenn@rzss.org.uk THE ROYAL ZOOLOGICAL SOCIETY OF SCOTLAND RZSS Edinburgh Zoo, Edinburgh EH12 6TS 0131 314 0300 rzss.org.uk < http:/-/www.rzss.org.uk/ > @RZSS < https://twitter.com/-rzss > /RZSSofficial < https://www.facebook.com/-RZSSofficial?ref=hl > REGISTERED CHARITY NUMBER: SC004064 [http://www.rzss.org.uk/downloads/-RZSS_brand_email_sig.jpg] < http://www.rzss.org.uk/ >

Scandinavia Biosystematics

ForBio - the Scandinavian Research School in Biosystematics is organising a training program for outgoing and incoming postdoctoral fellows to apply for European Commission H2020 MSCA Individual Fellowships.

The training program is open to potential outgoing and incoming fellows from research groups in systematic biology in Scandinavia, including systematics, taxonomy, phylogenetics, biogeography, etc. The target group are academically-engaged senior PhD students, postdocs and junior researchers. Including IF programs ER-ST (Standard European), ER-CAR (Career Restart Grant), ER-SE (Society and Enterprise), ER-RI (Reintegration), and GF (Global). We aim to have a mixed group of incoming and outgoing fellows.

The program runs from May 19th to the submission deadline of the H2020 MSCA-IF call on September 14th 2017. The training includes match-making between fellows and hosts, coaching, an intensive 3-day workshop at the Natural History Museum in Oslo, writing support, peer review, and liaison with EU coordination offices.

For more information about teachers, target group, course plan, costs and registration, see: http://-www.forbio.uio.no/events/courses/2017/MSCAIF.html For a list of potential hosts for incoming fellows, see: http://www.forbio.uio.no/events/courses/2017/-msca-if-hosts.html Registration: Fellows should register online and provide contact information of their host before May 19th. Registered fellows will be evaluated and notified by May 21st regarding acceptance and participation in the training program. Make sure the reserve the dates 12-14 June for the workshop.

Contact Hugo de Boer (hugo.deboer@nhm.uio.no) or Maria Capa (maria.capa@ntnu.no) for more information.

Hugo de Boer

Natural History Museum University of Oslo P.O. Box 1172 Blindern 0318 Oslo, Norway Phone: +47 22851875

Leader of ForBio - the Scandinavian Research School in Biosystematics www.nhm.uio.no/english/about/organization/research-collections/people/hugode/ www.forbio.uio.no/ h.d.boer@nhm.uio.no

SLU Uppsala QuantGenetics

We are looking for a highly motivated person that will work within a newly started project focused on climate-adapted poplars (Populus spp.) for Swedish and Baltic regions (CLAP, https://www.slu.se/clap). The postdoc (24 months fixed term employment) will do work in association genetics and quantitative genetics to study the genetic architecture of phenology traits as bud burst, bud set and growth cessation with the overall aim to develop molecular markers for breeding poplars varieties for use at northern latitudes. The applicant will conduct work in the lab, in the field and use genomic and phenotypic data for different types of quantitative genetic analyses.

Successful candidates will have a PhD degree in genetics or equivalent field. As postdoctoral appointments are career-developing positions for junior researchers, we are primarily looking for candidates with a doctoral degree that is three years old at most. The candidate should have proven expertise in genetics and be used to handle large genomic and/or phenotypic datasets. Prior experience of working with computational and/or statistical analyses in a quantitative genetics framework is thus highly desirable. Excellent proficiency in English is required, as English is the working language in the research group. A driving license is preferable, as the work will involve some fieldwork in remote areas. The project involves working within a larger research team of around ten researchers, so candidates should have an easy time working with others but also the ability to work independently with your own research topics. Creativity and drive are personal characteristics that are desirable due to the knowledge-driven aspect of the project. The PhD position is housed at the Department of Plant Biology, Swedish University of Agricultural Sciences in Uppsala, Sweden.

For mor information and instructions of how to apply see:

http://www.slu.se/en/about-slu/jobs-vacancies/read-more/?eng=1&Pid=5177 The Swedish University of Agricultural Sciences (SLU) is a research-intensive university that also offers unique degree programmes in for example rural development and natural resource management, environmental economics, animal science and landscape architecture. SLU has just over 3,000 employees, 5,000 students and has recently invested heavily in a modern, attractive environment on its campuses in Alnarp, UmeÃ¥ and Uppsala.

Pär K. Ingvarsson Professor, Plant genomics and breeding Department of Plant Biology Uppsala BioCenter Swedish University of Agricultural Sciences PO-Box 7080 SE-750 07 Uppsala, Sweden

par.ingvarsson@slu.se

StAndrews SocialEvolDigitalOrganisms

Schoolof Biology, University of St Andrews, Scotland. Salary: 32,004 - 36,001 per annum, Start Date: 1 July 2017, or as soon as possible, Fixed Term: until 31 May 2019

Applicationsare invited for a Research Fellow to work with Dr Andy Gardner at the University of St Andrews on the social evolution of digital organisms.

Thesuccessful candidate will develop a software platform for studying social evolution in digital organisms and will use this platform to conduct social evolutionary experiments on the evolution of cooperation. The project is very flexible and will be tailored to the skills, experience and interests of the successful candidate.

Thesuccessful candidate should have a good degree in biology, computer science, or in another relevant discipline and a PhD in computer science, evolutionary biology, or another relevant discipline. They should have strong computer programming ability and experience.

Thepost is available from 1 July 2017, or as soon as possible thereafter until 31 May 2019.

Applicationsare particularly welcome from women who are under-represented in Science posts at the University.

TheUniversity of St Andrews is committed to promoting equality, which is further demonstrated through its working on the Gender and Race Equality Charters and being awarded the Athena SWAN award for women in science, HR Excellence in Research Award and the LGBT Charter. More details on diversity online: http://www.st-andrews.ac.uk/hr/edi/diversityawards/ . Pleasequote ref: AR1936ML

ClosingDate: 19 May 2017

Moredetails and instructions for applying at: https://twitter.com/drandygardner/status/-853899032028209152 AndyGardner

– DrAndy Gardner Readerin Biology Universityof St Andrews DyersBrae StAndrews KY16 9TH UnitedKingdom

Email.andy.gardner@st-andrews.ac.uk Tel.+44 (0) 1334 463 385 Fax.+44 (0) 1334 463 366

andy.gardner@st-andrews.ac.uk

StockholmU EvolutionaryGenomics

A 2-year postdoctoral position in evolutionary genomics is currently available at Stockholm University and Science for Life Laboratory in Stockholm, Sweden.

This is a re-posting of an earlier ad - there was a problem with the link to the complete ad at the Stockholm University website in the previous posting

Link to the full ad: http://bit.ly/2r7YwcN Deadline May 19th, 2017

We are looking for a highly motivated postdoctoral researcher to work on a project concerning the population genomic consequences of plant mating system shifts and the impact of selection on linked sites on plant genomic variation. Whole-genome and whole-transcriptome sequence data sets from multiple plant species are already available, and more are currently being generated in the lab. The project offers plenty of opportunities for postdocs to pursue their own ideas using available genomic data. There is also a possibility to be involved in other ongoing projects in the lab, including analyses of cis-regulatory variation and divergence, or analyses of S-locus evolution.

Infrastructure and Environment The postdoctoral researcher will join a group of postdocs and PhD students led by Dr. Tanja Slotte (https://tanjaslottelab.se). For recent examples of our work, see e.g. Steige, Laenen et al. 2017 PNAS, Steige et al. 2015 MBE, or Slotte et al. 2013 Nature Genetics. The Slotte lab is part of the Dept. of Ecology, Environment and Plant Science at Stockholm University (http://su.se/deep/english/) and is located at Science for Life Laboratory in Stockholm (http://www.scilifelab.se), which holds considerable expertise in high-throughput sequencing technology and bioinformatics. The working atmosphere is international with English as the working language, and the position offers plenty of opportunities for scientific exchange with both genomicists, evolutionary biologists and ecologists at SciLifeLab and Stockholm University.

Main Responsibilities The position involves research on the population genomic effects of plant mating system shifts, and will include analysis of large-scale population genomic data, population genetic simulations, and de novo assembly and annotation of plant genomes. The position also includes responsibility for planning and conducting sampling of natural plant populations in the Mediterranean region.

Qualification Requirements Applicants are expected to hold a PhD, preferably in population genetics, evolutionary genetics, bioinformatics, or a related subject. Experience of analyses of large-scale population genomic data is required. Experience of population genetic simulations is beneficial. Coding skills and ability to work on a high-performance computing cluster are required. Experience of sampling of plant populations in the field is beneficial. A strong interest in mating system evolution, in particular transitions from outcrossing to self-fertilization, is beneficial.

Assessment In the appointment process, special attention will be given to research skills, in particular regarding analyses of large-scale population genomic data. The applicant should have proven expertise in genomics and be used to handle large genomic data sets (i.e. “next-generation sequencing” data). Documented scientific qualifications within the research field, such as first or joint-first author publication(s) are desirable. Excellent proficiency in English (the working language of the group) is required. The ideal candidate needs to be able to work well in a collaborative environment, as well as independently. Finally, creativity and drive are personal characteristics that are desirable.

Terms of Employment The position involves full-time employment for a maximum of two years. Start date immediately or as per agreement.

Application For full information on the positions, please see the ads on Stockholm University’s webpages (links below). Apply through Stockholm University’s recruitment system.

Postdoctoral Fellow in Evolutionary Genomics: http://bit.ly/2r7YwcN - Application deadline May 19th, 2017 - For this position, there is a requirement that the PhD degree should have been completed no more than three years before the application deadline.

Contact For further information, please contact Dr. Tanja Slotte directly at tanja.slotte@su.se

Tanja Slotte, Associate Senior Lecturer, SciLifeLab Fellow Department of Ecology, Environment and Plant Sciences Stockholm University

Email: Tanja.Slotte@su.se

Visiting Address: SciLifeLab Stockholm Tomtebodav. 23 a 171 65 Solna SWEDEN

“tanja.slotte@su.se” <tanja.slotte@su.se>

StockholmU ExperimentalEvolutionWithYeast

Postdoctoral position in Experimental Evolution with Yeast at Stockholm University, Sweden.

Project: Adaption in stressful environments

Host: Rike Stelkens Start date: September 2017 (negotiable) Application date: June 15 2017

Description: Candidates will use experimental evolution with the budding yeast Saccharomyces cerevisiae (and its relatives) as model organism to study evolutionary processes. The overall aim of the project is to develop an empirical system for studying adaptation in rapidly changing and stressful environments - a major challenge falling within the nexus of evolutionary genetics and conservation biology. Potential topics include but are not limited to 1) the effects of hybridization on rates and mechanisms of adaptation, 2) the genomic basis of hybrid fitness, and 3) the genomic basis of reproductive isolation.

Qualifications: I am looking for people with a strong interest in evolution, especially in speciation and conservation genetics. Ideally, you have experience in experimental evolution methods, molecular genetics/genomics techniques, bioinformatics, and you have knowledge of the principles of population and quantitative genetics and genomics. Prior training in Saccharomyces yeast cultivation are highly desirable. Candidates should be well-organized, good communicators, and happy to work in a team as well as independently. You must have a PhD in evolutionary biology, population genetics, or a similar subject. You should also have a strong desire to develop a successful and highly productive research career.

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

Application: Please send a statement of motivation including relevant expertise, a CV and the contact details of at least two references through this platform: http://www.su.se/english/about/vacancies/vacancies-new-list Further details on research in the department and staff: http://www.zoologi.su.se/en/index.php To discuss the role please contact Rike Stelkens by email: rike.stelkens@zoologi.su.se

Closing date for applications is 15 June 2017. Interviews will take place on Skype. Following that, shortlisted candidates may be invited (expenses paid) to visit the department to meet with colleagues and present their previous work.

References: Stelkens, Brockhurst, Hurst, and Greig, (2014). Hybridization facilitates evolutionary rescue. Evolutionary Applications 7, 1209Â’1217

Stelkens, Brockhurst, Hurst, Miller, and Greig, (2014). The effect of hybrid transgression on environmental tolerance in experimental yeast crosses. Journal of Evolutionary Biology 27, 2507-2519

Stelkens and Greig (2016). Fungal evolution: On the origin of yeast species. Nature Microbiology 1, 15017

Rike Stelkens <rike.stelkens@zoologi.su.se>

StonehillC QuantitativeGeneticsTeaching

NSF-funded post-doc/teaching post-doc position

The Bleakley lab is looking for a post-doctoral colleague to join an NSF-funded project on the quantitative genetics and physiology of cooperative antipredator behavior in guppies. The Bleakley Lab focuses on the quantitative genetics of social behavior, including indirect genetic effects (IGEs). The goals of the project are to characterize both the genetic architecture of cooperative antipredator behavior in populations of Trinidadian guppies that differ in intensity of depredation and the physiological and molecular mechanisms that underlie such social effects. In addition to our research goals, this NSF-funded project also seeks to develop active learning and lab materials to support introductory biology, evolution, and animal behavior courses. The applicant will have the opportunity to work with undergraduate researchers and teach one course per semester with close mentoring from Stonehill faculty to promote strong teaching skills for future potential career goals. This position is ideal for scientists interested in exploring career opportunities that incorporate research and teaching.

A Ph.D. in Biology or related field is required and experience teaching at the undergraduate level is preferred. Conceptually, individuals with a strong understanding of quantitative genetics will be favored. Candidates should have extremely strong organizational, written, and oral communication skills; be able to work both independently and as part of a collaborative team; and be strongly interested in developing as a teacher-scholar in an undergraduate-focused setting.

For further information, please feel free to contact Dr. Bronwyn (Heather) Bleakley (bbleakley@stonehill.edu; +1.508.565.1590).

Anticipated start date is August 1, 2017. Review of applications will begin immediately and will continue until the position is filled. Interested applicants should upload a curriculum vitae, a 1-2 page statement of research and teaching interests that explicitly describes professional qualifications for this position, and contact information for three references at https://jobs.stonehill.edu/. Review of applicants is ongoing. This is a fixed-term appointment funded for one year from the date of hire ywith the possibility of two additional years of funding, contingent on job performance and anticipated continuance of funding.

Founded by the Congregation of Holy Cross in 1948, Stonehill is a private Catholic college located just 22-miles from downtown Boston on a beautiful 384-acre campus in Easton, Massachusetts. With a student to faculty ratio of 13:1, the College engages its 2,500+ students in 80+ rigorous academic programs in the liberal arts, sciences, and pre-professional fields. To apply for the position, submit required documentation via the URL link: https://jobs.stonehill.edu/ Please email inquiries regarding this position to Prof. Bronwyn Bleakley, bbleakley@stonehill.edu. I'll also be at the Poeciliid Biologists, Animal Behavior Society, and Evolution meetings this summer to discuss the position in person.

Applicants who will enrich the diversity of the campus community are strongly encouraged to apply.

Stonehill College is an equal opportunity employer committed to diversity.

"Bleakley, Bronwyn H." <bbleakley@stonehill.edu>

SwanseaU PDF 2PhD FishEvolution

2 fully funded PhDs on Fish Ecology and Evolution at Swansea University

We are looking for candidates for 2 PhD positions with a first, upper second class honours or a Masters degree (Merit or above), in a relevant discipline. Field experience working with fish and some experience on the use of molecular and analytical methods (microsatellites, eDNA, SIA) would be desirable but not essential as the student will be fully trained and will become part of a large multi-disciplinary research group (FishBee http://fishbee.wixsite.com/fishbee).

PhD 1: Brown trout in the Falkland Islands: invasion ecology, population structure and genetic diversity

http://www.swansea.ac.uk/biosci/postgraduate/-phdopportunitiesandresearc htopics/brown-trout-in-the-falkland-islands/

PhD 2: Adaptive responses of fish to climate change

http://www.swansea.ac.uk/biosci/postgraduate/-phdopportunitiesandresearc htopics/adaptive-responses-of-fish-to-climate-change/

Informal enquires can be directed to Carlos Garcia de Leaniz(c.garciadeleaniz@swansea.ac.uk) or Sonia Consuegra

(s.consuegra@swansea.ac.uk).

Postdoctoral position in Molecular Analyses of Fish Connectivity A 3-year postdoctoral position is available at the Department of Biosciences at Swansea University as part of the AMBER project, which aims to provide a better understanding of the causes and consequences of stream fragmentation.

Rivers rank among some of the most threatened ecosystems in the world and improving stream connectivity has been flagged as one of the priorities for more efficient stream restoration. River fragmentation can result in rapid evolution of ecotypic differentiation and reproductive isolation of natural fish populations, but can also work as a measure of control of invasive species. This is one of two postdoctoral positions who will work as part of the EU-funded AMBER consortium ('Adaptive Management of Barriers in European Rivers'). The overarching goal of these positions is to develop better and more meaningful metrics of stream fragmentation and to apply them to European-wide datasets to quantify and predict current and future impacts of barriers on local stream biodiversity for a variety of taxa and across multiple spatial and temporal scales. The project will develop novel molecular and ecological metrics of stream fragmentation. It is based on the Singleton Campus within Biological Sciences (College of Science).

We are looking for a Postdoctoral Researcher with an excellent track record commensurate with their career stage, and experience working on freshwater ecosystems and with knowledge of metrics of habitat fragmentation and community connectivity. Specific expertise is also required on the application of molecular methods (eDNA, metabarcoding) to join the multidisciplinary AMBER research team (see www.amber.international).

