EvolDir

April 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.

—— / ——

Foreword 1

Conferences 2

GradStudentPositions 20

Jobs 54

Other 75

PostDocs 90

WorkshopsCourses 123

Instructions 147

Afterword 147

Conferences

Aarhus Denmark Probgen17 Sep18-20 2
Asilomar ASN Jan5-9 SympCall 3
Asilomar California AmerSocNat Jan5-9 RequestProposals 4
Bangalore StudentConservationScience Sep21-24 4
Barcelona CrustaceaGenomics Jun19-22 5
Blossin InsectEvolutionaryImmunity Aug28-Sep1 Extension 5
Calgary EvoDevo Aug19-23 6
ChicagoFieldMuseum PlantEvolution Apr8 6
Chize France EcologyBehaviour Jun19-23 DeadlineExt 7
Copenhagen RubiaceaeConference Sep11-14 7
Edinburgh ComplexTraitGenetics Mar17 8
Groningen ESEB Aug20-25 Earlybird 8
HalleSaale PlantEvolution May18-20 8
London BESMacro July5-7 9
London WildlifeConservation Mar14 9
LosAngeles MolluscAdaptation Jun20-22 10
Marseilles EBM21 Sep26-29 11
Montpellier GalaxyCommunity Jun26-30 11
NewHampshire MicrobialPopBiol Jul9-14 12
Portland Oregon MimulusCommunity Jun23 12
QueensU OE3C-17 May18-20 RegistrationClosesApr14 12
Roscoff HostParasiteInteractions Oct30-Nov3 13
Seattle GSA Macroevolution Oct22-25 14
Smithsonian Conservation Apr21-23 14
UCalgary EvoDevo Aug19-23 15
UEssex GenomicsEpigeneticsGeneRegulation Sep14 16
UFlorida GeneralScience May20 17
UNotreDame ArthropodGenomics Jun6-11 17
UNotreDame ArthropodGenomics Jun7-11 Registration 17
Winnipeg EcomorphologyDiversity May15-19 18
Yosemite Symbiosis May5-7 EarlyRegistrationDue . 18
Yosemite Symbiosis May5-7 SpacesOpen 19
Zurich PolygenicAdaptation Aug28-Sep1 20

Aarhus Denmark Probgen17 Sep18-20

Dear Colleagues,

We are pleased to announce the 3rd Probabilistic Modeling in Genomics Conference (ProbGen17), that will be held at Aarhus University, Denmark, from 18-20 Sept 2017.

The conference will cover probabilistic models, algorithms, and statistical methods across a broad range of applications in genetics and genomics. We invite abstract submissions on a range of topics including Population Genetics, Functional Genomics, Systems and Structural Biology, Methods for Genome-wide Association Studies, Causal inference in genetic studies, Assembly and Variant Identification, Phylogenetics, Natural Selection and Quantitative Genetics.

Alongside invited speakers, oral presentations will be selected from submitted abstracts. We particularly encourage abstract submissions from junior investigators, including postdoctoral fellows and graduate students.

Probgen was held previously in Cold Spring Harbor (2015), and Oxford (2016). It evolved from the success of previous similarly-themed workshops held at the HHMI Janelia Farm Research Campus (2013) and Merton College, Oxford (2014).

The conference talks and poster sessions will be held at the new Moesgaard Museum for archaeology and ethnography (MOMU) situated just 5 km out of Aarhus. Aarhus is most easily accessible from either Aarhus (AAR) or Billund (BLL) Airport that serves most major European cities.

The meeting will begin with an informal mixer on the evening of Sunday 17 September 2017 at Hotel Comwell [http://www.comwellaarhus.dk/] in central Aarhus. Talks will take place from Monday 18 September until lunchtime on Wednesday 20 September.

Registration will open soon. We have provisional capacity for ~200 participants; due to space limitations, registration will proceed on a first-come-first-served basis.

Important deadline: The early bird registration and abstract submission deadline is June 10th, 2017.

The conference venue webpage: www.moesgaardmuseum.dk/en/ The conference webpage can be found at http://conferences.au.dk/-probgen17/ Please send enquiries to probgen17@birc.au.dk

We would appreciate if you could circulate this announcement to your local colleagues and collaborators.

The organizers: Ida Moltke, University of Copenhagen Thomas Mailund, Aarhus University Thomas Bataillon, Aarhus University Mikkel H. Schierup, Aarhus University

Thomas Bataillon <tbata@birc.au.dk>

Asilomar ASN Jan5-9 SympCall

The American Society of Naturalists

Call for Symposia

ASN meeting at Asilomar, California

5-9 Jan 2018

The American Society of Naturalists invites symposium proposals for their stand-alone meeting, to be held at Asilomar in Monterey, California 5-9 January 2018. Two symposia will be chosen for this meeting, to run on separate days, in addition to a special symposium celebrating the 150th anniversary of the first publication of the American Naturalist. Proposals for the special anniversary symposium are being solicited separately.

Symposium topics should support the Society's goal to advance the conceptual unification of the biological sciences and further knowledge in evolution, ecology, behavior and organismal biology. Proposals are encouraged on topics that are synthetic, interdisciplinary or that address important emerging issues in evolution, ecology and behavior.

Proposals should include (1) a title; (2) a description of the symposium topic (one page); (3) a tentative list of speakers, including institutional affiliations; (4) a justification for the symposium explaining why the topic and speakers are appropriate for an ASN meeting, keeping in mind the broader goals of the society (http://-www.amnat.org/about/about-the-society.html); and (5) a statement that all proposed invited speakers have agreed to participate. Organizers should plan the symposia to run from approximately 1:30-5:30, and can divide this time amongst speakers as they wish, reserving time for a coffee break.

Proposals must be submitted by midnight Eastern Standard Time on March 31, 2017 by email (emilies@umn.edu) as a single pdf attachment, under subject heading: ASN Asilomar Symposium Proposal. Proposals that include women, young investigators and individuals from underrepresented groups are especially encouraged.

Please note that the society does not have the funds to pay for travel or lodging expenses of the chosen speakers. But, in exceptional circumstances we may consider requests to waive conference registration costs for junior participants in symposia. Regardless, there may be opportunities to seek external symposium funding.

The Society's selection committee will evaluate proposals based on the likelihood of attracting a substantial audience, the significance and timeliness of the topic, and on it being substantively different from recent symposia hosted by the Society. All applicants will be notified of the decision by late April 2017.

Emilie Snell-Rood

ASN Symposium Committee Chair

Department of Ecology, Evolution and Behavior

University of Minnesota

emilies@umn.edu

Asilomar California AmerSocNat Jan5-9 RequestProposals

Tocelebrate the 150th Anniversary of the first publication of The American Naturalist, there will be a special symposium at the stand-alone meeting of the American Society of Naturalists (January 5 - 9, 2018, Asilomar CA, USA). The symposium is titled “On the shoulders of giants: the future of The American Naturalist”. The goal of the symposium will be to show how major advances published in the journal’s history have laid the foundation for exciting new directions in evolutionary ecology and related fields. There will be time for six 30-minute talks, each highlighting a different concept from a classic American Naturalist paper, and where those ideas are headed next. We want the talks to place the original paper into its historic context, trace the subsequent development of the idea, and (crucially) show how the classic ideas connect to today’s cutting-edge research. Weare requesting proposals for talks. Each proposal should be no more than 250 words. Proposals should:

1) Identify what influential paper(s) from The American Naturalist’s past will be the starting point of the talk.

2) Briefly explain how that past paper influenced the direction of the field generally and the speaker’s career in particular.

3) Indicate how the speaker is using / developing / changing that classic paper’s ideas in their own current and future work. Inaddition to the 250 word limit, one figure and up to 5 references are allowed.

Talkproposals should be sent to Daniel Bolnick (danbolnick@austin.utexas.edu) by May 1. We expect to notify chosen speakers by June 1.

Weencourage junior researchers (post-docs, early-career faculty) to apply, and individuals from often underrepresented groups.

Thesociety does not have the funds to pay for travel or lodging expenses of the chosen speakers. But in exceptional circumstances ASM may consider appeals to waive conference registration fees for junior presenters who lack other means to cover conference costs.

Inaddition to this symposium, the American Society of Naturalists is separately seeking proposals for topics and speakers for two other organized symposia at the 2018 Asilomar meeting (contact Emilie Snell-Rood for details, emilies@umn.edu).

Dr.Daniel I. Bolnick

Professor Departmentof Integrative Biology Chair,Graduate Program in Ecology Evolution and Behavior OneUniversity Station C0990 Universityof Texas at Austin Austin,TX 78712

512-471-2824 fax512-471-3878 danbolnick@austin.utexas.edu

Labwebsite: https://bolnicklab.wordpress.com danbolnick@austin.utexas.edu

Bangalore StudentConservationScience Sep21-24

Dear all,

The Student Conference on Conservation Science (SCCS) - Bengaluru brings together young researchers in the science and practice of biodiversity conservation. The conference facilitates interaction, encourages exchange of research ideas and methods, sharing of knowledge and experience related to conserving wildlife and helps build contacts and capacity. As a sister conference to SCCS-Cambridge, SCCS-Bengaluru focuses on attracting student participants, primarily from countries in South and South-east Asia and Africa.

DATES:

The 2017 conference will be held at the JN Tata Auditorium, Indian Institute of Science, Bengaluru, from 21st to 24th September 2017.

* Early Bird registrations and Abstract submissions are now open on our website: http://www.sccs-bng.org * Abstract submissions are open for those who want to present either a talk or a poster.

* Students need to register and pay the conference fee before being able to submit an abstract. * Deadline for submitting abstracts is 3 April 2017.

You can view the Conference Flyer here: https://goo.gl/-LF0Hsh SCCS-Bengaluru is a four-day conference, where you can look forward to a host of long and short workshops (which are research focused and equip students with skills required for conservation), plenary talks by invited speakers, close to 25+ student talks and about 80 student poster presentations. Read the 2016 report here: https://goo.gl/LF0Hsh We will also have sessions on 'Who's Who in Conservation' and 'Birds of a Feather' for students to learn about the work done by a diversity of academic institutions and conservation organisations, to discover work and research opportunities they offer, and to network with students and scientists working on similar issues. Based on feedback from previous years we are working towards a slightly new format for this year's conference, so do keep a lookout for our announcements via email, our website, Facebook < https://www.facebook.com/sccsbangalore > and Twitter < https://twitter.com/sccsbng >.

For further information don't hesitate to contact us at sccs@sccs-bng.org.

Warm regards,

Shreekant Deodhar

Conference Administrator

On behalf of the Organizing Committee of SCCS-Bengaluru 2017

(Abinand Reddy, Abishek Harihar, Arshiya Bose, Kavita Isvaran, Krishnapriya Tamma, Ravi Chellam, Shomen Mukherjee and Tarsh Thekaekara)

SCCS - Bangalore <sccs@sccs-bng.org>

Barcelona CrustaceaGenomics Jun19-22

"Dear colleagues,

We organize a 2-day symposium on "Crustacean Genomics" within the TCS congress in Barcelona this summer (19th to 22nd June 2017).

The symposium will include talks on the use of Genomics in Physiology (19th June 2017) and Systematics and Evolution studies (20th June 2017), so we believe it might be of interest for a broad audience. You will find the preliminary program attached.

For more information and registration to this event, please visit the conference website at:

http://tcs2017barcelona.com/welcome.html Looking forward to meeting you in Barcelona. Best regards,

Guiomar Rotllant & Ferran Palero Organizing committee of the Crustacea genomics symposium"

You will find the preliminary program attached.

Thanks!

– Ferran

PALERO Ferran, Ph.D. M.Sc. Dept. Marine Ecology Centro de Estudios Avanzados de Blanes (CEAB-CSIC) C/ d'acces a la Cala St. Francesc, 14. 17300 Blanes SPAIN Tel: +34 972 33 61 01 (Ext: 277) E-mail : fpalero@ceab.csic.es // BPI - Biologie des Populations Introduites Institut Sophia Agrobiotech (INRA PACA) 400 route des Chappes. BP 167 06903 Sophia Antipolis cedex. FRANCE Tel: +33 (0)4 92 38 64 99 E-mail : fpalero@inra.fr Web: http://www.paca.inra.fr/-institut-sophia-agrobiotech/Equipes-de-recherche/BPI ResearcherID: A-7830-2012

Ferran Palero <fpalero@ceab.csic.es>

Blossin InsectEvolutionaryImmunity Aug28-Sep1 Extension

DEADLINE FOR ABSTRACT SUBMISSION EXTENDED TO 20TH MARCH

Please submit your abstract or register via the following link: http://rolffevolution.net/ecological-immunology-workshop-2017/ Ecological Immunology Workshop 2017 on:

'Insect immunity: genomics, microbiome, applications'

28th August to 1st September 2017 in Blossin (close to Berlin), Germany.

This workshop will bring together researchers interested in ecological immunology with a focus on insects, and with diverse scientific backgrounds ranging from molecular biology to ecology. The hallmark of these workshops, started in 2001, is the open atmosphere fostering free exchange by keeping it an affordable, small conference (100 participants). The format consists of eighteen invited speakers, contributed talks and a dedicated poster. Long breaks provide plenty of opportunity for informal exchange. Past workshops have initiated new collaborations and ideas focusing on frontier research that has not been published. The premises are basic but in a beautiful location conducive to the success of the meeting. We will be located at a lakeside, which at this time of the year offers great swimming and canoeing, and a small private bar at the harbour [http://www.blossin.de] . Registration fee includes accommodation and catering (all meals): https://goo.gl/forms/Rtz3ngliH3ZnGvyD2 Important dates Abstract submission extended until

20th March 2017 Registration closes at the latest on 31st March 2017 or when the maximum number or possible participants is reached, i.e. 100 persons. Final programme announcement is 31st July 2017.

Program and invited speakers

Genomics and functional work in the wild Seth Barribeau, University of Liverpool Nicole Gerardo, Emory University Brian Lazzaro, Cornell University Hinrich Schulenburg, University of Kiel Ann Tate, University of Texas Lumi Viljakainen, University of Oulu Chris Wheat, University of Stockholm

Host-symbiont interactions affecting host immunity Nichole Broderick, University of Connecticut Ewa Chrostek, MPI Infection Biology Ellen Decaesteker, University of Leuven Abdelaziz Heddi, INSA-Lyon Martin Kaltenpoth, University of Mainz David Schneider, Stanford University

Applying ecological immunology Lena Bayer-Wilfert, University of Essex Astrid Groot, University of Amsterdam Dino McMahon, Free University Berlin Brian Weiss, Yale University Ken Wilson, University of Lancaster

We are looking forward to welcoming you at the Ecological Immunology Workshop 2017.

Kind regards,

Organizing Committee Jens Rolff, Free University of Berlin Oliver Otti, University of Bayreuth Paul Schmid-Hempel, ETH Zurich Magdalena Nagel, Free University of Berlin

If you have any questions concerning the meeting please do not hesitate to e-mail us: oliver.otti@uni-bayreuth.de (program) magdalena.nagel@fu-berlin.de (travel and registration)

Dr. Oliver Otti Animal Population Ecology Animal Ecology I University of Bayreuth Universitätsstrasse 30 95440 Bayreuth Germany

phone: +49921552646 e-mail: oliver.otti@uni-bayreuth.de

web: Otti's homepage < http://www.bayceer.uni-bayreuth.de/toek1/de/mitarbeiter/mit/mitarbeiter_detail.php?id_obj=106154 >

Ecological Immunology Meeting 2017 in Blossin < http://rolffevolution.net/ecological-immunology-workshop-2017/ >

Oliver Otti <oliver.otti@uni-bayreuth.de>

Calgary EvoDevo Aug19-23

The Pan-American Society for Evolutionary Developmental Biology 2nd Biennial Meeting August 19-23, 2017

University of Calgary Alberta, Canada

Registration is now open for the 2nd Biennial EvoDevoPanAm Meeting, which will be held on the campus of the University of Calgary. Renew your membership and register for the meeting online, http://www.evodevopanam.org/2nd-biennial-meeting.html . Abstract submission and discounted rates are available through May 15.

Please visit http://www.evodevopanam.org/ for news and updates as the meeting approachs. And be sure to follow us on Facebook (https://www.facebook.com/EvoDevoPanAm) and on Twitter @EvoDevoPanAm!

-The EvoDevoPanAm Executive Board

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

ChicagoFieldMuseum PlantEvolution Apr8

Chicago Plant Science Symposium 2017 The Field Museum *Saturday April 8, 2017 * *10:00 AM - 7:00 PM*

We are pleased to announce the seventh year of the annual Chicago Plant Science Symposium. This series is designed bring together the plant science community of the greater Chicago area for a one day symposium that highlights the cutting edge of research in plant evolution, ecology, and conservation. The program will include lunch and a post-conference mixer. Best of all, registration is free!

The theme of the symposium this year is *"Genomic insights into plant ecology and evolution"*. We have invited a diverse set of speakers representing a wide range of research fields that are benefitting from the application of these new technologies and analytical methods.

Schedule

9:00-10:20 AM Registration, West Atrium

10:20-10:30 AM Patrick Herendeen, Chicago Botanic Garden Introductory remarks

10:30-11:15 AM Felix Grewe, The Field Museum Mitochondrial genome evolution: trends towards extreme complexity in the plant lineage

*11:15-12:00 AM Fay-Wei Li, Cornell University *The ferntastic genomes reveal unique evolution of ferns and cyanobacterial symbiosis

*12:00-1:15 PM Lunch, West Atrium * *1:15-2:00 PM Quentin Cronk, University of British Columbia *Tracking labile sex determining regions of plants using genomics and methylomics

*2:00-2:45 PM Alison Dawn Scott, University of Wisconsin *Polyploid evolution in Sequoioideae: The dawn of redwood phylogenomics

*2:45-3:30 PM Matt Johnson, Chicago Botanic Garden *Building a better tree and using it wisely: phylogenomic approaches in non-model organisms

*3:30-4:00 PM Coffee Break, West Atrium * *4:00-4:45 PM Emily Sessa, University of Florida *Taming Darwin's incubus: Phylogenetics and floral symmetry evolution of the Core Goodeniaceae

*4:45-5:30 PM Debashish Bhattacharya, Rutgers University *Greening of our planet: the long and short story of plastid endosymbiosis

5:30-7:00 PM Mixer, West Atrium

Registration: Registration is free, but we need to know who is coming to plan for lunch and refreshments.

To register simply respond to this message with your name and institution. You may also send questions to chicagoplantscience@gmail.com.

Organizers: Andrew Hipp, Patrick Herendeen and Richard Ree chicagoplantscience@gmail.com http://www.chicagoplantscience.org/ ahipp@mortonarb.org

---

Chize France EcologyBehaviour Jun19-23 DeadlineExt

Dear everyone,

We decide to extend the deadline of submission until the 1st April 2017.

Send us your abstract directly on the website of the conference : https://eb2017.sciencesconf.org/ For more information, you can also look at our teaser : https://vimeo.com/203603912 Regards, AREB

sophie.dupont93@gmail.com

Copenhagen RubiaceaeConference Sep11-14

VII International Rubiaceae and Gentianales Conference 11-14 September 2017 Carlsberg Academy, Copenhagen, Denmark

The Natural History Museum of Denmark invites you to Copenhagen from 11 to 14 September 2017 to participate in the Seventh International Rubiaceae and Gentianales Conference. The conference is an excellent opportunity for international researchers with a common interest in Rubiaceae and Gentianales to meet and interact. It will be a great opportunity to share exciting results, to spark vivid discussions, to exchange original ideas, and to initiate or strengthen international collaboration. We are looking forward to meeting you in Copenhagen!

ONLINE http://snm.ku.dk/english/research/conferences/vii-rubiaceae-gentianales/ DEADLINES Abstract submission and registration open: 1 February 2017 Abstract submission close: 1 May 2017 Registration close: 1 July 2017

PROGRAM Monday 11: Presentations and evening reception at the Natural History Museum of Denmark Tuesday 12: Presentations Wednesday 13: Presentations and conference dinner Thursday 14: Excursion to Møns Klint Friday 15: Optional visit to the Herbarium C

The conference fee includes coffee breaks, lunches, the reception, the conference dinner, and the excursion.

CONTACT viirubiaceae@gmail.co

brecht.verstraete@snm.ku.dk

Edinburgh ComplexTraitGenetics Mar17

Message for Evoldir:

The 12^th meeting of the Edinburgh Alliance for Complex Trait Genetics, sponsored by the Genetics Society, will be held on the afternoon of 17^th March 2017. Programme below.

It is free to attend but please register at https://-tinyurl.com/E-ACTG12 Chris Haley

Josephine Pemberton

for the E-ACTG Committee

***

Edinburgh Alliance for Complex Trait Genetics

12th meeting - Friday 17^th March, 2017

Royal Society of Edinburgh

22-26 George St., Edinburgh,EH2 2PQ

13.00 Arrival and registration

13.30 Session 1

13.30 Elizabeth Thompson (University of Washington) Mapping QTL using shared descent of genome

14.00 Xia Shen (Usher Institute of Population Health Sciences and Informatics) Beyond Mendelian randomization: Establishing causal relationships using GWAS results

14.30 David Hill (Centre for Cognitive Ageing and Cognitive Epidemiology) Shared genetic aetiology between personality and health and anthropometric traits

14.45 Gail Davies (Centre for Cognitive Ageing and Cognitive Epidemiology) Meta-analysis of GWAS of general cognitive function in the CHARGE-COGENT consortium

15.00 Tea

15.30 Frank Chan (Friedrich Miescher Laboratory of the Max Planck Society, Tubingen) Genomics of selection response for increased tibia length in the “Longshanks” mouse

16.00 Christos Palaiokostas (The Roslin Institute) Breeding disease resistant farmed fish using high-throughput sequencing

16.30 Tom Marchant (The Roslin Institute) Identifying genes for craniofacial morphology in dogs

17.00 David Clark (Usher Institute of Population Health Sciences and Informatics) Inbreeding depression in humans

17.30 Discussion and refreshments

***

PEMBERTON Josephine <J.Pemberton@ed.ac.uk>

Groningen ESEB Aug20-25 Earlybird

ESEB 2017 - biennial congress of the European Society for Evolutionary Biology August 20 - 25, Groningen, The Netherlands Website: www.eseb2017.nl Congress registration is still open at discounted early bird rates! EARLY BIRD REGISTRATION DEADLINE EXTENDED TO APRIL 14, 2017

ESEB office - office@eseb.org

office@eseb.org

HalleSaale PlantEvolution May18-20

PopBio2017 - 30th Conference of the Plant Population Biology Section of the Ecological Society of Germany, Austria and Switzerland (GfÃ-)

“Population Biology in a Changing World” http://-www.popbio2017.de/ We are very happy to invite you to the 30th PopBio conference, which will be held in Halle/Saale, Germany, from 18th to 20th May 2017.

PopBio 2017 will be hosted by the Helmholtz Centre for Environmental Research (UFZ), the Martin Luther University Halle-Wittenberg, and the German Centre for Integrative Biodiversity Research (iDiv).

Online registration and abstract submission is open now at: http://www.popbio2017.de/registration.html *** Deadline for abstract submission 31 March, 2017 *** PopBio is the annual international meeting for people working in the field of plant population biology and ecology. This years motto is “Population Biology in a Changing World”. We invite contributions in the subfields: - Plant demography - Population and evolutionary genetics - Pollination ecology - Mechanisms of biological invasions - Plant-pathogen and plant-herbivore interactions - Free topics

We expect that the conference will define the state of the art in plant population ecology, set the research agenda for the next years and give insights into novel tools to empower in particular young scientists to analyse population-ecological data.

We will have two and a half days of exciting presentations. An informal conference dinner will be offered on Friday. On Saturday afternoon, you can join the excursion to the Global Change Experimental Facility, GCEF, or to continental dry grasslands with unique flora on porphyry outcrops near Halle.

Keynotes: - Roberto Salguero-Gomez, Department of animal and plant sciences, University of Sheffield, UK “Life history currencies shape plant population performance worldwide” - Erin Mordecai, Department of Biology, Stanford University, USA “Impact of pathogens on plant species diversity in grassland communities” - Jeff Ollerton, Faculty of Arts, Science and Technology, University of Northampton, UK “The macroecology of wind and animal pollination” - Steve Keller, Department of Plant Biology, University of Vermont, USA “Climate adaptation past, present, and future: new insights from combining genomics and spatial modeling in forest trees” - Jane Catford, Centre for Biological Sciences, University of Southampton, UK “Using community ecology to understand invasive species and their impacts”

Timeline: - Deadline for abstract submission 31 March, 2017 (www.popbio2017.de) - Notification of abstract acceptance after 17 April, 2014 - Deadline for registration: 24 April, 2014 - Registration fees rise by 50 euro after 2 May, 2017

Special feature in Basic and Applied Ecology, BAAE: Presenters at PopBio2017 are invited to contribute to a special issue of Basic and Applied Ecology, the Journal of the Ecological Society of Germany, Austria and Switzerland (GFÃ-) which will be edited by Susanne Lachmuth, Stefan Michalski and Niek Scheepens.

The PopBio 2017 organization committee: Harald Auge, Helge Bruehlheide, Walter Durka, Isabell Hensen, Tiffany Knight, Susanne Lachmuth, Stefan Michalski

Conference secretary: Dr. Hildegard Feldmann F&U confirm, Permoserstr. 15, 04318 Leipzig, Germany

Fon: +49 341 235 2264 Fax: +49 341 235 2782 Email: popbio2017@fu-confirm.de

Susanne Lachmuth <susanne.lachmuth@botanik.uni-halle.de>

London BESMacro July5-7

The deadline for BES Macro 2017 registration, April 28, is rapidly approaching!

http://www.eventbrite.co.uk/e/bes-macro-2017-tickets-29074065312 BES Macro 2017 is the annual meeting of the British Ecological Society Macroecology (and macroevolution) Special Interest Group, and we hope you’ll join us for three days of macro-fun!

This year’s conference is 5-7 July at the Natural History Museum in London. We’ve got a great line up of speakers (see below) highlighting all kinds of macro-scale research as well as our annual student plenary, contributed talks, posters etc. Tickets are just 45 for students (and unemployed graduates) or 75 for non-students.

KEYNOTE SPEAKERS AND TOPICS

- David Nogues-Bravo < http://macroecology.ku.dk/-research/phylogeography/ > (CMEC) - extinction dynamics under climate change - Helene Morlon < http://www.biologie.ens.fr/phyloeco/index.html > (CNRS) - macroecology, macroevolution, modelling - Richard Pearson < https://www.ucl.ac.uk/cber/-pearson > (UCL) - climate change, SDMs, community ecology - Erin Saupe < https://www.earth.ox.ac.uk/-people/erin-saupe/ > (Oxford) - macroecology, palaeontology, marine inverts - Jana Vamosi < http://-homepages.ucalgary.ca/~jvamosi/ > (Calgary) - macroecology, macroevolution, plants

Hope to see you there!

The BES Macro committee

“cs16502@bristol.ac.uk” <cs16502@bristol.ac.uk>

London WildlifeConservation Mar14

Zoological Society of London, Regent’s Park, London NW1 4RY, UK; Tuesday 14 March 2017; 18:00-21:00

Immigrants to the rescue! How can immigration help save threatened wildlife populations?

Speakers: Richard Frankham; Mike Bruford; Jane Reid

Threatened species have invariably small and frequently isolated populations, and are thus characterized by increased inbreeding and depleted genetic variation. Increased inbreeding could lead to a reduction in reproduction and survival (inbreeding depression), which causes an immediate risk of extinction. Depleted genetic variation could compromise the ability of a species to adapt to an ever-changing environment, threatening its long-term survival. How to mitigate these adverse effects of small populations, and maintain a threatened species for short- and long-term survival, is a major task for conservation science. Supplementing genetically impoverished populations with external unrelated individuals (immigrants) can be a valuable strategy to counteract the negative effects of isolation. This 'genetic rescue' effect occurs because the addition of unrelated genomes increases diversity in the recipient population, reducing inbreeding and inbreeding depression. Genetic rescue has the added benefit of increasing population size and larger populations are less vulnerable to random events, such as a natural disaster or disease outbreak. Despite the potential benefits of genetic rescue for the management of threatened species, there have been fewer than twenty published studies of genetic rescue/restoration for conservation purposes. Why has there been such a low uptake?

The speakers will describe the hurdles, and illustrate how genetic rescue can be expedited through reintroduction and conservation programmes. Free and open to all https://www.zsl.org/science/whats-on/-immigrants-to-the-rescue-how-can-immigration-help-save-threatened-wildlife The Zoological Society of London is incorporated by Royal Charter Principal Office England. Company Number RC000749 Registered address: Regent's Park, London, England NW1 4RY Registered Charity in England and Wales no. 208728

Linda DaVolls <linda.davolls@zsl.org>

LosAngeles MolluscAdaptation Jun20-22

SYMPOSIA ANNOUNCEMENT 50th Annual Meeting, Western Society of Malacologists, Los Angeles, California https://www.eventbrite.com/e/western-society-of-malacologists-50th-annual-meeting-tickets-28744283927

Molluscs and Climate Change 20 June 2017 What are the effects of climate change on molluscs and the evidence molluscs give us regarding climate change? Appropriate topics for presentations include (but are not limited to) anthropogenic and naturally-caused changes, range changes or contractions because of long term ocean temperature changes or El Niño/La Niña conditions, influence of ocean acidification, global or local extinctions, invasions or introductions, and evidence from fossil/subfossil and indigenous midden sites.

Current Research in Fossil Mollusca 21 June 2017 The rich fossil record of molluscs lends itself to studies and interpretation of biostratigraphy, systematics, evolution, and paleoecology. We invite presentations concerning any fossil molluscan taxa with a local, regional, or worldwide focus. We also invite presentations about the work of museums in cataloging and preserving fossil molluscs.

Terrestrial Molluscs 22 June 2017 Terrestrial snails and slugs comprise nearly one third of known molluscs at estimates of 40,000 species. Much of this fauna, especially in Western North America, is poorly documented and/or under-studied. This symposium will highlight native and introduced land snails and slugs and current research that is elucidating aspects of their morphology, behavior, distribution, evolution, and conservation.

General Session 20, 21, 22 June 2017 Presentations concerning almost any aspect of molluscan biology, archeology, and anthropology are welcome.

We hope to see you in Los Angeles!

Abstracts: The closing date for abstracts is 14 April, 2017. Please submit abstracts (with length limited to 350 words including title and authors) in Times New Roman, 12 pt. as a .doc .or docx as an email with the subject line “WSM abstract [your last name]” to jvendett@nhm.org or jannvendetti@yahoo.com

Abstracts should include: - Indication of the author's preference that this presentation should be a poster or talk - Title: Concise and descriptive, bold font left justified - Author(s): Last name first, followed by initials, presenting author underlined, plain font, left justified - Author(s) affiliation: Include full postal address and email for all authors, italics, left justified - Main body: Use standard scientific English, avoid contractions, plain font, left justified - References (if necessary): Author(s), year, title, journal (not abbreviated), volume, inclusive pages

Talks will be limited to ten minutes plus five minutes for Q&A. Posters should not be larger than 40 x 30 inches.