More details are available at: http:/-/www.swansea.ac.uk/personnel/jobs/-details.php?nPostingID=4552&nPo stingTargetIDv90&optionR&sortÃSC&respnr=1&ID=QHUFK026203F3VBQB7VL-O8NXD&LOV4x14&LOV5y78&JOBADLG=UK&Resultsperpage &lg=UK&mask=suext

Informal enquires can be directed to Carlos Garcia de Leaniz (c.garciadeleaniz@swansea.ac.uk) or Sonia Consuegra (s.consuegra@swansea.ac.uk).

Closing Date: 30-05-2017

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Sonia Consuegra Professor of Evolutionary Ecology College of Science Swansea University Singleton Park SA2 8PP Swansea

Tel. +44 (0) 1792 602931

Email. S.Consuegra@swansea.ac.uk

"Consuegra S." <s.consuegra@swansea.ac.uk>

TexasAMU PlantBacteriaInteractions

Title: Postdoctoral Research Associate

FTE amount: $40,000-$47,500/year based on experience; 18 month duration

Employees supervised: Graduate students, undergraduate students, laboratory technicians

Discretion and independent judgement: Yes, 50%

Required Education: PhD in Biology, Ecology, Zoology, Entomology or a related field.

Required experience: Research or education experiences with high throughput sequencing, chemical ecology, and behavior.

Preferred experience: Formal training or education in behavioral, ecological, genetic, and statistical methods; especially as applied to the community ecology and behavioral ecology of microbes and arthropods.

Required special knowledge: Familiarity with basic laboratory protocols and procedures; must be computer literate; must be detail oriented and able to organize and prioritize work with minimal or no supervision; and able to multi-task and work cooperatively with others.

Preferred special knowledge: Ability to effectively communicate scientific findings in written and oral formats. Ability to utilize computing clusters, especially as it relates to modeling efforts relevant to interkingdom-interactions.

Duties: 75% Conduct research on the behavioral responses of arthropods in response to bacterial communities associated with a targeted resource; especially as it relates to interkingdom interactions with maize, peanut, and Aspergillus flavus or Aspergillus parasiticus; the individual will need to have a strong track record with high-throughput sequencing and metagenomic data analysis. Individuals will also be trained to conduct volatile assessments. This position will require the individual to coordinate with collaborators, students, and employees in the lab, department, and other locations; and supervise various undergraduate, graduate students and lab technicians.

15% Research to be reported and published in a timely manner to the funding agency (monthly due to granting agency mandate), as well as high-impact refereed journals and relevant conferences or proceedings; assist in writing competitive grant proposals; assist and participate in research conceptual development, innovative thinking and approaches to addressing interkingdom interactions and the role of quorum sensing, constructive and critical research planning and development, manuscript preparation and writing.

10% Other job related duties as required/needed to meet general research objectives.

You may view this announcement at https://greatjobs.tamu.edu by searching for NOV 10224. If you are interested in applying you MUST complete an on-line application and follow the directions to apply for this position (NOV10224) at the stated website. During the application process you will have the opportunity to attach a resume, cover letter, etc. FYI Â' all individuals must apply via this on-line application process. We CANNOT accept walk-ins or applications/resumes via email. If you have questions, please contact Mr. Robert Jensen (979-845-9739; r-jensen@tamu.edu)

Jeffery K. Tomberlin, PhD, D-ABFE Associate Professor & AgriLife Research Fellow

Director, TAMU Forensic & Investigative Sciences Program Chair, American Board of Forensic Entomology

2475 TAMU Department of Entomology Texas A&M University College Station TX, USA 77843

Phone: 979-845-9718 Fax: 979-845-6305 website: forensicentomology.tamu.edu Email: jktomberlin@tamu.edu

Jeffery Tomberlin <jktomberlin@tamu.edu>

TrinityCollegeDublin StatisticalGenetics

We are inviting applications for a Postdoctoral Research Fellowship in Statistical Genetics or related fields to work on the project: Investigating the Parental Role in Autism Spectrum Disorder through Rare and Common Sources of Variation.

Autism Spectrum Disorder (ASD) is a neurodevelopmental disorder that is known to be heritable. The disorder affects approximately 1% of the population and presents significant challenges for those affected and their families. ASD is not caused by a single gene mutation, but rather the effects of a number of genes contribute to the disorder. In the majority of cases though, no genetic cause has been identified. In general, when genetic material is passed from parents to their offspring the material functions regardless of its parental origin, but in some instances this is not the case and how the genetic material behaves is dependent on its parental origin. Evidence suggests that these parent-of-origin effects are present in ASD and the aim of this project is to investigate these effects.

Advances in technology have resulted in Next-Generation Sequencing (NGS) data becoming available that consists of both rare and common sources of variation in the genome. This data offers promising avenues for identification of the underlying genetic causes of ASD. Through an investigation of rare and common sources of parent-of-origin effects, we will explore the parental genetic role in ASD. In this project Bayesian statistical methods, that can incorporate prior information, will be developed to investigate rare and common inherited variation for parent-of-origin effects. These statistical methods will be applied to selected regions of the genome in ASD NGS datasets in order to further the understanding of the genetic mechanisms underlying ASD. This research has the potential to shed light on the missing heritability in ASD and ultimately offer insights into the genetic causes of ASD which will help improve ASD diagnoses and lead to advances in treatments. See also: https://jobs.tcd.ie/ Candidate The ideal candidate will have, or be about to be awarded, a PhD in statistical genetics, biostatistics, bioinformatics, computational biology or a related discipline together with previous experience in developing and applying Bayesian statistical models and handling large datasets. The successful candidate will join a highly interdisciplinary team in the Dept. of Psychiatry, Trinity College Dublin.

Duration and Salary The position is for a duration of 15 months. Starting salary at IUA Postdoctoral Researcher Level 2, Point 1, gross salary: 33,975 euro.

Closing Date The closing date for applications is the 26th of May, 2017.

To Apply Please send a CV to include the names and contact details of 3 referees together with a cover letter to Dr Eleisa Heron, eaheron@tcd.ie. Informal inquiries can also be addressed to Dr Eleisa Heron.

Shigeki Nakagome <NAKAGOMS@tcd.ie>

UArizona HostParasite

New Postdoc positions in host-parasite coevolution in the Schlenke Lab at the University of Arizona

Position summary: The Schlenke Lab studies host-parasite interactions using Drosophila (fruit flies) as model hosts. We are developing parasitoid wasps, which lay their eggs in fly larvae and consume their hosts from the inside out, as model parasites. Flies mount cellular and behavioral defense responses against wasps, but wasps have adaptations for finding host fly larvae, suppressing host cellular immunity, and manipulating host behavior. We use a variety of "omics" tools to understand the molecular genetics of fly cellular immunity and wasp virulence, as well as patterns of host immunity and pathogen virulence coevolution across fly and wasp phylogenies. For more information, visit our lab website at: https://cals.arizona.edu/research/schlenke/ We have current NSF and NIH funding, as well as startup from UA. We are looking to hire at least two new highly motivated, creative, and collaborative postdocs to work on this system. Our lab attempts to understand the fly-wasp interaction at multiple biological levels, and thus we are searching for candidates with diverse expertise, such as in evolutionary ecology, genetics, molecular and cell biology, immunology, neurobiology, and/or bioinformatics. Our lab is based at the University of Arizona in the Department of Entomology and the positions are available immediately. Feel free to contact Todd (schlenke@email.arizona.edu) with questions.

Duties and Responsibilities: Postdocs will be involved in all aspects of the research, from developing project ideas to experimental design to data analysis to publication. Although we have funding for these positions, postdocs will be expected to apply for their own funding as well. Postdocs will interact with and mentor graduate and undergraduate students, and will be involved in lab outreach activities. In regular consultation with Todd, postdocs will pursue a plan to enhance their professional growth and meet their future career goals.

Minimum qualifications: Ph.D. in a biological or computational subject. Good writing, communication, and critical thinking skills.

Preferred qualifications: Experience studying: Drosophila or other insects, host-parasite interactions, behavior, cell biology, cell culture, molecular biology techniques, microscopy, genetic mapping, genomics, statistics;

Salary: $47,659 annually (following the NIH postdoc pay scale)

Instructions: See the official ad at https://-uacareers.com/postings/18990. To apply please submit (1) a cover letter with a brief description of how this position would match your background and your career goals, (2) a CV, and (3) a list of three people that we can contact as professional references. Todd Schlenke University of Arizona Entomology Department (520) 621-7167

Todd Schlenke <schlenke@email.arizona.edu>

UArizona Phylogenomics

Postdoctoral Researcher in Phylogenomics: University of Arizona

The Wiens lab in the Department of Ecology and Evolutionary Biology at the University of Arizona is seeking a postdoctoral researcher for an NSF-funded project focusing on phylogenomics, phylogenetic methods, and frog ecomorph evolution. The primary role of the postdoc will be collecting and analyzing new phylogenomic data using ultraconserved elements (UCEs), and integrating these new data with existing molecular data for frogs. The postdoc will also be involved in testing general questions about phylogenomic methodology. The postdoc is expected to lead two major publications, present the results at meetings, and help supervise undergraduate researchers. The position is for approximately two years, starting in the summer or fall of 2017.

The candidate is expected to have a strong background in phylogenomics (specifically, phylogenetics with next-generation sequence data), with experience in both data collection and large-scale data analysis. Beneficial attributes would also include (a) experience with UCEs or similar approaches, (b) an interest in phylogenetic theory, and (c) familiarity with frogs and frog phylogeny.

The University of Arizona has one of the top ecology and evolution departments in the world, with considerable faculty expertise in phylogenomics, phylogenetic theory, molecular evolution, and evolutionary biology in general. Tucson is a very fun, affordable, and livable city (and is now a UNESCO World City of Gastronomy). It also has great weather and is surrounded by spectacular scenery (including numerous national parks and wilderness areas), and amazing biodiversity. It is also less than an hour from Mexico.

Minimum qualification is a Ph.D. in biology or related subjects. Preferred qualifications include experience with phylogenomic data collection and analysis, and some knowledge of phylogenetic theory and frogs.

Salary = $47,670 plus benefits

To apply please send: (1) a cover letter, including a brief summary of your relevant research experience, (2) a curriculum vitae, and (3) contact information (including e-mail and phone) for three references, preferably including your Ph.D. advisor and most recent postdoctoral advisor. Please send materials to John Wiens via e-mail: wiensj@email.arizona.edu. For full consideration, please apply by 26 May, 2017, but applications will be considered until the position is filled.

John J. Wiens

Professor

Department of Ecology and Evolutionary Biology

University of Arizona

Tucson, AZ 85721-0088

E-mail: wiensj@email.arizona.edu

Phone: 520-621-0337

http://www.wienslab.com/Home.html John J. Wiens, Professor Department of Ecology and Evolutionary Biology University of Arizona Tucson, AZ 85721-0088 Phone: 520-621-0337 Web: http://www.wienslab.com/Home.html "Wiens, John J - (wiensj)" <wiensj@email.arizona.edu>

UCalgary InfectiousDisease Bioinformatics

Dr. James Wasmuth in at the University of Calgary is accepting applications for a Postdoctoral Fellow (PDF) to work on a project using bioinformatics and evolutionary systems biology to study infectious disease agents.

The postdoctoral fellow (PDF) will analyse genomic, transcriptomic and metabolomic data generated from multiple species of parasites. The aim is to reconstruct and model the biochemical pathways to identify essential components that are potential targets for new anti-parasitic drugs. The successful PDF will work alongside PDFs recruited to complementary parts of the overall project, e.g. structural biochemistry and immunology. The PDF will benefit from joining the Host-Parasite Interactions training program (www.ucalgary.ca/-hpi), the Infection Biology VetMed research group (vet.ucalgary/infectious-disease-research) and the growing research focus in Bioinformatics at the University of Calgary (ucalgary.ca/bmb/faculty/research-area/genomics-proteomics-and-bioinformatics).

The successful candidate will have a PhD in Bioinformatics / Computational Biology. The individual must have demonstrable experience in a programing language, e.g. Perl, Python, Java, and its application to genome-scale data. Experience with the R programming language and/or network biology software is an advantage. Excellent written and oral communication skills are essential. University of Calgary postdoctoral scholar appointment guidelines state that the applicant must have been awarded a PhD or its equivalent within the five (5) years immediately preceding the PDF appointment or ten (10) years from the completion of an MD, DVM or equivalent.

Individuals interested in applying should submit a curriculum vitae, a cover letter including a statement of research interests and goals, and the names of three references to the email address below. Dr. Wasmuth will acknowledge receipt of the application package but only those applicants selected for interviews will be contacted. Review and interviews will begin from June 1st and continue until the post is filled.

James Wasmuth - jwasmuth@ucalgary.ca www.wasmuthlab.org The University of Calgary is a leading Canadian university located in the nation's most enterprising city. The university has a clear strategic direction to become one of Canada's top five research universities by 2016, where innovative teaching and groundbreaking research go hand in hand, and where we fully engage the communities we both serve and lead. The strategy is called Eyes High, inspired by our Gaelic motto, which translates to 'I will lift up my eyes.'

Named a cultural capital of Canada and one of the best places to live in the world, Calgary is a city of leaders - in business, community, philanthropy and volunteerism. Calgarians benefit from the strongest economy in the nation and enjoy more days of sunshine per year than any other major Canadian city. Calgary is less than an hour's drive from the majestic Rocky Mountains and boasts the most extensive urban pathway and bikeway network in North America.

All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. The University of Calgary respects, appreciates, and encourages diversity.

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

UCalifornia SanDiego GeneDriveEvolution

Kryazhimskiy Lab (http://sklab.science/) and Meyer Lab (http://labs.biology.ucsd.edu/meyer/) at UCSD seek to jointly hire a postdoctoral researcher to work on gene-drive evolution in yeast. The position starts in July 2017. It is initially a one-year position, with a possibility of extension.

We aim to address the following questions using S.cerevisiae as a model system:

1. How does a gene drive affect genetic variation in the population?

2. How does the genome adapt to the presence of an active genetic element?

3. How does the the presence of an active genetic element alter future evolutionary outcomes in the population?

4. How does the gene-drive efficiency change over time?

This project will be part of a larger international collaboration aimed at investigating properties of gene drives across a variety of systems.

An ideal candidate will

* Have a solid background in yeast genetics * Have experience with experimental evolution, Illumina full-genome sequencing and sequencing data analyses * Understand population genetics * Be interested in evolutionary biology and its applications

If you are interested in the position, please send (1) your CV with your current publication list and the names of 2 references; (2) your most significant publication or manuscript, and (3) a short cover letter to Sergey Kryazhimskiy <skryazhi@ucsd.edu> or Justin Meyer <jrmeyer@ucsd.edu>.

University of California San Diego has a large and vibrant biology community that spans multiple natural sciences departments and the medical school. UCSD is a home for the Center for Microbiome Innovation (http://jacobsschool.ucsd.edu/microbiome/-) led by Prof. Rob Knight and the recently created Tata Institute for Genetics and Society led by Prof. Ethan Bier (http://ucsdnews.ucsd.edu/feature/-active_genetics_goes_global).

Best regards,

Sergey Kryazhimskiy

Assistant Professor Section of Ecology, Behavior and Evolution Division of Biological Sciences University of California San Diego

"skryazhi@ucsd.edu" <skryazhi@ucsd.edu>

UCLA PopulationGenetics

Postdoctoral research position at UCLA in population genetics

A postdoctoral research position is available in the lab of Dr. Kirk Lohmueller in the Department of Ecology and Evolutionary Biology and the Department of Human Genetics at the University of California, Los Angeles. The Lohmueller lab studies genetic variation to address a variety of questions in evolutionary, medical, and forensic genetics. The lab focuses developing new statistical methods, deriving novel insights from theoretical models, and applying these methods and models to interpret genetic variation data from a variety of organisms.

The successful candidate will have substantial input in the specific nature of this research project. However, the project should broadly fit within the lab's goals of learning about demographic history from genetic variation data, understanding natural selection and deleterious mutations, or applying population genetic principles to the analysis of complex traits. Opportunities are available to analyze cutting edge next-generation sequencing data from a variety of organisms.

The Lohmueller lab is imbedded within a vibrant research community in population and medical genetics at UCLA. We enjoy interactions with many other labs in human genetics (Pasaniuc, Eskin, Freimer, Pajukanta, Sinsheimer, Sul), population genetics (Kruglyak, Sankararaman), functional genomics (Ernst), and evolutionary genomics of non-model organisms (Wayne, Smith, Shaffer, Sork). Further, we are part of the Institute for Quantitative and Computational Biosciences at UCLA (https://qcb.ucla.edu).

Additional information about our lab and research can be found at: https://www.eeb.ucla.edu/Faculty/-Lohmueller/ The position is available for 1 year and may be continued for an additional year contingent on successful progress and available funding. Salary will be competitive. The University of California offers a competitive benefits package including medical, dental, vision, life insurance, accidental death and dismemberment insurance, and short and long term disability insurance.

Candidates should have a recent Ph.D. (2014 onwards) in biology, genetics, computer science, bioinformatics, statistics, computational biology, or a related field. Knowledge of theoretical population genetics (e.g. coalescent theory, diffusion theory, forward simulations) is required. As this is a computational position, proficiency in programming in R, Perl, or Python, and shell scripting is essential. Programming experience in C/C++ is highly desired. Preference will be given to candidates with a strong publication record, evidence of substantial research productivity, and ability to successfully communicate scientific information.

Review of applications will begin immediately and will continue until the position is filled. The position is expected to start in Fall 2017, though specific dates are negotiable.

Interested candidates should send a CV, short (1-2 pages) description of research interests and ideas for possible projects, and contact information for 3 references to Kirk Lohmueller at klohmueller@ucla.edu. Informal inquiries are also welcome.