WSM membership is not required for submitting an abstract and/or poster but attending authors must register for the meeting at https://www.eventbrite.com/e/-western-society-of-malacologists-50th-annual-meeting-tickets-28744283927 Please feel free to share this announcement with colleagues, students, and anyone interested in fossil mollusk research.

Abstract submission guidelines are here: http://-/research.nhm.org/malacology/western-society-of-malacologists/ Jann Vendetti, Ph.D. Assistant Curator & Twila Bratcher Chair in Malacology Natural History Museum of Los Angeles County 900 Exposition Blvd. Los Angeles, CA 90007 Phone: 213-763-3380 http://-www.inaturalist.org/projects/slime www.nhm.org/slime Jann Vendetti <JVendett@nhm.org>

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=3D524 best regards

Pierre

“pierre.pontarotti@univ-amu.fr” <pierre.pontarotti@univ-amu.fr>

Montpellier GalaxyCommunity Jun26-30

2017 Galaxy Community Conference (GCC2017) 26-30 June 2017 Montpellier, France https://-gcc2017.sciencesconf.org/ –

The 2017 Galaxy Community Conference will bring together several hundred researchers working in and supporting data intensive life science research. There is no better place to share your work and learn from others that are addressing diverse questions and facing common challenges in data intensive biology. GCC participants work across the tree of life, come from around the world, and represent universities, research organizations, industry, medical schools and research hospitals.

GCC2017 will be in Montpellier, France, 26-30 June and will feature two days of presentations, discussions, poster sessions, lightning talks, computer demos, keynotes, and birds-of-a-feather meetups, all about data-intensive biology and the tools that support it. GCC2017 also includes data and coding hackathons, and two days of training covering 16 different topics. GCC2017 will be held at Le Corum Conference Centre in the heart of Montpellier, just 10km from the Mediterranean.

Abstract submission is now open. If you work in or support data intensive life science research then GCC2017 is an ideal opportunity to present your work. The deadline for oral presentations is Apr 15 (23:59 Paris local time), and posters and computer demonstration submission closes on May 27 (23:59 Paris local time). The Lightning talk submission deadline is June 23 (23:59 Paris time).

Early registration is also open and starts at less than 55€/ day for post-docs and students. You can also book low cost conference housing when you register. Travel fellowships are being offered by the Galaxy Community Fund for early career researchers that are travelling from afar.

About Galaxy Galaxy (https://galaxyproject.org/) is an open, web-based platform for data-intensive biomedical analysis used by tens of thousands of researchers around the world. It supports ad hoc exploration and analysis through scalable and repeatable data analysis pipelines for large research studies. Galaxy is available in over 90 free and publicly accessible web servers, on public and national cloud infrastructures, and is locally installed at hundreds, if not thousands, of research organisations around the world.

We hope to see you this summer in Montpellier!

Au revoir,

The GCC2017 Organising Committee

PS: Please redistribute this announcement to any interested groups.

clementsgalaxy@gmail.com

NewHampshire MicrobialPopBiol Jul9-14

The 2017 Microbial Population Biology Gordon Research Conference will be held from July 9-14, 2017, at the Proctor Academy in Andover NH, USA. The conference will bring together thought leaders from a spectrum of disciplines to present and discuss empirical data and theoretical concepts pertinent to the adaptive evolution of not only microbes, but all other forms of life. The conference is still open for registration but is filling up fast. To see the full program of the meeting and to apply - preferably before April 1, go here: http://www.grc.org/programs.aspx?id=3D12013 Dr. Eva Top, Professor, Dr. Larry Forney, Distinguished University Professor Co-Chairs

Institute for Bioinformatics and Evolutionary Studies Department of Biological Sciences, University of Idaho

"evatop@uidaho.edu" <evatop@uidaho.edu>

Portland Oregon MimulusCommunity Jun23

Dear Community

An International Mimulus meeting will be held June 23rd, just prior to the Evolution Meeting in Portland, OR. The meeting will be located at Portland State University. Thanks to Matt Streisfeld and Mitch Cruzan for securing a room for us!!!!

For details of the meeting, please see the website.

http://mimulusmeeting2017.wordpress.com/ As our community continues to grow, we need to adjust the meeting format accordingly. Instead of research talks, like previous meetings, we will instead have presenters that will summarize advances in Mimulus research over the last few years. We will also focus the afternoon part of the meeting on community building and organization. We will send out more details soon on how this will all work, but community input will be crucial for success. So that we can send you updates, we encourage registration for meeting ASAP, even if you are not sure if you can come:

https://docs.google.com/spreadsheets/d/1z0X8QC49tBpzUHgcalPgbbHipNBML 6nJZq7eIDmPGwE/edit#gid=0

Hope to see you all in Portland!!!!!!

David, Matt, Yaniv, Andrea, Josh, Yaowu, Paul (Organizers)

– David B. Lowry Assistant Professor Plant Biology Department Michigan State University Plant Biology Laboratories Room 268 517-432-4882 http://davidbryantlowry.wordpress.com/ "dlowry@msu.edu" <dlowry@msu.edu>

QueensU OE3C-17 May18-20 RegistrationClosesApr14

Where: Queen's U

What: OE3C'17

When: May 18th-20th, 2017

Header: Conference: OE3C'17, Registration closes April 14th 2017

Message: The Ontario Ecology and Evolution Colloquium 2017 (OE3C'17) call for abstracts and registration is now open to all researchers including undergraduates, graduate students, post doctoral fellows, and faculty. The event focuses primarily on ecology, ethology, and evolution, but is open to researchers in conservation biology, earth sciences, behavior, environmental sciences, genetics, molecular and cellular biology, and psychology. Researchers will be able to present a full 12 minute presentation, 5 minute lightning talk, or a poster.

The three day event will include 4 plenary speakers: Dr. Fran Bonier (Queen's University), Dr. Rowan Barrett (McGill University), Dr. Ben Evans (McMaster University), and Dr. Anne Bell (Ontario Nature). It will also include 2 breakfasts, 2 lunches, Friday dinner, coffee breaks, and social events on Thursday and Friday nights.

Registration cost is $82.62 and abstract submission and registration will close April 14th.

For more information about OE3C'17 visit us at www.queensu.ca/oe3c17/ or contact us at oe3c2017@gmail.com.

We are excited to welcome researchers from all across

Ontario, Quebec and Upstate New York to Queen's!

oe3c2017@gmail.com

Roscoff HostParasiteInteractions Oct30-Nov3

Dear all,

Registration is now 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 slots available for non-invited participants, some of which will be selected for a short oral presentation.

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

Andrea Graham & Ana Rivero

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

Ana Rivero (ana.rivero@cnrs.fr)

www.researchgate.net/profile/Ana_Rivero4 Maladies Infectieuses et Vecteurs: Ecologie, Génétique, Evolution et Contrôle (MIVEGEC)

IRD, 911 Avenue Agropolis,

34394 Montpellier, FRANCE

tel: +33 467 41 63 73, fax: +33 467 41 62 99

– 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

— / —

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

Seattle GSA Macroevolution Oct22-25

Dear All,

We are convening a topical session entitled "Biodiversity dynamics in the face of environmental change: Integrating paleontological and neontological approaches to macroevolution" at the 2017 Geological Society of America conference. The conference will be held 22-25 October in Seattle, Washington. Our session (T51) will focus on how environmental changes have shaped Earth's biodiversity through geologic time and how these macroevolutionary relationships might be used to understand the responses of extant species to current and projected environmental conditions. Invited speakers include Samantha Price (University of California, Davis), Andy Purvis (Natural History Museum London), and Jens-Christian Svenning (Aarhus University).

If you have a current project that fits the scope of our session we hope that you will consider submitting an abstract for consideration. Abstract submission will be open around April 1st, 2017 and close on August 1. We are keenly interested in putting together a slate of talks that span a diversity of disciplinary approaches and including presenters from neontological backgrounds who are interested in incorporating paleontological perspectives into their research. For more information about the conference: https://www.geosociety.org/GSA/Events/Annual_Meeting/GSA/Events/gsa2017.aspx.

If you have any questions please do not hesitate to contact us and if you know others who might be interested please consider forwarding this announcement to them.

Best wishes,Shan Huang (Senckenberg Biodiversity and Climate Research Centre, shan.huang@senckenberg.de) Paul Harnik (Franklin & Marshall College, paul.harnik@fandm.edu) Lee Hsiang Liow (Natural History Museum & Centre for Ecological and Evolutionary Synthesis, University of Oslo, l.h.liow@ibv.uio.no)

– Paul Harnik Department of Earth and Environment Franklin and Marshall College PO Box 3003 Lancaster, PA 17604-3003 Phone: 717-358-5946 Email: paul.harnik@fandm.edu

Paul Harnik <paul.harnik@fandm.edu>

Smithsonian Conservation Apr21-23

EARTH OPTIMISM SUMMIT - SMITHSONIAN INSTITUTION April 21-23, 2017 - Washington, DC Ronald Reagan Building and International Trade Center www.earthoptimism.si.edu Join 150 speakers and 1200 thought leaders, scientists, artists, environmentalists, and civic and business leaders to share stories of what's working in conservation. From how to tackle species extinction to inspiring communities to take action or securing the future of food, we'll explore how people around the world are making positive change for the planet!

REGISTER ON LINE < https://www.regonline.com/registration/Checkin.aspx?EventID=1927451 >: Early bird registration extended to March 10, 2017. Student registration code: EarthST (Must bring student ID to check-in). PROGRAM & SPEAKERS < http://earthoptimism.si.edu/calendar/summit/ >

Summit Fees: General Admission: $650 / Early Bird Rate: $575 Student Rate: $300 / Early Bird Student Rate: $250

NB: Admission to the Summit includes breakfast and lunch, bird-friendly coffee sessions, and some receptions each of the 3 days.

VIDEO COMPETITION - "CONSERVATION SUCCESS": Winners receive travel, lodging and registration for the three day Summit. Grand prize winner also receives $1000 Help celebrate Earth Optimism by creating a 2 minute video about your own conservation success story or highlighting one that needs to be told. All videos will be posted to the Earth Optimism You Tube channel and select videos will be shown at the Summit. The competition is open to undergraduate and graduate students. Visit this link for complete details and submission instructions < http://earthoptimism.si.edu/blogs/news/2017/02/02/earth-optimism-summit-announces-student-video-competition/ >. Deadline to submit your video is March 10th, 11:59 PM EST.

HACK A THON: Cash prizes (currently $5,000) If you are you a hacker, coder, maker, engineer, designer, entrepreneur, creative thinker or tinkerer, come celebrate Earth Optimism by creating solutions to challenging conservation problems in front of a global audience! Fifteen teams of 4 will compete by pitching their innovative solutions & prototypes to a crowd of potential supporters in an on-site event called Make for the Planet. Teams will have access to problem sets two weeks before the event, access to leading conservationists and innovators during the event, and access to equipment on site to create prototypes and models of hardware and/or software solutions to specific conservation problems. All participants will have full access to the Earth Optimism Summit. Apply to participate on-line at Conservation X Labs Make for the Planet website < https://www.makefortheplanet.com/ > no later than March 1, 11:59 PM EST. Space and registration is limited!

SPECIAL FEATURES at EARTH OPTIMISM SUMMIT An Innovation Commons of exhibits showcasing solutions. Streaming FacebookLive. Musical performances, film festival and networking events. Public events in Smithsonian museums and zoo (entrance fees may apply).

Please direct questions to ConservationCommons@si.edu

"Coyle, Brian J." <CoyleB@si.edu>

UCalgary EvoDevo Aug19-23

The Pan-American Society for Evolutionary Developmental Biology 2nd Biennial Meeting August 19-23, 2017

University of Calgary Alberta, Canada

Registration is now open for the 2nd Biennial EvoDevoPanAm Meeting, which will be held on the campus of the University of Calgary. Renew your membership and register for the meeting online at http://www.evodevopanam.org/2nd-biennial-meeting.html . Abstract submission and discounted rates are available through May 15.

Conference venue The meeting will take place in the MacEwan Conference and Event Center (MCEC) at the University of Calgary. MCEC is located minutes by local transportation from downtown Calgary, with easy access to Calgary International Airport. There is a food court adjoining the center which offers many quick meal choices and coffee shops, bars. Other amenities nearby include a pharmacy, medical/dental center, gym and pool. MCEC is a fully wheelchair-accessible facility.

Meeting Schedule The meeting will begin at 6 pm on Saturday, August 19th with keynote talks and an opening reception. The meeting will end on Tuesday, August 22nd with our Young Investigator and Lifetime Award talks in the evening (6:30-8:00 pm) and a closing reception to follow. A preliminary schedule of events can be found online at https://goo.gl/FG0LLN **Registration** Faculty or Postdoc from Central America, South America or the Caribbean: $130.00

Faculty from all other geographical regions (e.g., US, Canada, Europe, Asia, Australia): $260.00

Postdoc from all other geographical regions (e.g., US, Canada, Europe, Asia, Australia): $200.00

Student (undergraduate or graduate): $130.00

Accommodations We have arranged accommodation for delegates through the Alma Hotel, the University of Calgary's on-campus hotel and residence facility. There are several room options to choose from, including individual rooms and suites, shared two-bedroom apartments, and dormitory-style rooms. These housing options are on the UofC campus, a 3-5 minute walk from the MacEwan Conference and Event Center. We have also reserved rooms at the Best Western Village Inn, a 15 minute walk from the MCEC. For details on housing options and instructions on reserving accommodations, refer to the PDF at https://goo.gl/ueDzqS **Child care** Child care will be available Monday 21st to Wednesday 23rd. For children aged 1-5, we have a limited number of drop-in spots at Kids & Company's SmartTech location, a ~20 minute walk from campus. 80$/day includes three meals and age-appropriate activities. Hours are 6:30 am to 6:00 pm. For reservations contact Kelley Hodson at smarttech@kidsandcompany.com. For older children, the University of Calgary runs an excellent summer camp program, weekdays from 8am to 4pm. Visit the University of Calgary Camps website https://www.ucalgary.ca/activeliving/camps . PASEDB will offer a partial childcare subsidy to conference attendees with accompanying children who will be attending either the drop-in daycare or the summer camp programs during the meeting. Please contact treasurer@evodevopanam.org for additional information and to apply for the subsidy.

Arriving by Air Calgary's international airport (YYC) is located in the north-east quadrant of the city. If you need any help when you arrive at the airport, just ask one of the many airport greeter/volunteers you'll find around the airport. They are easy to find in their white cowboy hats and red vests, and are there to assist. Transportation to the University is available by shuttle services (http://www.yyc.com/en-us/travellerinfo/groundtransportation.aspx) or taxi. It's about a 25 minute ride, and will cost 40-45$ (http://www.yyc.com/en-us/travellerinfo/groundtransportation/taxis,sedans.aspx) All major car rental agencies are available at the airport http://www.yyc.com/en-us/travellerinfo/groundtransportation/carrentals.aspx Public transportation from the airport to the University is also available http://www.evodevopanam.org/2nd-biennial-meeting.html Parking on campus is available in several on-campus lots with a pay-per-entry fee of $7.

Associated Course Arrive early and attend the Transmitting Science course: GEOMETRIC MORPHOMETRICS in R. August 14th - 18th, 2017 - Banff Centre, University of Calgary, run by Dr. Julien Claude. During this course, concepts in

— / —

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

---

UEssex GenomicsEpigenetics-GeneRegulation
Sep14

Dear colleagues,

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 visit our webpage:

http://gate.essex.ac.uk/ Registration is free. Abstracts will be accepted for submission from the 3rd of April until the 2nd of June.

Please share this information 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

UFlorida GeneralScience May20

To All Students and Postdocs:

The graduate students and postdocs of the UF Whitney Laboratory for Marine Bioscience invite you to our 5th Annual Science by the Shore Symposium (formally Biology at the Beach) open to all scientific disciplines. This event will take place all day Saturday, May 20th, at the Whitney Lab, located in Saint Augustine, FL. Undergrads, graduate students and postdocs from many different departments and universities in the southeast attend, so anticipate learning from, and explaining your research to, a diverse audience united by scientific curiosity and the beach!

Presentation formats include 10 minute and 5 minute oral presentations, a traditional poster session, and a poster blitz (see registration website for more details). Prizes will be awarded for the best presentations. Registration is $25 (cash or check only the day of the event) and covers breakfast, lunch, dinner, and fun symposium giveaways. The deadline to register is May 6th, but attendance is limited, so please register early.

We look forward to you joining us for a fun, casual day at the beach where we can discuss diverse research topics, engage in outdoor activities, and get to know peers from outside our individual fields! If you have any questions, feel free to email me at sciencebytheshore@whitney.ufl.edu

REGISTRATION LINK: https://ufl.qualtrics.com/SE/-?SID=SV_6zdP6HYX7L1QzbL Casandra Newkirk, PhD Student University of Florida Fisheries and Aquatic Sciences

melissa.debiasse@gmail.com

UNotreDame ArthropodGenomics Jun6-11

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 6 - June 11, 2017 and is hosted by the Eck Institute for Global Health at the University of Notre Dame.

KEY DATES AND DEADLINES - 2017

March 31, 2017: Poster Abstracts due if you DO wish to be considered for a General Session Platform presentation

March 31, 2017: Travel Grant Deadline for consideration.

April 14, 2017: Early Registration Deadline

May 26, 2017: Poster Abstracts due if you DO NOT wish to be considered for a General Session Platform presentation

May 26, 2017: Hotel / Dorm Room Block Deadline

May 26, 2017: 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, accommodations, and travel grants. In case of questions contact:

Ashley Scott, ascott12@nd.edu Sarah Craig, craig.20@nd.edu Mary Ann McDowell, mcdowell.11@nd.edu

– 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 Registration

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.

KEY DATES AND DEADLINES - 2017

March 31, 2017: Poster Abstracts due if you DO wish to be considered for a General Session Platform presentation

Friday, March 31, 2017: Travel Grant Deadline for consideration.

April 14, 2017: Early Registration Deadline (reduced registration rate)

May 26, 2017: Poster Abstracts due if you DO NOT wish to be considered for a General Session Platform presentation

May 26, 2017: 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, accommodations, and travel grants. 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

Winnipeg EcomorphologyDiversity May15-19

The Comparative Morphology & Development (CMD) section of the Canadian Society of Zoologists (CSZ) invites you to attend the following joint symposium (with Integrative Ecology and Evolution, IEE) at the annual CSZ meeting:

May 15-19, 2017, in fabulous WINNIPEG, MANITOBA

MAIN SYMPOSIUM: "Ecomorphology & Diversity" (May 17, 2017)

SHARLENE SANTANA (Washington) *CMD* The role of morphology, performance, and behavior in the ecological diversification of bats

BEREN ROBINSON (Guelph) *CMD* Ecomechanics and plasticity of lamellar self-amputation in larval damselflies

SIMONE DES ROCHES (UC Santa Cruz) *CMD* Niche shifts, directional change, and ecological release in White Sands lizard ecomorphology

LUIS F. DE LEON (U Mass, Boston) *IEE* Ecomorphology and adaptive radiation in Darwin's finches

JILLIAN DETWILER (Manitoba) *IEE* Using integrative taxonomy to explore the diversity and host specificity of echinostome parasites

KAMAL KHIDAS (Canadian Museum of Nature) *IEE* Ecomorphology, resources utilization and distribution patterns in mammals

[Organized by Tim Higham (UC Riverside) & Mery Martinez-Garcia (Laurentian)]

FOR MORE DETAILS ABOUT THIS SYMPOSIUM, SEE:

http://www.biology.ualberta.ca/CMD/home.htm TO REGISTER, OR TO LEARN MORE ABOUT THE CSZ ANNUAL MEETING, SEE:

http://www.csz-scz2017.com/home.html EARLY REGISTRATION DEADLINE: Friday, March 31, 2017

CONTRIBUTED PAPERS: Spaces are also available for contributed papers in sessions organized by the CMD section. The deadline for submitting abstracts is barely 3 weeks away, so don't delay:

ABSTRACT SUBMISSION DEADLINE: Friday, March 31, 2017

FINAL REGISTRATION DEADLINE: Sunday, April 30, 2016

– A. Richard Palmer, FRSC Systematics and Evolution Group Department of Biological Sciences University of Alberta Edmonton, Alberta T6G 2E9 CANADA phone: (780) 492-3633 message: (780) 492-3308 FAX: (780) 492-9234 http://www.biology.ualberta.ca/-palmer/palmer.html Secretary-General Comparative Morphology & Development section Canadian Society of Zoologists: http://www.biology.ualberta.ca/CMD/-home.htm rich.palmer@ualberta.ca

Yosemite Symbiosis May5-7 EarlyRegistrationDue

Dear Colleagues,

The Seventh annual Yosemite Symbiosis Workshop will take place on May 5th-7th, 2017 at the Sierra Nevada Research Institute, Yosemite National Park. This has become a great venue for a diversity of symbiosis researchers. We hope to continue to attract a diverse group in 2017!

Keynote speaker 2017: Dr. Corrie Moreau from the Field Museum of Natural History.

Information about our meeting:

Why: Our continuing goal is to better integrate the broad groups of scientists that focus on symbiosis research. Yosemite serves as an ideal site as it is both beautiful and secluded. This will be our 7th annual meeting and we have been consistently attracting scientists from all over the country and overseas.

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

When: The talks and formal meeting will be held May 6-7, 2017, though we make accommodation arrangements available for attendees to arrive on Friday the 5th to provide opportunities to enjoy the park. Since time at the conference is limited, we ask attendees to submit an abstract and a preference (talk versus poster). Priority will be given to those presenting.

Abstract and early bird registration are due on March 6th, 2017.

Where: SNRS has a set of cabins in Wawona and all within a short walk of the conference room.

Costs: See details in the registration page. We will only be able to accept credit card payments this year. Your registration is not activated until you have completed the payment process. NOTE that the payment link is at the top of the registration page. The registration fee includes room and board.

The registration form for the 2017 Symbiosis Workshop is active: http://snri.ucmerced.edu/symbiosis Please direct any questions to the organizers: Joel Sachs joels@ucr.edu A. Carolin Frank cfrank3@ucmerced.edu

*Joel L. Sachs**, Associate Professor* 5406 Boyce Hall Department of Biology University of California, Riverside

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

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

Yosemite Symbiosis May5-7 SpacesOpen

We still have spaces open and there is still time to register!

Dear Colleagues,

The Seventh annual Yosemite Symbiosis Workshop will take place on May 5th-7th, 2017 at the Sierra Nevada Research Institute, Yosemite National Park. This has become a great venue for a diversity of symbiosis researchers. We hope to continue to attract a diverse group in 2017!

Keynote speaker 2017: Dr. Corrie Moreau from the Field Museum of Natural History.

Information about our meeting: Our continuing goal is to better integrate the broad groups of scientists that focus on symbiosis research. Yosemite serves as an ideal site as it is both beautiful and secluded. This will be our 7th annual meeting and we have been consistently attracting scientists from all over the country and overseas.

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

The talks and formal meeting will be held May 6-7, 2017, though we make accommodation arrangements available for attendees to arrive on Friday the 5th to provide opportunities to enjoy the park. Since time at the conference is limited, we ask attendees to submit an abstract and a preference (talk versus poster). Priority will be given to those presenting.

Where: SNRS has a set of cabins in Wawona and all within a short walk of the conference room.

Costs: See details in the registration page. We will only be able to accept credit card payments this year. Your registration is not activated until you have completed the payment process. NOTE that the payment link is at the top of the registration page. The registration fee includes room and board.

The registration form for the 2017 Symbiosis Workshop is active: http://snri.ucmerced.edu/symbiosis Please direct any questions to the organizers: Joel Sachs joels@ucr.edu A. Carolin Frank cfrank3@ucmerced.edu

–

*Joel L. Sachs**, Associate Professor* 5406 Boyce Hall Department of Biology University of California, Riverside

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

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

Zurich PolygenicAdaptation Aug28-Sep1

A Summer School and a Symposium will take place this summer in Zurich calling for students and scientists keen to learn and discuss about the most recent theory, methods and applications to detect the genomic signal of polygenic adaptation and understanding the role of epistasis in evolution.

The invited speakers include, Prof Nick Barton (IST Austria, Austria) Dr. Jeremy Berg (Columbia University, USA) Prof Ã-rjan Carlborg (Uppsala University, Sweden) Dr. Josephine Daub (University Pompeu Fabra, Barcelona, Spain) Prof. Frederic Guillaume (University of Zurich, Switzerland) Prof. Thomas Hansen (University of Oslo, Norway) Prof Joachim Hermisson (University of Vienna, Austria) Prof Sergey Kryazhimskiy (University of California San Diego, USA) Prof. John Mckay (Colorado State University, USA) Dr. Josh Payne (University of Zurich, Switzerland) Prof. Peter Visscher (Institute for Molecular Bioscience, Queensland, Australia) Prof. Sam Yeaman (University of Calgary, Canada)

For more information visit the event websites: Summer School on "Integrated methods to detect polygenic adaptation from genomic data"

28 Aug - 30 Aug 2017, WSL, Birmensdorf, Switzerland http://www.ieu.uzh.ch/en/teaching/Polygenic-Adaptation.html Symposium on the "Genomics of polygenic adaptation and the role of epistasis in evolution"

31 Aug - 1 Sep 2017, ETH Zentrum, Zurich, Switzerland http://www.evolution.uzh.ch/en/events/-symposium.html Informal inquiries may be addressed to Katalin Csillery at katalin.csillery@wsl.ch

Looking forward to seeing you this summer!

The organising committee: Dr Katalin Csillery (ETH Zurich & WSL Birmensdorf) Prof Dr Frederic Guillaume (University of Zurich) Dr Felix Gugerli (WSL Birmensdorf) Dr Christian Rellstab (WSL Birmensdorf) Dr Alejandra Rodriguez-Verdugo (ETH Zurich) Dr. Tony Weingril (University of Zurich) Prof Dr Alex Widmer (ETH Zurich) Dr. Debra Zuppinger-Dingley (University of Zurich)

Katalin Csillery <katalin.csillery@env.ethz.ch>

GradStudentPositions

CharlesU Prague EvolutionGenomicsFishesLASTCALL 21
KielU ComputationalEvolutionaryGenomics 22
LausanneU AntNetworksDisease 23
London GenomicTraitCorrelation 23
MacquarieU BehaviouralEvolution 24
MasseyU Bioinforamtics 25
MasseyU Bioinformatics 26
MaxPlanckInst Ploen EvolBiol 27
MaxPlanck Ploen 10 EvolutionaryBiol 27
McMasterU FishBehaviour 28
MichiganStateU PopGenomics 28
MonashU EvolutionaryBiology 29
MurrayStateU Kentucky PhenotypicPlasticity 30
Naturalis Netherlands PteropodEvolution 30
NewZealand FishSex 31
NewZealand SnapperSequencing 32
SouthDakotaStateU SustainablePollinationBiol 33
SouthernIllinoisU PoisonFrogEvolution 33
StAndrews EvolutionaryTheory 34
TrentU LaurentianU AmphibianPopGenetics 34
TrinityCollegeDublin HumanPopulationGenomics . . 35
UAberdeen ArchaeaEvolution 35
UAberdeen UK MicrobialEcologyEvolution 36
UAdelaide BioinformaticsandPaleogenomics 37
UBath ExperimentalEvolution 37
UHelsinki MathModellingEvolution 38
UHuddersfield ApodemusEvolutionaryGenomics . . . 39
ULeicester GeneticEpidemiologyBioinformatics 40
ULeicester GenomicsKinshipAncestryForensics 41
ULethbridge EvolutionaryNeurobiology 42
ULincoln UruguayEvolutionStudents 42
ULondon EvolTheoryApplied2Cancer 43
UmeaU ForestGenetics 43
UmeaU LandscapeGenetics 44
UNewSouthWales 2 FishEpigenetics EvolMed 44
UNotreDame EcologicalSpeciation 45
UOtago GenomicsParasiticMindControl 46
UOtago NewZealand PopGenTheory 47
UOtago NZ WeevilEvolution 47
UPadua Italy SexualSelectionGuppy 48
UppsalaU BirchPopulationGenomics 49
USalzburg Austria PollinatorAdaptation 50
UStAndrews DrosophilaSpeciationGenomics 51
USussex FloralEvolution new deadline 51
UUppsala PopulationGenomics 52
Vienna PopulationGenetics 52
WesternSydneyU 3 TephritidFruitFlies 53

CharlesU Prague EvolutionGenomicsFishesLASTCALL

LAST CALL: We are still searching for more highly motivated candidates for a Ph.D. position to join our project focused on molecular evolution of sensory genes in fishes. The selected Ph.D. candidate will become part of the research team within the framework of the project entitled: “Genomics of sensory adaptations: evolution of vision, smell and taste in fishes” funded by SNSF (Switzerland):

1) PhD position I: Molecular evolution of vision and olfaction in teleost fishes with the main focus on the elephant fishes (Mormyridae); methods: genomics, transcriptomics, stable isotope analysis; offered field work participation: Cameroon, Czech Republic

2) PhD position II: Transcriptomics and developmental plasticity of sensory systems in fishes; model groups: Cichlidae, Cyprinidae, deep-sea fishes; methods: genomics, transcriptomics, experimental biology; offered field work participation: Cameroon, Zambia, Czech Republic

Genomic and transcriptomic methods will be employed to identify molecular evolution and mechanisms of adaptation of sensory systems in fishes. The general research project aims to integrate the findings of molecular genetics with trophic ecology and developmental stages in different species and, therefore, it offers a great combination of field observation, experimental setups and laboratory approaches.

The research group is located in Prague (Czech Republic) and the Ph.D. students will process collected material, as well as will have an option to actively participate in the field sampling. Selected candidates are expected to actively participate in international conferences and produce research publications.

Start: October 2017, Duration: 4 years

Competitive salary is composed of the fulltime project position (240’000 CZK annually) + standard university scholarship (will start at 75’600 annually and raise up to 115’000 CZK according to the progress of the study duties; additional bonuses available for published research papers), which in total corresponds to the average national salary and sufficiently covers living expenses in the Czech Republic.

Required: motivation and enthusiasm for biology and science; fluency in English; a M.Sc. degree in biology or related fields (or to be finished until September 2017).

Desirable (but not necessary): previous experience with molecular genetic methods; (basic) bioinformatics skills (please highlight if you have any), experience with research projects evidenced by a (co)authorship of research papers or conference contributions.

Deadline: 31st March 2017 (the candidate has to be assigned to the position by mid-April).