The University of California is an equal opportunity/affirmative action employer.

"klohmueller@g.ucla.edu" <klohmueller@g.ucla.edu>

UC London StatisticalGenetics

Research ssociate in Statistical Genetics and Bioinformatics Ref: 1645026

We are seeking a talented postdoctoral biostatistician/statistical geneticist to investigate the genetic architecture of obesity and diabetes in animal models of these important human diseases. The principal duties involve the statistical genetic analysis of data arising from a study of obesity and diabetes in a population of outbred heterogeneous stock (HS) rats. The data comprise over 20 obesity and diabetes traits, transcriptome data from liver and adipose tissue and genome-wide genotype information collected in these animals. The analysis will use statistical genetic methods, previously developed by our group (Mott et al 2000 PNS, Yalcin et al 2005 Genetics, Durrant and Mott 2011 Genetics, Davies et al 2016 Nature Genetics) and others (eg Gatti et al 2014) to find regions of the genome that affect outcomes related to diabetes and obesity. Specifically, this person will identify quantitative trait loci (QTL) for both phenotypic and transcriptome data in order to determine the gene networks which correlate with disease.

This NIH-funded project is a collaboration between Richard Mott at University College London (UCL) (see https://iris.ucl.ac.uk/iris/browse/-profile?upi=RFMOT57) and Dr. Leah Solberg Woods at the Wake Forest School of Health, North Carolina US (see http://www.wakehealth.edu/Faculty/Solberg-Woods-Leah-Catherine.htm). The post-holder will join Richard Mott's group at UCL, a dynamic group working on quantitative and population genetics across a wide range of animal and plant species.

Our group is part of the Department of Genetics, Evolution and Environment (GEE) and the UCL Genetics Institute (UGI), a vibrant centre of excellence in medical, statistical and computational genetics, offering one of the most exciting work environments in the UK. GEE is a large and collegial Department, which embraces essentially all aspects of modern biology. The post is funded for 2.5 years in the first instance.

pplicants should have relevant scientific education (PhD degree in Biostatistics, Computational Biology, Statistical Genetics or related field), preferably with a publication track record. Knowledge of applied statistics using R and programming experience is necessary, as well as good written and oral communication skills.

For more details and to apply follow the link http://-tinyurl.com/kwaoj5h , or email r.mott@ucl.ac.uk

Closing Date 7th June 2017

r.mott@ucl.ac.uk

UExeter TransposonHostInteractions

Apostdoctoral researcher position is available in the lab of Dr Alex Hayward, Centre for Ecology and Conservation, College of Life and Environmental Sciences, University of Exeter, Cornwall Campus, UK.

Thesuccessful candidate will study host-transposon interactions using European butterflies as a model system. This will involve quantification of transposon evolutionary dynamics, including the contribution of transposons to the evolution of host genomic complexity and the potential role of transposons in speciation. The project is funded by a BBSRC David Phillips fellowship to Dr Hayward, and involves collaboration with Dr Konrad Lohse at the University of Edinburgh.

Qualifiedapplicants will have a strong interest and proven track-record in genomics, including strong bioinformatics skills. The post will include the analysis of whole genome sequencing data for multiple butterfly species. This will involve bioinformatic analyses such as genome assembly and annotation, transposon detection and quantification, and phylogenetic analyses. Applicants will be experienced in conducting bioinformatic analyses, including the use of scripting languages such as Perl, Ruby or Python. Competency in additional programming languages such as Java, and experience of database systems such as MySQL, is an additional merit. Applicants will possess a relevant PhD and be able to demonstrate sufficient knowledge in the discipline and of research methods and techniques to work within established research programmes.

Interestedcandidates are encourage to submit an online application via the university recruitment system:

https://jobs.exeter.ac.uk/hrpr_webrecruitment/-wrd/run/ETREC107GF.open?VACANCY_ID=-221089IPfH&WVID=3817591jNg&LANG=USA ThisBBSRC funded full-time post is available from 1 September 2017 initially for 1 year, with the possibility of extension for several years. Salary for appointments at Associate level: 28,452 to 32,958 per annum. Salary for appointments at Fellow level: 33,943 to 41,709, depending on qualifications and experience. The closing date for applications is 1st June 2017.

Forfurther information please contact Dr Alexander Hayward, e-mail: alex.hayward@ex.ac.uk

TheUniversity of Exeter is a Russell Group university that combines world-class research with very high levels of student satisfaction. Exeter has over 21,000 students from more than 130 different countries and is in the top 1% of universities in the world with 98% of its research rated as being of international quality. Our research focuses on some of the most fundamental issues facing humankind today. The College is working towards department Silver Athena SWAN awards as a commitment to providing equality of opportunity and advancing the representation of women in STEM/M subjects: science, technology, engineering, mathematics and medicine. We welcome applications from candidates interested in working part-time hours or job-sharing arrangements. The University of Exeter is an equal opportunity employer which is 'Positive about Disabled People'. Whilst all applicants will be judged on merit alone, we particularly welcome applications from groups currently underrepresented in the workforce.

DrAlexander Hayward Centrefor Ecology & Conservation Universityof Exeter, Penryn Campus alex.hayward@exeter.ac.uk Tel:+44 (0) 1326 259147 Researchprofile: http://biosciences.exeter.ac.uk/staff/-index.php?web_id=Alex_Hayward&tab=research Alex.Hayward@exeter.ac.uk

UJena Biodiverstiy

Postdoctoral fellowship on "Aquatic microbial ecology" as part of the wider iDiv (www.idiv.de) community at University Jena We seek an enthusiastic postdoc to join our multinational and interdisciplinary team (http://www.geomicrobiology.de/). More information here: https://www.idiv.de/fileadmin/-content/Vacancies_PDF/Vacancies_2017/123-2017-Kuesel_PD_2017_final.pdf Dr. Marten Winter Scientific Coordinator Synthesis Centre sDiv / Wissenschaftlicher Koordinator Sy nthesezentrum sDiv German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig Deutscher Platz 5e 04103 Leipzig Germany

"Winter, Marten" <marten.winter@idiv.de>

ULausanne ComplexTraitGenetics

Seeking an outstanding candidate for a postdoctoral researcher position at the Complex Trait Genetics Group, Department of Computational Biology, University of Lausanne.

The group

The Complex Trait Genetics Group (www.unil.ch/ctgg) is a newly established research group within the Department of Computational Biology at the University of Lausanne, led by Dr. Matthew Robinson. Our research is at the interface of human medical genetics, population genetics, and bioinformatics. The aim of our work is to develop innovative methods in the analysis of genetic data of complex traits to gain new insight into complex human disease. Our research is regularly published in top journals and within the next two years we expect to grow to a dynamic team of 3 post-doctoral research staff and two PhD students. The Department of Computational Biology is newly formed and consists of seven groups and additionally the candidate will being their position hosted within the Centre for Integrative Genomics, enabling maximum opportunities for collaboration and transfer of knowledge and ideas. The University of Lausanne is an internationally focussed university with close connection to the University Hospital (CHUV), a wide range of data resources, excellent computing facilities (VITAL-IT) and a beautiful setting.

The role

The applicant will work with the group leader on existing projects and is also expected to develop their own ideas and research program. Work will focus on the application and development of novel statistical genetics methods to aid our understanding of the genetic basis of common disease. There are a number of research projects available, including but not limited to: improving prediction of common complex disease in personalized medicine, Bayesian analysis of large scale genotype-phenotype data, understanding the genetic control of environmental variation, and utilizing multiple sources of genomics data to understand the genetic basis of disease. There are opportunities to work with large population-based data sets and to be part of research teams, to address individually developed and collaboratively generated research questions, and to supervise undergraduate and graduate students. The appointee will be supported in the development of independently driven research objectives.

The person

Applicants should possess PhD qualifications in relevant disciplines e.g. statistical genetics, quantitative genetics, bioinformatics, or other relevant areas. You should also have a strong desire to develop a successful and highly productive research career, good general research skills, excellent statistical and analytic skills, advanced computer programming skills, knowledge of the principles of population and quantitative genetics and genomics, very good writing abilities, and the capacity to work with multidisciplinary research teams.

The position

This is a full-time, fixed term appointment, initially for 12 months in the first instance, but with extension possible up to 5 years depending upon performance. The starting date is flexible.

How to apply

Further details can be found here: http://wp.unil.ch/-ctgg/recruitment/ To discuss the role please contact Matthew Robinson by email matthew.robinson@unil.ch

Applications should be a single PDF document containing a research statement, curriculum vitae, a publication list, a detailed response to the selection criteria, and contact details of three individuals who can provide academic references.

Applications should be sent to matthew.robinson@unil.ch

Closing date for applications is 19th May 2017. Interviews will take place on the 25th or 26th of May 2017 on Skype. Following that, shortlisted candidates may be invited (expenses paid) to visit the department to meet with colleagues and present their previous work.

Matthew R. Robinson | Complex Trait Genetics Group | Department of Computational Biology | Genopode office 3020 | University of Lausanne | CH-1015 | Lausanne, Switzerland | tel: +41 21 692 3916 | email: matthew.robinson@unil.ch www.unil.ch/ctgg Matthew Robinson <matthew.robinson@unil.ch>

ULausanne ComputationalEvolGenomics

SNSF postdoctoral position in computational evolutionary biology

Job information Date of start: 01.09.2017 or to be discussed Duration of contract: 1 year. This contract can be renewed twice for two years. The maximum duration is 5 years. Employment rate: 80% Workplace: Lausanne Dorigny

Job description The incredible diversity of insects makes them fascinating to study, with important applications in the characterisation of animal biology, the control of disease vectors and pests, and the conservation of threatened insects. Falling sequencing costs are improving genomic species sampling and enriching sources of functional data, challenging researchers to find innovative approaches to best exploit these data to bring new levels of depth and detail to our understanding of biology. Overcoming these challenges requires substantial methodological advances in data integration and interrogation, supported by robust computational infrastructures. With an initial focus on disease-vector mosquitoes, this SNSF-funded research project aims to exploit genomic evolutionary signatures to enhance the understanding of putative functions of thousands of currently uncharacterised genes from hundreds of organisms.

The successful candidate will be based at the Department of Ecology and Evolution of the University of Lausanne, under the supervision of Prof. Robert Waterhouse (www.rmwaterhouse.org). S/he will work very closely with a PhD student and will be responsible for implementing the core research project goals, particularly with respect to the development of computational infrastructures to ensure that predictive model building is dynamic, extensible, and responsive to the fast-accumulating genomics data, as well as helping to design and build collaborative analysis and visualisation tools. Skills in handling large datasets, statistical modelling, automated collating of different data types from disparate resources, knowledge of database design and management for efficient data integration and quality control, are therefore desirable. The successful candidate will also have the opportunity to gain teaching and mentoring experience through contributions to undergraduate and graduate teaching programmes and the supervision of student projects. A minimum of 50% of the working time will be devoted to personal research work and a maximum of 50% of the working time will be devoted to institutional tasks. The University of Lausanne offers a world-class international research environment with state-of-the-art facilities.

Your qualifications In order to complete our team, we are looking for someone with the following skills : Essential: Doctorate degree in computer science (with life sciences experience) or bioinformatics / computational biology Demonstrable programming skills and experience (e.g. Python, Perl, C/C++, R), including web technologies (e.g. Javascript, HTML, CSS) Confidence in large-scale statistical analyses Scientific research experience in genomics Strong teamwork and interdisciplinary skills Excellent spoken and written English proficiency Desirable: Interest in evolutionary genomics of arthropods Knowledge of arthropod biology

What the post offers you We offer a nice working place in a multicultural, diversified and dynamic academic environment, opportunities for professional training. Possibilities of continuous training, a lot of activities and other benefits to discover. Contact for further information For further information please contact Prof. Robert Waterhouse (robert.waterhouse@gmail.com)

Your application by 16.06.2017 Please, send your full application in Word or PDF. The complete application should contain : Motivation letter (max. one page) Curriculum vitae including lists of publications, conferences, and awards, and a detailed description of programming skills and experience with links to examples online (where relevant) Doctoral thesis summary (max. one page) The names and contact details of 2-3 referees Applications should be made exclusively online.

Robert Waterhouse <robert.waterhouse@gmail.com>

ULausanne PlantSexualDimorphism

Postdoc: genomics and transcriptomics of plant sexual dimorphism Department of Ecology and Evolution, University of Lausanne, Switzerland

(This is a are-posting of an earlier ad. The was a problem with the link for uploading applications; the link at the bottom of this message should work now.)

We are seeking a postdoc to work on a two-year project on the evolution of combined versus separate sexes (hermaphroditism vs. dioecy) and sexual dimorphism in flowering plants. The scope of the project can be tailored to the successful candidate's interests and expertise, but will likely involve genome and transcriptome analysis of: (1) experimental populations of an annual plant species that have undergone a rapid transition between dioecy and hermaphroditism; and (2) natural populations of several dioecious species that vary strongly in their expression of secondary sexual dimorphism. The project start date is somewhat flexible but is envisaged for 1 October, 2017.

The postdoc would join a team postdocs and PhD students working on aspects of sexual-system evolution in plants, with a current focus on sex-chromosome evolution and the evolution of sex allocation and sexually antagonistic traits. Details of the lab can be found at: http://www.unil.ch/dee/home/menuinst/research/-pannell-group.html The postdoc would have excellent opportunities for collaborations and discussions with the Swiss Institute of Bioinformatics, which has three groups within the department; see:

http://www.unil.ch/dee/home/menuinst/research.html The ideal candidate should have: (1) a passionate interest (and PhD) in evolutionary biology and population genetics; (2) experience and skills in the generation and analysis of genomic and transcriptomic NGS data; and (3) excellent communication skills. Experience and an interest in working with plants could be an advantage; however, while there will be some opportunity for field work in the Iberian Peninsula and/or South Africa involving work with plants, it is anticipated that most of the work will involve hypothesis testing based on sequence analysis.

The postdoc would be appointed for an initial period of one year, renewable for two years assuming satisfactory progress, and with the eventual possibility of renewal for a total of up to 5 years.

The Department of Ecology and Evolution has a lively intellectual and social life. Although the University of Lausanne is Francophone, the department is highly international, and all its research activity and, e.g., seminars are conducted in English. The city is culturally rich and occupies a beautiful setting on the shores of Lake Geneva, very close to the Swiss and French Alps.

Informal enquiries for further details of the aims of the project should be sent to John Pannell (john.pannell@unil.ch). Formal applications should include a cover letter detailing your research interests and experience, a CV, and the names of two or three referees, and should be submitted through the University of Lausanne platform (link given below). Please also send your application file as a single pdf email attachment to john.pannell@unil.ch. Applications received by 15 May will be given full consideration.

Application link:

https://career012.successfactors.eu/career?career%5fns=job%5flisting&company=universitdP&navBarLevel=JOB%5fSEARCH&rcm%5fsite%5flocale=en%5fUS&site=VjItZy84VGQ5U1B5c09CRGlJeTlzUHdlZz09%3f&career_job_req_id=9923&selected_lang=en_US&jobAlertController_jobAlertId=&jobAlertController_jobAlertName=&_s.crb=VwS6g6Ugj5OtKGzG4fyaZZWkQMI%3d John Pannell <John.Pannell@unil.ch>

ULiverpool EvolutionaryEcology

Dear All,

We are looking for a post-doctoral research associate to join a NERC-funded project investigating the impacts of climate-driven evolution on plantÂCsoil interactions and ecosystem functioning. To do so, the project will make use of the Buxton Climate Change Impacts Lab (BCCIL), where experimental climate change treatments have been applied to a natural grassland for 25 years (the longest-running climate change experiment in the UK). You will use a range of approaches, including experimental evolution, next generation sequencing, plantÂCsoil microcosm experiments and ecosystem functioning assays to explore the effects of field-based climate change treatments on microbial evolution, and subsequent impacts on plantÂCsoil interactions and ecosystem functioning.

Applicants must hold a PhD in either evolutionary biology or ecology, and have experience in carrying out (or leading) research in these areas. Prior experience with genomics or bioinformatics data handling/analysis, with fieldwork and with experimental approaches in evolution and ecology will also be advantageous. The project will be supported by a full-time technician. You will be based primarily in Dr Raj WhitlockÂÂs research group at Liverpool, but will also spend time in Dr Emma SayerÂÂs group at Lancaster University. Research in Dr WhitlockÂÂs group focuses on a wide range of issues in evolutionary ecology, including climate-driven evolution, the genetics and structure of ecological communities, and conservation genetics. Dr SayerÂÂs research group is interested in the responses of ecosystems to environmental change and plantÂCsoil interactions.

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/). Research spans the complete range of biological scales from genes to whole organisms, populations and ecosystems. IIB also houses stateÂ©\ofÂ©\theÂ©\art ÂÂºomicsÂÂ± facilities, including a genomics centre (more here: https://www.liverpool.ac.uk/integrative-biology/facilities-and-services/).

The post is available for 3 years from the time of appointment. The closing date for applications is June 2, 2017.

Full job description and application link: http://www.jobs.ac.uk/job/BBB951/postdoctoral-research-associate/ BCCIL: http://www.ecologicalcontinuitytrust.org/bccil Please include a cover letter, CV, and details for three referees. Informal enquiries can be sent to Raj Whitlock (r.whitlock@liverpool.ac.uk).