All questions and applications (CV + half-page motivation letter + contact details for one person who can be asked for a reference) should be sent directly to Zuzana Musilova (zuzmus@gmail.com - preferred, zuzana.musilova@natur.cuni.cz). Please indicate which position you're interested in. More info about the Division of Animal Evolutionary Biology, and Department of Zoology: http://web.natur.cuni.cz/-zoologie/biodiversity/index.php?page=musilova zuzmus@gmail.com

KielU ComputationalEvolutionaryGenomics

The Genomic Microbiology Group of Prof. Tal Dagan in the Institute of Microbiology at Kiel University, Germany, invites applications for a:

PhD position in computational evolutionary genomics

The position is offered within the International Max Planck Research School (IMPRS) for Evolutionary Biology

Application deadline is April 23, 2017.

Research topic: Evolutionary metagenomics of foraminifera residing in oxygen minimum zones

Benthic foraminifera are unicellular eukaryotes populating sediments of aquatic environments. Several species were shown to perform complete denitrification, a rare metabolic pathway foraminiferal denitrification pathway is yet unknown and a prokaryotic contribution has been suggested. Our current research comprises the analysis of metagenomes sequenced from foraminifera sampled in a hypoxic environment in Gullmarfjord (Sweden). Our results indicate that denitrification is performed, at least in part, by foraminifera-encoded proteins. This constitutes evidence for a rare eukaryotic pathway for nitrite resporation. The PhD candidate will take part in analyzing foraminifera metagenomes sampled in the Peruvian oxygen minimum zone with a focus on evolution of the denitrification pathway. The project requires background in molecular evolution and programming skills.

Research Group: The PhD candidate will work in the Genomic Microbiology group led by Prof. Tal Dagan (http://www.uni-kiel.de/genomik) that is focused on microbial genome evolution. The group is international and multidisciplinary with both computational and experimental working scientists. For enquiries regarding the position and research topic please contact Prof. Tal Dagan: tdagan@ifam.uni-kiel.de

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

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

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

The deadline for applications is April 23, 2017

The selection week will be held from June 26- 30 and

the program itself starts on September 18, 2017.

For information regarding the program contact: Dr. Kerstin Mehnert, August-Thienemann-Str. 2, 24306 Plon, Germany email: imprs@evolbio.mpg.de phone: +49(0)4522 763 233

The coordinator Kerstin Mehnert

The steering committee Tal Dagan, Thorsten Reusch, Hinrich Schulenburg, Eva Stukenbrock, Diethard Tautz and Arne Traulsen

"tdagan@ifam.uni-kiel.de" <tdagan@ifam.uni-kiel.de>

LausanneU AntNetworksDisease

PhD position at Lausanne University

I am looking to recruit a highly motivated PhD student to work on disease transmission in ant social networks at the Department of Ecology and Evolution (DEE) of Lausanne University, Switzerland. The position is fully funded for three years and starts in August 2017.

The successful candidate will work with a novel system, the queenless clonal raider ant Ooceraea biroi (formerly: Cerapachys biroi), to investigate the properties of social groups that increase resistance to pathogens (fungi, nematodes). The unusual biology of this species allows us to precisely control and replicate aspects of colony composition (e.g. size, genetic and demographic structure) that are thought to modulate interaction network structure, and therefore, disease spread. The student will use newly developed techniques for automated behavioral tracking in combination with experimental infections and/or molecular methods (RNAseq/qPCR) to study how ant colonies of different composition regulate behavior and immune function at the individual and group levels, and how this affects disease spread. Within this framework, the student will also be encouraged to develop her/his own research questions.

Candidates should have a Master's degree (or equivalent) and a background in evolution/ecology, behavior, epidemiology, systems biology or other relevant field. Motivation, curiosity, and an ability to work independently are essential. Experience working with social insects, programming, or standard wet-lab techniques would be advantageous but are not necessary. The working language of the group is English; proficiency with French is helpful but not required.

The successful applicant will join an international, interactive department with 20 groups working on a wide range of topics in evolution and ecology, including other labs working on social insects. Lausanne is a small but vibrant city located on the shore of Lake Geneva, less than one hour from the Alps. There are large student and international communities and the city is well connected to all major European cities.

To apply, please send a CV, a short (<1 page) cover letter describing your background and interests, and the name and contact information of 2-3 persons willing to provide recommendations to Yuko Ulrich (yuko.ulrich@gmail.com) by the end of March. Informal inquiries are also welcome.

Yuko Ulrich (main supervisor)

Laboratory of Social Evolution and Behavior (current address)

The Rockefeller University, New York

http://lab.rockefeller.edu/kronauer/members Useful links:

Lab webpage: https://www.ulrichlab.com/ DEE at Lausanne University: https://www.unil.ch/dee/en/-home.html The system: https://www.nytimes.com/-2017/01/23/science/gene-modified-ants.html Yuko Ulrich <yulrich@mail.rockefeller.edu>

London GenomicTraitCorrelation

A fully funded PhD studentship is currently available at Queen Mary University of London on ash genomics in an evolutionary context. The deadline for application to these studentships is Friday, March 31, 2017.

see: http://www.ashgenome.org/studentships Further details are as follows:

The genomic basis of disease resistance in plants - integrating within and among species data

Supervised by Dr Richard Buggs and Prof. Richard Nichols

Project Description

Ash dieback, caused by the fungal pathogen Hymenoscyphus fraxineus, is threatening populations of ash trees throughout Europe. This has sparked off an international research effort to develop ash trees with low susceptibility to the fungus. This PhD studentship, funded by Defra, provides an outstanding opportunity for a student with a strong background in genetics, bioinformatics or statistics to contribute to this effort, and develop methods that will be applicable to other plant-pathogen systems.

The PhD student will be based in the lab of Dr Richard Buggs, working with other students and postdocs on ash genomics in relation to ash dieback. This lab recently published a paper in Nature on the genome of the European ash tree, and its diversity in Europe. The lab has strong collaborations with many other organisations working on the same problem, including Forest Research, Teagasc, Royal Botanic Gardens Kew, Univerity of Copenhagen and Earlham Institute. We are currently sequencing and assembling the genomes of 30 ash worldwide species and testing them for resistance to ash dieback (see http://www.ashgenome.org). We are also analysing mass screening trials of European ash (Fraxinus excelsior) set up by Forest Research, where tens of thousands of trees from different locations in the UK are bing exposed to ash dieback infection in field trials in the south of England.

The student will be co-supervised by Prof. Richard Nichols, who has a long track record of research and novel statistical method development in population genetics. The student will conduct data analyses and develop methods aiming to uncover the genomic basis of tree susceptibility to pests or pathogens. He/she will analyse genomic data from within and between tree species, and develop new methods of analysis and data integration. The main datasets analysed will be for the genus Fraxinus but the methods developed will be applicable to a wide range of systems where the genomic basis of traits is sought.

The main criterion by which a student will be selected is scientific excellence. There is considerable scope for the project to be tailored to the skills and interests of the student, fitting with the broad research programme on ash dieback.

Funding Notes

This studentship is funded by the UK Department for Environment, Food and Rural Affairs. The award covers Home/EU tuition fees and a tax free annual stipend at Research Councils UK rates (pounds 16,296 in 2016/17).

Dr Richard Buggs | Reader in Evolutionary Genomics | School of Biological and Chemical Sciences, Queen Mary University of London, E1 4NS, United Kingdom | email: r.buggs@qmul.ac.uk | website: http://www.sbcs.qmul.ac.uk/staff/richardbuggs.html | office: +44(0)207 882 8441 | mobile: +44(0)772 992 0401 | twitter: @RJABuggs

Richard Buggs <r.buggs@qmul.ac.uk>

MacquarieU BehaviouralEvolution

4 PhD positions in Behavioural and Physiological Ecology

at Macquarie University, Sydney, Australia We are pleased to announce multiple opportunities available for a start from mid to late 2017

1: Adapting to a foreign climate: the reproductive ecology of the house sparrow in Australia The house sparrow (Passer domesticus) was introduced into Australia in the 1860's and has since become well established across a broad range of climates in both countries. This project will take advantage of this 'experimental' introduction to focus on behavioural and physiological adaptations to different climates through a field-based comparative approach. This research will complement our existing work on related questions in endemic Australian species and will provide insight into the capacity of avian species to adapt to changing climates. This project will involve periods of field-work in Broken Hill, Armidale and Hobart in Australia, along with a range of behavioural, molecular and physiological assays. The project will involve collaboration with other groups in Australia and the US.

2: The challenge of growing in a hot climate (in the zebra finch) In recent years we have characterised the very hot conditions in which zebra finches are raised (with nests often reaching temperatures over 40 degrees Celsius, as well as identifying adverse effects of these conditions on embryonic development, offspring growth, and adult sperm. This project is supported by an ARC funded project and will investigate the adaptations that this iconic and well-studied species has to deal with the extreme climate in which it lives. The project will take a variety of approaches including behavioural work, and assays of metabolism and physiology, and combine fieldwork and laboratory work. The project will be run in collaboration with Dr Christine Cooper (Curtin University, Western Australia), Prof. Pierre Deviche (Arizona State University, US), and Prof. Pat Monaghan (Glasgow, UK).

3: Social structuring and life-history in free-ranging domestic sheep In this project we will examine the importance of social structure and collective intelligence to life-history trade-offs and productivity in domestic sheep in the rangelands of Australia. The project will use tools from social network theory and spatial ecology to characterise individual and group behaviour and investigate their effect on individual quality and productivity (lambs and wool) in this challenging, but economically important part of Australia. The project will be based at Fowlers Gap (near Broken Hill in the arid zone) and require field work and well-developed analytical skills. This work will be run in collaboration with partners in the pastoral industry and be jointly supervised by Dr Stephan Leu (also at Macquarie University).

4: Parasite transmission dynamics in an Australian lizard This project will investigate the relationship between host spatial and social behaviour and bacterial transmission. It combines social network theory, spatial ecology and wildlife epidemiology to determine how different bacterial strains are transmitted through the population and how individual behaviour and consequently population social structure changes as a function of infection status. The project combines the analysis of a very comprehensive (already collected) dataset with scope for the student to develop his/her own ideas and conduct fieldwork. The student should be interested in social networks and disease modelling and have strong analytical skills. This project will be jointly supervised by Dr Stephan Leu and A/Prof Martin Whiting (both at Macquarie University). We also have strong relationships with disease modelling colleagues in the US.

Application The Department of Biological Sciences at Macquarie University is a vibrant environment which offers excellent support to postgraduate students. A Macquarie University Excellence in Research Scholarship has already been assigned to one of these projects, but there are other scholarship opportunities available to suitably competitive candidates. International candidates are welcome to apply for any of the projects listed above.

The 2014 MQRES full-time stipend rate is $26,682 pa tax exempt for 3 years (indexed annually). In addition to external grant support for projects, there is additional internal funding (up to $17,000) available to cover direct research expenses and conference travel. Applicants should ideally have a research-based MSc in a related discipline (with a minimum 50% research component), and additional relevant research experience, qualifications, and details of awards or prizes. For projects 1, 2, and 4 an ability to work in remote and harsh conditions as well as experience in capturing and handling animals is desirable. A driving licence is required for all projects. Applications should include 1) your CV, 2) a brief statement of your reasons for applying (max. 500 words) and the project you are applying

— / —

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

MasseyU Bioinforamtics

We have a scholarship for an enthusiastic and motivated individual who is interested in conducting a PhD research project in the areas of computational statistics and/or bioinformatics. Typical keywords to describe our research include, but are not limited to: network inference/analysis, causality, simulation strategies, genetic/genomic data, evolution, high-dimensional methods, probabilistic graphical models. Examples of recent projects conducted here are “Study of gene expression patterns in an allopolyploid species: a network approach”, “Inferring causality in complex systems from observations” or “Analysis of phenotype:genotype relationships in bacteria using machine learning”. Our approach is clearly interdisciplinary.

Background: The Statistics and Bioinformatics group at Massey is among the largest of its kind in New Zealand. It is part of the Institute of Fundamental Sciences (IFS), which gathers scientists from varied fields working on cutting edge problems within and across their disciplines. Strong links with other Institutes within Massey University and beyond are already established. Biological/agricultural research is one the strengths of Massey University, and this is a real opportunity to develop sound and original quantitative methodologies. There is a large, diverse and active community of PhD students and postdoctoral researchers at Massey. Excellent library, computing (locally or at the nationwide scale, e.g. NeSi, https://www.nesi.org.nz/) and other research support facilities, sustained programmes of research seminars and workshops are available to the successful candidate. It is against this backdrop that the successful candidate will be afforded agreed upon objectives and the motivation to develop original research with a balance of methodological developments in a quantitative subject and meaningful applications. The planned supervisory team currently consists of A/Prof Patrick Biggs, who has a prominent role in research in Bioinformatics at Massey and Dr Matthieu Vignes, who is a specialist in modern statistical computation strategies for biologically inspired problems. Depending on the interests of the student, and the agreed project, other faculty members may join the supervisory committee.

Candidate and conditions: The anticipated admission standard for this PhD position is a 1st class or high upper 2nd class Honours degree, or a Master's degree with merit or distinction, in Mathematics, Statistics, Computer Science, or a related quantitative discipline. Overseas qualifications of an equivalent standard are also acceptable. In addition, the candidate will have a marked taste for interdisciplinary research, the ability to work as a team member, and to organise their own tasks. Proficiency with at least one scientific language/software (R, Python, C/C++...) is highly desirable.

The studentship will be three years in duration and covers tuition fees at the domestic rates plus a tax-free stipend of NZ $25,000 per annum. In addition, some reasonable funds are available to students e.g. for travel to international conferences, or small equipment. There would be the possibility to gain some experience in teaching if desired. The location of the PhD is at the Manawatu campus of Massey University, in Palmerston North, a small, very affordable yet lively, enjoyable and culturally diverse city in the North Island of New Zealand.

The deadline for the application is 30/04/2017. Applications will be considered on a rolling basis until the studentship is filled. Apply as soon as possible to avoid disappointment! The ideal enrollment date is Sept 2017. For further information and informal discussions of potential projects please contact us (p.biggs@massey.ac.nz and/or m.vignes@massey.ac.nz).

Patrick J Biggs PhD Associate Professor of Genomics and Computational Biology Head of Bioinformatics | mEpiLab Infectious Disease Research Centre (IDReC) Institute of Veterinary, Animal and Biomedical Sciences – and – Bioinformatics and Statistics Group Institute of Fundamental Sciences Massey University | Palmerston North | New Zealand

Tel: +64 6 356 9099 ex 84597 Direct dial: +64 6 951 7597 | Fax: +64 6 355 7955 Email: p.biggs@massey.ac.nz

P.Biggs@massey.ac.nz

MasseyU Bioinformatics

We have a scholarship for an enthusiastic and motivated individual who is interested in conducting a PhD research project in the areas of computational statistics and/or bioinformatics. Typical keywords to describe our research include, but are not limited to: network inference/analysis, causality, simulation strategies, genetic/genomic data, evolution, high-dimensional methods, probabilistic graphical models. Examples of recent projects conducted here are "Study of gene expression patterns in an allopolyploid species: a network approach", "Inferring causality in complex systems from observations" or "Analysis of phenotype:genotype relationships in bacteria using machine learning". Our approach is clearly interdisciplinary.

Background: The Statistics and Bioinformatics group at Massey is among the largest of its kind in New Zealand. It is part of the Institute of Fundamental Sciences (IFS), which gathers scientists from varied fields working on cutting edge problems within and across their disciplines. Strong links with other Institutes within Massey University and beyond are already established. Biological/agricultural research is one the strengths of Massey University, and this is a real opportunity to develop sound and original quantitative methodologies. There is a large, diverse and active community of PhD students and postdoctoral researchers at Massey. Excellent library, computing (locally or at the nationwide scale, e.g. NeSi, https://www.nesi.org.nz/) and other research support facilities, sustained programmes of research seminars and workshops are available to the successful candidate. It is against this backdrop that the successful candidate will be afforded agreed upon objectives and the motivation to develop original research with a balance of methodological developments in a quantitative subject and meaningful applications. The planned supervisory team currently consists of A/Prof Patrick Biggs, who has a prominent role in research in Bioinformatics at Massey and Dr Matthieu Vignes, who is a specialist in modern statistical computation strategies for biologically inspired problems. Depending on the interests of the student, and the agreed project, other faculty members may join the supervisory committee.

Candidate and conditions: The anticipated admission standard for this PhD position is a 1st class or high upper 2nd class Honours degree, or a Master's degree with merit or distinction, in Mathematics, Statistics, Computer Science, or a related quantitative discipline. Overseas qualifications of an equivalent standard are also acceptable. In addition, the candidate will have a marked taste for interdisciplinary research, the ability to work as a team member, and to organise their own tasks. Proficiency with at least one scientific language/software (R, Python, C/C++...) is highly desirable.

The studentship will be three years in duration and covers tuition fees at the domestic rates plus a tax-free stipend of NZ $25,000 per annum. In addition, some reasonable funds are available to students e.g. for travel to international conferences, or small equipment.

There would be the possibility to gain some experience in teaching if desired. The location of the PhD is at the Manawatu campus of Massey University, in Palmerston North, a small, very affordable yet lively, enjoyable and culturally diverse city in the North Island of New Zealand.

The deadline for the application is 30/04/2017. Applications will be considered on a rolling basis until the studentship is filled. Apply as soon as possible to avoid disappointment! The ideal enrollment date is Sept 2017. For further information and informal discussions of potential projects please contact us (p.biggs@massey.ac.nz and/or m.vignes@massey.ac.nz).

Patrick J Biggs PhD Associate Professor of Genomics and Computational Biology Head of Bioinformatics | mEpiLab Infectious Disease Research Centre (IDReC) Institute of Veterinary, Animal and Biomedical Sciences – and – Bioinformatics and Statistics Group Institute of Fundamental Sciences Massey University | Palmerston North | New Zealand

Tel: +64 6 356 9099 ex 84597 Direct dial: +64 6 951 7597 | Fax: +64 6 355 7955 Email: p.biggs@massey.ac.nz

P.Biggs@massey.ac.nz

MaxPlanckInst Ploen EvolBiol

Weare seeking a motivated PhD student to join our research team working oneco-evolutionary dynamics at the Max Planck Institute for Evolutionary Biologyin Plön, Germany.

Weare looking for a highly motivated ecologist or evolutionary biologist tojoin our group Community Dynamics at the Max Planck institute for EvolutionaryBiology (http://web.evolbio.mpg.de/comdyn) and the Kiel EvolutionCenter (http://www.kec.uni-kiel.de). The ideal candidate is fascinatedby evolutionary and ecological questions, independent and creative.She/he has a background in evolutionary biology, population orcommunity ecology. A MSc (or equivalent) in Biology is required.

Thereis a continuing interest to identify the interactions and feedback dynamicsbetween ecological and evolutionary changes at the same time scale.This interest in eco-evolutionary dynamics is fuelled by the needto understand how populations and communities could adapt to rapid environmentalchange such as warming, invasion and pollution. Despite thispressing need to understand eco-evolutionary dynamics, they are notwell understood in complex systems. In the project we aim to (1) identifyrapid adaptive changes in coevolving host-virus populations in differentfood webs that differ in the types of species interactions and complexityand to (2) comprehend how the dynamics of adaptive changes alterthe ecological dynamics and potential feedbacks. We will combine controlledlaboratory experiments, whole genome sequencing of populations acrossdifferent time points and modeling to characterize and compare theadaptive dynamics and their consequences within the different food webs.For more information on potential the project contact Lutz Becks (lbecks@evolbio.mpg.de).

Theinstitute offers a stimulating international environment and anexcellent infrastructure with access to stateâă-art techniques.The town of Plön is in the middle of the Schleswig-Holstein lake-districtwithin a very attractive and touristic environment near the Baltic-Sea, close to the university towns of Lübeck and Kiel. Hamburg andLübeck are the closest airports.

Theposition is funded for three years. We ask applicants to send aPDF file containing their CV and letter of motivation as well ascontact information of two references by e-mail to Lutz Becks (mailto:lbecks@evolbio.mpg.de).We will begin reviewing applications startingMarch 22th until the position is filled.

TheMax Planck Society is an equal opportunity employer.

Dr.Lutz Becks CommunityDynamics Group MaxPlanck Institute for Evolutionary Biology AugustThienemann Str. 2 24306Plön Germany

Telephone:+49 4522 763 230

LutzBecks <lbecks@evolbio.mpg.de>

MaxPlanck Ploen 10 EvolutionaryBiol

International Max Planck Research School (IMPRS) for Evolutionary Biology is offering up to 10 PhD positions and fellwoships. Application deadline is April 23, 2017.

It is important that the application should be done via the online tool on our homepage http://www.evolbio.mpg.de/3017297/application . The International Max Planck Research School for Evolutionary Biology

is offering up to 10 PhD positions and fellowships.

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

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

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

The deadline for applications is April 23, 2017

The selection week will be held from June 26- 30 and

the program itself starts on September 18, 2017.

Contact: Dr. Kerstin Mehnert,

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

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

The coordinator

Kerstin Mehnert

The steering committee

Tal Dagan, Thorsten Reusch, Hinrich Schulenburg, Eva Stukenbrock, Diethard Tautz and Arne Traulsen

–

Dr. Kerstin Mehnert Scientific Coordinator IMPRS, Press and Public Relations, International Office

Max Planck Institute for Evolutionary Biology International Max Planck Research School (IMPRS) August-Thienemann-Str. 2 24306 Plon, Germany

phone: ++49 - (0)4522 - 763 - 233 fax: ++49 - (0)4522 - 763 - 351 e-mail: mehnert@evolbio.mpg.de

www.evolbio.mpg.de, www.evolbio.mpg.de/imprs

Kerstin Mehnert <mehnert@evolbio.mpg.de>

McMasterU FishBehaviour

Two graduate student positions (at either MSc or PhD levels) are available in the Aquatic Behavioural Ecology Laboratory (ABEL) at McMaster University. Specific research projects will be designed to best fit the applicant's strengths and interests. Projects will focus on our lab's long standing research interests on ecological and behavioural analyses of fish reproductive behaviour and will make use of a combination of field and laboratory studies to address questions about the evolution of social behaviour, breeding systems and human impacts on animal behaviour.

If interested, please contact Dr. Sigal Balshine (sigal@mcmaster.ca) with a statement of interest, transcript and curriculum vitae.

Sigal Balshine Professor Department of Psychology, Neuroscience & Behaviour McMaster University 1280 Main St. West Hamilton,ON L8S 4K1 Canada Phone:905-525-9140 ext. 23024 FAX:905-529-6225 Email:sigal@mcmaster.ca http://abel.mcmaster.ca

"Balshine,Sigal" <sigal@mcmaster.ca>

MichiganStateU PopGenomics

Graduate Student-PhD, forest pathology (genetics/genomics)

Position Description:

The Forest Pathology Lab at Michigan State University (East Lansing, MI) is accepting applications for a graduate student (PhD level) to start as a research assistant in the Summer of 2017 and to enroll for Fall 2017. We are looking for a highly-motivated individual to study the population genomics of Ceratocystis fagacearum, the pathogen behind the devastating disease of oaks "oak wilt". This is a unique opportunity to combine traditional plant pathology research (microscopy, field and culture work) with molecular and bioinformatics approaches (PCR, qPCR and genome resequencing analyses). The candidate will identify the population structure of C. fagacearum in the US and evaluate known assays and, if required, develop novel molecular assays to detect the pathogen. Furthermore, the candidate will investigate seasonal variation in infection of red oak by C. fagacearum and seasonal variation in red oak susceptibility. The candidate will be part of a larger project focused on identifying high-risk periods of C. fagacearum transmission and infection in Michigan. For further information please go to the following web link: https://forestpathology.msu.edu/research/-oak-wilt/ . The Graduate student will have the option of a degree from either the Department of Plant, Soil and Microbial Sciences or the Department of Forestry, depending on their interests. The student will be supported with three years of stipend, tuition waiver and health insurance. Additional fellowship opportunities for graduate students at Michigan State University are also available.

Position Requirements:

The ideal applicant will have an MSc and experience and interest in molecular biology of tree pathogens, particularly in population genetics/genomics and detection assays. Applicants must have a degree in a relevant area, including plant pathology, forestry, mycology, genomics, bioinformatics, physiology, biochemistry, microbiology, botany, or other biological sciences. They should be self-motivated, have strong interpersonal skills and be capable of working in a multidisciplinary team. They must be able to perform experiments independently and write scientific publications and other documents. Applicants with prior experience in next-gen sequencing, bioinformatics, pcr and qPCR are encouraged to apply. Excellent communication, reading, and writing skills in English are also desired. The selected candidate must meet eligibility requirements for work in the U.S. by the start date. Additionally, candidates will need to meet the minimum requirements outlined by Michigan State University's Graduate program (https://grad.msu.edu/-).

Instructions For Applying:

If you are interested in this position please contact Dr. Monique Sakalidis via email at sakalidi@msu.edu. Include a short statement of interest, your CV and the contact details of three references. To be accepted into the graduate program you will need to apply through the MSU Graduate School https://grad.msu.edu/apply. Applications must be received by April 20^th, 2017 to receive full consideration.

Specific information regarding the Plant pathology graduate program please see http://www.psm.msu.edu/-degree_cerficate_programs . Specific information regarding the Forestry graduate program please see http://www.for.msu.edu/graduate/-important_information_for_graduate_appl icants.

Organization Description:

MSU is an equal opportunity employer and the Department Plant, Soil and Microbial Sciences and the Department of Forestry is committed to promoting diversity in research.

Organization Website: www.msu.edu Closing Date: April 20^th 2017

Monique Sakalidis <sakalidi@msu.edu>

MonashU EvolutionaryBiology

The School of Biological Sciences at Monash University is taking applications for PhD students (see the advertisement, below). Monash has a strong community of evolutionary biologists, including labs focusing on evolutionary population and quantitative genetics, evolutionary physiology, biogeography, behavioral ecology, and many other areas. Further information on how to apply can be found here:

http://www.monash.edu/science/schools/biological-sciences/postgrad/how-to-apply ——

PhD positions at the School of Biological Sciences, Monash University, Melbourne, Australia

Scholarships are available for enthusiastic and talented students looking to undertake study in the areas of Biosecurity, Cellular & Developmental Genetics, Disease Control & Genetics, Ecology, Evolutionary Biology, Global Change & Conservation, and Microbiology.

Scholarships covering tuition fees and providing a living allowance of AUD $26,682 per year are available to both Australian and international students. Students are also supported to attend an international conference during their PhD and as part of the Monash Doctoral Program are provided with professional development and training opportunities, to complement their research project.

Monash University is the largest university in Australia and is consistently ranked in the top 100 universities in the world and is ranked in the top 50 for Biological Sciences. The School of Biological Sciences provides an outstanding scientific environment in which to undertake a PhD. It is home to world-renowned researchers in a range of biological disciplines providing a highly collaborative and supportive environment. We have a large and dynamic postgraduate community with students drawn from a wide range of nationalities, cultures, and backgrounds. This creates a productive scientific environment as well as an active social atmosphere.

Academic Requirements: MSc (research) or BSc or equivalent degree including a research project of at least 6 months full time (or equivalent) duration.

English language requirements; IELTS 6.5 overall (no less than 6 in any category), TOEFL ibt 91 (at least 25 writing, 22 for speaking, reading, listening); or to be from, or have a tertiary qualification with at least 2 years study from, a country with English as the primary language.

Interested applicants should visit http://monash.edu/-biologyphd for more information and to identify a potential supervisor.

Applications close 31st May 2017â euro Â

tim.connallon@monash.edu

MurrayStateU Kentucky PhenotypicPlasticity

Graduate position (M.S.) in phenotypic plasticity and evolution of animal behavior.

The Beckers' lab at Murray State University accepts M.S. student interested in phenotypic plasticity and evolution of animal behavior starting in the fall of 2017. Our lab works on male calling and female preference behavior in two of the very few Orthopteran species that display environmentally-induced call plasticity. We use crickets and katydids as model organisms to address our questions. Our research is focused primarily on behavior, but will soon extend in a collaborative effort its focus to the underlying molecular underpinnings responsible for behavioral diversity. We seek an enthusiastic and driven student to join our lab, who has a B.S. in biology, ecology, evolution, or related discipline. Teaching assistantships are available.

To apply or for inquires please send email to: obeckers@murraystate.edu

For applications, please attach a letter of application indicating your research interests and career goals and a curriculum vitae including undergraduate GPA and, if available, GRE scores. Review of applications starts immediately and continues until the position is filled. Thank you for your interest.

Find more information on Dr. Beckers' research here (faculty directory):

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

Oliver Beckers <obeckers@murraystate.edu>

Naturalis Netherlands PteropodEvolution

Two PhD positions are available to study pteropods (planktonic gastropods) and the impact of ocean acidification at Naturalis Biodiversity Center (Netherlands)

http://www.naturalis.nl/nl/over-ons/organisatie/-werken-bij-ons/phd- student-pteropods-ocean-acidification/

The closing date for applications is March 16, 2017.

The focus of Naturalis is biodiversity. Naturalis curates a collection of 37 million specimens; this is one of the world's largest natural history collections. We present the history of our planet and the diversity of life on Earth with permanent and temporary exhibitions, educational programmes and websites. Our research and education are maintained at a high academic level.

Two PhD positions are available within the Vidi project of Dr. Katja Peijnenburg to study planktonic gastropods in the Marine Biodiversity group at the Naturalis Biodiversity Center (Leiden, the Netherlands). PhD project 1 will focus on assessing the adaptive potential of pteropods using a population genomics approach. PhD project 2 will focus on quantifying calcification and vulnerability to ocean acidification of shelled pteropods using 3D morphometric techniques and field experiments.

Successful candidates should have a Master's degree with an interest in ecology, evolution, oceanography, marine biology, or a related field. Excellent command of the English language (written and verbal) is required. The ideal candidates will be highly motivated and organised, with a demonstrated capacity for multidisciplinary research. For PhD project 1, experience with next generation sequencing and data analyses is a distinct advantage. For PhD project 2, knowledge of morphometric methods and advanced statistics is a distinct advantage.

We offer a full-time contract for a period of one year, to be extended with three years after a successful first year evaluation, and a salary of circa euro 2.670,- gross per month. The successful candidates will be employed by Naturalis in Leiden, and the PhD theses will be defended at the University of Amsterdam. Naturalis Biodiversity Center promotes gender equality and wants to enhance the diversity of staff members.

Information on how to apply: http://www.naturalis.nl/nl/over-ons/organisatie/werken-bij-ons/phd- student-pteropods-ocean-acidification/

Feel free to contact Katja Peijnenburg if you have questions about the positions. Katja.Peijnenburg@naturalis.nl. https://science.naturalis.nl/en/people/scientists/katja-peijnenburg/ https://www.researchgate.net/job/884998_PhD_position_to_study_pteropods _and_the_impact_of_ocean_acidification

“K.T.C.A.Peijnenburg@uva.nl”
<K.T.C.A.Peijnenburg@uva.nl>

NewZealand FishSex

Project opportunity BSc (Hons) or Masters

Investigating the molecular basis of sex in snapper

Maren Wellenreuther (Plant and Food Research, Nelson, New Zealand) and Neil Gemmell (University of Otago, Dunedin, New Zealand)

Project Description: Aquaculture provides half the seafood consumed worldwide, and is expected to increase substantially as wild fisheries have little or no scope for increased production. New Zealand has the potential to be a major producer; however, a lack of domesticated species is one factor that hinders development and profitability. Plant and Food Research aims to enhance production of New Zealand’s aquaculture sector by developing accelerated breeding approaches for native marine finfish species. Our main target species is the culturally and commercially important Australasian snapper (Chrysophrys auratus), a species that we have been breeding for over 10 years and for which we can reliably produce a large numbers of juveniles.

The ability to control sex is one of the most important factors for the commercialisation and efficient propagation of new fish species due to influences on reproduction, growth and product quality. Snapper have no heterochromosomes and are sexually monomorphic and it is not known how sex determination is achieved. Histological sexing is also complicated as juvenile snapper have a bisexual gonad with an ovarian lumen from which ovaries or testes develop. Differentiation to ovaries progresses in all fish until 7 months. Subsequently half of the fish continues to develop their ovaries, while the other half starts to develop testis until maturation at around 3 years. Plant and Food Research has recently assembled the snapper genome and transcriptome, and generated whole genome re-sequencing and GBS data that can be mined for genomic regions associated with sex. The aim of this research project is to i) utilise these whole genome and transcriptome sequence data to investigate the molecular basis for sexual determination in snapper and, ii) develop markers that can be used to determine sex early in snapper life history. Investigations will initially focus on a comparative genomics approach that utilises knowledge about sex determining genes from other species and mining the available genomic resources for their presence. Gene expression data from snapper at different ontogenetic time stages will also be generated and used to gain insights into the functional roles of potential sex determining genes. Finally, we will use the GBS data available to search for sex specific SNPs. Based on this knowledge, candidate sex specific markers will be developed and trialled in a number of snapper of known sex from across the species geographic range. The generation of a sex marker for snapper will improve broodstock management and enables to develop appropriate breeding schemes.

The Ideal Candidate: We are seeking an outstanding student with broad interests in genetics to conduct research into the genetic basis of sex determination in snapper. Although a good level of bioinformatic skills would be required to complete this project, a highly motivated student should be able to learn suitable Linux and scripting to undertake this task. Some background in statistics or programming would be an advantage, but training will be provided through the Plant and Food bioinformatics team, with support from the Gemmell lab While the project would be largely computational analysis, it would also involve RNA sampling and extraction. This is an opportunity to work more closely with industry, and would involve some time working at the Plant and Food Research hatchery in Nelson.

The project compartmentalises so there is prospect for this to be developed as either a BSc (Hons) or an MSc degree. Applications should include a curriculum vitae, academic transcripts, contact details of two academic referees and a cover letter that states why the candidate is interested in the position and how their qualifications and experience make them a good fit for the proposed research. Please email with completed applications and for any additional information Dr Maren Wellenreuther (Maren.Wellenreuther@plantandfood.co.nz) and Professor Neil Gemmell (neil.gemmell@otago.ac.nz).Closing date for applications is the end of March 2017.

Maren Wellenreuther Senior Scientist

T: +64 3 989 7658 F: +64 3 546 7049 E: maren.wellenreuther@plantandfood.co.nz www.plantandfood.co.nz The New Zealand Institute for Plant & Food Research Limited

Postal Address: Plant & Food Research Box 5114, Port Nelson, Nelson, 7043, New Zealand Physical Address: Plant & Food Research Seafood Research Unit, 300 Wakefield Quay, Port Nelson, Nelson, 7010, New Zealand

Maren.Wellenreuther@plantandfood.co.nz

NewZealand SnapperSequencing

PhD Project Opportunity

Testing for Fishing-Induced Evolution using Genotyping-by-Sequencing of Ancient and Modern Snapper

We are seeking a highly-motivated PhD student for a project that aims to test for fishing-induced evolution in New Zealand Snapper (Chrysophrys auratus) using Genotyping-by-Sequencing (GBS) of modern and ancient DNA.

Project Supervisors Dr. Peter Ritchie, Victoria University of Wellington (VUW), New Zealand Dr. Nic Rawlence, Department of Zoology, University of Otago, New Zealand Dr. Maren Wellenreuther, Plant and Food Research (PFR), Nelson, New Zealand

Fishing typically targets larger individuals and thus has the potential to increase the reproductive success of small fish that mature early. Numerous studies have reported a decrease in the average size of heavily fished species and the age of maturation, but there is uncertainty about whether this is caused by directional selection on allele frequencies (evolutionary change). The overall goal of this PhD project is to test for fishing-induced evolution in New Zealand snapper by comparing DNA isolated from contemporary populations, to the DNA isolated from bones of pre-industrial fish samples. New Zealand has a unique record of snapper bones that have been preserved in prehistoric New Zealand middens (i.e. places where food remains were dumped or buried). The successful candidate for this project will be responsible for collecting a GBS dataset of genome-wide SNPs using DNA extracted from contemporary samples. This position will be based at Victoria University of Wellington (New Zealand). The data set collected from contemporary samples will be combined with a comparable dataset recovered from snapper ancient DNA that will be obtained by researchers at the Otago Palaeogenetics Laboratory. The complete physical isolation of the ancient and modern part of the project will ensure there is minimal risk of cross-contamination. This ambitious and innovative approach will provide the level of resolution needed to identify genomic regions that have experienced selection and make precise population genetic and demographic inferences possible.

PhD Project Aims 1. To test whether size-selective industrial fishing is associated with a signature of genetic selection, 2. Determine levels of genetic diversity and differentiation, 3. Test for loci under selection and adaptive genetic variation.

This project will provide an excellent opportunity to develop skills in the areas of genomics, bioinformatics and population genetics, and how they can be used to support sustainable harvesting. The PhD student will gain experience working with collaborators in New Zealand (Professor Hamish Spencer), Australia (Professor Mike Bunce), and Norway (Dr. Bastiaan Star). The PhD student will be a member of a highly active and collaborative group of researchers, and help develop population genomics and an understanding of how human activity is changing the environment.

The successful candidate will be a highly-motivated researcher, with a strong background and interest in genomics and molecular evolution. Experience with a coding and/or scripting languages will be an advantage. This position will be based at Victoria University of Wellington and comes with a three-year scholarship that provides a stipend (NZ$27,500 pa) and university tuition fees. This project is supported by the New Zealand Marsden Fund.

Applicants should send a CV, contact details of two academic referees and a cover letter that states why you are interested in the position and how your qualifications and experience make you a good fit for the proposed research. Send these to Peter Ritchie (E-mail: Peter.Ritchie@vuw.ac.nz). Candidate selection will begin May, but applications will be considered until the position is filled. The ideal starting date is 1 July 2017. International applicants with strong academic record are encouraged to apply. For more information about studying at VUW and the entry requirements for the PhD program please see http://www.victoria.ac.nz/-

study/programmes-courses/postgraduates/phds-doctorates Also on https://www.findaphd.com/-search/ProjectDetails.aspx?PJID=84854 Peter Ritchie <Peter.Ritchie@vuw.ac.nz>

SouthDakotaStateU SustainablePollinationBiol

Master'sResearch Degree opportunity in the CB Fenster lab, South Dakota State University: Pollination Biology in an Agricultural Landscape

Starting Date: Preferably end of May 2017

Pollinator service is globally associated with increased crop yield. Furthermore, flowering field crops (i.e., oilseeds, legumes) contribute to the maintenance of ecosystem services, providing nectar and pollen resources for pollinators. The student opportunity is to participate with a team to investigate the role of pollinators in yield of a new crop,ÃBrassica carinataÃand how that crop can impact bee health. This team, in addition to myself, includes insect ecologists (Jon Lundgren), plant landscape ecologists (Henning Nottebrock), economists (James Stone, Heidi Sieverding) and extension personnel (Amanda Bachmann). More specifically, we will quantify plant-pollinator interaction at different scales to understand the contribution of carinata to sustaining native pollinators, honey bees and honey yield. Finally, we will determine parameters to estimate the economic impact of carinata in terms of yield, honey production, and sustainability of native pollinators.

Location: Department of Biology and Microbiology, South Dakota State University, Brookings, South Dakota. Brookings is a small, but vibrant community with easy access to culture and the outdoors. More information about the Department of Biology and MicrobiologyÃatÃSDSU can be found at: http://www.sdstate.edu/biology-and-microbiology Requirements: The ideal student should embraceÃfield-based research as well as have some background or interest in large data and or landscape approaches. Most importantly, you shouldÃbe passionate about biology and the questions being pursed at theÃCBFenster lab. Specifically for this project, one should have an interest in sustainable agriculture and the consequences of various land-use polices for ecosystem services. Generally, students who work with me either have or develop a broad understanding of statistics. Foreign students need to meet English language requirements.

I encourage you to contact me, if interested at: charles.fenster@sdstate.eduMore information can be found at the CBFenster lab website: https://charlesbfenster.wordpress.com/ and here you can also find links to all of the collaborators. Please include in your email: * brief description of your research interests* concrete evidence of interest in this project* experience related to this project * CV Funding options are available for both US and International students.

https://charlesbfenster.wordpress.com/ CharlesB. Fenster, Professor

Departmentof Biology and Microbiology

AgriculturalExperiment Station

SouthDakota State University

Brookings,South Dakota 57007

Office:Berg Agricultural Hall, 1148 College Avenue, Rm 310

Phone:(605) 688 4453

Charles.Fenster@sdstate.edu

SouthernIllinoisU PoisonFrogEvolution

Evolution of South American Poison frogs (genus Ameerega) Zoology Department, Southern Illinois University, Carbondale, IL, USA

A graduate position (either Masters or PhD) is available to study the evolution of South American poison dart frogs (genus Ameerega). Neotropical poison frogs are a species-rich family (Dendrobatidae) that exhibit a diversity of mating systems, parental care strategies and phenotypes. The Brown lab is looking for a student to develop a research program studying ANY core aspect of the lab's research. Topics could include color/pattern evolution, phylogeography/ biogeography, systematics and speciation (to name a few). The ideal student will be prepared to conduct field-based research, have some experience in molecular ecology/population genetics, genomic and/or geospatial analyses. Several trips to South America and lab work is fully funded.

For more information on the Brown Lab please visit the lab website at: http://www.jasonleebrown.org and the Zoology Department at SIUC http://www.zoology.siu.edu. Students will find all the brains of a nationally ranked research university and all the heart of a small college at SIUC.

Carbondale is located in southern Illinois and provides a close link to many forested areas and lakes. The regional landscapes varies from bottomlands to uplands with rolling hills, bluffs, and rugged topography. This makes it perfect home for outdoor lovers (when they are not in the rainforest of S. America).

Interested students are encouraged to contact Dr. Brown (jason.brown@siu.edu). Please include a brief description of your research interests, a CV, and names of two references (with contact info). Competitive funding options are available. US and Canadian students only. For full consideration, application due date is April 15th, 2017. Applications will be evaluated as they are received. Start date of position is August 2017 (or earlier).

"jason.brown@siu.edu" <jason.brown@siu.edu>

StAndrews EvolutionaryTheory

PHD IN EVOLUTIONARY THEORY

A PhD position is available in the group of Dr. Carolin Kosiol at the Centre of Biological Diversity of the University of St. Andrews/Scotland. The position will be funded for 3.5 years.

The PhD project is part of a larger project entitled "Genome-wide molecular dating". 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 my group, we have developed an allele-frequency based approach called Polymorphism-Aware Phylogenetic Models (PoMo, De Maio, et al., 2015, Schrempf et al., 2016). While standard phylogenetic models treat substitutions as instantaneous events, PoMo describes them as gradual: substitutions require first a mutation introducing a new rare allele, followed by a series of changes in allele frequency. This innovation accounted for many problems in classical phylogenetics, such as incomplete lineage sorting and shared ancestral polymorphisms that cause the tree topology to vary along the genome. In this project, we plan to expand this approach to infer population trees that can be used for molecular dating as well as model of character evolution that allow for polymorphism in traits along the tree.

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 before the deadline on the 27th March 2017. Further information can be found at https://synergy.st-andrews.ac.uk/research/phd-study/phd-study-projects/phd-study-cbd-projects/

"ck202@st-andrews.ac.uk" <ck202@st-andrews.ac.uk>

TrentU LaurentianU AmphibianPopGenetics

PhD positions available - Amphibian occupancy patterns, population genetics, and disease dynamics

Funded by a Strategic NSERC grant, we are seeking PhD students to complete our team on research related to the detection and monitoring of amphibians and their pathogens (chytrid fungus, ranavirus) in Canada. Using environmental DNA as a basis for the research, the team will conduct: 1) Habitat occupancy modeling for amphibians and their pathogens; 2) Analysis of the evolutionary dynamics of pathogens and amphibian hosts; 3) Assessment of potential synergistic interactions between pathogens and aquatic contaminants; and 4) Modeling the drivers of amphibian population decline. Students will develop research projects that fit within the context of the broader program, such as: Validation of eDNA for detecting amphibians; Assessment of ranavirus pathogenicity; Chytrid fungus evolutionary dynamics; and Modeling drivers of amphibian occupancy. We are seeking students to initiate their research in Spring or Fall 2017, with the research to be conducted across southern Ontario. Interested applicants should submit a letter of interest, CV, unofficial transcripts and names of 3 references to: Dennis Murray, Trent University, dennismurray@trentu.ca (www.dennismurray@trentu.ca) or David Lesbarreres, Laurentian University dlesbarreres@laurentian.ca (http://gearg.jimdo.com/people/-head/).

"dlesbarreres@laurentian.ca"
<dlesbarreres@laurentian.ca>

TrinityCollegeDublin HumanPopulationGenomics

We are seeking a highly motivated PhD student for a research project in the population genomics of Native Americans from South America. Please find details of the position: https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=84325&LID=367 Shigeki Nakagome, PhD Ussher Assistant Professor in Genomic Medicine School of Medicine, Faculty of Health Sciences Trinity College Dublin, the University of Dublin Tel: +353-1-896-3260 E-mail: nakagoms@tcd.ie

Shigeki Nakagome <NAKAGOMS@tcd.ie>

UAberdeen ArchaeaEvolution

UAberdeen.Archaea

Funded PhD studentship in microbial ecology and/or microbial evolution at the University of Aberdeen (UK).

A 3.5-year PhD studentship in microbial ecology and/or microbial evolution, starting in May 2017 at the earliest, is now open for application at the University of Aberdeen, Scotland, UK. The deadline for applications is April 10th 2016 and there is no restriction regarding the nationality of the applicants (no fee incurred for non-EU nationals).

The project will be designed with the PhD supervisors depending on the interest of the applicant, including on microbial ecology, evolution, physiology and/or bioinformatics. The PhD project will target ey scientific questions with a special focus on Thaumarchaeota to align with the research thematic of the University of Aberdeen Nitrification Group.

Thaumarchaeota form an abundant and ubiquitous phylum of archaea on Earth. They perform a critical ecosystem function, ammonia oxidation to nitrite, which is subsequently oxidised to nitrate in the process of nitrification. Ammonia oxidisers limit nitrification, and thereby play a central role in the global N cycle. In soil, they lead to considerable loss of N fertiliser, nitrate leaching into groundwaters and production of greenhouse gases. Thaumarchaeotal cultivation is in its infancy, especially that of soil Thaumarchaeota, but is currently being achieved employing a combination of DNA-SIP soil incubations, innovative cultivation approaches and single-cell genomics and metagenomics. These approaches are being applied in the University of Aberdeen Nitrification Group to study environmental adaptation of these microbes in soil. In recent years, our research has demonstrated that pH is a ey factor controlling the composition of the soil Thaumarchaeota community, which plays an important role in nitrification in acidic soils. In addition to influencing extant thaumarchaeotal niche specialisation, pH has also influenced their diversification and patterns of lineage formation through deep evolutionary time. The existence of several ecologically coherent dominant phylogenetic lineages ('pH-adapted lineages') has also been demonstrated and several mechanisms of specialisation for acidophilic growth have been suggested for the thaumarchaeotal strains acquired in the laboratory. Finally, our research expands to other Thaumarchaeota that do not perform ammonia oxidation in order to understand the evolution of these physiological metabolisms.

The University of Aberdeen Nitrification Group, headed by Prof. James Prosser (https://www.abdn.ac.u/-ibes/people/profiles/j.prosser) and Dr Cécile Gubry-Rangin (https://www.abdn.ac.uk/ibes/people/profiles/-c.rangin), is a well-established group with world-wide recognised reputation in microbial ecology and a high-impact track record.

The PhD student will join a dynamic team of researchers within the Institute of Biological and Environmental Sciences (https://www.abdn.ac.u/ibes/) and the School of Biological Sciences (http://www.abdn.ac.uk/sbs/). The University of Aberdeen (UoA) was ranked 1st in the UK by the 'Agriculture, Veterinary and Food Science' REF2014 exercise and provides an excellent scientific environment. In addition, the University of Aberdeen provides state-of-the-art technological support facilities with a unique single-cell genomics platform, highly-specialised cytometry and genomic platforms, an exclusive thaumarchaeotal culture collection, molecular and environmental facilities and a High Performance Computing system. The University of Aberdeen also provides diverse training opportunities for all aspects of research and for transferable academic and generic skills. The academic requirement for entry is a first or upper second class degree or equivalent.

For any inquiry, please send an email describing your research interests directly to the principal investigator Dr Cécile Gubry-Rangin (c.rangin@abdn.ac.u).

Application Process: Formal application should be made as described on: http://www.abdn.ac.u/clsm/-graduate/research/terrestrial-environment-1407.php Dr Cécile Gubry-Rangin, URF Institute of Biological & Environmental Sciences Cruicshank Building, Room 1.13 University of Aberdeen St Machar Drive Aberdeen AB24 3UU

c.rangin@abdn.ac.uk

Tel. +44(0)1224 273662

c.rangin@abdn.ac.uk

UAberdeen UK MicrobialEcologyEvolution

UAberdeenUK.MicrobialEcologyEvolution

Funded PhD studentship in microbial ecology at the University of Aberdeen (UK): ?Unravelling the metabolic versatility and diversity of abundant but unexplored terrestrial Thaumarchaeota?.

A 4-year PhD studentship in microbial ecology, starting in March 2017 at the earliest, is now open for application at the University of Aberdeen, Scotland, UK. The deadline for applications is March 17th 2016 and this studentship is available to UK and EU nationals (providing funding for tuition fees and stipend). The PhD project is funded by the Royal Society and will target key scientific questions with a special focus on Thaumarchaeota to align with the research thematic of the University of Aberdeen Nitrification Group.

The vast microbial diversity in natural environments underpins the global ecosystem functioning on earth. The central aim of this project is to understand the largely underexplored physiological and ecological processes that generate high microbial functional diversity in nature, with a special focus on a functionally important group of archaea, the Thaumarchaeota, that play a key role in the nitrogen cycle. Their high diversity and abundance, together with our recent demonstration of the influence of pH on both niche specialisation (Gubry-Rangin et al., 2011; Vico-Oton et al., 2016) and lineage formation through deep evolutionary time (Gubry-Rangin et al., 2015), provide an excellent system to address this aim. The paucity of cultivated representatives has severely limited their investigation, but this restriction can now be alleviated by major recent technical innovations in single cell genome sequencing and cultivation techniques (informed by genomic data) enabling physiological studies (Lehtovirta-Morley et al., 2011; 2016). Better knowledge about an abundant, globally distributed but unexplored and uncultivated group of Thaumarchaeota that dominate ammonia oxidiser communities in many agricultural neutral and alkaline soils seems crucial to unravel their ecophysiology and contribution to soil nitrification and greenhouse gas emission. By using a single-cell genomics-driven cultivation approach, the physiological mechanisms implicated in thaumarchaeotal alkaline adaptation will be determined, and novel isolates will in turn allow further experimental physiological studies. The suggested mechanisms allowing growth, activity and preferential selection over the other nitrifying communities will finally be tested in many alkaline soils. This ambitious project will strongly impact on our fundamental knowledge of the general integrated ecological-functional mechanisms of adaptation that generate high microbial diversity in nature, using Thaumarchaeota as a model.

The University of Aberdeen Nitrification Group, headed by Prof. James Prosser (https://www.abdn.ac.uk/-ibes/people/profiles/j.prosser) and Dr C?cile Gubry-Rangin (https://www.abdn.ac.uk/ibes/people/profiles/-c.rangin), is a well-established group with world-wide recognised reputation in microbial ecology and a high-impact track record.

The PhD student will join a dynamic team of researchers within the Institute of Biological and Environmental Sciences (https://www.abdn.ac.uk/ibes/) and the School of Biological Sciences (http://www.abdn.ac.uk/sbs/). The University of Aberdeen (UoA) was ranked 1st in the UK by the ?Agriculture, Veterinary and Food Science? REF2014 exercise and provides an excellent scientific environment. In addition, the University of Aberdeen provides state-of-the-art technological support facilities with a unique single-cell genomics platform, highly-specialised cytometry and genomic platforms, an exclusive thaumarchaeotal culture collection, molecular and environmental facilities and a High Performance Computing system. The University of Aberdeen also provides diverse training opportunities for all aspects of research and for transferable academic and generic skills. The academic requirement for entry is a first or upper second class degree or equivalent.

Application Process: Formal application should be made as described on https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=83998 . References: Gubry-Rangin C, Hai B, Quince C, Engel M, Thompson BC, James P, Schloter M, Griffiths RI, Prosser JI, Nicol GW. (2011) Niche specialization of terrestrial archaeal ammonia oxidizers. Proc Natl Acad Sci USA 108(52):21206-21211.

Gubry-Rangin C, Kratsch C, Williams TA, McHardy AC, Embley TM, Prosser JI, Macqueen DJ. (2015) Coupling of diversification and pH adaptation during the evolution of terrestrial Thaumarchaeota. Proc Natl Acad Sci USA 112(30):9370-9375.

— / —

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

UAdelaide BioinformaticsandPaleogenomics

2 PhDs in bioinformatics and paleogenomics using ancient DNA

Two (2) PhD positions are available at the Australian Centre for Ancient DNA (ACAD; adelaide.edu.au/acad). We seek highly motivated students to join our dynamic research team in one of the world's leading ancient DNA centres. Candidates must have a 1st Class Honours or MSc degree, an excellent undergraduate academic record and meet the English Language Proficiency requirement. The call is open to international and domestic students with a background in bioinformatics, programming or population/quantitative/statistical genetics. In addition, a passion for history and archaeology is desirable along with demonstrable analytical skills. The projects are high profile (ACAD's publications; adelaide.edu.au/acad/publications/) and will suit hard-working and self-motivated candidates equipped with good skills in critical and independent thinking. Training will focus on the analysis of Next-Generation Sequencing data with a special emphasis on the utilisation and expansion of population genetics, quantitative genetics, and phylogeny methods for paleogenomic data. Successful candidates will also have the opportunity to assist in the development and application of cutting-edge reference genome approaches for humans and other organisms. Training opportunities to advance wet-laboratory techniques can be offered in parallel.

Great computational skills are required and a successful candidate would be competent in:

- Data analysis and management skills

- Fluency in using Linux systems, with a good hands-on experience with Bash scripting

- Advanced programming in a scripting language such as Python and/or R

- Querying a SQL databases

This is a great opportunity to study abroad (for international candidates) as Adelaide is a vibrant cosmopolitan city with a Mediterranean climate guaranteeing a great lifestyle. Interested applicants are encouraged to send a resume, a cover letter and a list with full contact details of three referees to Dr Yassine Souilmi (yassine.souilmi@adelaide.edu.au).

ACAD collaborates with a team of high-profile international researchers from Europe and the USA, and successful applicants will be co-supervised by Prof. Alan Cooper, Dr. Yassine Souilmi, Dr. Raymond Tobler and Dr. Stephen Richards at ACAD, School of Biological Sciences, University of Adelaide.

Note that the Australian Department of Immigration and the University of Adelaide expect international applicants to meet the English Language Proficiency (ELP) requirements. See below for details of the ELP. The ELP is based on high scores in IELTS (International English Language Testing System) or TOEFL (Test of English as a Foreign Language). For further information, please refer to this link (http://www.international.adelaide.edu.au/apply/admission/).

Yassine Souilmi <yassine.souilmi@adelaide.edu.au>

UBath ExperimentalEvolution

Fully funded 4-year PhD position in experimental evolution at the University of Bath (UK).

Application deadline: 24/04/2017

Apply here: https://www.findaphd.com/search/ProjectDetails.aspx?PJID=84040&LIDi >> The Role of Environmental Change in Gene Regulatory Network Evolution

Supervisors: Dr Tiffany Taylor < http://www.bath.ac.uk/bio-sci/contacts/academics/tiffany-taylor/ >; Prof Laurence Hurst < http://www.bath.ac.uk/bio-sci/contacts/academics/laurence_hurst/ >

How does novelty arise in evolution? Does environmental change drive genome complexity, and if so how? These are central questions in evolutionary biology, and they are the questions that drive research in our lab.

Using a combination of molecular genetic manipulations/analyses and experimental evolution, within the context of gene regulatory networks (GRNs) you will explore whether more complex GRNs promote survival and create opportunities for innovation in changeable environments. This project will conduct experiments with a genetically modified common soil bacterium that has had the 'master switch' of the flagellar network deleted. Firstly, it will address the role that gene duplication plays in the evolution of complex gene networks. It will do this by observing the divergence between duplicated genes from a different network that is capable of 'mending' flagellar function (1). Secondly, it will test the hypothesis that more complex networks provide a fitness benefit in less predictable environments (2). It will do this by using genetically manipulated bacteria with stepwise increases in network complexity and evolve them in static and changing environments. Lastly, it will look across a range of bacteria of the same species, which inhabit different environments, to link life-histories with network architecture (3).

Location: This project will be conducted under the direct supervision of Dr Tiffany Taylor with co-supervision from Prof Laurence Hurst, and based at the Department of Biology and Biochemistry at the University of Bath (UK) in the new Milner Centre for Evolution (http://www.bath.ac.uk/groups/milner-centre-for-evolution/). The Milner Centre is a new research centre focused on doing ground breaking research that addresses major questions in evolutionary biology. The Milner Genomics Centre provides on-site facilities and expertise for genome sequencing and analysis for evolution research, and the world-class researchers at the centre creates a vibrant research culture that ensures support and training for the next generation of evolutionary biologist.

Requirements: This is a fully-funded PhD studentship. We are looking for a biology graduate who has a strong interest in genetics and evolution. Some practical experience in microbiology and molecular techniques is highly desired but training will be provided. The successful candidate will be enthusiastic, highly motivated, independent, have experience in microbiology, molecular biology or evolutionary biology (or a combination), and have a relevant degree. The applicant must meet the standard University of Bath English language requirements.

Planned start date: 2 October 2017.

For informal enquiries, please contact Tiffany Taylor <T.B.Taylor@bath.ac.uk>

Funding notes: Funding is available for up to 4 years for an excellent UK/EU student. The studentship will include Home/EU tuition fees and a stipend of 14,553 (2017/18 rate). Applicants who are classed as Overseas for fee-paying purposes are not eligible to receive the funding.

T.B.Taylor@bath.ac.uk

UHelsinki MathModellingEvolution

Graduate position for a PhD in mathematical modelling in evolution and development:

1.Job/ project description:

The main objectives of the PhD project is to:

Develop computational models of organ development (morphogenesis and pattern formation) and their evolution in mammalian teeth, hair or Drosophila wing.

The research will take place in the Center of Excellence in Experimental and computational developmental biology of the Biotechnology Institute of the Helsinki University under the supervision of Isaac Salazar-Ciudad.

Embryonic development is one of the most amazing phenomena in life. During development a single cell transforms into a complex functional organism made of many cells, different cell types and a specific spatial distribution of those in space. How embryos organize themselves so that each cell ends up located in a specific position in the body is the central question of pattern formation and morphogenesis. This process involves the interaction of many genes in complex networks and the interaction of those with cells' and tissue's mechanical properties. In addition, this process is now widely acknowledged to be crucial to understand evolution since any change in the phenotype in evolution (e.g. morphology) would be first a change in the developmental process by which this phenotype is produced. Understanding development, thus, would allows us to understand which phenotypic variation can arise in populations due to genetic mutation (the so called genotype-phenotype map) and that, together with natural selection, would determine the direction of evolution. Understanding this link between development and evolution is a central aspect of the research in Salazar-Ciudad group.

Computational models are important tools to understand how gene networks interact with cell and tissue mechanical properties in development. There is currently a huge amount of data on how genes interact during development but data alone do not directly lead to understanding. The large number of genes involved, the complexity of the gene networks and cell and tissue mechanics in development require the building of precise quantitative hypotheses, the building of mathematical models to explore the consequences of these hypotheses and the comparison between models' predictions and well designed quantitative experiments. The center of experimental and computational developmental biology is a pioneering center combining models and experiments with this approach. In that sense the PhD will include collaborating with experimental developmental biologists, bioinformaticians, populational and quantitative geneticists, systems biologists, mathematicians, paleontologists and other evolutionary biologists.

The modeling will focus on integrating gene network regulation, cell-cell communication, cell mechanical interactions and developmental mechanisms in general and, optionally, artifical in silico evolution.

2. Requirements:

The applicant must be a biologists preferably with a strong background in either evolutionary biology, developmental biology or theoretical biology. Some knowledge of ecology, zoology, cell and molecular biology are also desirable.

Bioinformaticians, systems biologists or computer biologists that do not have a degree in biology or a strong background in biology will not be considered (e.g. no engineers or computer scientists).

Programming skills or a willingness to acquire them is required.

The most important requirement is a strong interest and motivation on science, embryonic development and evolution. A capacity for creative and critical thinking is also required.

3. Description of the position:

The fellowship will be for a period of up to 3-4 years (100% research work: no teaching involved).

The purpose of the fellowship is research training leading to the successful completion of a PhD degree.

Salary according to Finnish PhD student salaries.

4. The application must include:

-Application letter including a statement of interests

-CV (summarizing degrees obtained, subjects included in degree and

grades, average grade)

-Application should be sent to Isaac Salazar-Ciudad by email:

isaac.salazar@helsinki.fi

Foreign applicants are advised to attach an explanation of their university's grading system. No official documents are required for the application first stage but these may be required latter on.

5. Examples of recent publications by Isaac Salazar-Ciudad group.

-Salazar-Ciudad I1, MarÃn-Riera M. Adaptive dynamics under

development-based genotype-phenotype maps.

Nature. 2013 May 16;497(7449):361-4.