Best wishes,

Raj Whitlock & Emma Sayer

– Dr Raj Whitlock Institute of Integrative Biology University of Liverpool The Biosciences Building Crown Street Liverpool L69 7ZB UK

Email:r.whitlock@liverpool.ac.uk Tel:0044 (0) 151 7954519 –

r.whitlock@liverpool.ac.uk

UMelbourne StatisticalGenomics

Post-doc - Statistical Genomics (2 positions) University of Melbourne

Position Title: Research Fellow Statistical Genomics Employer: University of Melbourne Location: Main (Parkville) Campus, Melbourne, Australia Classification: Research Fellow Level B Salary: AUD $98,775 - $117,290 per annum plus 9.5% superannuation Work Type: Full time Duration: Fixed term, 3 years Closing Date: 5pm (Melbourne time) Wednesday 14 June 2017

I am currently recruiting two senior post-doctoral research fellows in statistical genomics.

*** Please note that excellent candidates with a strong statistical background from any quantitative scientific discipline (e.g. physics, engineering, etc) are encouraged to apply. ***

For further details please see below, and/or:

http://jobs.unimelb.edu.au/caw/en/job/890905/research-fellow-statistical-genomics-2-positions Best wishes,

Stephen

– A/Prof. Stephen Leslie Associate Professor of Statistical Genomics Centre for Systems Genomics Schools of Mathematics and Statistics, and BioSciences, The University of Melbourne Honorary Fellow, Murdoch Childrens Research Institute A: Building 184, Royal Parade, University of Melbourne, Parkville 3010, Victoria, Australia T: +61 3 8344 0441 | M: +61 407 264 734 E: stephen.leslie@unimelb.edu.au | W: http://sysgen.unimelb.edu.au/ —–

Applications are invited for two post-doctoral researchers to join the Statistical Genomics Group in the Centre for Systems Genomics, University of Melbourne, headed by Associate Professor Stephen Leslie. The group's work focuses on methodological developments for the analysis of high throughput genetic data and the application of these methods to studies of disease and natural population variation. These methods typically combine modern computationally-intensive statistical approaches with insights from population genetics models. Specifically the group works on statistical methods for imputing immune system (and other) genes from incomplete genetic data; the application of these methods to studies of autoimmune and other diseases; methods for detecting and controlling for population stratification; and understanding the causes and consequences of genetic variation in populations. The group has strong established collaborations with the Donnelly and McVean groups at the Wellcome Trust Centre for Human Genetics in Oxford.

The positions involve working on problems at the cutting edge of human genetics, and represent an exciting opportunity for a statistical geneticist, or someone with a strong statistical background and skills wishing to move into this field. The successful applicants will focus on developing methods to type HLA, KIR and other immune system related loci from genomic data. They will further apply these methods to studies of auto-immune and other disease, with a particular focus on psoriasis. They will work directly on projects arising from the collaboration between the Leslie group and A/Prof. Wilson Liao at UCSF, investigating the role of HLA and KIR in psoriasis. The appointees will also contribute to the group's other research projects as directed by A/Prof. Leslie. They will be encouraged to develop their independent research projects where appropriate, as long as they are generally consistent with the research priorities of the Leslie group and the Centre for Systems Genomics as a whole.

We are seeking highly motivated scientists, with a PhD in statistics or a closely related area. Applications are encouraged from people who can demonstrate a strong statistical or other quantitative background and wish to move into statistical genetics research. Ideally you will have experience of genetic analyses but this is not essential. You must have considerable programming experience with a low level language (e.g. C, C++) and preferably also with the statistical software R. The successful applicants will have an aptitude for visualizing data, problem solving and careful statistical analysis. They should be able to work alone and collaboratively, and be able to digest and communicate scientific ideas effectively. The positions are available for three years.

The Research Fellows will be located in the Centre for Systems Genomics, a joint initiative of the Faculty of Science and the Faculty of Medicine, Dentistry and Health Sciences. The positions will report to A/Prof. Stephen Leslie, Associate Professor of Statistical Genomics, and the appointees will be part of the Leslie Group.

Informal enquires can be directed to Stephen Leslie (stephen.leslie@unimelb.edu.au).

The position description and information on how to apply can be obtained from:

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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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UMinnesota EvolutionaryGenetics

MULTIPLE POSTDOC POSITIONS [see website https://brandvainlab.wordpress.com/2017/05/11/multiple-postdoc-positions/]

In the Brandvain Lab (that's us), at the University of Minnesota - St Paul. We combine population and quantitative genomic theory with the analysis of genomic, phenotypic, and comparative data sets to address evolutionary questions. The postdoc(s) will work with Yaniv (and collaborators) to help develop and execute a research project related to our areas of interest (see publications). I am also happy to support candidates interested in developing NSF Plant Genome, NSF Broadening Participation, or USDA postdoctoral fellowship applications concerning these projects or projects of mutual interest. Some ongoing work is described below:

- *Plant mating system speciation* The postdoc on this collaborative (with Dave and Emma) project would develop novel population genetic theory and generate / analyze population genomic datasets.

- *Speciation genomics and hybridization* We develop theory to learn when we expect reproductive isolation to arise, and how to learn about the action of recent selection in hybridizing populations. The interested postdoc will have the opportunity to develop theory and to analyze population genomic data from numerous taxa. see also Suzanne's postdoc advert [https://sites.google.com/site/mcgaughlab/postdoc-opportunities]

- *The interface of micro and macroevolution*. The lab has an interest in how population genetic process impact diversification. An interested postdoc could work with Yaniv and James on theoretical problems in Phylogenetic GWAS - i.e. when to expect them and how to find them, or with Yaniv and Emma on developing theory to connect the evolution of reproductive isolation to the diversification rate.

- *Quantitative genomics and inferring recent selection*. A potential postdoc with Yaniv and Suzanne would develop theory to learn about recent selection on quantitative traits from deeply sequenced and heavily phenotyped populations, and could put this theory to practice by analyzing numerous potential datasets. see also Suzanne's postdoc advert [https://sites.google.com/site/mcgaughlab/postdoc-opportunities]

- *Even more*: Mating system evolution, Genomic conflict., denovo domestication..

Start Date is Flexible. Send inquiries + CV and research interests to Yaniv (ybrandva AT UMN dot EDU) before July first. I would also love to talk to interested postdocs at Evolution or SMBE meeting this summer. We aim to build a diverse and engage group scholars, here in the twin cities (which is a great place to live!).

The lab has many ongoing collaborations and/or opportunities for collaboration with Suzanne McGaugh, David Moeller, Emma Goldberg, James Pease, Kevin Smith, Candice Hirsch, Peter Tiffin (and moreÂ) +

ybrandva@umn.edu

UMinnesota PopulationEvolutionaryGenomics

We have a postdoc open in the McGaugh lab. Start-date is flexible (prefer sooner) and there is some flexibility with the scientific goals as well. The general goals are to 1) analyze ~120 resequenced genomes for complex demography, admixture, and local adaptation between cave and surface fish, 2) conduct multiple high-resolution QTL maps of sleep loss and circadian deregulation in cavefish, and 3) collaborate with the Brandvain lab on modeling project focused on genomic signature of admixture and a separate project focused on understanding loci effect size in wild populations.

Please send inquiries and CV to smcgaugh@umn.edu

Principal Duties and Responsibilities 90% Computational genomics, sample collection, writing manuscripts, animal husbandry and DNA extraction Analyzing next-generation sequencing data, keeping detailed notes and logs of the analyses, and keeping well-annotated code that was written for those analyses to ensure future replication of the work.

Conduct phenotyping, genotyping, and analyses of fish for a large-scale QTL experiment.

Submit permits, conduct field-work, and extract DNA for population genomic analyses.

Maintain fish and basic molecular lab work to confirm results of next generation sequence analysis.

Participate in small projects that may or may not be directly related research, but aid in other's projects in the lab and help generate preliminary data for grant submissions. This may also include mentoring of undergraduate and graduate students.

Write and submit at least one manuscript per year that presents results of the analysis conducted in the McGaugh lab. Help in the preparation of other lab-wide manuscripts and analyses for those manuscripts.

5% Lab maintenance, safety, supplies and systems administration In charge of daily function and operation of the McGaugh lab including the purchasing of supplies, maintenance of a safe and productive physical and computational environment.

5%- Lab citizen Attend lab meetings (and do associated readings), attend relevant lectures and training sessions. Assist other lab/community members.

Minimum Qualifications A PhD in genomics, evolution, genetics, or related fields. Experience with next-gen sequence data and a unix/command line interface. Experience with or willingness to learn scripting/programming languages including R, python, and/or C++ Demonstrated ability to produce high-quality publications A desire to help lead an integrative and motivated group of young scientists Patience, dedication, flexibility, and enthusiasm Excellent communication skills

Preferred Qualifications Strong knowledge of population genetics, genomics Interest in aging, stress, and recombination. Experience with international fieldwork and caving At least minimal understanding of Spanish or willingness to learn basics prior to fieldwork.

Suzanne McGaugh <suzanne.mcgaugh@gmail.com>

U Missouri QuantitativeGenetics

The Beissinger Lab is seeking an outstanding individual for a postdoctoral position in the Plant Genetics Research unit with the USDA Agricultural Research Service at the University of Missouri, Columbia. Our primary focus is understanding the evolution of quantitative traits in maize and related models. Our research utilizes a wide assortment of model species therefore individuals with experience in any species are encouraged to apply. We seek a candidate who will develop approaches to quantify epistasis using novel maize and algae—Epistasis Mapping Populations, refine methodology to estimate the number of loci contributing to variation for quantitative traits, and/or implement genomic prediction pipelines incorporating evolutionary annotations. The ideal candidate will be familiar with at least one coding language (ie R or Python), and will be proficient in statistics and mathematics. If interested, please send a cover letter and CV to Tim Beissinger:— beissingert@missouri.edu, or get in touch on Twitter: @timbeissinger. Informal inquiries are welcome.

Website: www.beissingerlab.org Kindly, Tim Beissinger USDA & Divisions of Plant and Biological—Sciences University of Missouri beissingert@missouri.edu http://beissingerlab.org

"beissingert@missouri.edu" <beissingert@missouri.edu>

UNevada Reno BioinformaticsNGS

POSTDOCTORAL POSITION IN MOLECULAR EVOLUTION AND NEXT GENERATION SEQUENCING AT THE UNIVERSITY OF NEVADA, RENO

The Alvarez-Ponce lab at the University of Nevada, Reno, is seeking a postdoctoral researcher to work on an USFWS funded project on the population genomics of Mycoplasma agassizii and Mycoplasma testudineum, two pathogens of the endangered desert tortoise. The successful candidate will conduct bioinformatic analyses to analyze dozens of NGS datasets and characterize the genomic diversity of both species. Research will be conducted in close collaboration with the labs of Dick Tracy and Ken Hunter (University of Nevada, Reno), and Franziska Sandmeier (Colorado State University).

Information about the Alvarez-Ponce lab can be found at www.genomeevol.wordpress.com The appointment will be for 12 months, with the possibility of extension depending on performance and funds availability.

Ideal candidates are those with: - A PhD in Biology, Computer Science or a related field. - Experience with bioinformatics analyses, including programming in any scripting language (e.g. PERL or Python). - Experience with Next Generation Sequencing. - A strong interest in Molecular Evolution. - Evidence of excellence and productivity in research. - Good communication and interpersonal skills.

Candidates should e-mail the following information to Dr. David Alvarez-Ponce (dap@unr.edu) as a single PDF: - An application letter, addressing the applicant's motivation for the position, and how their experience and skills fulfill the requirements listed above. - A full CV. - Contact information for 2 or 3 potential referees.

The University of Nevada, Reno is a Tier I institution offering a highly productive research environment, including outstanding core facilities in genomics and bioinformatics. The Biology Department has a growing and highly interactive evolutionary genomics research community. Reno is located in the Sierra Nevada mountains near Lake Tahoe, and has been recently rated as one of the best small cities in the US for outdoor recreation and overall quality of life.

Please circulate this post among suitable candidates.

– David Alvarez-Ponce, PhD Assistant Professor Department of Biology University of Nevada, Reno Max Fleischmann Agriculture Building, office 140B Tel.: (775) 682-5735 www.genomeevol.wordpress.com david.alvarez.ponce@gmail.com

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UPennsylvania GroupBehavior

Postdoctoral position in the evolution of group behavior

I am looking to hire a postdoc to study the emergence of group behaviors and collective identities. Anyone with an interest in any aspect to this problem is encouraged to apply. This could include (but is not limited to) those with expertise in (i) the development of mathematical models of social behavior based in evolutionary game theory, (ii) the application of machine learning approaches to make inferences about group behaviors from large, noisy datasets or (iii) the development of novel experimental approaches such as online games to test theories about the emergence of group behaviors.

The appointment will be initially for 1 year, with the possibility of reappointment for a further 2 years, and will be based at the University of Pennsylvania. The successful applicant will be strongly encouraged to develop their own research program under the aegis of the DARPA Next Generation Social Sciences project (https://news.upenn.edu/news/penn-led-team-receives-darpa-support-develop-next-generation-social-science) and to interact and collaborate with other groups involved in this research.

To apply, please send a two paragraph summary research proposal on the emergence of group behaviors and/or collective identities, a CV and contact information for 1-2 references via email to: alstew@sas.upenn.edu

The University of Pennsylvania is an EOE/Affirmative Action employer. Applications are welcome from candidates of any nationality. People from under-represented minorities are especially encouraged to apply

Please send enquiries to: alstew@sas.upenn.edu

"alstew@sas.upenn.edu" <alstew@sas.upenn.edu>

UPennsylvania MicrobialPopulationGenomics

Postdoctoral Researcher University of Pennsylvania, Department of Biology

The Evolution and Ecology of Disease Systems laboratory at the University of Pennsylvania is searching for a postdoctoral researcher to enable microbial population genomics by advancing the selective whole genome amplification (SWGA) protocol development pipeline. Microbial population genomic research is often hindered by the practicalities of obtaining samples with sufficient amounts of relatively pure microbial genomic DNA for next-generation sequencing. The goals of this project are to reduce the technical barriers that currently prevent researchers from collecting populations of whole genome sequences from microbes by developing an efficient selective whole genome amplification (SWGA) development pipeline that can create SWGA protocols to rapidly and cheaply amplify the genome of any focal microbial species, even if the focal microbial genome constitutes only a miniscule fraction of the sample (which often contains contaminating DNA from the host and other organisms). For more information on SWGA, see: https://www.ncbi.nlm.nih.gov/pubmed/28190880 https://www.ncbi.nlm.nih.gov/pubmed/28334194 https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4804174/ https://www.ncbi.nlm.nih.gov/pubmed/25096321 The main duties of the postdoctoral researcher will be designing and troubleshooting advanced molecular tools, processing and analyzing next generation sequence data including quality control and bioinformatics, and interfacing with computer scientists to identify criteria that can improve protocol efficacy. The ideal candidate should have experience designing and troubleshooting advanced molecular protocols, working with genomic data, and have enthusiasm for evolutionary based questions. This post is part of a larger project on the population genomics of microbial pathogens that includes researchers at Penn and other universities around the world.

The Department of Biology has a long-standing tradition of maintaining an integrated research and educational program across all basic biological sciences including Ecology and Evolution, Plant Sciences, Molecular and Cellular Biology, Genomics, and Neuroscience. The Department values interdisciplinary research, collaboration, and collegiality, emphasizing Life in its Natural Context. The University of Pennsylvania has a strong group of evolutionary biologists that frequently interact with each other and with an accomplished group of microbiologists in the Medical and Veterinary schools. Unlikely many universities, the proximity of the medical, veterinary, and arts and science schools are centrally located on the Philadelphia campus, which promotes a cross-talk and collaboration. The University of Pennsylvania is an equal opportunity employer. Minorities, women, individuals with disabilities, and protected veterans are encouraged to apply.

The position is available as early as Summer 2017. Salary is commensurate with experience based on the NIH guidelines.

To apply, please send (1) a cover letter outlining your previous experiences that make you suited for this position as well as your research, training, and career goals, (2) CV, and (3) Contact information for 3 references via email to dbrisson@sas.upenn.edu.

Please send enquiries to dbrisson@sas.upenn.edu

Dustin Brisson, Associate Professor Director, Evolution and Ecology of Disease Systems Laboratory Department of Biology University of Pennsylvania Philadelphia PA 19104-6018 http://www.bio.upenn.edu/faculty/brisson/ https://sites.sas.upenn.edu/brisson-lab/ dbrisson@sas.upenn.edu

"Brisson, Dustin" <dbrisson@sas.upenn.edu>

UppsalaU ArchaeaMetagenomics

Postdoctoral researcher in metagenomics and comparative genomics of archaea

Uppsala University, Department of Cell and Molecular Biology

Uppsala University is an international research university focused on the development of science and education. Our most important assets are all the individuals who with their curiosity and their dedication make Uppsala University one of Sweden's most exciting work places. Uppsala University has 40,000 students, 7,000 employees and a turnover of SEK 6,5 billion.

A postdoctoral researcher position is available at Uppsala University in the group of Dr. Anja Spang, which is based at the Department of Cell and Molecular Biology (Uppsala University, Sweden). The position, which is funded by a VR starting grant (to Anja Spang), is offered for a two-year period. The postdoc will be part of the research team of Associate Professor Thijs Ettema (see http://www.ettemalab.org/) at Uppsala University.

Dr. Spang has a key interest in the role of symbiosis in the evolution of life on Earth ranging from the origin of the eukaryotic cell to symbiotic relationships between different extant microbial groups, such as syntrophic and symbiotic interactions involving archaeal partners.

Therefore, a particular focus of her current research lies in the study of the evolution, cell biology, ecology and phylogenetic diversity of archaea affiliating with the tentative DPANN superphylum, which comprises lineages with extremely small genomes and cell sizes.

Metagenomics, comparative genomics and phylogenomic approaches have proven extremely useful to reconstruct genomes of the uncultivated microbial majority and comparatively analyze their genomic potential and evolution. In this regard, advanced bioinformatics and data science based approaches are increasingly necessary to adequately analyze the vast amount of genomic data, that has recently been generated.

Duties: The project is focused on the development and use of novel metagenomics approaches including sophisticated binning methodologies, that will allow to obtain highly complete, non-redundant genomes of deep-branching archaea affiliating with the DPANN superphylum. In addition, sophisticated phylogenomic and comparative approaches, will be applied and further developed to model genome evolution (and reduction) in the archaea.

Qualifications required: The successful applicant has a Ph.D. in computational biology, bioinformatics, phylogenomics, microbial genomics, molecular and/or evolutionary biology or related fields, and should preferably have knowledge and experience in high throughput genomic technologies including metagenomics. Experience in the use of the command line and Unix as well as in the application of programming languages such as R, Python and/or Perl are required. Finally, good command of English, spoken as well as written, is a prerequisite.

Applicants should have completed their doctorate within three years before the application deadline. If there are special reasons, Ph.D.

may have been awarded previously. Special reasons include leave of absence due to illness, parental leave, etc. The application must include three named referees with the necessary contact details, a Curriculum Vitae, a motivation letter (1 page) and a description of your past research (1 page).

For further information about the position contact Anja Spang (anja.spang@icm.uu.se). Please submit your application by 30th of May 2017, UFV-PA 2017/1421.

We decline offers of recruitment and advertising help.

See also: https://uu.mynetworkglobal.com/en/what:job/jobID:148992 Anja Spang <anja.spang@icm.uu.se>

USouthernCalifornia EvolMitochondriaSexAging

POSTDOCTORAL POSITION TO STUDY MITOCHONDRIAL EFFECTS ON SEX-SPECIFIC AGING IN TIGRIOPUS CALIFORNICUS

The position is available in the lab of Suzanne Edmands in the Department of Biological Sciences at the University of Southern California (lab website: https://dornsife.usc.edu/labs/edmands/).

The goal of this federally-funded project is to use the copepod Tigriopus californicus to understand effects of mitochondria and mitonuclear interactions on sex-specific aging. The postdoc would be involved in setting up and maintaining interpopulation crosses and quantifying fitness components, mitochondrial content and deletion ratios, oxidative stress markers and gene expression. The ideal candidate would have a strong background in evolutionary genetics, with experience in transcriptomics (including WGCNA), quantitative PCR and bioinformatics. The position is available for 2 years with a start date as early as August 2017.

Please submit application materials to: https://usccareers.usc.edu/job/los-angeles/postdoctoral-scholar-research-associate/1209/4515089 Consideration of applications will continue until the position is filled. For any questions, contact Suzanne Edmands: sedmands@usc.edu

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Suzanne Edmands Professor Department of Biological Sciences 3616 Trousdale Parkway, AHF 130 University of Southern California Los Angeles, CA 90089 (213)740-5548 http://dornsife.usc.edu/labs/edmands/ “sedmands@usc.edu” <sedmands@usc.edu>

UTromso EnvironmentalDNA

Four-year Postdoc with opportunity for permanent position as Associate Professor

Application deadline: May 31^st 2017

The research group for genetics at the Norwegian College of Fishery Science (NCFS), UiT The Arctic University of Norway (in beautiful Tromsø), seeks a motivated, collaborative, and ambitious scientist for a four-year postdoctoral position within environmental DNA (eDNA) and metabarcoding. The position offers the opportunity to qualify for a permanent Associate Professor position in the group. The position is a part of a strategic commitment to strengthen the capacity for aquaculture related research at NCFS/UiT.

The successful candidate will be responsible for developing approaches and applications of eDNA analysis within aquaculture to improve profitability, the management, and reduce the environmental impact. This includes proof-of-concept studies and in situ experiments at fish farms. The successful candidate is expected to establish a strong research program within novel genetic methods for surveying and monitoring in aquaculture and in the environment. Responsibilities also include teaching genetics (in the broadest sense), supervision of undergraduate and graduate students, and contribution to educational outreach and dissemination, at UIT and to the industry and society in general.

Qualification requirements: Doctoral degree in genetics or related subject areas (e.g. molecular ecology) and a strong research record. The ideal candidate should have a background in metabarcoding, the related bioinformatics, and experience with the use of diagnostic markers for qualitative and quantitative characterization of environmental DNA. Experience with relevant field and laboratory protocols used for analysis of environmental DNA is needed, and knowledge in theory and methods used in population genetics and taxonomy is an advantage. Knowledge about the aquaculture industry, the biology of Arctic and sub-Arctic fishes, experience in teaching relevant subjects, and the ability to obtain external funding is also considered a strength.

Please read the full posting for complete details pertinent to the position at: https://www.jobbnorge.no/ledigestillinger/stilling/137876/postdoctoral-fellow-for-tenure-track-position-in-genetics-at-the-norwegian-college-of-fishery-science, and follow the application instructions therein.

Kim PrÃbel, Ph.D. Associate Professor Norwegian College of Fishery Science UiT The Arctic University of Norway N-9037 Tromsø, Norway Office: (+ 47) 776 46107 Mobile: (+47) 454 36415 E-mail: kim.praebel@uit.no

kim.praebel@uit.no

UWashington Bothell MicrobialEvolution

A postdoctoral research position in microbial evolution is available in the Hillesland lab at University of Washington Bothell. This position is part of an NSF-funded grant to determine the population genetics governing the evolutionary dynamics of two mutualists during the first 3000 generations of their adaptation to obligate mutualism. In previous work, the Hillesland lab propagated the bacteria Desulfovibrio vulgaris and the archaeon Methanococcus maripaludis for thousands of generations in conditions requiring their cooperation. The postdoctoral researcher will investigate the impact of both inter and intra-genomic epistasis on evolutionary trajectories of these populations. She or he will also assist the PI in teaching undergraduates how to combine genetic manipulation and experimentation to identify and characterize adaptations of D. vulgaris or M. maripaludis.

The successful candidate will have a strong background in either evolutionary biology or microbiology and a PhD in a related field, and will demonstrate a strong interest in understanding evolutionary processes in a community context. Candidates that have experience in population genetics, in genetic manipulation of bacteria or archaea, or in anaerobic techniques, are encouraged to apply.

This postdoctoral position provides the opportunity to engage in scholarly activities with researchers in the greater Seattle area while living in a thriving metropolitan area in the Pacific Northwest. The Hillesland lab (https://sites.google.com/a/uw.edu/hillesland-lab/-home) is located in the Division of Biological Sciences in the new School of STEM at University of Washington Bothell, which is about 15 miles from the UW Seattle campus. The Division of Biological Sciences has a highly interactive group of 12 full-time faculty with expertise in ecology, evolution, physiology, computational biology, cellular biology, animal behavior, and neuroscience. The postdoctoral scholar may also participate in regular seminars and research discussions on the Seattle campus. The School of STEM and Division of Biological Sciences values innovative student-centered teaching and high quality research that engages undergraduate researchers. Mentored teaching opportunities are available for postdoctoral researchers that are interested in developing as teacher-scholars.

To apply for this position, please submit a copy of your CV, the names and contact information for three references, and a cover letter that explains i) why you are interested in this particular research project and position, ii) why you are qualified for the position, iii) your career goals, and how you expect this position to help you achieve those goals. Application materials should be sent in a single pdf to Dr. Kristina Hillesland at hilleskl@uw.edu. Applications will be reviewed as they are received until the position has been filled.

Kristina Hillesland

Assistant professor Biological Sciences School of STEM University of Washington, Bothell Bothell WA 98011

“(Kristina Hillesland” <hilleskl@uw.edu>

UWaterloo CompBiology

This position is funded by the SOSCIP program, and will involve a project on biomarker detection and analysis from metagenomes. Please see the additional information at this link: https://www.soscip.org/wp-content/-uploads/2017/05/ SOSCIP_MetagenomBio.pdf

Trevor C. Charles, Ph.D. Professor, Department of Biology University of Waterloo 200 University Avenue West Waterloo, ON N2L 3G1 CANADA tel: 519 888 4567 x35606 @trevorcharles

Trevor Charles <trevor.charles@uwaterloo.ca>

UWisconsin FungalDiseaseInBats

Microbiologist/Molecular Biologist: Wisconsin

Agency

University of Wisconsin, Department of Pathobiological Sciences

*Location *

Madison, Wisconsin

Job Category

Post Doctoral Appointments

Salary

$47,476.00 (annual salary)

Last Date to Apply

6/31/2017

Description

POST-DOCTORAL RESEARCH POSITION studying the mechanisms of resistance to white-nose syndrome (WNS), an emerging disease of bats caused by the fungus *Pseudogymnoascus destructans*. Two years of funding is available through the University of Wisconsin's Department of Pathobiological Sciences and the USGS National Wildlife Health Center located in Madison, WI. The primary objective of this project is to determine the biotic and abiotic properties of soil that reduce the abundance of infectious *P. destructans* in the environment. The specific objectives pertaining to WNS are to: 1) identify cave soils that suppress *P. destructans*, 2) characterize microbial communities and soil properties that may suppress *P. destructans* in the environment, and 3) investigate the potential to manipulate soils so that they are less conducive for the survival of *P. destructans*. The USGS National Wildlife Health Center conducts diagnostic work and research on numerous aspects of WNS and other wildlife diseases, and the selected candidate may have opportunities to work on additional projects as time and funding permit.

Qualifications

Qualified applicants should have a recent (last 1-3 years) Ph.D. with an emphasis in microbiology, molecular biology, genetics, or a similar discipline. Applicants must have 1) a record of research and publications, 2) experience with next-generation sequencing, metagenomics, and microbial community analyses, 3) proficiency with real-time PCR, 4) ability to work independently and solve project objectives with limited assistance, 5) good written and oral communication skills, 6) ability to work with other scientists, and 7) interest in disease ecology. Experience with culturing bacteria and fungi from environmental samples and/or analysis of soil properties is preferred but not required. Interested applicants should send a cover letter outlining experience, research interests, and relevant coursework; a curriculum vitae; and contact information for three references to Dr. Jeffrey Lorch, US Geological Survey - National Wildlife Health Center at jlorch@usgs.gov. Applicants should apply by May 31, 2017 to ensure consideration; however, applications will be accepted until position is filled. Start date may be negotiable. Applicants that have applied to this position will automatically be considered without the need to resubmit another application.

Contact Person

Jeffrey Lorch

Contact eMail jlorch@usgs.gov

"Lorch, Jeffrey" <jlorch@usgs.gov>

UZurich 2 ExptEvolutionaryBiol

Postdocs in computational or experimental evolutionary biology Postdoctoral fellowships in evolutionary biology are available in the laboratory of Andreas Wagner at the University of Zurich. The Wagner lab studies biological evolution on all levels of organization, from genes, genomes, and genetic networks to whole organisms. Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and life's fundamental organizational principles. Ongoing work in the lab includes computational analyses of genetic networks and of the evolution of metabolic diversity, the directed evolution of enzymes, and laboratory evolution of microbes (e.g., Bratulic et al. PNAS 2015; Aguilar-Rodriguez et al., Nature Ecology and Evolution 2017). A sample of the laboratory's research can be found at http://www.ieu.uzh.ch/wagner/ . We are looking for an individual who has received his or her PhD within the last five years, who is highly self-motivated and can work independently on a project that he or she will help develop. A successful computational biology candidate will have extensive experience in analyzing high throughput DNA sequence data, functional genomic data, or in computational or mathematical modeling of regulatory or metabolic systems. A successful experimental candidate will have a strong background in molecular cloning, microbiological techniques, DNA sequence analysis, and preferably experience with fluorescent proteins. Applicants without a demonstrated interest in evolutionary biology cannot be considered further. The position offers a highly competitive salary of up to three years on annually renewable contracts.

The working language in the laboratory is English. German skills, although helpful, are not essential. Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file merged from the following parts to annette.schmid@ieu.uzh.ch: CV including publication list, academic transcripts, a statement of research interests not exceeding three pages, and three academic references. Please include the word "PDOC17" in the subject line. Applications will be considered until May 25, 2017, or until the position is filled, whichever comes first. The position is available from the summer or fall of 2017.

Annette Schmid Administrative Assistant of Prof. A. Wagner University of Zurich Institute of Evolutionary Biology and Environmental Studies Wagner lab, Y27-J52 Winterthurerstrasse 190 CH-8057 Zurich Switzerland Mail to: annette.schmid@ieu.uzh.ch Phone +41 (0)44 635 61 42 Fax +41 (0)44 635 61 44 at the office on Monday and Thursday

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Postdoc in experimental evolutionary biology to study protein innovation

A postdoctoral fellowship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. We are looking for a researcher to study the evolution of new protein functions through directed evolution, and in particular the role that genetic robustness play for evolutionary innovation. Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and life's fundamental organizational principles. Ongoing work in the lab ranges from the directed evolution of enzymes to laboratory evolution of microbes and computational analyses of genetic networks (e.g., Bratulic et al. PNAS2015; Aguilar-Rodríguez et al., Nature Ecology and Evolution2017). A sample of the laboratory's research can be found at http://www.ieu.uzh.ch/wagner/ . We are looking for an individual who has received his or her PhD within the last five years, who is highly self-motivated and can work independently on a project that he or she will help develop.The successful candidate will have a strong background in molecular cloning, flow cytometry, and microbiological techniques. Experience with fluorescent proteins, as well as with computational analysis of high-throughput DNA sequence data will be a plus. Applicants without a demonstrated interest in evolutionary biology cannot be considered further. The position offers a highly competitive salary of up to three years on annually renewable contracts.

The working language in the laboratory is English. German skills, although helpful, are not essential. Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file merged from the following parts to annette.schmid@ieu.uzh.ch: CV including publication list, academic transcripts, a statement of research interests not exceeding three pages, and three academic references. Please include the

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WorkshopsCourses

Aussois France SoftwarePopGen Sep11-15

Dear colleagues,

It is our pleasure to announce that the third edition of the SSMPG summer school (Software and Statistical Methods for Population Genetics) will take place in Aussois (Savoie, France) from September 11 to September 15, 2017.

The aim of the summer school is to provide a comprehensive overview on software and statistical methods for detecting genes involved in local adaptation. Lecture notes and software demos will be given during the summer school. In addition to software demos, a data challenge will be organized to promote learning. By working in groups, participants will be asked to analyse simulated and challenging datasets. The objective is to find adaptive loci using the different software presented at the summer school.

More details about the summer school are available in the website of Grenoble Alpes Data Institute: https://goo.gl/sc09pA The deadline for registration is July 28, 2017.

Michael Blum (Univ Grenoble Alpes)

Michael Blum <michael.blum@univ-grenoble-alpes.fr>

Bari Italy AdvancedComputational-Metagenomics Jun19-23

ELIXIR-IIB Summer School in Advanced Computational Metagenomics < https://elixir-iib-training.github.io/website/miscellaneous/metagenomics-bari-2017-description.html >

DEADLINES EXTENSION:- early registration: 19 May 2017 - late registration: 9 June 2017

*** room availability at the UNA Hotel Regina is guaranteed only up to May 5th. People who want to attend the school can book the room at the Hotel before the school registration deadline. For room reservation at the at the special rate for school attendants, please send an e-mail to Stella (stella@meeting-planner.it) within May 5th.

The school will focus on the computational aspects of metagenomics analysis including reference databases, software and data retrieval and submission. The investigation of microbial communities will be discussed with an overview on real projects cases, both in ecological, clinical and nutrition fields. During the practical sessions students will learn how to analyse meta-barcoding and shotgun data from Next Generation Sequencing experiments and to perform statistical inference on them.

Target audience

This course is aimed at researchers involved or embarking upon bioinformatic analysis in metagenomic projects.

During the course, you will learn about:

Analysis of meta-barcoding sequence data; Analysis of shotgun Metagenomics sequence data; Functional annotation of metagenomic data; Methods for statistical comparisons of multiple metagenomic samples. Learning objectives

After this course you should be able to:

Choose and accomplish the most appropriate approach to analyse taxonomic composition and function of your metagenomics data; Perform metagenomic data submission and retrieval; Use statistical tools for comparative analysis of multiple samples; Use methods for pathway and network analysis in metagenomics projects.

A two-day workshop will precede a three-day intense training school where experts in the field will be delivering interdisciplinary training in computational metagenomics.

We offer three different registration options:

1. Workshop only 2. Three-day school only 3. Both events

You can find here < https://elixir-iib-training.github.io/website/2017/06/19/metagenomics-workshop-and-school-bari.html > full details - including fees and a registration form.

The workshop is open to all and will be able to host up to 100 people, whereas the intensive hands-on training course, for organisational and logistic reasons, is restricted to max 40 attendants.

IMPORTANT DATES: - Workshop: 19-20 June, 2017 - School: 21-23 June, 2017

VENUE: University of Bari, Italy

Speakers: - Duccio Cavalieri (University of Florence, IT) - Guy Cochrane (EBI, UK) - Carlotta De Filippo (IBIMET-CNR, IT) - Graziano Pesole (IBBE-CNR and University of Bari, IT) - Maurizio Sanguinetti (Catholic University of Rome, IT) - Nicola Segata (University of Trento, IT) - Gabriel Valiente (Technical University of Catalonia, SP) - Nills Peder Willansen (The Arctic University of Norway, NO) - Rob Finn (EBI, UK)

Summer School's instructors: - Marc Rosello & Guy Cochrane (EBI, UK); - Bruno Fosso & Monica Santamaria (IBBE-CNR, IT) - Gabriel Valiente (Technical University of Catalonia, SP) - Matteo Chiara (University of Milan, IT) - Rob Finn (EBI, UK)

Should you have any questions, please, do not hesitate to contact us: domenica.delia@gmail.com <domenicadelia@gmail.com> allegra.via@gmail.com enza.colonna@gmail.com

Best regards,

Domenica on behalf of the ELIXIR-IIB Training Team

vincenza.colonna@igb.cnr.it

Berlin BioinformaticsWithLinux 31Jul-4Aug deadline

Dear all,

we still have a few spots left for the course "Introduction to Linux and workflows for biologists".

https://www.physalia-courses.org/courses/course1/
Dates: 31 July-4 August 2017

Application deadline is: June 30th, 2017 (first-come, first-served)

Instructor: Dr. Martin Jones (founder, Python for Biologists).