-Salazar-Ciudad I, Jernvall J. A computational model of teeth and

the developmental origins of morphological variation. Nature. 2010

Mar 25;464(7288):583-6.

6. Interested candidates should check our group webpage:

http://www.biocenter.helsinki.fi/salazar/index.html

— / —

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

---

UHuddersfield ApodemusEvolutionaryGenomics

A 3-year PhD studentship in evolutionary genomics of wood and yellow-necked mice (Apodemus flavicollis and sylvaticus), starting in September 2017, is now open for applications at the University of Huddersfield, West Yorkshire, UK. The deadline for applications is 26th March 2017. The studentship is funded by the University of Huddersfield and available to UK and EU nationals.

Rodents from the genus Apodemus are the most common mammals in the Palearctic and an attractive subject for evolutionary and molecular studies: they are likely to be under multitude of selective pressures in different habitats, they contribute to the spread of Lyme disease and tick-borne encephalitis and harbour extra ("B") chromosomes. However, the genomic and genetic resources for their studies remain very limited.

We are a young and small research group that has recently embarked on establishing phylogenetic and phylogeographic relationships between Apodemus populations in Europe based on whole-genome genotypes. Thanks to collaboration with researchers in Poland, Germany and Belgium we are presently acquiring and analysing whole-genome high-density genotyping data (ddRAD-seq) from hundreds of individuals across Europe. Analysis of this data will inform future directions of our studies: phylogeography of sylvaticus and flavicolis, diversity and divergence of their populations, SNP-based genetic maps and whole-genome scans for signatures of positive selection.

We are looking for an independent candidate with keen interest in evolution and computational approaches to study genetic variation on a population scale. Familiarity with UNIX/Linux, command line or R is a plus, as is research experience, preferably on a master's level, but strong B.Sc. graduates are also encouraged to apply. Majority of the project involves computational analyses of large datasets, but it has a small wet-lab component, such as preparation of DNA and/or RNA sequencing libraries.

The PhD student will be associated with the Evolutionary and Environmental Genomics Group at the Department of Biological Sciences and embedded with PhD students in the Leverhulme Doctoral Training Centre who work on human and cattle phylogeography, archaeoentomology, yeast transposable elements and evolution of choanoflagellates using genomic approaches. The studentship requires candidates to undertake small teaching duties during the PhD. For more information about us and our work, please go to https://bryklab.net/-research/ and https://www.hud.ac.uk/ourstaff/profile/-index.php?staffid=1409 . To apply, send an email outlining your motivation and experience to j.bryk@hud.ac.uk (CC'd to f.cross@hud.ac.uk), including a CV and the names of two referees. You also need to complete an on-line application at http://halo.hud.ac.uk/-pgr_onlineapps/. For more details about the application process please go to https://www.findaphd.com/search/-PhDDetails.aspx?CAID=3062. Candidates are also encouraged to contact the project's supervisor, Dr Jarek Bryk, directly with informal questions and requests at j.bryk@hud.ac.uk. University of Huddersfield inspiring tomorrow's professionals.

J.Bryk@hud.ac.uk

ULeicester GeneticEpidemiologyBioinformatics

The following 3 year PhD studentship is being re-advertised for a September 2017 start.

Title: Using genetic epidemiology to understand the role of complex genetic variation of immune system genes in respiratory health and disease

Supervised by Dr Louise Wain and Dr Ed Hollox (Department of Genetics)

The studentship is for 3 years and will commence in September 2017. The student will be based in the Department of Health Sciences.

Respiratory disease is a major public health concern and the third leading cause of death globally. Genome-wide association studies (GWAS) have identified multiple regions of the genome associated with respiratory health and disease and amongst these, one of the strongest signals of association is in the Human Leukocyte Antigen (HLA) region gene cluster on chromosome 6 which encodes proteins with essential roles in the immune system. However, the HLA region is complex and understanding the mechanisms underlying the genetic signals of association in this region requires sophisticated analytical approaches. Bespoke computational methods which measure variation of the HLA region, and of other clusters of functionally-related genes, at both the genetic and protein level, have been developed. This project will involve applying these methods to large general population cohorts to explore both the direct and interactive effects of variation at immune gene clusters on respiratory traits and disease. The student will develop computational research skills at the interface of genetics, statistics and computer science which will equip them for a career in the exciting and fast-moving field of genetic epidemiology. A background in bioinformatics, genetics or statistics is preferred and a keen interest and aptitude for developing further skills in all of those areas, and in the use of high performance computing to analyse very large data sets, is essential.

Closing date for applications: 31st March 2017

https://www.findaphd.com/search/-ProjectDetails.aspx?PJID=81829 http://-www2.le.ac.uk/research-degrees/funding/mbp "Batini, Chiara (Dr.)" <cb334@leicester.ac.uk>

ULeicester GenomicsKinshipAncestryForensics

Project supervisors: Professor Nuala Sheehan - Department of Health Sciences; Professor Mark Jobling - Department of Genetics

University of registration: University of Leicester

Non-Academic partner: Dr Martin Blythe - DNA WorldWide Group

Project title: Next-generation kinship deduction for forensic and genealogical analysis

We seek a highly-motivated student with an interest in statistics, genomics, population genetics and/or forensic genetics, to work with us and our industrial partner DNA WorldWide (https://www.dna-worldwide.com), a direct-to-consumer DNA testing company offering ancestry, paternity and kinship testing.

The use of DNA analysis to determine familial relationships between human individuals is well established. For close (first-degree) pairwise relationships as targeted in the paternity test, a small number of polymorphic markers (the short-tandem repeats [STRs] also used in forensic individual identification) is analysed, and probabilities of true paternity can be established with near certainty. However, there is also a need in some applications to estimate more distant kin relationships: in forensic casework 'familial searching' exploits the fact that a perpetrator and their relative(s) are expected to share 'similar' DNA profiles, which can provide investigative information when the relative(s) are in the National DNA Database but the perpetrator is not; in immigration cases a claim of relationship may need to be validated in order to allow entry to the UK; in genealogical research participants may have specific hypotheses about their relationships which they wish to support via DNA evidence. The kinship estimation problem is more difficult in these cases because with each additional generation that separates two individuals, the expected proportion of the genome shared identical by descent (IBD) halves. Additional power can be gained by increasing the number of DNA markers analysed, for example by using genome-wide SNP chips.

The project proposed here addresses these issues by exploring the potential of NGS forensic multiplexes and genome-wide SNP data in relationship estimation, using real-world data. Forensically relevant data will be generated by typing either the Promega Powerseq or Illumina Forenseq multiplex on existing pedigree DNA resources (e.g. CEPH families; French-Canadian deep-rooting pedigrees). Anonymised genome-wide SNP data will be obtained from DNA WorldWide (consenting clients, and a dataset of 72 individuals from 9 pedigrees). Both the forensic multiplexes and the genome-wide data (based on the HumanOmniExpressExome-8 chip) include uniparentally-inherited markers (Y chromosome, mitochondrial DNA) as well as biparentally-inherited (autosomal) markers. A novel feature of this project is to investigate efficient incorporation of such data with SNP-based likelihood estimates by considering haplotype frequencies and possible pedigree structures including sex. A key issue will be to understand the sensitivity of relationship estimation to allele frequencies, and a number of approaches will be taken, including the use of internal frequencies from the data themselves, data from public resources such as HapMap, or our own datasets. Consideration will also be given to population structure, admixture and the effects of linkage disequilibrium. Detailed sensitivity analyses will be carried out through extensive simulation studies.

Closing date for applications: 31st March 2017

Check eligibilty and apply here: https://www2.warwick.ac.uk/fac/cross_fac/mibtp/pgstudy/phd_opportunities/application/ Please note:

Students will be part of the Midlands Integrative Biosciences Training Partnership (MIBTP), a BBSRC-funded Doctoral Training Partnership between the Universities of Warwick, Birmingham and Leicester. iCASE students must fulfil the MIBTP entry requirements and will join the MIBTP cohort for the taught modules and masterclasses during the first term. Students can then start their PhD project in Jan 2018 but must complete a 3-month miniproject (at a non-home institution) before the end of their first year. They will remain as an integral part of the MIBTP cohort and take part in the core networking activities and transferable skills training.

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

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

ULethbridge EvolutionaryNeurobiology

MSc and PhD positions in evolutionary neurobiology

Our lab uses a combination of approaches to understand evolutionary differences in brain size and anatomy across vertebrates. We are now seeking students interested in pursuing a graduate degree (MSc or PhD) in the evolutionary neurobiology of birds and mammals (http://scholar.ulethbridge.ca/iwaniuk/home). Much of our current research focuses on the effects of sexual selection and sociality on brain anatomy and neurochemistry in ground squirrels, but many other projects are available on birds, other mammals and fish.

Located at the University of Lethbridge, the Iwaniuk lab has a large comparative bird brain collection and direct access to a range of microscopy equipment. Dedicated lab facilities include microtome, cryostat, fluorescent microscope, a digital slide scanner for creating 'virtual' slides, and the latest in stereology and neuron tracing software. Confocal and electron microscopy are also available within the Canadian Centre for Behavioural Neuroscience at the University of Lethbridge. Field research is supported by a brand new 4x4 field vehicle and mobile lab for preparing samples. Our fieldwork takes us to the Rocky Mountains, foothills and prairie regions of western Canada, depending on the species being studied. Opportunities are available for students to collaborate with researchers at other institutions in Canada, the USA, Australia and elsewhere as well as travel to national and international conferences.

The University of Lethbridge offers competitive scholarship funding, including tuition waivers, for applicants based on grades and research experience. Potential students must have a background in biology, psychology or neuroscience, some research experience and a valid driver's license.

To apply, send: 1) a c.v.; 2) unofficial copies of academic transcripts; and 3) a brief description of your research interests to: andrew.iwaniuk@uleth.ca. Applications will be evaluated as soon as they are received. Start dates are flexible, but there are deadlines set by the university for graduate student applications. For more details see: https://www.uleth.ca/graduate-studies/

“theresa.burg@uleth.ca” <theresa.burg@uleth.ca>

ULincoln UruguayEvolutionStudents

Header: ULincoln (UK), Fully-funded PhD Scholarship (Uruguay)

A new programme of scholarships to conduct PhD studies in Life Sciences has recently been agreed between the University of Lincoln (UK) and the Uruguay National Agency for Research and Innovation (ANII - Agencia Nacional de Investigacion e Innovacion). This programme consists of full 3-year PhD scholarships for citizens of Uruguay only, which cover University fees and a subsistence bursary.

Funding will be awarded to applicants working on the following areas of research (broadly defined - please contact potential supervisors in these fields to discuss projects in more details): Environmental Sciences and Climate Change Biology, Conservation of Biodiversity, Evolution and Ecology, Biomedicine, Macroecology, Molecular Biology and Genetics, Molecular Nanotechnology, Biophysics, Clinical and Veterinary Animal Behaviour, Animal Welfare.

Application Process and Requirements include: (1) Must be a citizen of Uruguay, (2) Have already obtained a BSc (or equivalent) degree in an area relevant to the research fields described above. A minimum of a UK equivalent to a 2:1 award is required to enter the application process, (3) As part of the application process the applicant must complete and submit their application to the University of Lincoln using the online application system, (4) The applications must include a copy of the applicant's CV and a one page research statement describing research interests, ambition and briefly outline a research project.

Submission of applications for 2017 entry are now open. The deadline for applications via the University of Lincoln is 11^th May 2017.

For additional information regarding this scholarship please contact:

Dr Daniel Pincheira-Donoso

School of Life Sciences

University of Lincoln E-mail: DPincheiraDonoso@lincoln.ac.uk Web: http://-selectiondynamics.weebly.com/ Telephone +44(0)1522 835025

Daniel Pincheira-Donoso

Senior Lecturer in Evolutionary Biology

Laboratory of Evolutionary Ecology of Adaptations

School of Life Sciences

Joseph Banks Laboratories

University of Lincoln

Brayford Campus

Lincoln, LN6 7DL

United Kingdom

Office Tel: +44(0) 1522 835025

Office: JBL 1W12

E-mail: DPincheiraDonoso@lincoln.ac.uk

Lab Website: http://selectiondynamics.weebly.com/ The University of Lincoln, located in the heart of the city of Lincoln, has established an international reputation based on high student satisfaction, excellent graduate employment and world-class research.

Daniel Pincheira-Donoso <dpincheiradonoso@lincoln.ac.uk>

ULondon EvolTheoryApplied2Cancer

Fully funded position with stipend. EU and other overseas candidates welcome.

There is a repertoire of theory in evolutionary ecology to explain the rate and nature of adaptation to sudden changes in the environment, particularly pesticide use and rapid climate change. This body of evolutionary theory is strongly analogous to that needed to explain the emergence of resistance during cancer therapy - both involve a sudden new selective regime (temperature, presence of a pesticide or drug). In this PhD project, we propose to translate this theory to understand the development of resistant clones in cancer, and then to construct new treatment regimes that are designed to forestall or even prevent their emergence. The project will involve theory development, and then bioinformatic analysis of human cancer data and in vitro evolution experiments to critically evaluate the theoretical predictions.

This is an interdisciplinary collaboration between

Prof Nichols (Evolutionary Genetics) and http://www.sbcs.qmul.ac.uk/staff/richardnichols.html Prof Graham (Cancer biology) https://sites.google.com/site/nottrevorgraham/lab-members Further details

Richard Nichols r.a.nichols@qmul.ac.uk Trevor Graham t.graham@qmul.ac.uk

Richard Nichols <richard.alan.nichols@googlemail.com>

UmeaU ForestGenetics

PhD student position in forest genetics

The Department of Ecology and Environmental Science (EMG), UmeÃ¥ Plant Science Center (UPSC) and the Swedish Forest Research Institute (Skogforsk) jointly open a 5-year PhD position within the industrial graduate student research school in forest genetics and biotechnology at UPSC. Application deadline is 20th April, 2017.

Project description The future supply of biomass will come mostly from planted forests. In Sweden, almost all the regeneration material used in pine and spruce reforestation are supplied by tree breeding programs and seed orchards. It is thus critical that seed orchards function well, producing high seed yield and breeding gain but also a genetic base to support increased biomass production and resilience to future conditions. This project investigates: 1) how seed orchard design and management practices affect the genetic composition and diversity of seed crops; and 2) how seed orchard establishment and seed deployment strategy affect pine and spruce forestsÂ adaptation and productivity in their northern range.

This project is in close collaboration with Skogforsk. The position is for 5 years and defined as 80% research time at EMG, UmeÃ¥ University, and 20% at Skogforsk.

Qualifications We seek a candidate with academic background in population genetics, forest genetics and breeding, or molecular ecology. Knowledge of genetic data analyses, bioinformatics, and experience of high-throughput sequencing techniques are strong merits. The candidate should be highly motivated, independent and collaborative, and have a very good command in both oral and written English. The position includes interactions with the Swedish forestry sector. Evaluation will be based on the individual letter, quality and relevance of master program and publication, the interview, and the candidate's performance in a literature essay given after the interview.

Prerequisites for PhD studies include 240 ECTS credits of higher education studies of which 60 ECTS credits should be on an advanced level (Master level), or an equivalent qualification from abroad. This position specifically requires 120 ECTS credits in a subject relevant for ecology.

Application The application should include: . A short letter (max 2 pages) describing your research interests and why you are interested in the position . CV, including academic achievements . Digital copies of Bachelor/Master thesis . publications . Certificates from higher education and other documentation that supports your application . Contact information to three reference persons.

Your application must be registered in UmeÃ¥ University's e-recruitment system MyNetwork Pro (at http://www.umu.se/om-universitetet/lediga-jobb/) no later than 20th April 2017.

Other information The principle supervisors to this project are Prof. Xiao-Ru Wang (xiao-ru.wang@umu.se) from EMG, and Prof. Bengt Andersson Gull (bengt.anderssongull@skogforsk.se) from Skogforsk.

Salary: According to agreements for PhD students at UmeÃ¥ University.

The Department of Ecology and Environment Sciences, UmeÃ¥ University, performs research and research education in ecology, environmental science and physical geography. The department has ~150 co-workers of which ~30 are PhD students. (www.emg.umu.se)

Skogforsk is funded by the forest industry and the state. The demand-driven applied research includes a wide variety of fields, such as forest technology, raw-material utilization, environmental impact and conservation, forest tree breeding, logistics, forest bioenergy and silviculture. The institute has about 120 employees, of which 80 are researchers. (www.skogforsk.se)

Xiao-Ru Wang

Xiao-Ru Wang <xiao-ru.wang@umu.se>

UmeaU LandscapeGenetics

We are seeking candidates for a PhD student position in ecology with focus on landscape genetics at UmeÃ¥ University. The project will use recent conceptual and methodological advances in genetics and spatial ecology to study patterns in gene flow in riverine plants and how these are influenced by landscape structure and obstruction of dispersal pathways by dams.

Information about the position and how to apply, English version: https://umu.mynetworkglobal.com/en/what:job/jobID:134617/where:4/ Information about the position and how to apply, Swedish version: https://umu.mynetworkglobal.com/se/what:job/jobID:134617/where:4/ Please circulate to qualified candidates!

The last day to apply is April 18, 2017.

best,

Roland Jansson and Xiao-Ru Wang

Roland Jansson Dept. of Ecology and Environmental Science UmeÃ¥ University SE-901 87 UmeÃ¥ Sweden Phone +46-90-7869573 alt +46-70-3686605 http://www.emg.umu.se/english/about-the-department/staff/jansson-roland Roland Jansson <roland.jansson@umu.se>

UNewSouthWales 2 FishEpigenetics EvolMed

A PhD position: Transgenerational non-genetic (epigenetic) effects in zebrafish at I-DEEL, E&ERC, UNSW, Australia

It is increasingly clear that non-genetic (epigenetic) parental effects influence not only the phenotypes of offspring but also those of grand-offspring. However, we still know very little about the extent of this effect in the subsequent generations, and its specific mechanisms.

The project will use a zebrafish model to close this gap in our understanding of transgenerational non-genetic effects by taking an integrative evolutionary framework.

Our group (http://www.i-deel.org/) is seeking a PhD candidate to take on this project. The candidate will conduct experiments using zebrafish to investigate how parental conditions can transgenerationally influence subsequent generations; we especially focus on behavioural traits. We have access to a state-of-the-art zebrafish facility and molecular facility in collaboration with Dr. Dan Hasselson at the Garvan Institute of Medical Research (www.garvan.org.au). There, we have developed a high-throughput behavioural phenotyping system. High quality behavioural data will be combined with cutting edge molecular data (individual-based transcriptome and methylation data) to explore the impact of parental environments on subsequent offspring behaviour. We also employ modern genome editing techniques (CRISPR, TALEN) to manipulate parental genomes and thus the potential molecular mechanisms under investigation.

This project is challenging and uniquely interdisciplinary, by mixing molecular genetics, evolutionary biology, behavioural ecology and statistical modeling. Therefore, the candidate will learn not only molecular techniques but also advanced statistical and computational methods. There are also opportunities for the candidate to develop their own PhD project with us. Note that our lab conducts many meta-analyses, comparative analyses and computer simulation work so these kind of projects can be blended into the PhD thesis.

Please read our webpage to see the wide range of research we conduct (www.i-deel.org). Here are some relevant papers.

O'Dea, R. E., Noble, D. W. A., Johnson, S.L., Hesselson, D.

& Nakagawa, S. (2016) The role of non-genetic inheritance in evolutionary rescue: epigenetic buffering, heritable bet hedging, and epigenetic traps. Environmental Epigenetics. 2:1-12 Chatterjee, A., Ozaki, Y., Stockwell, P. A. Horsfiled, J. A., Morison I. M. & Nakagawa, S. (2013) Mapping the zebrafish brain methylome using reduced representation bisulfite sequencing. Epigenetics. 8: 979-989

APPLICATION PROCEDURE: (1) DISCUSS: Email letter with CV, academic record, and details of two academic referees, to A/Prof Shinichi Nakagawa (s.nakagawa@unsw.edu.au). Your letter should explain how your results are sufficient to allow application for a SCHOLARSHIP at UNSW (see below). At this point we cannot provide funding for a PhD from other sources, so you need to qualify for a scholarship (see below) or bring your own funding to work with us.

(2) PhD CANDIDACY APPLICATION: Requirements for PhD are BSc (Hons 1), MSc, or equivalent along with solid research and communication skills.

For application timing and details, see: https://research.unsw.edu.au/how-apply-enrol-research-degree (3a) PhD SCHOLARSHIP APPLICATION - LOCAL: Citizens or permanent residents of Australia/NZ, apply for APA and UPA at UNSW. You will need to have completed a research degree (e.g. MSc or BSc Honours research year), with results which are equivalent to 85% or higher, in order to be competitive for these scholarships. Publications in ISI-listed international journals will also help. For application timing and details see: https://research.unsw.edu.au/postgraduate-research-scholarships (3b) PhD SCHOLARSHIP APPLICATION - INTERNATIONAL: Applicants who are NOT citizens or permanent residents of Australia/NZ, can apply for IPRS and UIPA at UNSW. In order to be competitive for these scholarships, you will need to have completed a research degree (e.g. a full year of research in either MSc or BSc-Honours), with results which are equivalent to 95% or higher for the research component of the degree. Note that a coursework MSc is NOT acceptable.

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/ —–

— / —

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

---

UNotreDame EcologicalSpeciation

The Jeff Feder lab in the Department of Biological Sciences at the University of Notre Dame, in Notre Dame, Indiana has a graduate student position available for studying the genomics of ecological adaptation and speciation in insects. Our research has both laboratory and field components, spanning the realms of ecology and evolution from experimental manipulation studies to high throughput DNA sequencing, focused on discerning the adaptive basis of speciation and its genomic underpinnings. Ideally, we seek individuals with experience in bioinformatics and candidates with past research experience (e.g., in a master's program), for the position. However, all highly motivated students are encouraged to apply. The Department provides graduate students with generous stipend support and benefits. To apply please e-mail a CV, personal statement of interest, and contact information for three references to feder.2@nd.edu.

For additional information about our lab and graduate program, please see http://federlab.nd.edu/- and http://biology.nd.edu/graduate/graduate-studies-overview/, respectively.

"mdoellma@nd.edu" <mdoellma@nd.edu>

UOtago GenomicsParasiticMindControl

PhD Project Opportunity

Parasitic Puppeteers - How do They Pull the Strings? We are currently seeking at least one, but potentially several PhD students with interests in genetics, evolution, parasitology and neuroscience to investigate the molecular mechanisms through which parasitic worms alter the behaviour of their insect hosts.

Project Description Parasites can have profound effects on the animal hosts they invade, manipulating host biology with exquisite precision to enhance host-to-host transmission. One of the most extraordinary of these host manipulations is the water-seeking behaviour that some nematodes and hairworms induce in their hosts so that the worms might exit the host and reproduce. The process is the stuff of science fiction; the worm hijacks the host's central nervous system forcing it to seek water. Once water is found the adult worm, often many times the size of the host, emerges, sacrificing the host. This amazing alteration in behaviour is induced by parasitic worms spanning two phyla (Nematoda and Nematomorpha) and is observed in a variety of arthropod hosts, notably crickets, weta, earwigs, and sandhoppers, leading us to hypothesise that a common and conserved mechanism is being utilised by the parasites to induce this behaviour in their hosts. Here we propose to couple field and laboratory studies of two phylogenetically distinct hosts and their parasites, with powerful genomic and bioinformatic comparisons to elucidate the trigger and genetic cascade through which these parasitic puppeteers elicit this highly conserved, yet astonishing behavioural response.

The project emerges from a new Marsden Grant headed by Professor Neil Gemmell (Anatomy) in collaboration with Professor Robert Poulin (Zoology) and will be based in the Gemmell laboratory at the University of Otago.

The Ideal Candidate The ideal candidate will possess experience in molecular genetics/genomics, evolutionary biology and bioinformatics. Knowledge of NGS approaches and analyses us desirable, while past work in comparative genomics and an interest in parasitology and neurobiology may be helpful. They candidate will be motivated and organized, with a demonstrated capacity to master the broad skill set necessary for the successful completion of a research project. They will be collegial and able to work alongside a wide variety of people. In addition they will have a strong commitment to academic and research excellence. Minimum qualifications: B.Sc. (Hons) and/or M.Sc. in Genetics, Genomics, Molecular Biology or equivalent with an A average or better.

Scholarship Funding: Financial support is expected to be available for a high achieving student with an A average or better via a University of Otago or Departmental scholarship see http://www.otago.ac.nz/study/-scholarships/).

Eligibility: The University of Otago and Departmental scholarships are open to all nationalities. However, overseas candidates for whom English is not a first language must satisfy the English Language Requirements of the University < http://www.otago.ac.nz/international/-postgraduate/index.html#englishlanguage > to be eligible for study (see). Other international eligibility criteria are here < http://www.otago.ac.nz/international/-postgraduate/otago002221.html >.

How to Apply: Interested applicants are encouraged to make informal enquiries to Professor Neil Gemmell. Please send your Curriculum Vitae, a copy of your academic transcript, a sample of your written scientific work and the names of three referees with a covering letter to:

Professor Neil J. Gemmell e-mail: neil.gemmell@otago.ac.nz

Further information Gemmell lab < http://gemmell-lab.otago.ac.nz/ >

Applications close on the 28/4/2017. It would be desirable if the successful applicant were able to start by mid 2017.

Neil Gemmell <neil.gemmell@otago.ac.nz>

UOtago NewZealand PopGenTheory

PhD in Epigenetic Theory

A PhD position is available within the Department of Zoology at the University of Otago in Dunedin, New Zealand. This position in the laboratory of Professor Hamish G. Spencer is funded by the Marsden Fund of the Royal Society of New Zealand. A scholarship covering fees plus a tax-free stipend of NZ$27,500 per year is available for three years.

The project is part of a larger project entitled "Epigenetics and Evolutionary Theory." Just as natural populations exhibit genetic variation, so too do they harbour epigenetic variation, some of which is transmitted from one generation to the next. This project asks how we can explain this transgenerationally inherited epigenetic variation in natural populations and what might be the consequences for evolution. The candidate will construct and analyse novel mathematical models to investigate these matters, validating these models with data from real examples, and using the models to make novel predictions about the properties of epigenetic variation in nature.

The successful candidate will have a strong interest in applying quantitative methods in biology. They will have a degree in biology and/or mathematics (or a related field) that included a research component (e.g., a dissertation or a thesis). The degree (e.g., BSc(Hons), MSc) will have been awarded with first-class honours/distinction.

Our research group and the wider Department includes world-class research staff, facilities and strong international collaborations, offering excellent opportunities to gain a variety of highly pertinent research and technical skills.

For details about living in Dunedin, in the South Island of New Zealand, see http://www.otago.ac.nz/-humanresources/join-otago/lifestyle-and-culture/dunedin/index.html

As part of your application, please submit a CV, a transcript of your university grades, a personal statement of suitability and the names and contact details of two referees to Professor Hamish Spencer (hamish.spencer@otago.ac.nz).

Applications will close on 9 April 2017.

Hamish Spencer <hamish.spencer@otago.ac.nz>

UOtago NZ WeevilEvolution

PhD Project Opportunity Available to Investigate the Reproductive Ecology of Clover Root Weevils to Inform New Biocontrol Strategies

We are currently seeking at least one PhD student with interests in genetics, evolution, and behavioural ecology to conduct research into the reproductive ecology of clover root weevil and its implications for an exciting new pest management method called the Trojan female technique.

Project Description: Maternally inherited mitochondrial DNA can accumulate mutations deleterious to males so long as the mutations are neutral for females - a phenomenon dubbed "Mother's curse". Often these mutations reduce male fertility. Recently it was recognised that this male-fertility-reducing curse could, in theory, be cast upon invasive pests through an approach known as the 'Trojan female technique' (TFT). The TFT involves finding male-fertility-reducing mitochondrial mutations, breeding up populations of the female carriers in captivity, then releasing them into the field where their infertile male progeny reduce reproduction of the wild population. The TFT concept has recently been proven in laboratory trials and we are now working towards the world-first field implementation against a New Zealand pasture pest called clover root weevil.

The efficacy of the TFT will be partly dependent on the reproductive ecology of clover root weevil: How often does a female mate, and with how many males? How long does she store sperm for? Which male's sperm does she use to fertilise her eggs? Can she choose? Is sperm from males that carry one or more deleterious mitochondrial mutations equally competitive with the sperm of wild-type males? Answers to these and related questions are critical for optimally implementing the TFT against clover root weevil and other similar pests.

The project emerges from a new MBIE Smart Ideas grant headed by Dr Craig Phillips (AgResearch, Lincoln) in collaboration with Prof Neil Gemmell (Otago), Dr Damian Dowling (Monash University, Australia) and Dr Dan Tompkins (Landcare Research, Dunedin). The PhD position will be based predominantly based at AgResearch Lincoln with a requirement to also spend time in the Gemmell laboratory at the University of Otago.

The Ideal Candidate: The ideal candidate will possess experience in molecular genetics, genomics and evolutionary genetics, likely with direct application in addressing questions relating to mating systems and mate choice. Knowledge of entomology, microscopy and molecular genetic approaches and analyses will be a distinct advantage. The successful candidate will be motivated and organised, with a demonstrated capacity to master the broad skill set necessary for the successful completion of a research project. They will be a competent laboratory worker, experienced in all routine molecular genetic techniques, and computer literate with familiarity with database management and statistical analyses.

Minimum qualifications: B.Sc. (Hons) and/or M.Sc. in genetics, genomics, molecular biology, behavioural ecology or equivalent with an A average or better.

Scholarship Funding: Financial support is available for a high achieving student with an A average or better via an AgResearch stipend, and the candidate may also be eligible for University of Otago scholarships.

Eligibility: The AgResearch and University of Otago scholarships are open to all nationalities. However, overseas candidates for whom English is not a first language must satisfy the English Language Requirements of the University < http://www.otago.ac.nz/international/-postgraduate/index.html#englishlanguage > to be eligible for study.

How to Apply: Interested applicants are encouraged to make informal enquiries to Professor Neil Gemmell. Please send your Curriculum Vitae, a copy of your academic transcript, a sample of your written scientific work and the names of three referees with a covering letter to:

Professor Neil J. Gemmell e-mail: neil.gemmell@otago.ac.nz

Further information: Gemmell lab < http://gemmell-lab.otago.ac.nz >

Applications close on the 28th May and it would be desirable if the successful applicant were able to start by mid 2017.

Professor Neil J. Gemmell Head of Department Department of Anatomy | School of Biomedical Sciences | University of Otago Te Tari Kikokiko | Te Kura Mâtai Rongoâ-Koiora | Te Whare Wânanga o Otâgo Tel: 64 3 479 6373 Fax: 64 3 479 7254 Mail: PO Box 56, Dunedin 9054, New Zealand Address: 270 Great King Street, Dunedin 9016, New Zealand Web: www.otago.ac.nz/-anatomy [http://www.otago.ac.nz/otago634585.jpg] Neil Gemmell <neil.gemmell@otago.ac.nz>

UPadua Italy SexualSelectionGuppy

PhD scholarship for a project on sexual selection in guppies (Poecilia reticulata)

Supervisor Andrea Pilastro, University of Padova, Italy

Application Process:

The University of Padova, Italy, offers 15 PhD positions to non-Italian students (deadline March 28, 2017, see: http://www.unipd.it/en/research/doctoral-degrees-phd-programmes/phd-courses-fees-grants-and-benefits#). The scholarships is 13.638 euros per year for 3 years, but it comes with full board and free lodging (at the University residences and canteens), so basic costs of living are covered. Furthermore, the fellowship will be increased by 50% during periods spent abroad (which need to be approved by the PhD School board) in other research institutions for study and research.

Padova is a lively town, close to the Venice, the Adriatic see and the Dolomites, and hosts about 50000 undergraduate and 1400 graduate students. Our PhD School in Biosciences (http://dottorato.biologia.unipd.it/) enrols approx 50 PhD students and adopt English as working language.

Selection of candidates is based on CV, proposed research plan and recommendation letters from two previous supervisors. Preliminary agreement on the research project with a supervisor at U Padua (that will cover research funds) is also an important selection criterion. Selection will be completed

The U Padua usually receives about 500 applications for the 15 positions. Competition may therefore be hard, although really eligible applicants (with good CV, two reference letters and a project agreement) are usually a small fraction of the total applicants.

The list of the candidates that will get a fellowship will be published by 26th June 2017. Succesful candidates will have to confirm their will to enroll by July 3rd 2017 and courses will start on

Any graduate student interested in doing a PhD in my lab in the topic described below is encouraged to contact me (andrea.pilastro@unipd.it), by sending a brief CV and a statement of research interests. Deadline for applications is March 28, 2017. Below a brief, general description of the proposed research topic.

Proposed project

Interaction between pre- and post-mating episodes of sexual selection in a variable environment

In polyandrous species, sexual selection acts on reproductive traits during both pre- and post-mating episodes of selection. While the scientific literature exploring these two episodes singularly is vast, we are just starting to explore how the overall variance (the potential for 'total sexual selection' to act) in reproductive success can be decomposed into its pre- and post-mating components (see Devigili et al 2015, 2016 for some recent study). In particular, although there is strong evidence that ecological and social factors can modify singular components of the sexual selection process, very little experimental work has actually explored how total sexual selection is affected by variations in ecological factors. Modifications in the strength and direction of the relationships between traits involved in mating and fertilization success would have important evolutionary implications (e.g. maintenance of additive genetic variation in sexual traits, genetic befits of mate choice, contribution of sexual selection to adaptation to environmental changes). Following established experimental protocols (Devigili et al. 2015), we will use replicated populations of guppies (Poecilia reticulata) to investigate how experimentally manipulated environmental and social factors affect the level of polyandry, variances in mating rate and competitive fertilization success. Traits associated with mating and fertilization success are well known in this species (Evans et al. 2003; Pilastro et al. 2004; Devigili et al. 2016) and will allow a trait-based analyses of selection across a range of conditions.

Devigili, A., A. Di Nisio, A. Grapputo, and A. Pilastro. 2016. Directional postcopulatory sexual selection is associated with female sperm storage in Trinidadian guppies. Evolution 70:1829-1843. Devigili, A., J. P. Evans, A. Di Nisio, and A. Pilastro. 2015. Multivariate selection drives concordant patterns of pre- and postcopulatory sexual selection in a livebearing fish. Nat. Commun. 6:8291. Evans, J. P., L. Zane, S. Francescato, and A. Pilastro. 2003. Directional postcopulatory sexual selection revealed by artificial insemination. Nature 421:360-363. Pilastro, A., M. Simonato, A. Bisazza, and J. P. Evans. 2004. Cryptic female preference for colorful males in guppies. Evolution 58:665-669.

More publications of th eresearch group can be found at:

— / —

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

---

UppsalaU BirchPopulationGenomics

PhD Position in birch population genomics at the Department of Ecology and Genetics, Evolutionary Biology Centre, Uppsala University, Sweden

The Department of Ecology and Genetics, which is part of the Evolutionary Biology Centre, is an international environment with more than 200 coworkers. The Department research and education span from evolutionary ecology and genetics to studies of ecosystems. The Evolutionary Biology Centre is one of the world's largest workplaces for evolutionary biologists and is an excellent research environment with a wide range of topics in evolution and ecology. Our graduate school offers a creative and stimulating environment and offers a rich variety of seminars, journal clubs, courses and possibilities to interact with other scholars and students. The environment is international with English as the primary language at the department. For more information, see www.ieg.uu.se . Project description: Natural occurrence of polyploidy, inter-specific hybridization and the ability to propagate asexually, together with accelerated flowering (less than 1 year) and a relatively small genome size of 440 Mb with a recent reference genome sequence, make birches ideal for evolutionary biology studies in trees. In the present project, we will investigate the relative contributions of hybridization, population history and selection to local adaptation and thereby address the response of Swedish birch populations to global warming. The work will combine population genomic studies of hybridization and local adaptation along latitudinal gradients with controlled experiments of the response of birches to elevated temperatures. These new data, together with data from birch breeding programs, will be used to evaluate the potential of genomic selection for developing advanced breeding material better adapted to the forthcoming environmental conditions.

The applicant will be involved in material collection, DNA extraction, bioinformatics, growth chamber experiments and populations genetic analysis. The work will be coupled to the ongoing EU project GENTREE, which studies local adaptation of trees at European scale in seven species. In this way there will be possibilities to expand the PhD project in new directions. The work will be co-led by Dr. Jarkko Salojarvi at University of Helsinki. The project is supported by the Swedish Research Council Formas and Dr. Martin Lascoux is the main supervisor.

Qualifications: A relevant master degree in biology, genetics, ecology or equivalent. We are looking for a candidate that is motivated, highly reliable, driven and well-organized, and has a broad interest in evolutionary biology. Experience of laboratory work and bioinformatics and using Linux is needed. Previous experience of quantitative/molecular/population genetics and programming (e.g. R, Matlab, C, Perl, Python) is a merit. You should have the capacity to express yourself well in speech and writing in English. Because the holder of this position will interact closely with other lab members, we put emphasis on personal ability, independence and ability to collaborate.

Position: The graduate program covers four years of full-time study. The position can be combined with teaching or other duties at the department (maximum 20%), which prolongs the employment with the corresponding time. The salary will be set according to local agreements. Rules governing PhD candidates are set out in the Higher Education Ordinance Chapter 5, – 1-7 and in Uppsala university's rules and guidelines http://regler.uu.se/Rules_and_regulations_in_English/. More information about postgraduate studies at Uppsala University is available at http://www.teknat.uu.se/education/postgraduate/ . Application: The application should include 1) a letter describing yourself, your research interests, why you want to do a PhD and why you are suitable for the current position, 2) a CV 3), a short description of your education, 4) an authorized copy of your Master's degree and course grades, 5) the names and email addresses of at least two referees, 6) relevant publications including Master's thesis. The application should be written in English.

Uppsala University aims for gender balance and diversity in all activities in order to achieve a higher quality at all levels of the organization. We therefore welcome applicants of any gender and with different birth background, functionality and life experience.

Starting: As soon as possible or as otherwise agreed.

For further information about the position please contact

Professor Martin Lascoux, e-mail: martin.lascoux@ebc.uu.se, tel. 018-471 6416.

More information about the research: https://lascouxlab.wordpress.com/people/

— / —

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

---

USalzburg Austria PollinatorAdaptation

The Department of Ecology & Evolution at the University of Salzburg is offering

2 PhD positions for three years each

in the FWF-funded project "Local pollinator adaptation in deceptive Arum maculatum" (Project leaders: Stefan Dötterl, Hans-Peter Comes, Anja Hörger)

This project aims to identify 1) the ecological roles of floral scent in the plant-pollinator interaction between brood-site deceptive Arum maculatum and its main pollinators, Psychoda phalaenoides and Psycha grisescens; and 2) the likely differential selective influence of each moth fly species and its olfactory preferences on inflorescence scent divergence between European A. maculatum populations along a latitudinal gradient covering areas north and south of the Alps. The project will be pursued along three axes. First, it will study the geographic patterns of pollinators trapped in comparison to the inflorescence scents emitted. Second, it will study the mechanisms of pollinator attraction by looking which molecule(s) within the blend is(are) responsible for deceiving the two main pollinator species. Finally, it will test for the involvement of inflorescence scent in the divergent local adaptation of A. maculatum by using both ecological-experimental and genomic approaches.

One of the doctoral researchers will be mainly responsible for the ecological and chemo-ecological approaches (dynamic headspace, gas chromatography / mass spectrometry; electroantennographic detection, behavioral assays, multivariate statistical analyses), the second student will focus on the genomic approaches (Rad-seq, meta-barcoding, bioinformatics) and correlative analyses (ecological-genomic). Both students are expected to perform field work (scent sampling, pollinator observations, reciprocal transplants) and supervise field assistants.

The successful applicants should be highly motivated, proficient in English language and scientific writing, and have a research focus in one or more of the following fields of research: a) pollination biology; b) chemical ecology; c) population genetics/genomics. An MSc, diploma degree or equivalent in Botany, Zoology, Ecology, Genetics, Molecular Biology or Evolutionary Ecology is required. Previous field and lab experience and/or bioinformatics skills are of advantage.

The monthly gross salary is c. 2071 EUR (14 months of payment per year). The University of Salzburg offers excellent research facilities, and a very pleasant working and living environment in a beautiful landscape with numerous lakes and mountains.

Please send your application (letter of motivation, CV, certificates, contacts of two potential referees) in electronic form as a single pdf file to Univ.-Prof. Dr. Stefan Dötterl, Stefan.Doetterl@sbg.ac.at. Please also indicate your preference for the ecological or the genomic project. The start date is scheduled for April 2017. The positions will be filled as soon as suitable applicants are found. In case you have any requests, please contact Univ.-Prof. Dr. Stefan Dötterl.

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

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

Hörger Anja <anja.hoerger@sbg.ac.at>

UStAndrews DrosophilaSpeciationGenomics

We would like to advertise a PhD project at the University of St Andrews.

PhD studentship: Genomic predictors of reproductive isolation in Drosophila

We are looking for a talented and motivated student (UK or EU) to undertake a four-year PhD at the University of St Andrews, Scotland. Project details below. Interested applicants are encouraged to contact the primary supervisor, Prof. Mike Ritchie, via email (mgr@st-andrews.ac.uk) before the application deadline on March 27th.

Project summary

Reproductive isolation has long been recognised as a key step in the process of speciation. The Biological Species concept argues that isolation needs to be complete between 'good' species, but most recent research suggests that this is far too stringent a criterion. Advances in the availability and methods of analysis of genomes allow us to detect and quantify variation in gene flow not only between species, but also between genomic regions within species. Much new data is emerging on patterns of genomic divergence. This project will examine predictors of these patterns of divergence using both existing and novel genomic data, in combination with data on the ecology and measures of pre- and post-mating reproductive isolation. The data will come from Drosophila, which has a relatively well understood genome, and detailed compilations of the strength of different types of reproductive isolation exist. The student will integrate existing and new genomic data into this database and use novel analytical techniques to determine genetic divergence and gene flow between different genomic regions. Do similar patterns of genomic divergence correlate with sexual or post-mating isolation? Do both influence sex-chromosomes versus autosomes similarly? Do ecological generalists show different patterns from specialists? Do patterns differ between sympatry and allopatry, and how often do we detect gene flow in sympatric species? Co-supervisor1, Konrad Lohse (Edinburgh), has developed new methods to detect introgression and regions of admixture from such genomic data. Co-supervisor 2, Oscar Gaggiotti (St Andrews), has developed methods to detect genomic outliers while controlling for population history and ecological covariates. Both will advise and help the student apply such techniques to the data. The lead supervisor, Michael Ritchie, brings extensive experience of speciation in this group.

Prof. Mike Ritchie Centre for Biological Diversity, School of Biology, University of St Andrews, Fife. Scotland KY16 9TH UK 0 (+44 outside UK) 1334 463495 http://www.st-andrews.ac.uk/-profile/mgr http://scholar.google.co.uk/citations?user=JSkvwMsAAAAJ&hl Email: mgr@st-andrews.ac.uk

LOHSE Konrad <klohse@exseed.ed.ac.uk>

USussex FloralEvolution new deadline

Deadline extended for this PhD opportunity:

* PhD position available to study flower evolution during range expansions at the University of Sussex*

Supervisor: Maria Clara Castellanos (www.sussex.ac.uk/lifesci/plant-evolutionary-ecology-lab)

co-supervisor: Dave Goulson (www.sussex.ac.uk/lifesci/-goulsonlab) co-supervisor: Jeff Ollerton (University of Northampton)

We are looking for an enthusiastic student interested in pollination and floral evolution to explore how new pollinator environments on different continents can generate floral evolutionary innovation during plant invasions. The project will use several plant species that can be studied in their native and new ranges, and combine field work in South and Central America and/or southern Europe, molecular work and greenhouse studies to understand how plants deal with changes in their pollinators. For further details on the project please visit http://www.sussex.ac.uk/study/phd/fees-and-scholarships/scholarships/view/759 .The student will be part of the vibrant Evolution, Behaviour and Environment subject group within the University of Sussex; our campus is located within a national park, 10 minutes from the seashore city of Brighton.

This 3.5-years fully funded studentship is open to UK and EU citizens. The successful applicant will have a strong interest in plant evolutionary ecology; experience with field work and/or molecular biology will be a plus. A driving licence and availability and interest in performing field work in the UK and abroad are essential. The closing date for applications is 25th April 2017. Applications should be submitted through Sussex University's graduate application system: http://www.sussex.ac.uk/study/phd/apply. Please include a CV, statement of interest and the names and email addresses of two academic referees. The expected starting date is in September 2017. Email me for informal enquiries: m.c.castellanos@sussex.ac.uk.

Maria Clara Castellanos <M.C.Castellanos@sussex.ac.uk>

UUppsala PopulationGenomics

A PhD student position in population genomics is available at the department of Organismal Biology, Uppsala University.

Closing date: 2017-04-30

Project description: The demographic history of many species is currently being addressed with modern computational methods combined with population genomic data, especially humans that often function as a model organism in this respect. In order to understand population divergence processes, concepts of effective population size, population structure and genetic diversity become important. Linking effective population size as a function of time to population divergence and structure is a major challenge for modern population genomics and computational biology. The proposed project focuses on trying to disentangle population structure and divergence from population size (both effective and census) changes. The project will investigate these processes using large-scale population genomic data from humans and archaic humans such as Neandertals.

The project is part of a larger program that links theoretical population genetics, genomics and human evolution. The successful candidate will work in Professor Mattias Jakobsson research group together with Dr. Per Sjödin. The group consists of ~25 researchers (senior scientist, postdocs, graduate students and research engineers) with different areas of expertise. The research at the Jakobsson lab focus on population genetics and human evolution and the lab uses a combination of mathematical studies of population genetic models and computational approaches to understand the complex patterns of large-scale human genetic variation and their implications for human demographic and evolutionary history. In particular, the research focuses on understanding human evolution using genetic information from both recent and ancient individuals, developing statistical methods for analyzing large genomic data, and searching for genes targeted by selection.

Qualifications: A master degree (or equivalent) in a relevant field is required. The ideal candidate is highly motivated with thorough education in quantitative disciplines, such as statistical/quantitative/population genetics, bioinformatics, computer science, statistics, mathematics and with a strong interest in population genetics and human evolution.

For further information about the position please see http://www.iob.uu.se/about-us/join-us/?positionId=-3D141314 or contact Professor Mattias Jakobsson mattias.jakobsson@ebc.uu.se, +46 18 471 6449.

"Per.Sjodin@ebc.uu.se" <Per.Sjodin@ebc.uu.se>

Vienna PopulationGenetics

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

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 – 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

WesternSydneyU 3 TephritidFruitFlies

Three PhD Positions, Hawkesbury Institute for the Environment, Western Sydney University, Australia

Three PhD scholarships are available for highly motivated and driven candidates to study the ecology and evolution of entomopathogens and endosymbionts of Australian tephritid fruit flies. The general aims of the projects are to characterise the diversity and impact of entomopathogens (EPNs, fungi, bacteria and viruses), the interactions with their hosts and endosymbionts (including Wolbachia). Research will include laboratory experiments and field studies in different environments from central New South Wales to northern Queensland, Australia.

The PhD candidates will be based at the Hawkesbury Institute for the Environment (HIE) (https://www.westernsydney.edu.au/hie) in Richmond, NSW, with placements with collaborating research and industry partners. HIE is a recently established research institute within Western Sydney University. HIE has rapidly built a strong research reputation in ecology and evolution, and houses a team of over 50 academic research scientists and over 50 PhD students with access to a unique suite of world-class research facilities.

The PhD positions form part of the HIE node of the Australian Research Council (ARC) funded Industrial Transformation Training Centre (ITTC) for Fruit Fly Biosecurity and Innovation (http://www.fruitflyittc.edu.au). This ITTC is cross-institutional (in collaboration with Macquarie University and Queensland University of Technology), and the focus of the team at HIE is to investigate the potential for new microbial control of Australian tephritid pest fruit flies, including Australia's most significant pest, Queensland fruit fly Bactrocera tryoni.

Three research projects are available to highly motivated candidates in the areas below: Interactions of entomopathogens and Australian fruit fly. Wolbachia and other endosymbionts of Australian fruit fly. Biotic mortality factors of Australian fruit fly across different regions.

For more information about the projects and application process please visit the website below: https://www.westernsydney.edu.au/graduate_research_school/-

grs/scholarships/ current_scholarships

Application deadline: 19 March 2017 (please direct late applications to Markus Riegler).

For further information please contact Associate Professor Markus Riegler <m.riegler@westernsydney.edu.au>

Markus Riegler <M.Riegler@westernsydney.edu.au>

Jobs

23andMe . . . 54
BrownU AnatomyTeacher . . . 55
ClemsonU 2 Lecturer Genetics . . . 55
DukeU FullTimeTeachingAssistant . . . 56
GeorgeWashingtonU Bioinformatics . . . 57
ImperialC London PollinatorEvolutionaryEcol . . . 58
LaTrobeU Australia GenomicPlantBreeding . . . 58
LUOMUS UHelsinki InsectCurator . . . 59
NewYorkU ResearchScientist EvolGenetics . . . 60
OhioStateU CropGeneticsGenomics . . . 61
OmahaZoo GeneticsResAssist Bioinformatics . . . 62
QueenMaryU EvolNeurobiology . . . 63
SouthDakotaStateU WildlifeConservation . . . 63
Tromso Norway FishEvolution . . . 64
UCalgary ComputationalBiol DeadlineExt . . . 65
UCatolicadeChile 2 EvolutionaryBiol . . . 66
UCentralFlorida CoastalDiseaseEvolution . . . 67
UEdinburgh BioinformaticsHairColour . . . 67
UGreifswald EvolutionaryMathematics . . . 67
UGreifswald SciAssist18Mnths EvolutionVibrationalCommunication . . . 68
UGrenobleAlpes 3yr EvolutionaryDataScience . . . 69
UKansas ResAsst Drosophila ComplexTraits . . . 69
UMaryland Tech InvertPopGenetics . . . 70
UppsalaU QuantitativeGeneticsGenomics . . . 71
UPrague PlantEvolutionSystematics . . . 71
UTromso FishEvolution . . . 72
UUtah Genetics LabManager . . . 72
Virginia DirectorResearchCenter Bioinformatics . . . 73
WSLBirmensdorf EnvironmentalGenomics . . . 74
Xishuangbanna TropicalBotanicalGarden ResearchPositions . . . 75

23andMe

23andMe's mission is to help people access, understand, and benefit from the human genome. We are a group of passionate individuals excited to push the boundaries of what's possible to help turn genetic insight into better health and personal understanding.

Our Research Team prides itself on driving cutting edge, industrial-scale science to make an impact that belies the team's size, in an environment and culture that fosters creativity, innovation, collaboration, and fun.

More than 80% of our customers consent to participate in research, and as a result of their participation, we have one of the largest recontactable, genotyped, and phenotyped research cohorts in the world. The scope and breadth of our vision means that most of the methods and tools necessary to unlock the potential of this unique resource for discovery have yet to be developed.

Our science has garnered the respect of many members of the broader scientific community. For a list of our publications, see www.23andme.com/publications/-for-scientists/ . Join us! Visit our Careers page (www.23andMe.com/careers) to learn more about these open positions:

- Scientist, Research Communications - Bioinformaticist - Computational Biologist, Ancestry R&D - Scientist/Senior Scientist, Statistical Genetics - Scientist/Senior Scientist, Survey Methodology - Scientist/Senior Scientist, Health R&D - Senior Computational Biologist - Biostatistician

pfontanillas@23andme.com

BrownU AnatomyTeacher

Alpert Medical School and Department of Ecology and Evolutionary Biology Brown University

Anatomy Lecturer

The Alpert Medical School at Brown University is seeking a full-time faculty member at the rank of Lecturer (non-tenure track) with teaching responsibilities in dissection-based human anatomy. The successful applicant will: 1) team-teach anatomy for medical students, including lecture, prosection preparation and presentation, dissection labs, and training teaching assistants; 2) coordinate the anatomy component of the new Gateways to Medicine, Health Care, and Research Program (MasterÂ^{1}s and Certificate students); 3) team-teach anatomy for physician assistant students from Bryant University, both lecture and dissection; 4) organize, manage and supervise the anatomy outreach program including visits, tours, and use of the lab by clinical groups.

Qualifications: Ph.D., M.D., D.O. or equivalent doctoral degree and experience in dissection-based human anatomy required. At least two years teaching experience in dissection-based human anatomy preferred.

The successful applicant will join a cohesive team of anatomy faculty including Dale Ritter (Director), Stephen Gatesy, Thomas Roberts and Elizabeth Brainerd. Review of applications will begin March 15, 2017 and will continue until the position is filled. The anticipated start date is June 1, 2017. Salary will be commensurate with experience and competitive for non-tenure track faculty in medical education. Please apply through the Interfolio system [http://apply.interfolio.com/40284] and include a letter of application, curriculum vitae, and statement of teaching experience and interest, and the names and contact information for four references.

Brown University is committed to fostering a diverse and inclusive academic global community; as an EEO/AA employer, Brown considers applicants for employment without regard to, and does not discriminate on the basis of, gender, race, protected veteran status, disability, or any other legally protected status.

“holbrook@rowan.edu” <holbrook@rowan.edu>

ClemsonU 2 Lecturer Genetics

Clemson University: College of Science: Genetics & Biochemistry Lecturer Location: 154 Robert F Poole Closes: Apr 15, 2017 at 11:59 PM Eastern Time (GMT-4 hours)

Two full-time, nine-month LECTURER positions for the instruction and development of teaching laboratories in genetics and biochemistry. One lecturer will have expertise in the area of Biochemistry and a second will have expertise in the area of Genetics. Both Lecturers will be responsible for the sophomore integrated biochemistry/genetics laboratory course GEN/BCHM 3040 Molecular Biology Lab. The Biochemistry Lecturer will also be responsible for the upper level biochemistry laboratory courses, BCHM 4330 Physical Approach to Biochemistry Lab and BCHM 4340 Biochemistry of Metabolism Lab, while the Genetics Lecturer will be responsible for the upper level genetics laboratory courses, GEN 4210 Molecular Genetics and Gene Regulation Lab and GEN 4110 Population and Quantitative Genetics Lab. A Ph.D. in a relevant discipline is required and experience in teaching and laboratory course development at the college level is preferred. Expected start date is July 1, 2017. This is a renewable, non-tenure track position with opportunity for promotion. Salary level will be commensurate with education and experience and a benefits package is included.

Qualifications One lecturer will have expertise in the area of Biochemistry and a second will have expertise in the area of Genetics. A Ph.D. in a relevant discipline is required and experience in teaching and laboratory course development at the college level is preferred.

Application Instructions To apply, please submit an electronic application (submitted as a single PDF) that includes a cover letter, curriculum vitae, names and contact information for three persons from whom a letter of reference can be requested, and a statement of teaching philosophy to Interfolio at (insert Interfolio web address and job # for Genetics position) or (insert Interfolio web address and job # for Biochemistry position). Appropriately qualified individuals may apply for both positions by submitting an application to each. To ensure full consideration, please submit applications by April 14, 2017.

https://apply.interfolio.com/41087 Amy Lawton-Rauh, PhD Associate Professor, Department of Genetics and Biochemistry; Faculty Senate Vice President/President-Elect

Clemson University 316 Biosystems Research Complex, 105 Collings Drive, Clemson SC 29634-0318

Office +1.864.656.1507 | Skype amy.lawton.rauh | amylr@clemson.edu | popquantgenomics.org | twitter.com/alawtonrauh < http://twitter.com/-CUSoA_Clemson >| | clemson.edu/genbiochem < http://www.clemson.edu/genbiochem > | ros-breed.org/about <mailto:amylr@clemson.edu> | clemson.edu/glimpse/?pR60 < http://-clemson.academia.edu/PeterLaurence >

Amy Lawton-Rauh <amylr@clemson.edu>

DukeU FullTimeTeachingAssistant

Information about the full-time teaching/prep positions in Biology 202L course “Genetics and Evolution,” Duke University

Position description: Work full time (40 hours/week) as a teaching assistant and laboratory prep assistant in the introductory biology program for the 2017-2018 academic year. The position has two main components, teaching and behind-the-scenes laboratory preparation.

Teaching component: The primary teaching responsibility of the position is to lead laboratory sections of up to 16 students in the Biology Department’s genetics and evolution Gateway course, Biology 202L. Each Biology 202L section meets weekly for 2.5 hours for a combined hands-on laboratory/problem-based learning session. Additional teaching responsibilities include (a) attending and taking notes at all course lectures including the weekly large discussion section, (b) grading weekly student written assignments, (c) helping with the preparation and grading of in-class quizzes and mid-semester hourly and final exams, and (d) assisting students during office hours and otherwise mentoring students as beginning biologists.

Teaching assistants should plan to be in Durham early the week of August 21, 2017, and are expected to participate in a teacher-training workshop before the fall semester begins. TAs also attend weekly prep sessions during the semester on Mondays.

Prep component: The second set of duties associated with the position is to assist in the preparatory work for the teaching labs in Biology 201L and 202L, as determined by the Lab Administrator. Responsibilities include setting up and putting away equipment and specimens for laboratory exercises, maintaining supplies in lab rooms between sections, cleaning glassware, assisting with field collection of live specimens, and helping to care for a diverse collection of invertebrate animals in salt-water aquaria. The lab prep workload is likely to require some evening (until 10 PM) and/or early morning (8 AM) work.

Salary: The projected salary for the position is $17,500 or commensurate with experience. Employment begins on August 21, 2017 and ends May 11, 2018, with most of the winter and spring breaks off, with payment made in 9 equal amounts on the 25th of each month starting in September and ending in May. Full-time teaching/prep employees are eligible for health plans made available by the University.

Qualifications: Applicants should have a bachelor’s degree with a strong, varied background in biology, especially genetics and evolution, with a superior science GPA. A very important attribute is a high level of energy and an enthusiasm for teaching genetics and evolution. Prior enrollment with good grades in Duke University courses Biology 25L (introductory biology), 118 (genetics), 116 (evolution), 102L/202L (genetics and evolution), or the equivalent(s), and experience teaching are highly desirable; experience tending Drosophila is a plus. Teaching assistants in Biology 202L are expected to be actively engaged with their students in all aspects of the course and to serve as role models and mentors. Because they are a vital part of the gateway biology teaching team both in the classroom and behind the scenes, full-time assistants must be willing to commit themselves fully to the responsibilities of the position described above and as determined by the faculty members in charge of the gateway course. US citizens only. Duke is an Equal Opportunity and Affirmative Action employer.

Interviews and Application Process: Formal interviews are planned to begin after April 5, 2017. Hiring decisions will be made on a rolling basis thereafter, continuing as necessary.

Interested applicants should provide (a) a cover letter, (b) a transcript(s), and (c) a resume with the names of two references (preferably at Duke for Duke students or alumni) to Julie Noor. These may be emailed to jkfnoor@duke.edu, delivered to her mailbox in the Department of Biology (BioSci 138), or mailed to her at the Department of Biology, Box 90338, Duke University, Durham, NC 27708-0338. To be assured of consideration, applications should be submitted by April 5, 2017, although later applications will be considered if all positions haven't been filled.

For more information contact Julie Noor by e-mail at jkfnoor@.duke.edu

Mohamed Noor <noor@duke.edu>

GeorgeWashingtonU Bioinformatics

Computational Biology Institute

Department of Epidemiology and Biostatistics

Milken Institute School of Public Health

The George Washington University

The Computational Biology Institute and the Department of Epidemiology and Biostatistics of the GW Milken Institute School of Public Health are recruiting for 1-2 full-time tenure track or tenured faculty at the rank of Assistant or Associate Professor. The successful candidate(s) will develop a program of sponsored research with the Computational Biology Institute, and teach and mentor graduate students in the Department of Epidemiology and Biostatistics. Academic rank, salary and employment position are competitive and will be commensurate with experience. GW has a strong commitment to achieving diversity among faculty and staff, and accordingly we encourage applications from members of underrepresented populations.

The Computational Biology Institute seeks faculty members to establish externally funded, internationally recognized, and interdisciplinary research programs in bioinformatics and/or computational biology in an area such as genome analysis, biodiversity informatics, translational medicine, public health, cancer, neurobiology and systems biology developing methods to address 'big data' issues from a computational perspective.

The Department of Epidemiology and Biostatistics oversees the MPH, MS and PhD programs in epidemiology, MPH program in biostatistics, and the MS program in public health microbiology and emerging infectious diseases. The Department collaborates with the Department of Statistics for the MS and PhD programs in biostatistics.

Basic Qualifications: Applicants must have an MD or PhD conferred prior to the time of application in Bioinformatics, Computational Biology, Computer Science, Mathematics, Genomics, Epidemiology or a related discipline, with postdoctoral research experience; as well as experience publishing in peer-reviewed journals, proposing and/or implementing funded research, and teaching graduate and/or undergraduate courses in their area of expertise.

Responsibilities: The successful candidates will devote approximately 50% of their efforts to obtaining, implementing or overseeing funded research, and 50% to teaching, mentoring, and educational administration.

Application Procedure: Applicants should complete the online faculty application at http://www.gwu.jobs/postings/40652 and submit the following documents: 1) a curriculum vitae; 2) a statement of research interest to include accomplishments and future plans; and 3) a statement of teaching interest to include mentoring interest. Only complete applications will be considered. Review of applications will begin on March 29, 2017 and will continue until the positions are filled.