Martin started his programming career by learning Perl during the course of his PhD in evolutionary biology, and started teaching other people to program soon after. He is author of two text books, Python for Biologists [http://www.amazon.com/Python-Biologists-complete-programming-beginners/dp/1492346136/] and Advanced Python for Biologists [http://www.amazon.com/Advanced-Python-Biologists-Martin-Jones/dp/1495244377/] . Overview

Most high-throughput bioinformatics work these days takes place on the Linux command line. The programs which do the majority of the computational heavy lifting genome assemblers, read mappers, and annotation tools are designed to work best when used with a command-line interface. Because the command line can be an intimidating environment, many biologists learn the bare minimum needed to get their analysis tools working. This means that they miss out on the power of Linux to customize their environment and automate many parts of the bioinformatics workflow. This course will introduce the Linux command line environment from scratch and teach students how to make the most of its tools to achieve a high level of productivity when working with biological data.

Intended audience

This workshop is aimed at researchers and technical workers with a background in biology who want to learn to use the Linux operating system and the command line environment. No previous experience of Linux is required.

Course Programme

https://www.physalia-courses.org/courses/course1/-curriculum/ Monday 31th - Classes from 09:30 to 17:30

Session 1 - The design of Linux

In the first session we briefly cover the design of Linux: how is it different from Windows/OSX and how is it best used? We'll then jump straight onto the command line and learn about the layout of the Linux filesystem and how to navigate it. We'll describe Linux's file permission system (which often trips up beginners), how paths work, and how we actually run programs on the command line. We'll learn a few tricks for using the command line more efficiently, and how to deal with programs that are misbehaving. We'll finish this session by looking at the built in help system and how to read and interpret manual pages.

Session 2 - System management

We'll first look at a few command line tools for monitoring the status of the system and keeping track of what's happening to processor power, memory, and disk space. We'll go over the process of installing new software from the built in repositories (which is easy) and from source code downloads (which is trickier). We'll also introduce some tools for benchmarking software (measuring the time/memory requirements of processing large datasets).

Tuesday 1sh - Classes from 09:30 to 17:30

Session 3 - Manipulating tabular data

Many data types we want to work with in bioinformatics are stored as tabular plain text files, and here we learn all about manipulating tabular data on the command line. We'll start with simple things like extracting columns, filtering and sorting, searching for text before moving on to more complex tasks like searching for duplicated values, summarizing large files, and combining simple tools into long commands.

Session 4 - Constructing pipelines

In this session we will look at the various tools Linux has for constructing pipelines out of individual commands. Aliases, shell redirection, pipes, and shell scripting will all be introduced here. We'll also look at a couple of specific tools to help with running tools on multiple processors, and for monitoring the progress of long running tasks.

Wednesday 2nd - Classes from 09:30 to 17:30

Session 5 - EMBOSS

EMBOSS is a suite of bioinformatics command-line tools explicitly designed to work in the Linux paradigm. We'll get an overview of the different sequence data formats that we might expect to work with, and put what we learned about shell scripting to biological use by building a pipeline to compare codon usage across two collections of DNA sequences.

Session 6 - Using a Linux server

Often in bioinformatics we'll be working on a Linux server rather than our own computer typically because we need access to more computing power, or to specialized tools and datasets. In this session we'll

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Berlin RAD-seq Dec4-8

Reduced representation genome sequencing (RADseq) data analysis for population genetics, association studies and phylogenetics

Dates

4-8 December 2017

https://www.physalia-courses.org/courses/course16/ INSTRUCTORS

Dr. Naiara Rodriguez-Ezpeleta https://www.physalia-courses.org/instructors/t19/ (Senior Researcher, Marine Research Division, AZTI, Spain)

https://www.physalia-courses.org/instructors/t19/ Dr. Josephine Paris https://www.physalia-courses.org/-instructors/t21/ (University of Exeter, UK)

https://www.physalia-courses.org/instructors/t21/ COURSE OVERVIEW

Reduced representation genome sequencing methods are revolutionizing evolutionary analyses of non-model organisms. Several data generation and data analysis protocols have been developed to generate thousands of sequence variants in hundreds of individuals at relative low cost and speed. 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.

WORKSHOP FORMAT

The workshop will be delivered over the course of five days. Each day will include an introductory lecture with class discussion of key concepts. The remainder of each day will consist of practical hands-on sessions. These sessions will involve a combination of both mirroring exercises with the instructor to demonstrate a skill as well as applying these skills on your own to complete individual exercises. After and during each exercise, interpretation of results will be discussed as a group.

WHO SHOULD ATTEND

This workshop is aimed at researchers and technical workers who are generating and/or analyzing reduced representation genome sequencing data (RAD-seq, ddRAD, 2bRAD, GBS,Â). 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.

REQUIREMENTS

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.

CURRICULUM

Monday 4th- Classes from 09:30 to 17:30

Lecture 1- Introduction to high-throughput reduced representation data

Lab 1-Computer environment set up and introduction to UNIX

Lab 2- High-throughput data quality assessment

Tuesday 5th-Classes from 09:30 to 17:30

Lecture 2- Overview of reduced representation library sequencing data analysis strategies: considerations depending of each case study

Lab 3- Data preprocessing

Wednesday 6th-Classes from 09:30 to 17:30

Lecture 3- De novo and reference based loci assembly and informative marker selection

Lab 4- De novo loci assembly

Lab 5- Reference genome based loci assembly

Thursday 7th-Classes from 09:30 to 17:30

Lecture 4- Applications of reduced representation sequencing data to population genetics, genome wide association studies and phylogenetics

Lab 6- From assembled loci to informative marker selection

Friday 8th-Classes from 09:30 to 17:30

Lecture 5-Review. Questions and Answers. Open discussion.

Lab 7 -Continue previous unfinished exercises or work on your own data

Further information:

The cost is 480 euros (VAT included) including course material and refreshments. We also offer an all-inclusive package at 745 euros (VAT included), which includes course material, refreshments, accommodation and meals.

–

Carlo Pecoraro, Ph.D

Physalia-courses Coordinator

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mobile: +49 15771084054

https://groups.google.com/forum/#!forum/physalia-courses

Berlin TrinityRNAseq Jun12-16 2

Dear all,

we have the last 4 spots left for the course “ Using the Trinity Framework for De novo Transcriptome Assembly, Annotation, and Downstream Expression Studies https://www.physalia-courses.org/courses/course11/ ”, 12-16 June 2017, Berlin (Germany).

https://www.physalia-courses.org/courses/course11/
https://www.physalia-courses.org/courses/course3/ .

Registration deadline: May 12th, 2017

Instructor: Brian Haas (Senior Computational Biologist at the Broad Institute of MIT & Harvard; https:/-

/www.physalia-courses.org/instructors/t12/ https://www.physalia-courses.org/instructors/t14/).

Course Overview:

RNA-Seq technology has been transformative in our ability to explore gene content and gene expression in all realms of biology, and de novo transcriptome assembly has enabled opportunities to expand transcriptome analysis to non-model organisms. This workshop provides an overview of modern applications of transcriptome sequencing and popular tools and algorithms for exploring transcript reconstruction and expression analysis in a genome-free manner, leveraging the Trinity software and analysis framework. Attendees will perform quality assessment of Illumina RNA-Seq data, assemble a transcriptome using Trinity, quantify transcript expression, leverage Bioconductor tools for differential expression analysis, and apply Trinotate to functionally annotate transcripts. Additional methods will be explored for characterizing the assembled transcriptome and revealing biological findings.

Intended Audience:

This workshop is aimed primarily at biologist researchers that have basic bioinformatics skills and are pursuing RNA-Seq projects in non-model organisms. Attendees will gain skills needed to successfully approach transcriptome sequencing, de novo transcriptome assembly, expression analysis, and functional annotation as applied to organisms lacking a high quality reference genome sequence.

Teaching format:

The workshop will be delivered over the course of four and a half days, with each session entailing lectures followed by practical hands-on sessions. Most all computing will be done on the cloud and attendees will use their own laptop computers with the Google Chrome web browser providing all the necessary interfaces to the cloud computing environment, including the linux command terminal.

Assumed background for the participants:

Basic experience with linux command-line execution and execution of bioinformatics tools would be helpful. We will begin the course with a review of basic linux commands and operations as a refresher. No programming or scripting knowledge is required.

Curriculum:

Day 1: Intro to the Trinity RNA-Seq workshop

* Intro to RNA-Seq * Intro to next-gen sequence analysis * Overview of unix and workshop setup o Practical: exploring the computational infrastructure * Read quality assessment and trimming o Practical: using FASTQC and TRIMMOMATIC

Day 2: Trinity de novo assembly, expression quantitation, and assembly QC

* Overview of Trinity de novo transcriptome assembly o Practical: assemble rna-seq data using Trinity * Intro to expression quantification using RNA-Seq o Practical: quantify expression for Trinity assembly * Initial data exploration: assembly quality, and QC samples and replicates o Practical: using IGV o Practical: replicate correlation matrix and PCA

Day 3: Differential expression analysis

* Overview of statistical methods for differential expression (DE). o Practical: using Bioconductor tools for DE analysis. * Transcript clustering and expression profiling o Practical: generating heatmaps and extracting transcript clusters.

Day 4: Functional annotation and Functional enrichment studies

* Overview of methods for functional annotation o Practical: applying Trinotate to find coding regions in transcripts and predict biological function. * Overview of functional enrichment analysis o Practical: applying GOseq to identify significantly enriched Gene Ontology categories among transcript clusters.

Day 5: Review and custom data analyses

Further information:

There are two packages available:

* "only-course" at 530 euros (VAT included), including all course materials and refreshments; * " all-inclusive" at 795 euros (VAT included), including all course materials, refreshments, meals and accommodation.

–

Carlo Pecoraro, Ph.D

Physalia-courses Coordinator

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mobile: +49 15771084054

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Bordeaux Holobionts Nov6-8

Interdisciplinary Workshop on Holobionts November 6-8, 2017 University of Bordeaux. Bordeaux, France < https://www.immuconcept.org/holobiont-workshop/ > Organizers: Derek Skillings and Thomas Pradeu

Microbes play a significant role in the evolution, development, health, and ecological interactions of multicellular organisms. The importance of microbial interactions is now widely recognized and at the center of many new research initiatives across the life sciences. Part of this emerging research has focused on reconceptualizing all macroorganisms as "holobionts", defined as a host and all its microbial symbionts, with the genomic complement of all partners becoming the "hologenome". There has been extensive debate about the importance and need for such a reconceptualization, and how it will shape research and our understanding of the living world moving forward.

This workshop will bring together researchers from diverse disciplines (microbiology, evolutionary biology, ecology, pathology, neuroscience, medicine, philosophy) working on holobionts and host-microbe associations, in order to foster interdisciplinary communication, investigate whether there are any particular insights or fruitful general principles that emerge from investigations across fields, and hopefully stimulate collaborative research for the future.

If you would like to participate by giving a talk, please submit an abstract or prospectus (up to 1000 words) by going to the link on the workshop website. Submissions should be prepared for blind review and uploaded by the Abstract Deadline: July 16, 2017.

Registration for the workshop by October 1st, 2017 is required, but free. Follow the website for further updates.

Confirmed Speakers: John Cryan - University College Cork John Dupré- University of Exeter Ruth Gates - Hawaii Institute of Marine Biology Carmen Lía Murall - CNRS, University of Montpellier Forest Rohwer - San Diego State University Pamela Schnupf - Pasteur Institute Philippe Vandenkoornhuyse - University of Rennes

This workshop is part of the Immunity, DEvelopment and the Microbiota (IDEM) project, an ERC-funded project located at the interface of philosophy of biology and biology (ERC Grant #637647, PI: Thomas Pradeu).

derek.skillings@gmail.com

cE3c Portugal Biology

Subject: Portugal-cE3c-Course: three advanced courses with deadlines end May-June2017

cE3c - Centre for Ecology, Evolution and Environmental Changes is organizing several Advanced Courses: see below the three with closer deadlines (last before summer holidays!).

Additional informations at: http://-ce3c.ciencias.ulisboa.pt/training/?cat=8 —

Lichens as a tool for interpretation of environmental changes

taught by Pedro Pinho, Paula Matos, Silvana Munzi et al.| July 10-14 2017 @ Lisbon, Portugal

Objectives: With this course, we aim at providing the participants with the basics of lichen biology and ecology, biomonitoring and data analysis methods to allow the use of lichens for the interpretation of the environmental conditions and the development of a responsible scientific-based environmental management.

Course coordinator Pedro Pinho (paplopes@fc.ul.pt) Post-Doc at the Centre for Ecology, Evolution and Environmental Changes (cE3c) (http://-ce3c.ciencias.ulisboa.pt/member/pedro-pinho)

Intended audience This course will be open to a maximum number of 18 participants, being directed to PhD or MSc students in Ecology, Environmental Studies, Geography or related areas, and postdocs and other professionals working in related topics. Minimum formation: Bachelor in Biology, Natural Science or related areas.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of fees for other participants see the programme details (access link below)

Deadline for applications: May 31, 2017

Candidates should send a short CV and motivation letter to lichenscourse@fc.ul.pt

For additional details about the course and to know how to register, go to http://ce3c.ciencias.ulisboa.pt/training/?cat=8 or http://lichens.fc.ul.pt/ For more information about the course, please contact by email: Pedro Pinho (paplopes@fc.ul.pt)

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Practical Course on Phylogeography

organized by Octavio Paulo| July 3-7 2017 @ Lisbon, Portugal

Objectives: Phylogeography is one of the recent scientific areas emergent from the dissemination of highthrouput technologies of sequencing starting in the 90's of the XXth century, with the consequent development of intraspecific genetic variance analysis and its geographic distribution. The analysis of phylogeographic data allows to study the processes of population differentiation and the underlying evolutionary and demographic history. Applications of this body of knowledge go from conservation genetics to the study of the evolution of species and populations. This course is aimed at students and professionals that intend to get started on phylogeographic analysis as well as researchers already with some experience that want to deepen or update their knowledge in the field. The course involves theoretical classes as well as hands-on practical sessions using software. Participants are encouraged to bring their own sequence data for analysis.

Course instructor Octavio Paulo (octavio.paulo@fc.ul.pt) Assistant Professor at the Faculty of Sciences of the University of Lisbon, researcher at the Centre for Ecology, Evolution and Environmental Changes (cE3c - http://ce3c.fc.ul.pt/), Coordinator of the Computational Biology & Population Genomics Group (http://cobig2.com)

Intended audience This course will be open to a maximum number of 20 participants. Minimum formation: Bachelor in Biology or related area.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of fees for other participants see the programme details (access link below).

Deadline for applications: June 9, 2017

Candidates should send a short CV and motivation letter to Octavio Paulo (octavio.paulo@fc.ul.pt)

For additional details about the programme of the course, fees and to know how to register, click here, and access the specific course http://ce3c.ciencias.ulisboa.pt/training/?cat=8 For more information about the course, please contact: octavio.paulo@fc.ul.pt

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Big Data - knowledge extraction from biological databases

Taught by Teresa Nogueira | July 10-14 2017

Objectives: This five days intensive course aims at familiarizing the attendees with the unix environment and shell scripting. The participants will develop and implement querying algorithms in order to generate metadata for analysis.

Course instructor

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Finland MathematicalEcology Aug2018

Advance Announcement: THE HELSINKI SUMMER SCHOOL ON MATHEMATICAL ECOLOGY AND EVOLUTION 2018

Dear Colleagues,

We are glad to announce the 2018 edition of The Helsinki Summer School on Mathematical Ecology and Evolution, an EMS-ESMTB School in Applied Mathematics. The school will be held next year, between 19 and 26 August 2018 in Turku, Finland, and will be part of the EMS Year of Mathematical Biology < http://euro-math-soc.eu/year-mathematical-biology-2018 >.

The core program consists of five series of lectures:

Karl Sigmund (University of Vienna): Evolutionary game theory Odo Diekmann (Utrecht University): Renewal equations in population biology Sebastian Schreiber (University of California, Davis): Coexistence in variable environments Ellen Baake (University of Bielefeld): Probabilistic models and ancestral processes in population genetics Hans Heesterbeek (Utrecht University): Ecology of infectious diseases

All young researchers working in mathematical ecology can apply from all countries, especially from Europe and the Mediterranean. The school is aimed at graduate students of mathematics, but we also welcome students of biology with sufficient background in mathematics, as well as advanced undergraduates and postdocs.

The application period will start in late 2017. For more information, see the school's webpage https://wiki.helsinki.fi/display/BioMath/The+Helsinki+Summer+School+on+Mathematical+Ecology+and+Evolution+2018 With best regards, Eva Kisdi

"eva.kisdi@helsinki.fi" <eva.kisdi@helsinki.fi>

Groningen ESEB2017 Aug20-25 DrosophilaPopulationGenomics

ESEB 2017 Satellite Workshop in Groningen: "ESEB STN - The European Drosophila Population Genomics Consortium (DrosEU)"

Dear Colleagues:

We would like to kindly invite you to participate in a satellite discussion workshop on Drosophila population genomics and evolution, held during the ESEB 2017 meeting in Groningen (16th Congress of the European Society for Evolutionary Biology, 20-25 August 2017; Groningen, The Netherlands; http://www.eseb2017.nl).