For further information about the Computational Biology Institute at George Washington University, please see https://cbi.gwu.edu/ .Additional information about the Milken Institute School of Public Health can be found at http://publichealth.gwu.edu/ and the Department of Epidemiology & Biostatistics http://publichealth.gwu.edu/departments/epidemiology-and-biostatistics . The university is an Equal Employment Opportunity/Affirmative Action employer that does not unlawfully discriminate in any of its programs or activities on the basis of race, color, religion, sex, national origin, age, disability, veteran status, sexual orientation, gender identity expression, or on any other basis prohibited by applicable law.

Employment offers are contingent on the satisfactory outcome of a standard background screening.

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

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

ImperialC London PollinatorEvolutionaryEcol

Research Associate in Insect Pollinator Evolutionary Ecology Imperial College London, UK - Department of Life Sciences, Faculty of Natural Sciences

Closing date 6 April 2017 (Midnight GMT)

A NERC funded Research Associate position is available for 33 months in the research group of Dr Richard Gill at Imperial College London's Silwood Park campus, to investigate insect pollinator responses to a century of land-use change. This position will primarily focus on population trait evolution of insect pollinators, and the investigation of stress induced effects on bee behaviour and colony fitness. The position will involve collaborating with researchers at the Natural History Museum London who will generate complementary genomic datasets, and involve work with curators from a number of UK museums to analyse insect specimens and with researchers from NHM London, Queen Mary University of London, Northampton University and Christchurch University (New Zealand).

The Gill group's aim is to better understand how insect pollinator populations (primarily bees) respond to landscape change, and how they adapt to newly emerging environments and the impact on measures of fitness. The successful candidate will focus on addressing two primary questions (i) whether there are regional adaptations in response to differential land-use change (LUC) and (ii) whether specific factors associated with agricultural LUC place a constraint on social bee colony development and fitness. This will involve analysis of morphological variation using museum specimens, investigating phenological change from archival records, and undertaking manipulation experiments alongside behavioural observations. As part of this NERC project, Prof Ian Barnes and Dr Selina Brace (@NHM London) will be focusing on the recovery and analysis of ancient DNA from museum specimens and we intend for the successful candidate to also contribute to this aspect of the project.

You should hold a PhD (or equivalent) in a Biological Science. You will have a background in evolution and/or ecology, with experience in the analysis of trait variation. You will also have experience of husbandry, handling or monitoring animals in the laboratory and/or field. You will also have experience in experimental design and will have the ability to analyse large data sets in addition to a proven track record of publishing quality research. Previous experience in using any of the following methods is desirable: micro-CT scanning technology, geometric morphometrics, observation of animal behaviour and collections-based research.

This full-time, fixed-term post has a start date of 19 June 2017 (but with some flexibility). Informal enquiries should be directed to Dr Richard Gill at r.gill@imperial.ac.uk and further details of the Gill research group can be found at: https://www.imperial.ac.uk/people/r.gill . The preferred method of application is online via our website http://www3.imperial.ac.uk/employment (please select "Job Search" then enter the job title or vacancy reference number including spaces - NS 2017 045 LH - into "Keywords"). Please complete and upload an application form as directed. If you are unable to apply online, please contact Christine Short by email c.j.short@imperial.ac.uk, to request an application form.

Salary: 36,070 - 43,350 per annum (maximum starting salary 36,070)

"Gill, Richard J" <r.gill@imperial.ac.uk>

LaTrobeU Australia GenomicPlantBreeding

Are you a plant breeder/quantitative geneticist who is passionate about genomic plant breeding? Do you want to work in a group that develops new methods and applies them directly to increase genetic gain for growers in Australia and globally? Then you should think about joining my growing group.

We are currently looking for a Senior Research Scientist and a Research Scientist. Both positions require strong skills and experience in quantitative genetics, genomics, and candidates should be familiar with computer programming. A major theme for these positions is to investigate the long-term impact on genetic gain and diversity of novel plant breeding programs using empirical data and computer simulations.

The positions will report to me (Hans Daetwyler). There will also be opportunities to collaborate with other team leaders including Assoc. Prof. Matt Hayden, Dr. Noel Cogan, and Prof Mike Goddard. Senior Research Scientist (closes March 19, 2017) §Fixed Term / Full Time - 3

Years §Bundoora location, AgriBio, La Trobe University Campus

more info at https://jobs.careers.vic.gov.au/jobs/VG-022151 We are seeking a motivated and experienced quantitative geneticist for an exciting new role underpinning our strategy to accelerate the rate of genetic gain in plant breeding. You will be responsible for coordinating and delivering research within large plant breeding research projects, primarily focused on plant breeding program designs that utilise genomic and optimal haploid value selection. An important focus will be to develop stochastic computer simulations to underpin breeding program choice within Agriculture Victoria and for commercial partners.

We are looking for an experienced researcher with excellent organisational skills, preferably with a background in the use of genomic data for breeding outcomes in general and specifically for genomic selection, as well as a foundation in computer programming. Publications in key international journals are expected and encouraged, as is supervision of staff and PhD students.

You will also have a strong commitment to the values of collaboration, accountability, delivery, and a passion for science. The position offers a unique opportunity to fast track the latest research in plant genetics and genomics into industry application with a large commercial partner.

The successful applicant will work effectively as a member of a team, enjoy flexible working arrangements and undertake a wide variety of work across the division.

Research Scientist (closes March 12, 2017) §Fixed Term / Full Time - 3 Years §Bundoora location, AgriBio, La Trobe University Campus

more info at https://jobs.careers.vic.gov.au/jobs/VG-022152 The Research Scientist Computational Biology will develop tools enabling faster genetic gain for important crop and forage species through research on genomic and optimal haploid value selection, with a focus on developing stochastic computer simulations that underpin breeding program choice within Agriculture Victoria and for commercial partners. The role is required to deliver on specific research milestones for large, collaborative, industry co-funded projects. In this position you will develop novel genomic breeding programs that will be the foundation for breeding and pre-breeding programs in Australia and abroad. Communicating key results and new methodologies to industry, and engaging with industry partners will also be a key part of the role. Publications in key international journals are expected and encouraged. The position offers a unique opportunity to fast track the latest research in genetics and genomics into industry application. You will be expected to support other scientists as well as PhD students working in the same area and build a collaborative culture.

For a confidential discussion, please call or email Hans Daetwyler on +61 (0)3 9032 7037. hans.daetwyler@ecodev.vic.gov.au The Department of Economic Development, Jobs, Transport and Resources is an equal opportunity employer and welcomes applicants from a diverse range of backgrounds.

We assist successful candidates with attaining work visas.

Best wishes, Hans

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

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

hans.daetwyler@ecodev.vic.gov.au

LUOMUS UHelsinki InsectCurator

The Finnish Museum of Natural History LUOMUS (www.luomus.fi/en) is an independent institute of the University of Helsinki and the national museum in the field of natural history in Finland. The museum's duties are to amass, maintain, and display its collections, and to conduct related research, particularly in the field of species-level biodiversity. The collections serve research, teaching, and public education in biology, geology, and biodiversity, and form part of the international network of natural history repositories. The Finnish Museum of Natural History, established in 1988, has four units: Zoology, Botany, Natural Sciences, and General Services. The institution has a staff of c. 130, of which 40 work in the Zoology Unit. The entomological collections of the Unit comprise c. 9 million specimens from all over the world. Close to half of the insects are from Finland, and there are extensive collections from e.g. the northern Palearctic region and sub-Saharan Africa. The collections are particularly rich in Lepidoptera, Coleoptera, Hymenoptera, and Diptera.

The Finnish Museum of Natural History invites applications for a permanent position of

Senior Curator

specialising in the systematics and biogeography of insects. The appointment will begin on 1 November 2017 or as mutually agreed.

The duties of the senior curator will include independent research in collection-based systematics and zoogeography, acting as a superior for the Entomology Team as well as managing, amassing, and developing the scientific collections together with the other team members. As an expert in the field, the senior curator will participate in the museum's international collaboration and community engagement in the field, as well as tasks related to teaching, e.g., the development of Bachelor's and Master's programmes and digital learning environments. The senior curator is expected to be active in obtaining external funding and in supervising research students and junior colleagues.

According to the Regulations of the University of Helsinki, an appointee to a senior curatorship shall hold a doctoral degree and have top-level scholarly qualifications, experience in leading research, proven success in obtaining external funding, as well as the documentation of international cooperation in the research field that the appointee represents.

Experience in working with scientific collections, pedagogical training, participation in university teaching and supervision, good leadership skills, and an inclination to team work as well as experience of societal interaction and knowledge of Finland's nature and fauna are considered further assets.

The official languages of the University of Helsinki are Finnish and Swedish. According to the Government Decree on Universities, senior curators must be proficient in Finnish. They must also have at least satisfactory spoken and written skills in Swedish. Foreign citizens, non-native Finnish citizens or citizens who have not been educated in Finnish or Swedish may be exempted from this requirement without a separate application. To successfully attend to the duties of the position, the appointee must also have good skills in English.

The senior curator's salary will be based on level 8-9 of the job requirement scheme for teaching and research personnel in the salary system of Finnish universities. In addition, the appointee will be paid a salary component based on personal work performance. The gross monthly salary will be approximately 5 100-6 100 euros, depending on the appointee's career stage and scholarly qualifications.

Applicants are requested to submit their application as one single pdf file which includes the following documents:

1) An English language CV

2) An English language report (max. 3 pages) on the applicant's previous research activities and acquired external funding, and a brief plan on how the applicant intends to develop and focus his or her research and its funding in the future

3) A report (max. 3 pages) of experience and merits which are of relevance for the evaluation of other skills relevant for the position (e.g. leadership, collection work, supervision and teaching). Please refer to the criteria for the assessment of teaching skills: http://www.helsinki.fi/bio/faculty/materials/-Teaching_skills_evaluation_matrix2012.pdf 4) A numbered English language list of publications and other works with which the applicant wishes to demonstrate his or her competence and merits

Or, alternatively, an academic portfolio containing the above documents and information (for instructions, please see http://www.helsinki.fi/recruitment/-academicportfolio.html /

— / —

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

---

NewYorkU ResearchScientist EvolGenetics

NYU Evolutionary Genetics Research Scientist

The Rockman Lab at NYU seeks to hire a senior research scientist. We use quantitative genetics and genomics to study the molecular and evolutionary causes of phenotypic variation, with a focus on developmental and life-history phenotypes.

The research scientist will collaborate with postdocs on three funded projects in the lab: Genetic dissection of developmental variation in Streblospio benedicti, a polychaete annelid Construction of a genetic mapping panel in the diatom Seminavis robusta Analysis of complex-trait genetic architectures in outbreeding and selfing Caenorhabditis nematodes

Applicants should have experience with the wet-bench components of NGS library construction and associated methods (e.g., qPCR, bioanalyzer, covaris, etc.), including RNA-seq and reduced-representation methods for genomic DNA. The ideal candidate is highly organized and enthusiastic about experimental marine biology and evolutionary genetics and genomics.

Core responsibilities of the research scientist will include: - Perform experimental crosses in diatoms, annelids, and nematodes - Construct sequencing libraries for genetics and genomics projects - Help develop new phenotyping assays - Participate in the design of experiments - Maintain annelid and diatom stocks and associated databases - Prepare media (worm plates, diatom media, polychaete food, artificial seawater, buffers, etc) - Order supplies and manage inventory - Keep detailed lab notebooks - Participate in lab meetings - Help write up results for publication

This is a full-time position with an initial 1-year appointment, with subsequent reappointment available. The lab is located in Greenwich Village, a block from Washington Square Park, convenient to transit and everything else. Employment comes with a full benefits package.

NYU is an equal opportunity employer. We work in New York because we value diversity.

Please send a CV and cover letter to mrockman@nyu.edu. We aim to fill this position before May.

"mrockman@nyu.edu" <mrockman@nyu.edu>

OhioStateU CropGeneticsGenomics

https://hcs.osu.edu/about-us/open-faculty-positions
Position: Genetics, Genomics, and Breeding of Horticultural Crops

Rank: Assistant Professor

Departments: Horticulture and Crop Science

Description

The Department of Horticulture and Crop Science in The College of Food, Agriculture and Environmental Sciences (CFAES) at The Ohio State University (OSU) seeks applicants for a 9-month tenure-track faculty position at the Assistant Professor level in genetics, genomics, and breeding of cultivated plants, whose scholarly interests focus on the programmatic field of applied genetics and genomics. The successful candidate should have demonstrated skills in developing an extramurally funded, innovative research program pertinent to the breeding of cultivated plants, such as germplasm development, seed biology and/or trait analyses. Applicants who focus on vegetable, small fruit, or medicinal plant breeding and link fundamental and genome-wide questions with applied outcomes to cultivar improvement are particularly encouraged to apply.

Candidates should have a strong record of research accomplishments and a commitment to teaching. The successful candidate is expected to contribute to the undergraduate and graduate education with at least 2 classes (5-7 credit hours) per academic year to support the department's core teaching program and to engage in new interdisciplinary teaching collaborations with other departments. There will also be opportunities to develop new courses based on the candidate's expertise.

This position is located at OSU's main campus in Columbus, Ohio. OSU has a large and strong plant research community, with outstanding interdisciplinary undergraduate and graduate programs and excellent core facilities on the main campus in Columbus and the Ohio Agricultural Research and Development Center (OARDC) in Wooster. Collaborations are facilitated by multiple Centers and Programs including the Food Innovation Center, Center for Applied Plant Sciences, and Translational Plant Sciences Graduate Program.

Candidates are expected to have a Ph.D. degree in plant breeding and genetics or related field, evidence of scholarly productivity in publications, university teaching experience, demonstrated excellence in communication, experience in interdisciplinary collaborations, ability to obtain extramural funding, and interest and/or experience in mentoring or working with members of underrepresented populations.

Contact: Ginger Koozer koozer.2@osu.edu

full description: https://hcs.osu.edu/sites/hcs/files/imce/images/Genetics%20Genomics%20and%20Breeding%20of%20horticultural%20Crops%20pd.pdf

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

OmahaZoo GeneticsResAssist Bioinformatics

Genetics Research Assistant

Job Description:

Applications are invited for a Genetics Research Assistant (Bioinformatics) in the Conservation Genetics Department at Omaha's Henry Doorly Zoo & Aquarium (http://www.omahazoo.com/careers/). The Bioinformatics Technician will participate in ongoing molecular and bioinformatics research. Importantly, the technician will utilize sophisticated computer programs during the analysis of datasets from next generation sequencing. This technician will develop high-throughput solutions to improve scalability of in-house genetic interpretation tools. The technician will be responsible for developing a pipeline for genomic analyses and database monitoring and maintenance. Early-career technicians will have the opportunity to gain on-the-job training regarding bioinformatics.

Duties:

The Bioinformatics Technician will confer with research staff to determine data needs and programming requirements and to provide assistance with database-related research activities. Importantly, the technician will utilize bioinformatics techniques to analyze or manipulate large datasets from next generation sequencing in a Unix/Linux environment. Sophisticated computer programs will be used to gather, analyze, and track data regarding biological functions or characteristics in order to gain a better understanding of computational evolutionary biology and comparative genomics. The technician will develop high throughput solutions to improve scalability of in-house genetic interpretation tools. Duties will involve writing or modifying existing computer code to perform analysis of high-throughput sequencing data including the analysis of whole genome sequencing data. The technician will need to develop a pipeline for genomic analyses as well as a system for monitoring database performance and perform any necessary maintenance, upgrades, or repairs. Ultimately the technician will complete statistical analyses and prepare reports on related findings. Additionally, the technician will assist multiple research projects as well as routine maintenance within the laboratory. Participation in group activities such as grant preparation and reporting, literature searches, and manuscript writing efforts will be expected. All laboratory staff will maintain cleanliness and sanitation while complying with safety procedures in their employed laboratories. Duties will include non-research activities such as facility maintenance and outside work.

Qualifications:

Ideally, the Bioinformatics Technician will have a thorough knowledge of bioinformatics, molecular genetics and related techniques, and have a good understanding of biological sciences. Experience in bioinformatics and next-generation sequencing is highly preferred. A Bachelor's degree in the Genomics, Genetics, Bioinformatics or Computer Science or related field is required. Ideal candidates will have proficiency in Linux, Bash, and scripting experience in Python (BioPython), Perl (BioPerl), Julia, or R. C, C++, PHP, and Java competency is a plus. Knowledge of parallel processing, and computing would be beneficial.

Start Date:

Flexible, ideally mid-April 2017

Application:

Please visit http://www.omahazoo.com/careers/ for full job description and to formally apply. Applicants should include a cover letter describing previous experience, a resume, and the names and contact information for a few professional or academic references. Please also send a copy of your application materials to Dr. Edward Louis Jr. at genetics@omahazoo.com

Review of applications will begin immediately and will continue until the position is filled.

From: Genetics Department Sent: Wednesday, March 1, 2017 9:24:10 AM To: Golding@McMaster.CA Subject: EvolDir -for announcement section

Postdoctoral Fellow - Madagascar Biodiversity Genomics

Job Description:

Omaha's Henry Doorly Zoo & Aquarium Department of Conservation Genetics (OHDZA-CG) based in Omaha, Nebraska, is seeking a post-doctoral researcher with interest/expertise in the generation and analysis of next-generation sequencing data of lemurs, tortoises, and other taxa from Madagascar.

Duties:

The successful applicant will be proficient in the construction genomic libraries and in solution hybridization methodologies for high throughput sequencing as well as all relevant analysis of large datasets, and manage next-generation sequence workflows. This individual will be responsible for development, implementation, and support of software applications related to variant detection and interpretation from high-throughput experiments involving multiple species of lemurs, tortoises, and taxa from Madagascar. Assembly of whole genomes is in-progress, but will likely require additional analysis pertinent to specific research projects. Interested candidates

— / —

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

---

QueenMaryU EvolNeurobiology

Lecturerin Neurobiology Schoolof Biological and Chemical Sciences QueenMary University of London

We'relooking to hire a lecturer in Neurobiology to join our Nanchang joint programme. The search is for a world-class neurobiologist in the broad sense, including researchers with interests in comparative/evolutionary neurobiology, evolution and physiology of neuropeptide signalling, behavioural neurobiology, and developmental neurobiology.

Thepost involves teaching for 4-6 weeks in Nanchang, China, and the setting up of a leading research group at QMUL's campus in London.

Deadline:17 March 2017

Fulldetails: http://bit.ly/QMUL-Neurobiology Mariodos Reis

Lecturer@QMUL mariodosreis.wordpress.com

m.dosreisbarros@qmul.ac.uk

SouthDakotaStateU WildlifeConservation

Assistant Professor/Wildlife Ecologist (50% teaching, 50% research/full time, 9 month position) Department of Natural Resource Management South Dakota State University

The Department of Natural Resource Management (NRM) at South Dakota State University invites applications for a full-time, tenure-track, 9-month position (50% teaching, 50% research) at the rank of Assistant Professor with expertise in Wildlife Ecology and Management, beginning fall 2017. We seek a talented colleague who will contribute to teaching excellence in the department and will build an external, competitively-funded research program with an emphasis on wildlife ecology and management in natural and/or captive environments. The candidate should address fundamental questions about ecology and life histories of wildlife to inform and benefit current issues and future management practices.

The NRM Department houses undergraduate programs in Ecology and Environmental Science, Natural Resource Law Enforcement, Rangeland Ecology and Management, and Wildlife and Fisheries Sciences. The department has 21 faculty (20 tenured/tenure-track and 1 non-tenure-track) and 4 Extension Field Specialists. It is also the home of the USGS South Dakota Cooperative Fish and Wildlife Research Unit (3 research scientists). In addition, the department is promotion and tenure home for 3 faculty members in the Geospatial Sciences Center of Excellence. The department's faculty have diverse teaching, research, and extension appointments. Departmental research facilities include the Oak Lake Biological station (30 minutes from campus), the Wildlife Research Unit (one mile from campus) for captive field studies that include enclosures for animals, field plots, aquatic research space, storage and upkeep of field research gear (research space and lab space is housed in various buildings at this unit). The department is also home to the C.A. Taylor Herbarium, fully databased South Dakota State Aquatic Invertebrate Collection, bird, amphibian, reptile, and mammal collections.

RESPONSIBILITIES: The successful candidate will be expected to be active in research and contribute to a nationally recognized applied wildlife research program which includes competing successfully for extramural sources of funds, and publishing in national/international peer-reviewed journals. The candidate will contribute to advising and professional development of M.S. and Ph.D. students. The candidate will teach courses in principles of wildlife management and introductory biometry as well as contribute to team-taught courses in natural resource management field techniques and habitat conservation and management. Participation in service associated with wildlife management is expected, including involvement with professional organizations and student organizations affiliated with the department.

MINIMUM QUALIFICATIONS: The successful candidate will have completed a Ph.D. in a research area germane to Wildlife Ecology, Wildlife Management, or closely related discipline prior to March 2017. The successful candidate will have strong quantitative skills and a publication record commensurate with experience. Candidates must be enthusiastic scientists and teachers with the ability to develop excellent communication skills (verbal, written, and electronic). Applicant must demonstrate the ability to work cooperatively with other faculty, extension field specialists, state and federal wildlife biologists, producers, and other clientele.

PREFERRED QUALIFICATIONS: We prefer a candidate with post-doctoral experience and an established record of external competitive grant funding with accompanying publications in nationally/internationally recognized peer-reviewed journals; experience in grant budget management; demonstrated interest and experience in teaching; and an expert skill set in addressing questions pertinent to the ecology and life histories of wildlife that inform and benefit current issues and future management practices.

SALARY: Commensurate with qualifications and experience.

UNIVERSITY/COMMUNITY: South Dakota State University, founded in 1881, is the state's land grant institution and its largest and most comprehensive institution of higher learning. It is a designated Carnegie Research University-High Intensity and is an APLU Innovation and Economic Prosperity University. Current enrollment is approximately 12,500 students. SDSU and the NRM department offer research and teaching opportunities at four field stations, two with equipped laboratories and long-term data sets. Additionally, the SDSU Functional Genomics Core Facility facilitates interdisciplinary gene function research and training.

South Dakota State University is located in Brookings, on the east-central border of South Dakota. Brookings is an economically vibrant and welcoming college town of approximately 23,000 residents. The city has an excellent

— / —

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

---

Tromso Norway FishEvolution

*Associate Professor in fish biology- *UIT The Arctic University of Norway**

The research group for genetics at the The Norwegian College of Fishery Science < http://en.uit.no/om/enhet/forsiden?p_dimension_id=88166 > (NCFS), UiT The Arctic University of Norway (in beautiful Tromsø), seeks a motivated, collaborative, and ambitious scientist for a permanent position as Associate professor in fish biology (12 month's salary). The position is a part of a strategic commitment to strengthen the capacity for aquaculture related research at NCFS/UiT.

Research emphases of the position include two or more of the following themes: 1) Biological and genetic interactions between aquaculture and natural systems; 2) Biological and genetic effects of climate change for the aquaculture industry; 3) Evaluation and assessment of biodiversity in relation to area planning and sustainability of aquaculture activities; 4) Conservation biology with focus on maintaining local adaptations in aquaculture and natural systems/species. Responsibilities also include teaching fish biology, 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 fish biology and a strong research record.The ideal candidate should have a background and experience in classic fish biology, modern molecular taxonomy, and principles related to speciation in fishes. Knowledge of the use of environmental DNA in studies of biodiversity, population genomic methods, fish anatomy and/or fish physiology, as well as documented ability to secure external funding for research are an advantage. Experience in teaching relevant subjects is needed.

Please read the full posting for complete details pertinent to the position at: https://www.jobbnorge.no/en/available-jobs/job/135757/associate-professor-in-fish-biology-at-the-faculty-of-biosciences-fishery-and-economics, and follow the application instructions therein.

For further information, please contact: Group leader, Associate Professor Kim PrÃbel, kim.praebel@uit.no, Professor Ragnar L. Olsen, ragnar.olsen@uit.no, or head of department Kathrine

TveiterÃ¥s, kathrine.tveiteras@uit.no._ _ < http://www.life.illinois.edu/ccheng/ >

c-cheng@illinois.edu

UCalgary ComputationalBiol DeadlineExt

The University of Calgary invites applications for a full-time Professor faculty position with Tenure to join a dynamic group of investigators as part of the Biomedical Engineering (BME) Calgary Initiative. BME Calgary brings together researchers from multiple faculties across campus with external stakeholders, including government and industry participants, to benefit from a team-based approach for tackling current and future BME challenges in Alberta, Canada and worldwide. Biomedical Engineering at the University of Calgary involves more than 100 faculty members across six faculties, with current annual research funding exceeding $45M. The university has made significant investments in Biomedical Engineering to date, including the allocation of four Tier 1 and five Tier 2 Canada Research Chairs. Engineering Solutions for Health: Biomedical Engineering is one of six strategic research priorities of the University of Calgary. A strong culture of collaboration and cross-disciplinary research excellence is enabled by significant research infrastructure located in multiple centers across campus. The university operates a multi-faculty Biomedical Engineering Graduate Program, hosts a Biomedical Engineering-related NSERC-CREATE training program, and delivers a Biomedical Engineering Specialization in conjunction with 6 engineering majors in the Schulich School of Engineering. Please visit our website (http://www.ucalgary.ca/bme) for more information.

The successful candidate will be placed in a joint position, depending on their background, in the Faculty of Science, and/or Schulich School of Engineering, and/or Cumming School of Medicine. Applicants must have earned a Ph.D. in biomedical engineering or equivalent. It is expected that the successful candidate will provide evidence of:

- Outstanding and innovative world-class research which has made a major impact in their field - International recognition as a leader in their field - Superior track record in attracting and supervising graduate students and postdoctoral fellows - Strong service and/or leadership record - Excellent teaching record The applicant should propose an original, innovative research program of the highest quality. The successful candidate will be nominated for an NSERC Tier 1 Canada Research Chair, created by the Government of Canada to position Canada as a world leader in research. This Chair will directly support the successful candidate's research program.

Exceptional candidates must have a research focus in Biomedical Engineering with particular interest in:

- Development of computational biology or bioinformatics algorithms, tools or software for the analysis of large multivariate datasets, including biosensor, imaging, human genome, transcriptome, epigenome, microbiome, or physiome - Biological network behaviors, such as gene regulatory networks, protein interactions, and epigenetic effects, as approached through experimental, computational, and analytical methods. - Big data/machine learning methods, analytics, visualization, software and modeling applied to emerging areas of biomedical engineering or biological science - Development and application of precision diagnostic and therapeutic technology, through computational, genomic, and pervasive data sensing and collecting techniques

The successful candidate will join an established multidisciplinary and inter-Faculty team of biomedical engineers, scientists, clinicians, nurses and veterinarians whose fundamental research activities, support collaborative health-related research problems. The position provides an opportunity to establish a vigorous, sustainable, externally-funded research program, contribute to teaching and graduate student supervision, and participate in leadership of BME related research, education and service. This is an excellent opportunity to build and develop an innovative research program within a dynamic and collaborative environment. A competitive salary and an attractive start-up package will be provided.

The University of Calgary is committed to supporting Biomedical Engineering as a strategic research theme within the context of the Eyes High vision to become one of Canada's top 5 research universities. The successful candidate possesses the attributes and desire to lead research initiatives within this interdisciplinary area at the University of Calgary, to build on current strengths, to develop strategy for future growth and promote program development combined with both student engagement and experience.

The Schulich School of Engineering is committed to fostering diversity through cultivating an environment where people with a variety of backgrounds, genders, interests and talents feel welcome and included. In 2016, the Schulich School of Engineering was recognized with the KNOVO Award of Distinction to honour school's commitment to diversity and equity.

— / —

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

UCatolicadeChile 2 EvolutionaryBiol

The Pontifica Universidad Católica de Chile invites applications to two tenure-track Assistant Professor positions, affiliated to the Department of Ecology at the Faculty of Biological Sciences.

*Description of the Department of Ecology and the Positions *

The Department of Ecology (DECOL) includes 20 researchers some of which have joint appointments with the Faculty of Physics, Engineering, and Political Sciences & Geography. The DECOL is a diverse department that includes among its members, researchers from Argentina, Australia, USA, France, México and Uruguay. They participate in both undergraduate (Licentiate in Biology and Marine Biology) and graduate teaching (PhD in Biological Sciences / Ecology). In terms of research, the DECOL has identified interdisciplinary science as one of its priorities and the analyses of the impact of Global Change upon biodiversity and sustainability as its major cross-cutting themes.

In general, we are searching for creative, productive and collaborative scientists whose work addresses fundamental questions in Ecology and/or Evolution that fit within the general profile of DECOL outlined above. However, for one of these positions priority will be given to applicants with the capacity to develop a research program in the area of Ecology and/or Evolution of marine organisms, specifically macroalgae.

*Position Responsabilities: *

The selected applicants should:

1) develop an independent research program, and lead research projects in the area of Ecology and/or Evolution with emphasis in any level of ecological integration (from molecules to ecosystems) and using experimental, correlational and/or theoretical approaches.

2) generate interactions with researchers within DECOL, and potentially, from other Departments of the Faculty of Biological Sciences and/or other Faculties within the University.

3) He/she should be prepared to teach courses at the undergraduate and graduate level and according to the needs of DECOL.

Application requirements:

Applicants should have a PhD and Postdoctoral experience. At least one of these should be in Ecology or Evolution. The applicant should show capacity to carry out an independent research program and obtain competitive, extramural funding. Teaching experience at undergraduate and/or graduate level is desirable.

Selection Criteria:

Academic trajectory and quality of the scientific production of the applicant

Experience in interdisciplinary work

Academic references

Potential for integration into the academic activities of DECOL and the Faculty of Biological Sciences.

Application Process:

§TO APPLY, COMPLETE THE APPLICATION FORM *AVAILABLE UPON REQUEST FROM: *Prof. Xavier Figueroa, Academic Secretary of the Faculty of Biological Sciences. E- mail: secretaria.academica@bio.puc.cl

§Request at least three letters of recommendation that make reference to the trajectory and academic credentials of the candidate. These should be sent directly to the Academic Secretary of the Faculty of Biological Sciences at the following E- mail: secretaria.academica@bio.puc.cl

Applicants should send all application materials by E-mail to Prof. Xavier Figueroa, Academic Secretary, Faculty of Biological Sciences, Pontificia Universidad Católica de Chile, E- mail: secretaria.academica@bio.puc.cl

*Deadline for Applications: April 27, 2017 at 17:00. *

– Sylvain Faugeron

UMI3614 Evolutionary Biology and Ecology of Algae Departamento de Ecología Facultad de Ciencias Biologicas Pontificia Universidad Catolica de Chile Av. Bernardo O'Higgins 340 Santiago - Chile +56-223 54 26 47 sfaugeron@bio.puc.cl

Sylvain Faugeron <sfaugeron@bio.puc.cl>

UCentralFlorida CoastalDiseaseEvolution

Sustainable Coastal Systems Cluster

Coastal Disease Ecologist

Applicants for an Assistant/Associate Professor position in coastal disease ecology must have a Ph.D. from an accredited institution, relevant post-doctoral training, and show a demonstrated ability, or strong potential, to maintain a vigorous, extramurally-funded research program. Preference will be given to candidates whose research interests focus on the ecology of infectious diseases in natural coastal ecosystems (not aquaculture systems) and who uses innovative approaches, including modeling and empirical field and laboratory work, to address fundamental ecological or evolutionary questions about any coastal host-pathogen systems regardless of taxonomic group. Potential research questions may include, but are not limited to, the ecology of emerging coastal diseases and the intersection of disease and anthropogenic stressors, such as climate change, pollution, habitat loss, or invasive species. Strong interdisciplinary skills, experience working at the interface of social and biological sciences, strong quantitative and excellent communication and interpersonal skills are essential. Proven track records of publication in refereed journals of high quality and acquisition of research funding are highly desirable.