The workshop will be held on Thursday 24 August in the afternoon; please see the conference program for details. The workshop is open to all interested ESEB participants/evolutionary biologists.

The main aim of the workshop is to present the work and objectives of the European Drosophila Population Genomics Consortium (DrosEU), which is funded by an ESEB Special Topics Network (STN) grant, to the ESEB/evolutionary biology community and in to discuss future developments/collaborations in the field of Drosophila adaptation genomics.

The DrosEU consortium, founded in 2013, consists of approx. 70 scientists from Europe and beyond: over the past few years, we have been sampling and sequencing a large number of European Drosophila melanogaster populations through space and time. The overarching goal of DrosEU is to foster the integration and exchange of population genomic information and data in the Drosophila system and to cooperate closely in collecting, generating and analyzing genomic and environmental data for numerous Drosophila populations across Europe and beyond in order to gain a better understanding of adaptation. DrosEU is also closely collaborating with the US-based Drosophila Real Time Evolution Consortium (Dros-RTEC) (http://web.sas.upenn.edu/paul-schmidt-lab/dros-rtec).

More information on DrosEU can be here: http://eseb.org/prizes-funding/special-topic-networks/european-drosophila-population-genomics-network-droseu/ or at https://sites.google.com/site/droseuweb/ . We are looking forward to seeing you in Groningen!

Best wishes, Josefa González, Martin Kapun, and Thomas Flatt.

Organizers (on behalf of DrosEU):

Josefa González Institute of Evolutionary Biology CSIC-Universitat Pompeu Fabra Barcelona, Spain josefa.gonzalez@ibe.upf-csic.es www.biologiaevolutiva.org/gonzalez_lab Thomas Flatt Department of Ecology and Evolution University of Lausanne Lausanne, Switzerland

Martin Kapun Department of Ecology and Evolution University of Lausanne Lausanne, Switzerland

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

E-mail: Thomas.Flatt@unil.ch Office: +41 21 692 4203 Fax: +41 21 692 4165

Web: https://www.unil.ch/dee/home/menuinst/people/group-leaders/prof-thomas-flatt.html Mechanisms of Life History Evolution: http://ukcatalogue.oup.com/product/9780199568765.do Thomas Flatt <thomas.flatt@unil.ch>

Lausanne Statistical Genetics Sep4-15

SWISS INSTITUTE IN STATISTICAL GENETICS

MODULE 1 - BAYESIAN STATISTICS FOR GENETICS

WHERE? University of Lausanne WHEN? 4-6 September 2017

ORGANIZERS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INSTRUCTORS: Prof. Jonathan Wakefield (University of Washington - US) & Prof. Ken Rice (University of

Washington - US)

INFO & REGISTRATION: https://www.cuso.ch/activity/?p28&uid350 DESCRIPTION: The use of Bayesian methods in genetics has a long history. In this introductory module we will begin by discussing introductory probability. We will then describe Bayesian approaches to binomial proportions, multinomial proportions, two-sample comparisons (binomial, Poisson, normal), the linear model, and Monte Carlo methods of summarization. Advanced topics will be touched on, including hierarchical models, generalized linear models, and missing data. Illustrative applications will include: Hardy-Weinberg testing and estimation, detection of allele-specific expression, QTL mapping, testing in genome-wide association studies, mixture models, multiple testing in high throughput genomics.

MODULE 2 - POPULATION GENETIC DATA ANALYSIS

WHERE? University of Lausanne WHEN? 6-8 September 2017

ORGANIZERS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INSTRUCTORS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INFO & REGISTRATION: https://www.cuso.ch/activity/?p28&uid351 DESCRIPTION: A unified treatment for the analysis of discrete genetic data, starting with estimates and sample variances of allele frequencies to illustrate genetic vs statistical sampling and Bayesian approaches. A detailed look at Hardy-Weinberg and linkage disequilibrium, including the use of exact tests with mid-p-values and a new look at X-chromosome Hardy- Weinberg testing. A new characterization of population structure with F-statistics, based on allelic matching within and between populations with individual relationship estimation as a special case. Analyses illustrated with applications to forensic science and association mapping, with particular reference to rare variants.

MODULE 3 - QUANTITATIVE GENETICS

WHERE? University of Lausanne WHEN? 11-13 September 2017

ORGANIZERS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INSTRUCTORS: Prof. Bruce Walsh (University of Arizona - US) & Prof. Guilherme J. M. Rosa (University of Wisconsin - US)

INFO & REGISTRATION: https://www.cuso.ch/activity/?p28&uid744 DESCRIPTION: Quantitative Genetics is the analysis of complex characters where both genetic and environment factors contribute to trait variation. Since this includes most traits of interest, such as disease susceptibility, crop yield, growth and reproduction in animals, human and animal behavior, and all gene expression data (transcriptome and proteome), a working knowledge of quantitative genetics is critical in diverse fields from plant and animal breeding, human genetics, genomics, behavior, to ecology and evolutionary biology. The course will cover the basics of quantitative genetics including: genetic basis for complex traits, population genetic assumptions including detection of admixture, Fisher's variance decomposition, covariance between relatives, calculation of the numerator relationship matrix based on IBD alleles and an arbitrary pedigree, the genomic relationship matrix based on AIS alleles, heritability in the broad and narrow sense, inbreeding and crossbreeding, and response to selection. Also an introduction to advanced topics such as: Mixed Models, Best Linear Unbiased Prediction (BLUP), Genomic selection (GBLUP), Genome Wide Association Analysis (GWAS), QTL mapping, detection of selection from genomic data, correlated characters; and the multivariate response to selection.

MODULE 4 - MIXED MODELS IN QUANTITATIVE GENETICS

WHERE? University of Lausanne WHEN? 13-15 September 2017

ORGANIZERS: Prof. Jérôme Goudet (University of Lausanne - CH) & Prof. Bruce Weir (University of Washington - US)

INSTRUCTORS: Prof. Bruce Walsh (University of Arizona - US) & Prof. Guilherme J. M. Rosa (University of Wisconsin - US)

INFO & REGISTRATION: https://www.cuso.ch/activity/?p28&uid745 DESCRIPTION: "Mixed models" refers to the analysis of linear models with arbitrary (co)variance structures among and within random effects and may be due to such factors as relationships or shared environments, cytoplasm, maternal effects and history. Mixed models are utilized in

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LeedsUK EssentialComputingSkillsForMolBiol Jul3-5

Next Generation Biologists: Essential Computing Skills for Molecular Biology is a BBSRC-STARs programme-funded project to introduce and train researchers in the essential skills and best practices in scientific computing and bioinformatics. The format of the materials and the nature of the delivery will be based on the successful "Software Carpentry" (http://software-carpentry.org/-) blended-learning model where students learn by developing skills through hands-on live coding and peer programming sessions led by experienced Software Carpentry instructors and supported by a small team of helpers.

AUDIENCE The first workshop is aimed at researchers with little or no experience in programming and data analysis who nevertheless need these approaches in their research.

ORGANISERS AND INSTRUCTORS The main organisers of the workshops are Dr Mary J. O'Connell (@Evol_Molly), Dr Martin Callaghan (both at the University of Leeds) and Dr Jarek Bryk (@jarekbryk at the University of Huddersfield). Drs Callaghan and Bryk are Software Carpentry Instructors. The project is a joint initiative of the University of Leeds and the University of Huddersfield.

PRELIMINARY PROGRAMME Monday Introduction to the fundamentals of UNIX shell, software development and best practices, delivered using Python but easily transferable to other programming languages.

Tuesday Introduction to fundamentals of R with R Studio, including data and analysis reproducibility, concluded with example analysis of high-throughput data.

Wednesday A "hackathon" day, during which participants will use skills learned in earlier days to solve a real-life data analysis problem of their choosing.

DATE The first workshop will be run on the 3rd-5th July 2017 (Monday to Wednesday inclusive).

VENUE The first workshop will take place at the University of Leeds, UK.

COSTS The workshop is free of charge for all BBSRC-funded researchers, as well as staff and students from the Universities of Leeds and Huddersfield. For all other participants a course fee of Â£170 will apply that will need to be paid before the workshop begins. Travel and accommodation costs are *not* covered by the organisers.

HOW TO APPLY To apply for a place on the workshop, prepare a maximum one-page long curriculum vitae and a 200 word statement detailing why this course if of particular importance to your current research. Please combine the two *into a single pdf file* and send it to Dr Mary J. O'Connell at m.oconnell[at]leeds.ac.uk *by midnight 15th June 2016*. The workshop will be limited to 25 participants. The selection committee will notify successful applicants by the end of 16th June.

More details about the project and the workshop are available on our website at http://nextgenbiologists.org. We are also on Twitter at @nextgenbiol (the "l" is important :-).

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âBryk

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University of Huddersfield inspiring tomorrow's professionals.

Jarek Bryk <J.Bryk@hud.ac.uk> Jarek Bryk <J.Bryk@hud.ac.uk>

London BayesianPhylodynamics Jul24-28

Dear colleagues,

We are pleased to announce the Taming the BEAST 2017 workshop on Bayesian phylogenetic and phylodynamics analyses

Date: Monday 24 July - Friday 28 July 2017 Venue: London School of Hygiene and Tropical Medicine, Keppel Street, London, WC1E 7HT, UK

Taming the BEAST is a workshop focused on BEAST2, an open-source software package for Bayesian phylogenetic analyses of molecular sequences. The workshop consists of invited talks, lectures and hands-on tutorials by prominent experts in the field. This workshop aims at equipping participants with the skills and core knowledge necessary to confidently perform phylogenetic and phylodynamics analyses of their own. It is open to scientists of any level interested in the analysis of genomic data and molecular evolution.

Invited speakers: Alexei Drummond, University of Auckland; Nuno Faria, University of Oxford; Oliver Pybus, University of Oxford; Tanja Stadler, ETH Zürich; Tim Vaughan, University of Auckland; Erik Volz, Imperial College London

Program: The program can be seen at the following link: https://taming-the-beast.github.io/workshops/ Registration fee: 245 + fees. Lunch and snacks will be provided. Registration deadline: Monday 12 June 2017 Accommodation: Participants are asked to arrange their own accommodation. For a selection of recommended hotels and/or hostels nearby the School please view the hotels list < https://www.tripadvisor.co.uk/HotelsNear-g186338-d7888549-London_School_of_Hygiene_Tropical_Medicine-London_England.html >.

Contact: Stephane Hue Email: Stephane.Hue@lshtm.ac.uk

For more information and how to apply, please visit: http://www.lshtm.ac.uk/newsevents/events/-2017/07/taming-the-beast-2017 This workshop is organised in collaboration with ETH Zürich and the LSHTM Centre for Mathematical Modelling of Infectious Diseases

Stephane.Hue@lshtm.ac.uk

LundU AnimalMigration Oct16-27

Dear all,

We like to announce that on the 16th-27th of October the two-week long international PhD course in Ecology of Animal Migration will be held at the Department of Biology at Lund University, Sweden. Here follows a short overview of the course. For more information and registration, please visit the course home page (link attached further down). Please consider passing this to interested PhD students.

Overview

Animals move across different spatial and temporal scales either as part of their daily life or as part of seasonal migrations to exploit resources in the environment. Well known examples are the global scale seasonal migrations in birds, sea turtles, fish and mammals, such as whales and wildebeests. Also movements at smaller scales occur, such as the vertical movements in plankton, the dispersal in soil collembolans and movements of pollinating insects. But what are the ecological causes and evolutionary consequences of animal movements?

During this two-week course you will get insight in a number of different methods and approaches to study the migration of birds, insects, fish, amphibians and mammals, ranging from experimental studies in the laboratory to tracking long-distance migration in wild animals. Lectures will be given by international authorities in the field as well as by researchers in the CAnMove Group at Lund University.

http://www.canmove.lu.se/courses-workshops/courses/-ecology-of-animal-migration-2017 Kind regards,

Linus Hedh

Student coordinator

Linus Hedh

PhD student

Department of Biology Ecology Building Sölvegatan 37 SE-223 62 Lund Sweden +46 766 444 660

Linus Hedh <linus.hedh@biol.lu.se>

MDIBL Maine EnvironmentalGenomics Jul8-15

Subject: The Summer Workshop on Population-Scale Genomic Studies of Environmental Stress (EnGen 2017), July 8- July 15, with scholarships still available

REGISTER SOON; scholarships and places are now very limited

Next-Generation Summer Course in Environmental Genomics at the Mount Desert Island Biological Laboratory

A technical course that provides participants with the skills needed to generate and analyze modern sequence data (DNA, RNA) through a hands-on approach that utilizes novel data to guide research into how environmental conditions affect gene responses and the fitness of organisms while accounting for population structure.

Date: July 8- July 15, 2017. Number of participants: Restricted to 25. Only $300 registration fee!

We are pleased to announce that this course is now supported by the National Institutes of Health through the Big Data To Knowledge (BD2K) Program. Therefore, scholarships are available for US citizens or permanent residents, including room and board.

https://mdibl.org/course/environmental-genomics/ Please contact John Colbourne (J.K.Colbourne@bham.ac.uk) and Joe Shaw (joeshaw@indiana.edu) if you are a non-US citizen or permanent resident wanting to participate.

The faculty at MDI Biological Lab is pleased to again offer a training course in Environmental Genomics, aiming to better understand technologies and approaches used to discover how gene function is influenced by environmental conditions while accounting for variation that exists within and among natural populations. This course is built on the paradigm that the research field will most effectively grow by properly designing large-scale experiments enabled by drastically increased sample-throughput and lower sequencing costs. Most importantly, the bioinformatics challenges of manipulating and analyzing population-level genomics data must be addressed.â€â€

This course is designed to train the next-generation of environmental scientists, which have included in past years: university professors, postdoctoral researchers, doctoral students and government scientists, representing institutions from North America and Europe. Most responded in the departure survey that the course curriculum, choice of technologies, and effectiveness provided sufficient training to either begin or enlarge an environmental genomics project in their own laboratories. All reported that they would recommend this course to a colleague.

â€â€This course trains researchers to design studies, and to collect and analyze RNA-Seq gene expression data. Daphnia is used for training because of its growing use as a model system for environmental genomics and for improving environmental health protection, yet the skills learned during the course will be applicable to all study systems with maturing genomics resources, including humans. Much time is devoted to guiding the current and future projects of attendees.

â€â€Ultimately, participants will be better positioned to incorporate these technologies into their own research laboratories, while better understanding how functional genomics and automation can be applied to ecology, evolution and environmental toxicology.â€

Mount Desert Island Biological Laboratory Old Bar Harbor Rd., Salisbury Cove, ME 04672 MDIBL - http://www.mdibl.org j.k.colbourne@bham.ac.uk

Montana PopulationGenomicsDataAnalysis Sep25-30

ConGen: Population Genomics Data Analysis Course and Workshop

Theme: Applications of Next Gen Sequencing Data to Understand Population Structure, Adaptive Evolution, and Environmental Influences on Genomic Variation.

Instructors include: Louis Benatchez, Eric Anderson, Tiago Antao, Brian Hand, Paul Hohenlohe, Marty Kardos, Tabatha Graves, Joanna Kelley, Gordon Luikart, Mike Schwartz?, Robin Waples, Diane Whited, and more.

When: September 25-30, 2017, Flathead Lake Biological Station, Polson, Montana

For details on ConGen-2017: see http://www.umt.edu/sell/cps/congen2017/ Past courses: see Andrews & Luikart 2014, http://onlinelibrary.wiley.com/doi/10.1111/mec.12686/abstract and Benestan et al.

2016: http://onlinelibrary.wiley.com/doi/10.1111/-mec.13647/full; ConGen 2013 - dinner by the lake

Objective: To provide training in conceptual and practical aspects of data analysis for understanding the population and evolutionary genomics of natural and managed populations. Emphasis will be on next generation sequence data analysis (RADs, exon capture, and whole genome sequence analyses) and interpretation of output from recent novel statistical approaches and software programs. The course include discussions (in a workshop like format) among young researchers (student participants) and >10 leaders in population genomics (instructors) to help develop our next generation of conservation and evolutionary geneticists.

Who should apply: Advanced Undergrads, Ph.D. students, post-docs, faculty, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. Participation will be limited to 25-30 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own NGS data to analyze.

"Luikart, Gordon" <gordon.luikart@mso.umt.edu>

Oslo Biosystematics Jun12-14

ForBio - the Scandinavian Research School in Biosystematics is organising a training program for outgoing and incoming postdoctoral fellows to apply for European Commission H2020 MSCA Individual Fellowships.

The training program is open to potential outgoing and incoming fellows from research groups in systematic biology in Scandinavia, including systematics, taxonomy, phylogenetics, biogeography, etc. The target group are academically-engaged senior PhD students, postdocs and junior researchers. Including IF programs ER-ST (Standard European), ER-CAR (Career Restart Grant), ER-SE (Society and Enterprise), ER-RI (Reintegration), and GF (Global). We aim to have a mixed group of incoming and outgoing fellows.

The program runs from May 19th to the submission deadline of the H2020 MSCA-IF call on September 14th 2017. The training includes match-making between fellows and hosts, coaching, an intensive 3-day workshop at the Natural History Museum in Oslo, writing support, peer review, and liaison with EU coordination offices.

For more information about teachers, target group, course plan, costs and registration, see: http://-www.forbio.uio.no/events/courses/2017/MSCAIF.html For a list of potential hosts for incoming fellows, see: http://www.forbio.uio.no/events/courses/2017/msca-if-hosts.html Registration: Fellows should register online and provide contact information of their host before May 19th. Registered fellows will be evaluated and notified by May 21st regarding acceptance and participation in the training program. Make sure the reserve the dates 12-14 June for the workshop.

Contact Hugo de Boer (hugo.deboer@nhm.uio.no) or Maria Capa (maria.capa@ntnu.no) for more information.

Hugo de Boer Natural History Museum University of Oslo P.O. Box 1172 Blindern 0318 Oslo, Norway Phone: +47 22851875 Leader of ForBio - the Scandinavian Research School in Biosystematics www.nhm.uio.no/english/about/organization/research-collections/people/h ugode/ www.forbio.uio.no/ Hugo de Boer <h.d.boer@nhm.uio.no>

Sicily Italy EnvironmentalDNAMetabarcoding Sep3-9

Dear All,

I am very pleased to announce the first International Course in Environmental DNA and Metabarcoding, Understanding Aquatic Biodiversity, organised in collaboration with the Sicily Center for International Education (SCIE), Italy and the University of Salford, UK.

Dates 3-9 September

Program - 7 days/6 nights

Number of participants - (25 max)

Program Fee per Student - euro 1290

Venue - SCIE Center, Sicily, Italy www.sciecenter.org Course Description:

Environmental DNA (eDNA) coupled with metabarcoding represents a powerful tool to investigate ecosystem complexity and reveal hidden biodiversity.

This novel approach is revolutionising the way we assess and monitor aquatic ecosystems.

This course will provide the students with the basic knowledge and skills required to apply the eDNA metabarcoding approach in aquatic environments.

The course program includes a combination of lectures, field activities in the Plemmirio Marine Protected Area, lab-work and data analysis to provide the students with a thorough understanding of the use of eDNA in molecular ecology, with hands-on experience.

This program is aimed to postgraduate students (masters and PhD students), postdoctoral and early-career researchers.

The course will be held on the scenic island of Ortigia, the historic centre of Siracusa in Sicily, Italy.

Course Lecturers:

Prof. Stefano Mariani, University of Salford, United Kingdom

http://www.marianilab.org/stefano-mariani Dr. Owen S. Wangensteen, University of Salford, United Kingdom

http://www.marianilab.org/owen-wangensteen-1 Judith Bakker, MSc., University of Salford, United Kingdom

http://www.marianilab.org/judith-bakker Dr. Alexia Massa-Gallucci, SCIE Center, Italy

http://sciecenter.org/about/ Course Content:

What is eDNA. The role and usefulness of eDNA for the study of aquatic biodiversity. Application of eDNA.

Sampling methods and strategies. Sample storage, transport and processing.

Analysis of samples: extraction of DNA. Choice of primers, species-specific vs multispecies approaches. Metabarcoding. PCR-free approaches.

eDNA metabarcoding: library preparation and sequencing.

eDNA metabarcoding: bioinformatics.

Down-stream ecological analysis.

Powers and pitfalls of eDNA. The Future of eDNA.

Application and Course Fees

Application by May 26th 2017 at info@sciecenter.org

To apply send a letter of support from your academic supervisor and a half page letter of intention detailing your research interests and experience and how you would envisage employing eDNA in your current or future project.

Fee per student euro 1290 includes:

Accommodation in B&B, welcome and farewell dinners, refreshments during the course, transport to the fieldwork site, general liability insurance, certificae of participation, tuition, SCIE Center 24 hour support.

For more information, enquiries and booking:

Email: info@sciecenter.org web: www.sciecenter.org tel.: +39 366 1907984

Please share this information with people who might be interested.

Best regards,

Dr. Alexia Massa-Gallucci.

Dr. Alexia Massa-Gallucci Course Coordinator for Environmental Science, SCIE (Sicily Centre for International Education), Via Landolina 5, 96100 Siracusa Italy

massagalluccia@sciecenter.org

www.sciecenter.org Alexia Massa Gallucci <alexia.massagallucci@gmail.com>

UCambridge SystemsBiol Jul17-21

Dear Colleagues,

Apologies for multiple postings. Please help forward it to other potentially interested attendees. This is the final call for participation for the 4th International Synthetic and Systems Biology Summer School (SSBSS 2017) on July 17-21, 2017 at the University of Cambridge, UK.

Call for Participation

Submission system is open, and can be found here: http://www.taosciences.it/ssbss/#application-form applicants will be notified of acceptance within a few days of application submission.

Call for Abstracts

We are still accepting abstract submissions for posters and oral presentations to be presented during the poster sessions and the talk sessions. Abstracts can be uploaded to EasyChair and authors will be notified of acceptance within a few days of abstract submission: https://easychair.org/conferences/?conf=ssbss2017 Please register and join us at the University of Cambridge for SSBSS 2017! More details about the conference can be found below and at the SSBSS 2017 web site: http://www.taosciences.it/ssbss/ We hope to see you there!

Thanks! SSBSS 2017 Organizing Committee

INVITED SPEAKERS

Antonino Cattaneo, Scuola Normale Superiore Pisa, Italy Jasmin Fisher, Microsoft Research & Cambridge Systems Biology Centre, UK Carole Goble, University of Manchester, UK Jim Haseloff, University of Cambridge, UK Jay Keasling, University of California, Berkeley, USA Edda Klipp, Humboldt University, Germany Natalio Krasnogor, Newcastle University, UK Markus Ralser, University of Cambridge, UK & The Francis Crick Institute, UK Uwe Sauer, Institute of Molecular Systems Biology, ETH Zurich, Switzerland Gill Stephens, The University of Nottingham, UK Mike Stubbington, EMBL-EBI, Cambridge UK Eriko Takano, University of Manchester, UK Sarah Teichmann, Wellcome Trust Sanger Institute & EMBL, European Bioinformatics Inst., UK

Talks Talks Matteo Barberis, University of Amsterdam, The Netherlands Other speakers will be announced soon.

Industrial Panel Jonathan Chesnut, Thermo Fisher Scientific Inc., USA Other speakers will be announced soon.

TOPICS

Applications of Synthetic & Systems Biology Biological Design Automation Computational/Mathematical Modelling and Design Computer Aided Design Directed Evolution Designing and Writing Genomes DNA Synthesis, Assembly, and Sequencing High Throughput Design Space Exploration Industrial Applications of Synthetic & Systems Biology Mammalian Synthetic Biology Metabolic Engineering Microbial Synthetic Biology / Microbiome Engineering Molecular Programming Omics Science and Synthetic & Systems Biology Pedagogical/Educational Tools Plant Synthetic Biology Protein Engineering Synthetic & Systems Biology for Cell Culture and Medical Applications Synthetic & Systems Biology of Industrial Microorganisms

SCIENTIFIC COMMITTEE

Giuseppe Nicosia, University of Catania, Italy Richard Allmendinger, The University of Manchester, UK Matteo Barberis, University of Amsterdam, The Netherlands Yaakov (Kobi) Benenson, Synthetic Biology Group@Department of Biosystems Science and Engineering, ETH Zurich, Basel, Switzerland Leonidas Bleris, Bioengineering Department, The University of Texas at Dallas, USA Paola Branduardi, University of Milano Bicocca, Italy Michele Ceccarelli, University of Sannio, Italy Jole Costanza, Italian Institute of Technology, Italy Domitilla Del Vecchio, Department of Mechanical Engineering, MIT, USA Diego Di Bernardo, Telethon Institute of Genetics & Medicine TIGEM & U. of Napoli “Federico II”, Italy Barbara Di Camillo, University of Padova, Italy Barbara Di Ventura, Synthetic Biology Group - BioQuant/DKFZ, Heidelberg, Germany Simone Furini, University of Siena, Italy Emanuele Domenico Giordano, University of Bologna, Italy J. Gootenberg, Feng Zhang and Aviv Regev Groups, Department of Systems Biology, Harvard Medical School, Harvard University, USA Guido Grandi, University Trento, Italy Mario Guarracino, ICAR-CNR, Italy Markus Herrgard, Novo Nordisk Foundation Center for Biosustainability, Technical University of Denmark, Denmark Paolo Magni, University of Pavia, Italy Donato Malerba University of Bari, Italy Vincenzo Manca, University of Verona, Italy Nelson Marmiroli, University of Parma, Italy Giancarlo Mauri, University of Milano Bicocca and SYSBIO - Center of Systems Biology, Italy Enzo Medico, IRCC - Candiolo and University of Torino, Italy Giuseppe Narzisi, New York Genome Center, USA Wieslaw Nowak, Nicholas Copernicus University, Poland Gennaro Piccialli, University of Napoli Federico II, Italy Danilo Porro, University of Milano Bicocca, Italy Francesco Ricci, University of Rome “Tor Vergata”, Italy Nicola Segata, University of Trento, Italy Gianna Maria Toffolo, University of Padova, Italy

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UK IntroToPythonForBiologists Nov27-Dec1

INTRODUCTION TO PYTHON FOR BIOLOGISTS http://www.prinformatics.com/course/introduction-to-python-for-biologis ts-ipyb04/ This course is being delivered by Dr Martin Jones, an expert in Python and author of two text books, Python for Biologists [http://www.amazon.com/Python-Biologists-complete-programming-beginners /dp/1492346136/] Advanced Python for Biologists [http://www.amazon.com/Advanced-Python-Biologists-Martin-Jones/dp/14952 44377/].

Prices start at Â£475 and accommodation packages can be added for an additional Â£260, includes all meals and accommodation on site for the week, arrival Sunday before the course starts) Course overview: Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. This workshop is aimed at complete beginners and assumes no prior programming experience. It gives an overview of the language with an emphasis on practical problem-solving, using examples and exercises drawn from various aspects of bioinformatics work. After completing the workshop, students should be in a position to (1) apply the skills they have learned to tackle problems in their own research and (2) continue their Python education in a self-directed way.

Intended audience: This workshop is aimed at all researchers and technical workers with a background in biology who want to learn programming. The syllabus has been planned with complete beginners in mind; people with previous programming experience are welcome to attend as a refresher but may find the pace a bit slow.

Teaching format: The workshop is delivered over ten half-day sessions (see the detailed curriculum below). Each session consists of roughly a one hour lecture followed by two hours of practical exercises, with breaks at the organizer's discretion. There will also be plenty of time for students to discuss their own problems and data.

Assumed background: Students should have enough biological background to appreciate the examples and exercise problems (i.e. they should know about DNA and protein sequences, what translation is, and what introns and exons are). No previous programming experience or computer skills (beyond the ability to use a text editor) are necessary, but you'll need to have a laptop with Python installed.

Curriculum:

Monday 27th Module 1: Introduction.

We will start with a general introduction to Python and explain why it is useful and how learning to program can benefit your research. Some time will be taken to explain the format of the course. We will outline the edit-run-fix cycle of software development and talk about how to avoid common text editing errors. In this session, we also check that the computing infrastructure for the rest of the course is in place.â€Core concepts introduced: source code; text editors; whitespace; syntax and syntax error; and Python versions.

Module 2: Output and text manipulation.

This session will show students how to write very simple programs that produce output to the terminal and in doing so become comfortable with editing and running Python code. This session also introduces many of the technical terms that we'll rely on in future sessions. We will run through some examples of tools for working with text and show how they work in the context of biological sequence manipulation. We also cover different types of errors and error messages and learn how to go about fixing them methodically.â€Core concepts introduced: terminals; standard output; variables and naming;â€strings and characters; special characters; output formatting; statements; functions; methods; arguments; comments.

Tuesday 28th

Module 3: File IO and user interfaces.

We will discuss about the importance of files in bioinformatics pipelines and workflows during this session, and we then explore the Python interfaces for reading from and writing to files. This involves introducing the idea of types and objects and a bit of discussion about how Python interacts with the operating system. The practical session is spent combining the techniques from session 2 with the file IO tools to create basic file-processing scripts.â€Core concepts introduced: objects and classes; paths and folders; relationships between variables and values; text and binary files; newlines.

Module 4: Flow control 1: loops.

A discussion of the limitations of the techniques learned in session 3 quickly reveals that flow control is required to write more sophisticated file-processing programs, at this point we will progress on to the concept of loops. We look at the way in which Python loops

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UK NicheModelling Oct16-20

Ecological niche modelling using R (ENMR01)

Delivered by Dr. Neftali Sillero

http://www.prstatistics.com/course/ecological-niche-modelling-using-r-enmr01/ This course will run from 16th - 20th October 2017 at SCENE field station, Loch Lomond national park, Scotland

Applying niche modelling to the field of evolutionary biology has increased in recent years. It is especially important for field of ecological speciation, sympatric speciation, resource specialisation and studying how organisms and traits may evolve/cope with rapid changes to the environment such as those caused by climate change.

Ecological niche, species distribution, habitat distribution, or climatic envelope models are different names for similar mechanistic or correlative models, empirical or mathematical approaches to the ecological niche of a species, where different types of ecogeographical variables (environmental, topographical, human) are related with a species physiological data or geographical locations, in order to identify the factors limiting and defining the species' niche. ENMs have become popular due to the need for efficiency in the design and implementation of conservation management.

The course will cover the base theory of ecological niche modelling and its main methodologies. By the end of this 5-day practical course, attendees will have the capacity to perform ecological niche models and understand their results, as well as to choose and apply the correct methodology depending on the aim of their type of study and data.

The course will be mainly practical, with some theoretical lectures. All modelling processes and calculations will be performed with R, the free software environment for statistical computing and graphics (http://www.r-project.org/). Attendees will learn to use modelling algorithms like Maxent, Bioclim, Domain, and logistic regressions, and R packages for computing ENMs like Dismo and Biomod2. Also, students will learn to compare different ecological niche models using the Ecospat package.

Course content is as follows

Monday 16th Elementary concepts on Ecological Niche Modelling Module 1: Introduction to ENM theory. Definition of ecological niche model; introduction to species ecological niche theory, types of ecological niches, types of ENM, diagram BAM, ENMs as approximations to species' niches. Module 2: Problems and limitations on ENM. Assumptions and uncertainties, equilibrium concept, niche conservatism, autocorrelation and intensity, sample size, correlation of environmental variables, size and form of study area, thresholds, model validation, model projections. Module 3: Methods on ENM. Mechanistic and correlative models. Overlap Analysis, Biomod, Domain, Habitat, Distance of Mahalanobis, ENFA, GARP, Maxent, Logistic regression, Generalised Linear Models, Generalised Additive Models, Generalised Boosted Regression Models, Random Forest, Support Vector Machines, Artificial Neural Network. Module 4: Conceptual and practice steps to calculate ENM. How to make an ENM step-by-step. Module 5: Applications of ENM. Ecological niche identification, Identification of contact zones, Integration with genetical data, Species expansions, Species invasions, Dispersion hypotheses, Species conservation status, Prediction of future conservation problems, Projection to future and past climate change scenarios, Modelling past species, Modelling species richness, Road-kills, Diseases, Windmills, Location of protected areas.

Tuesday 17th Prepare environmental variables and run ecological niche models with dismo package. Module 6: Preparing variables. Choosing environmental data sources, Downloading variables, Clipping variables, Aggregating variables, Checking pixel size, Checking raster limits, Checking NoData, Correlating variables. Module 7: Dismo practice. How to run an ENM using the R package dismo.

Wednesday 18th Run ecological niche models with Biomod2 package and Maxent. Module 8: Biomod2 practice. How to run an ENM using the R package Biomod2. Module 9: Maxent practice. How to run an ENM using the R packages dismo and Biomod2 as well as Maxent software.

Thursday 19th Compare ecological niche models with ecospat. Module 10: Ecospat practice. Compare statistically two different ecological niche models using the R package Ecospat. Module 11: Students' talks. Attendees will have the opportunity to present their own data and analyse which is the best way to successfully obtain an ENM.

Friday 20th Run ecological niche models with your own data. Module 12: Final practical. In this practical, the students will run ENM with their own data or with a new dataset, applying all the methods showed during the previous days.

Please email any inquiries to oliverhooker@prstatistics.com or visit our

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Venice EvoDevo Sep18-21

Summer School on Evolutionary Developmental Biology Conceptual and Methodological Foundations

5th Edition: Process Thinking for Evo-Devo

Venice, September 18th-21st 2017

Organizers: Alessandro Minelli, Gerd B. Müller and Giuseppe Fusco School director: Johannes Jaeger

School sponsors: Istituto Veneto di Scienze, Lettere ed Arti (IVSLA), Venice and Konrad Lorenz Institute for Evolution and Cognition Research (KLI), Vienna.

Location: Istituto Veneto di Scienze, Lettere ed Arti, Palazzo Franchetti, Venice

Taching panel: Johannes Jaeger (School Director, KLI Klosterneuburg, Austria), Scott Gilbert (Swarthmore College, Swarthmore, PA, U.S.A.), James DiFrisco (KLI Klosterneuburg, Austria), Nick Monk (University of Sheffield, U.K.), Berta Verd (KLI Klosterneuburg, Austria), Ron Jenner (Natural History Museum, London, U.K.), Graham Budd (University of Uppsala, Sweden), Stuart Kauffman (Institute for Systems Biology, Seattle, WA, U.S.A.)

Deadline for applications: May 30th 2017

For details, visit http://www.istitutoveneto.org/-EDB2017/ Giuseppe Fusco Department of Biology University of Padova Via U. Bassi 58/B I-35131 Padova Italy tel. +39.049.827.6238 fax +39.049.827.6230 e-mail giuseppe.fusco@unipd.it webpage http://www.biologia.unipd.it/giuseppe.fusco

Giuseppe Fusco <giuseppe.fusco@unipd.it>

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.