Candidates must apply on-line at http://-www.jobswithucf.com/postings/46716 (Position #38660) and attach the following materials: a cover letter, curriculum vitae, teaching statement, research statement, and contact information for three professional references. In the cover letter candidates should address their background in their discipline and should identify the department(s) for their potential tenure home. In the research statement candidates should include descriptions of their successful interdisciplinary research collaborations and how their current and future research can contribute to the cluster's overall interdisciplinary objectives.

The search committee will review applications on an on-going basis until the position is filled.

The University of Central Florida, with more than 63,000 students, has grown in quality, diversity, and reputation in its first 50 years and is committed to being inclusive and diverse by building a faculty who are a reflection of the students they teach. For more information about this position please contact the Sustainable Coastal Systems Cluster search committee Chair, Dr. Graham Worthy at CoastalCluster@ucf.edu

Anna Savage <Anna.Savage@ucf.edu>

UEdinburgh BioinformaticsHairColour

Dear All,

There is an exciting opportunity to study the genetics of hair colour in humans at the MRC-HGU at the University of Edinburgh. We are looking for a driven bioinformatian/statiscal geneticsts that would like to work within a very multidisciplinary team. Further information can be found at https://www.vacancies.ed.ac.uk/ Vacancy reference 038148. Please, address informal inquires to Albert Tenesa < albert.tenesa@ed.ac.uk> or Ian Jackson ian.jackson@igmm.ed.ac.uk.

Best wishes, Albert

TENESA Albert <Albert.Tenesa@ed.ac.uk>

UGreifswald EvolutionaryMathematics

Dear readers of EvolDir,

At the institute of Mathematics and Computer Science at the University of Greifswald (Germany), we have an open permanent position (50 %, TVL-13) as a teaching and research assistant with teaching obligations of 7 hours per week (note that one of our research focusses is biomathematics, which is why I am posting this job offer here, too! Please see below for more details). The application deadline is the 1st of April. The aspired research area is not restricted, so we are open to interested applicants of all areas of mathematics as long as he or she fits into the general research areas of our institute. Note that the main focus of this position is teaching. For more details on the position, please visit our website: https://www.uni-greifswald.de/universitaet/-information/stellenausschreibungen/oeffentlichestellenausschreibungen/wissenschaftliches-personal/-institut-fuer-mathematik-und-informatik-17sa05/ Note that the website also contains an English version (you just need to scroll down).

We accept applications via mail or via email (one single PDF please).

Greifswald is a beautiful town located at the Baltic Sea, a popular holiday region. Student life here is vibrant, and the university has a long tradition - in fact, it is one of the oldest universities of Europe. Our institute is one of only a few places in Germany where students can study biomathematics already at an undergraduate level, which is why this study program attracts students from all over Germany. Therefore, the majority of our institute's students study biomathematics, but we also have pure mathematics students as well as students who want to become maths teachers. However, our institute also does a lot of teaching for students of other subjects that are not directly linked to our institute, e.g. students of natural sciences.

Kind regards,

Mareike Fischer

–

Prof. Dr. Mareike Fischer

Biomathematics and Stochastics

Ernst-Moritz-Arndt-University Greifswald Institute for Mathematics and Computer Science Walther-Rathenau-Str. 47 17487 Greifswald Germany

Tel: +49 (0) 3834 864643

Mareike Fischer <email@mareikefischer.de>

UGreifswald SciAssist18Mnths EvolutionVibrationalCommunication

Scientific assistant position - Vibrational Communication in Mantophasmatodea

Application deadline: 20.03.2017

A scientific assistant position (65% TV-L E13, 18 months contract) is available at the University of Greifswald, in the group of Dr. Monika Eberhard, Zoological Institute and Museum, General and Systematic Zoology (chair: Prof. Gabriele Uhl). The successful candidate will join the DFG-funded research project

Vibrational Communication Signals in Mantophasmatodea: Species Recognition, Sexual Selection, and Population Differentiation.

We are investigating the vibrational signals of Mantophasmatodea-species that occur in several populations at different localities in the Western Cape Region, South Africa, a biodiversity hotspot. Variability of vibrational calls and morphological characters, as well as genetic diversity using microsatellite markers will be investigated in populations of the same species to reveal the present state of population differentiation of Mantophasmatodea in the Western Cape. Behavioural experiments will be conducted to assess the decisive cues within vibrational communication calls, which are used for species recognition. Field studies (in cooperation with University of Cape Town) will allow for optimized seminatural laboratory setups. This will provide insight into the role vibrational communication might play for population differentiation and speciation in Mantophasmatodea. Further possibilities of research include anatomical studies, behavioural trials or phylogenetic analyses. The position is open for early stage researchers (postgraduate or postdoc) or very dedicated Bachelor with Honours.

The highly motivated candidate will use genetic analyses (microsatellites, sequencing), morphological methods (light microscopy, SEM, microCT), and behavioural trials (video, laser-doppler-vibrometry). Strong background in at least one of these skills would be advantageous.

Requirements: - Either B.Sc. degree + Honours, M.Sc., or higher, in Biology (Zoology, Ecology, Behavioural or Evolutionary Biology) - Strong background in Evolutionary Biology - Practical experience in at least two of the following areas: DNA-analysis (microsatellites, sequencing), behavioural studies (field and laboratory; preferably with invertebrates), Ecology (population dynamics), morphology (SEM, micro-CT) - Very good English skills (written and spoken) - Willingness to stay in South Africa for a longer time period (ca. 6-8 weeks) - Experience in analysis programs for the required datasets and statistics are an advantage

The position is available from April 2017 until filled.

For more information please contact Monika Eberhard and send your application in one PDF (letter of motivation, CV, contact details of two academic referees, and summary of final thesis) with the reference number 17/Wi09 via email to

Universität Greifswald, Zoologisches Institut und Museum Dr. Monika Eberhard J.-S.-Bachstraße 11-12 17489 Greifswald

E-mail: monika.eberhard@uni-greifswald.de

Monika Eberhard <monika.eberhard@uni-greifswald.de>

UGrenobleAlpes 3yr EvolutionaryDataScience

Université Grenoble Alpes invites applications for a 3-year junior research chair in Data Science for Life Sciences starting in October 2017. The objective is to recruit an outstanding candidate motivated in developing or applying data science methodology to Life Sciences.

We are looking for candidates that will accelerate the uptake of data science analytics in Life Sciences. Through his/her research activities in one of the research groups at Université Grenoble Alpes, the successful candidate should demonstrate the benefits of data science and modern data analytics in Life Sciences. His/her research applications in Life Sciences can concern bioinformatics, epidemiology, evolutionary biology, and neuroscience. His/her activities at Université Grenoble Alpes should in particular help demonstrating how open-source scientific software or new collaborative approaches (e.g. hackaton, data challenges) contribute to successful interdisciplinary research. Candidates for this position should be either - a life scientist with experience in applying modern data analytics in his/her field and/or experience in open source scientific software development. - or a data scientist (computer science, machine learning, optimization, signal processing, statistics) with a proven track record in biological applications and a strong motivation for advancing knowledge in Life Sciences.

The research chair is funded by the Grenoble Alpes Data Institute, which promotes applications of data science in several scientific domains. The Grenoble Alpes Data Institute seeks to leverage methodological advances in machine learning, signal processing, statistics, and computational sciences to provide actionable tools for addressing concrete scientific challenges. Research must be conducted in one of the labs affiliated with the Grenoble Alpes Data Institute (https://goo.gl/wzzmQx).

Interested applicants should send their application to application-datachair@univ-grenoble-alpes.fr before May, 21st 2017. Before application, we encourage candidates to contact contact-datachair@univ-grenoble-alpes.fr to discuss about potential labs where the research project can be carried out. Application files should include a two page research project, a curriculum vitae, and a list of publications and references. Short-listed candidates will be interviewed in June.

Annual gross salary ranges from 30,000 to 35,00 euros. The position is endowed with equipment and travel resources. The research chair will be employed by Université Grenoble Alpes that is a major player in higher education and research in France (http://www.univ-grenoble-alpes.fr/en/). The position is located in Grenoble, which is a university town located in a beautiful alpine environment.

Michael BLUM CNRS Senior Researcher Tel: +33 (0)4 56 52 00 65 michael.blum@imag.fr http://-membres-timc.imag.fr/Michael.Blum/ Michael Blum <michael.blum@univ-grenoble-alpes.fr>

UKansas ResAsst Drosophila ComplexTraits

A research assistant position is available in my lab at KU to work on flies and complex traits. The position will involve both fly work and molecular biology (including approaches using high-throughput sequencing), and might be great for someone interested in gathering more research experience before going to graduate school. Experience with flies would be a plus, but isn't required. The formal announcement, and links to the institutional employment website are provided below. Feel free to email me with any questions. Stuart Macdonald (sjmac@ku.edu)

A research assistant position is available in the Macdonald lab in the Department of Molecular Biosciences at KU. The Macdonald group explores the genetic basis of complex phenotypic variation using Drosophila as a model system. The successful candidate will help maintain a panel of fly lines, supervise and carry out large-scale phenotyping screens, and generate next-generation sequencing libraries for various genomics applications. We are looking for an enthusiastic and organized individual who is willing to learn new skills, and has excellent oral and written communication skills. Previous research assistants in the Macdonald group have undertaken independent research projects and been authors on research publications from the lab. The position is funded through a multi-year NIH grant and has an anticipated start date of July 1, 2017 (although this is negotiable).

Required qualifications include a Bachelor's degree in biology (or a related field) by the time of appointment, and some experience with laboratory molecular biology techniques. Prior experience with flies and/or next generation sequencing library construction would be a plus.

For a complete announcement and to apply online, go to https://employment.ku.edu/staff/8336BR Please direct any questions about the position to Stuart Macdonald (sjmac@ku.edu).

A complete online application includes the following materials: A CV/resume, a cover letter outlining relevant experience, and contact information (phone/email/address) for three referees. Initial review of applications begins 1 May 2017 and will continue until the position is filled.

The University of Kansas prohibits discrimination on the basis of race, color, ethnicity, religion, sex, national origin, age, ancestry, disability, status as a veteran, sexual orientation, marital status, parental status, gender identity, gender expression, genetic information and retaliation in the University's programs and activities. Access to information regarding equal opportunity and diversity worksite posters is available at http://www.humanresources.ku.edu/policies_procedures/category_details/index.aspx?category=8 or you may contact 785-864-4946 or employ@ku.edu for alternate access options. Any inquiries regarding the nondiscrimination policies should be directed to: Executive Director of the Office of Institutional Opportunity and Access, IOA@ku.edu, 1246 W. Campus Road, Room 153A, Lawrence, KS, 66045, (785)864-6414, 711 TTY.

Dr. Stuart J. Macdonald Department of Molecular Biosciences 4043 Haworth Hall 1200 Sunnyside Avenue University of Kansas Lawrence KS 66045

office: 785-864-5362 lab: 785-864-5777 fax: 785-864-5321 email: sjmac@ku.edu web: FlyRILs.org

"sjmac@ku.edu" <sjmac@ku.edu>

UMaryland Tech InvertPopGenetics

Faculty Research Assistant

The University of Maryland Center for Environmental Science (UMCES) is seeking applicants for a technician position in the Plough Laboratory (http://geronimo.hpl.umces.edu/lplough/)at the Horn Point Laboratory (HPL) in Cambridge MD.

The position will be a full-time Faculty Research Assistant (BA or BS degree required) in support of grant-funded projects related to the population genetic analyses of estuarine and marine animals, particularly invertebrates (blue crabs, oysters). Laboratory duties will include tissue preservation and DNA extraction, environmental DNA sampling, quantitative PCR and analysis, and preparation of genomic libraries for next-generation sequencing (NGS). The technician may also be involved in field work (local) collecting animals on small craft or from shore, and will assist with finfish care and shellfish culturing at HPL. Finally, the technician will be expected to assist in data organization/analysis and preparation of reports/manuscripts.

Required skills include: laboratory experience in molecular genetics (e.g. PCR, agarose gel electrophoresis, DNA extraction; ideally in a research setting), handling of large datasets in spreadsheets, and familiarity/experience with biostatistical analysis using software such as R or similar. A willingness to be in the field for short periods of time (day trips) and to manage live cultures of larvae or fish is also required. Ideal applicants will have some prior experience preparing next generation sequencing libraries and some familiarity with UNIX/Linux for command-line processing of genomic data sets. Some experience with animal culture or care (especially larval shellfish culture) is also a plus. Funding is currently available for two years with additional time possible dependent on future funding. Salary will be commensurate with experience and a comprehensive benefits package is available.

Email a single PDF containing a letter of interest, resume or curriculum vitae, and contact information for three professional references to: (ploughfrajob@umces.edu), Subject: Faculty Research Assistant.

To receive full consideration, apply by March 31, 2017.

UMCES is an AA/EOE institution. Individuals with disabilities, veterans, women, and minorities are encouraged to apply.

Wennett Jones-Johnson, M.S. Program Management Specialist-HR UMCES Horn Point Laboratory 410.221.8241

Wennett Jones-Johnson <wjonesjohnson@umces.edu>

UppsalaU QuantitativeGeneticsGenomics

Tenure track position as Assistant Professor in Quantitative Genetics and Genomics at Uppsala University

Department of Ecology and Genetics, program in evolutionary biology, Evolutionary Biology Centre

World-leading research in the interface of ecology, evolution and genomics is conducted at the Evolutionary Biology Centre of Uppsala University. One particular area of strength is genomic research geared towards evolutionary processes such as speciation, local adaptation and evolution of fitness traits. It remains a challenge to connect genotype and phenotype in research aimed at understanding the genetic basis of traits in natural populations. Genome scans and genome-wide association studies (GWAS) are important tools in this respect and build on large-scale genomic analyses of population samples. The genetics of quantitative traits is closely associated to such research. We are now seeking a highly competitive candidate with interests and competence combining quantitative genetics and genomics.

The position is for four years and can then be tenured. Specifically, 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. Applicants who have obtained a doctoral degree or achieved the equivalent competence in seven (7) years or less prior to the end of the application period will be given priority.

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. The university has 40,000 students, 7,000 employees and a turnover of SEK 6,5 billion. The Evolutionary Biology Centre is one of the strongest research environments at Uppsala University, as for example illustrated by hosting a large number of ERC grantees, including at Starting, Consolidator and Advanced levels.

You are welcome to submit your application no later than 2 April 2017, UFV-PA 2017/364. Please use the following link to get further information about the position including how to apply http://uu.se/en/about-uu/join-us/details/?positionId=139356 For further information about the position, please contact professor Hans Ellegren, hans.ellegren@ebc.uu.se

Hans Ellegren <hans.ellegren@ebc.uu.se>

UPrague PlantEvolutionSystematics

Assistant Professor of Plant Evolution and Systematics Department of Botany, Charles University, Prague, Czech Republic Deadline: 31st March 2017

We are seeking an experienced independent researcher to join the academic staff of the Department of Botany, Faculty of Science, Charles University, Prague. The successful candidate will become member of the Vascular Plant Unit, a research team addressing a broad range of evolutionary questions in vascular plants such as evolution through genome duplication, breeding system variation, phylogenomics and phylogeography incl. potential practical implications for plant conservation and biodiversity assessment (taxonomy).

We offer - a full institutionally-funded position for min 3 years in rates markedly exceeding the average Czech salary - academic career growth and perspective of extension into a long-term contract - support for establishment in foreign language environment - support for submission of Czech and international grant proposals - work in an inspiring academic environment in daily contact with students in the historical centre of the UNESCO heritage site of Prague

We require - strong scientific track record including regular publications in international journals - full scientific independence, enthusiasm for team building and collaboration - experience in grant project management - moderate teaching load (the extent negotiable) - supervision of Master and PhD students

Desirable but not required - experience from a working environment outside the Czech Republic - experience with evolutionary research in vascular plants (e.g., population genetics, genomics, phylogenomics) - good background in statistical analysis of ecological and/or molecular data - teaching experience in the academic environment

Please, send your CV, list of publications, contact of two referees, a short motivation letter specifying your major motivation how to contribute the research environment at the Dept. of Botany (https://botany.natur.cuni.cz/-cevnate), legalized copy of PhD certificate by March 31st 2017 to the Faculty of Science, Charles University, Albertov 6, CZ-12843, Prague. For questions regarding the position requirements and the application submission process please contact the Head of the Vascular Plant Unit at the Department of Botany, Dr. TomáÂ¹ Fér (tomas.fer@natur.cuni.cz).

The position is available from September 2017, with negotiable starting date.

– Tomas Fer tomas.fer@natur.cuni.cz +420-221951661

tomasfer@natur.cuni.cz

UTromso FishEvolution

Associate professor in fish biology

Application deadline: April 30^th 2017

The research group for genetics at The Norwegian College of Fishery Science (NCFS), UiT The Arctic University of Norway (in beautiful Tromsø), seeks for a motivated, collaborative, and ambitious candidate for a vacant permanent position as Associate professor in fish biology.

The position is expected to emphasize two or more of the following research themes: 1) Biological and genetic interactions between aquaculture and natural systems; 2) Biological and genetic effects of climate change for the aquaculture industry; 3) Evaluation and assessment of biodiversity in relation to area planning and sustainability of aquaculture activities; 4) Conservation biology with focus on maintaining local adaptations in aquaculture and natural systems/species. The position is assigned teaching within fish biology, as well as supervision of master and PhD candidates. The successful candidate is further expected to contribute with outreach and dissemination, at UIT and to the industry and society in general.

Qualification requirements: Doctoral degree in fish biology and scientific merits beyond this. Experience within modern fish biology and within fish taxonomy and diversity. It is advisable to have experience within classic fish biology, an understanding of principles related to speciation in fishes and experience with modern molecular taxonomy. Knowledge of population genomic methods, the use of environmental DNA in studies of biodiversity, fish anatomy and/or fish physiology is an advantage. The applicant must have a strong track-record, documented ability to receive external funding for research, and experience in teaching relevant subjects.

As this posting is a short summary of the complete job posting, please read the full posting and apply via: https://www.jobbnorge.no/en/available-jobs/-job/135757/associate-professor-in-fish-biology-at-the-faculty-of-biosciences-fishery-and-economics Kim PrÃbel, Ph.D. Associate Professor Group leader, Genetics 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

UUtah Genetics LabManager

The Chow Lab in the Department of Human Genetics at the University of Utah School of Medicine is hiring a new technician or lab manager:

Apply here: https://utah.peopleadmin.com/postings/-61290 Target Start Date June/July.

Job Summary: Assists with the daily operations of the lab, including but not limited to, training new members, assisting in lab projects, maintenance, and ordering. There will be an opportunity to perform independent research. Previous experience with genetics and molecular biology or biochemistry is strongly preferred. Experience with Drosophila maintenance is a plus, but not required. Must be willing to work with mice. The laboratory of Dr. Clement Chow in the Dept. of Human Genetics is seeking a lab technician to aid in projects related to genetic variation and disease. Research in the Chow lab utilizes the fruit fly Drosophila, mouse, and cell culture. The candidate will work independently and together with other researchers in the lab to study specific aspects of how genetic variation impacts human disease. Please see www.ChowLab.org for more details.

Qualifications: Bachelor's degree in biology, chemistry, or other scientific disciplines in a related field or equivalency required; knowledge of complex laboratory techniques, equipment, terminology, materials and substances. Skilled in the use of laboratory equipment, ability to create and analyze statistical calculations and prepare reports required; and demonstrated human relations and effective communication skills also required. OSHA training and certification in animal care and use or the willingness to complete the certification may be required by some departments.

Responsibilities: 1. Works together with researchers in the lab to further the goals of specific projects. 2. Operates and maintains laboratory equipment and microscopes. 3. Troubleshoot basic molecular biology procedures 4. Ensures that the lab is stocked and supply orders are placed when needed. 5. Maintains the Drosophila lab stocks 6. Maintains a detailed and well organized laboratory notebook. 7. May assist in mouse colony maintenance 8. May assist in supervision of undergraduate researchers 9. May engage in independent research 10. May coauthor research papers and publications

Clement Chow <cchow@genetics.utah.edu>

Virginia DirectorResearchCenter Bioinformatics

Director,Center for the Study of Biological Complexity Richmond,Virginia Rank:Associate to Full Professor

VCULife Sciences seeks a Director of the Center for the Study of BiologicalComplexity (CSBC). VCU Life Sciences is a Universityâmatrix organizationthat promotes Life Sciences Research and Education. CSBC has beenin existence for 15 years and offers undergraduate and graduate degreesin bioinformatics. Administrative offices are on the Monroe Park campus.Degree programs are Bachelor of Science in Bioinformatics, Master ofScience in Bioinformatics with a traditional thesis and a nonâdegreeoption (Professional Master's program). Doctoral students have a specializedtrack in the Integrative Life Sciences doctoral program, which alsooperates under VCU Life Sciences. The new director would be expected tobring their own research program, but also recruit a diversified set of juniortenureâfaculty, increasing the research portfolio with extramuralfunding and expanding enrollment in the existing degree programs.

VirginiaCommonwealth University is a major, urban public research universitywith national and international rankings in sponsored research. VCUis designated as a research university with very high research activity bythe Carnegie Classification of Institutions of Higher Education and is recognizedas a communityâinstitution by the Carnegie Foundation. VCUtakes great pride in its commitment to creating a campus community that embracesdiverse perspectives, cultures, experiences and people. Located in downtownRichmond, VCU enrolls more than 31,000 students in 226 degree and certificateprograms in the arts, sciences and humanities. Sixtyâof theprograms are unique in Virginia, many of them crossing the disciplines ofVCU's 13 schools and one college. Medical College of Virginia Hospitals andthe health sciences schools including the Schools of Medicine, Dentistry,Nursing, Pharmacy and Allied Health Professions comprise VCU MedicalCenter, one of the nation's leading academic medical centers. Today,VCU serves an integral role in the economic health of the city of Richmondand the region by educating the current and future workforce, advancingresearch, and enhancing patient care. VCU, its health system and otherrelated entities have assets of approximately $3.0 billion, which includes$840 million in endowment funds.

Responsibilities

- Represent the Center to Life Sciences, the University, and the community (local,regional, and national).

- Provide scholarly leadership by maintaining independent research program andgraduate student mentorship.

- Supervise 10 fullâterm and tenured/tenureâresearch and teachingfaculty. Assign specific teaching and service responsibilities to faculty.

- Supervise fullâclassified staff members who run the Center for High PerformanceComputing (CHiPC).

- Assume primary responsibility for recruitment, retention, tenure and promotion,and compliance with university guidelines regarding faculty appointments.

- Negotiate and supervise the departmental budget.

- Grow enrollment in BNFO degree programs (B.S., M.S.) with over 120 graduateand undergraduate majors and a curricula comprised of 30+ courses.

- Build on existing crossâinitiatives to strengthen linkages acrosscampus.

RequiredQualifications

- Doctoral degree in related discipline from an accredited university

- Ten years of experience in discipline

- Tenured faculty member at a research active institution.

- Demonstrated experience working in and fostering a diverse faculty, staff,and student environment or commitment to do so as a faculty member atVCU

PreferredQualifications

- Demonstrated commitment to undergraduate and graduate education

- Current federal research funding

- Demonstration of ability to recruit tenure track faculty and support research

- Demonstrated experiencein budget management

- Excellent leadership, communication and interpersonal skills

ApplicationProcess

Ifinterested, please apply online at https://www.vcujobs.com/postings/58027 tosubmit cover letter, application, CV, and a list of three references. Foradditional information, please contact Paul Fawcett, Ph.D. at paul.fawcett@vcuhealth.org.

Projectedstart date is July 1, 2017. This position offers a competitive salary,startâ, and relocation package.

VirginiaCommonwealth University is an equal opportunity, affirmative actionuniversity providing access to education and employment without regardto race, color, religion, national origin, age, sex, political affiliation,veteran status, genetic information, sexual orientation, genderidentity, gender expression, or disability.

RodneyJ. Dyer, PhD Departmentof Biology Centerfor Environmental Studies VirginiaCommonwealth University http://dyerlab.bio.vcu.edu

— / —

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

---

WSLBirmensdorf EnvironmentalGenomics

See job posting online and find link for uploading your application: https://apply.refline.ch/273855/0687/pub/1/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 Research Unit Biodiversity and Conservation Biology studies the diversity of life in its various forms, from genetic diversity to the diversity of species and ecosystems as well as their interactions. To strengthen our team in ecological genetics, starting July 1, 2017, or later, we are searching a

TENURE TRACK SCIENTIST IN ENVIRONMENTAL GENOMICS (80%?100%)

You are responsible for the design and execution of the studies on the interrelationship of genomic and environmental variation, focusing on forest trees, alpine plants and conservation-relevant animal species. Together with the group leader, you will acquire third-party funding at international and national levels. You will carry out these research projects in collaboration with technical staff, publish the results in high-ranking international journals and present them at international conferences. Contributions to applied research projects and outreach activities are also expected. You have a PhD degree in biology or environmental sciences, an excellent international reputation in the field and a strong background in ecological genetics and evolutionary biology. You are competent in the analysis of genomic and environmental data and their relationship, and provide skills in written and oral scientific publication. You are ambitious and highly motivated, demonstrate a high level of collaborative, interdisciplinary competence, and are experienced in guiding technical staff during molecular-genetic lab work.

Please send your complete application to Monika Lips, Human Resources WSL. Felix Gugerli, felix.gugerli@wsl.ch, and Rolf Holderegger, phone +41 (0)44 739 25 27 or rolf.holderegger@wsl.ch, will be happy to answer any questions or 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 Kuenzle, PhD Senior Scientist / Head "Ecological Genetics" Swiss Federal Research Institute WSL Research Unit Biodiversity & Conservation Biology Zuercherstrasse 111 CH-8903 Birmensdorf

SWITZERLAND

phone: +41-(0)44-739-2590 fax: +41-(0)44-739-2215 http://www.wsl.ch/info/mitarbeitende/gugerli/index=5FEN "felix.gugerli@wsl.ch" <felix.gugerli@wsl.ch>

Xishuangbanna TropicalBotanicalGarden ResearchPositions

I have several positions available for researchers keen to carry out some exciting research in a very healthy environment.

In my group, I have the following positions open at moment (1) 2 Positions of assistant or associate professor (2) 3 Postdoc positions Please forward this information to anyone who might be interested. The job advertisements are available at: http://english.xtbg.cas.cn/ju/ The call will be open until the positions are filled.

Best wishes, Harald

Prof Harald Schneider, PhD FLS 1. Xishuangbanna Tropical Botanical Garden, Centre for Integrative Conservation, Chinese Academy of Sciences 2. Department of Life Sciences Natural History Museum, London SW7 5BD, UK

erin.tripp@colorado.edu

Other

1000 Genomes TeachingTools 76
5000OmmenPrize EvolutionAndMedicine NominateYourArticle 76
Avian Plasma Progesterone levels 76
BloodCapillaries For DNA Extraction 76
Cairns Australia VolFieldAssist FairyWrens 77
Caymans YouPay MarineConservationFieldAssist . . 77
DukeU SummerInternshipOpportunity 79
DukeU SummerInternshipOpportunity 2 79
ESEB SpecialTopicsNetworks CallDeadlineMar31 . . 80
MaxPlanckInst Seewiesen 2Vol SexualSelectionParrots 81
Melbourne VolFieldAssist Mistnetting 81
PacBio Competition BombardierBeetle 82
PacBio Competition Dingo 82
PacBio Competition PinkPigeon 83
PacBio Competition SeaSlug 83
Phyloseminar FordDoolittle March28 84
Phyloseminar MartaCasanellas Apr26 84
PossibleGrants ForScienceExchange 85
Pyrenees VolFieldAssist PlantSpeciation 85
RohlfMorphometricsMedal CallForNominations 86
SocStudyEvol GradStudentCouncil 86
Software NextGeneration RAxML Released 86
SSB Grad Student Research Grant 87
Sweden VolFieldAssit AvianEvolEcol MayJune 87
ULausanne SIBVirtualSeminar LaurentExcoffier TODAY 88
ULausanne SIBVirtualSeminar LExcoffier Mar29 . . 88
USaskatchewan 4Interns GroundSquirrel 88
US NatlMedalScience CallNominations 89
Volunteer TeachingEvolutionInNepal 90

1000 Genomes TeachingTools

Hi All,

As a follow up to my previous request for any teaching tools using 1000 genomes in the classroom, the following noble souls shared their teaching resources with me. They have all agreed to be contacted if you are interested in their documents/ideas.

Vikram Chhatre vchhatre@uwyo.edu Daryn Stover dastover@asu.edu Max Taub taubd@southwestern.edu David Remington dlreming@uncg.edu

– Diane Ramos, PhD

Associate Professor Natural Sciences Department Daemen College 4380 Main St. Amherst, NY 14226

Duns Scotus 329 dramos@daemen.edu 716.839.8560

“dramos@daemen.edu” <dramos@daemen.edu>

5000OmmenPrize EvolutionAndMedicine NominateYourArticle

Nominations are open now for the

$5000

2016 Omenn Prize for the best article published in 2016 in any scientific journal on a topic related to evolution in the context of medicine and public health. Self nominations are encouraged. Deadline March 31, 2017. https://evolutionarymedicine.org/-funding-and-awards/gil-omenn-prize/ The prize will be awarded at the 2017 annual meeting of The International Society for Evolution, Medicine & Public Health, August 18-21 in Groningen, Netherlands. https://-evolutionarymedicine.org/2017-isemph-meeting/ The prize, provided by the generosity of Gilbert S. Omenn, will be awarded to the first author of the winning article. Authors are encouraged to nominate their own articles, but nominations of articles by others are also welcome.

Any relevant peer-reviewed article with a publication date of 2016 for the final version of the article is eligible, but the prize is intended for work that uses evolutionary principles to advance understanding of a disease or disease process. The prize committee will give priority to articles with implications for human health, but many basic science or theoretical articles have such implications.

The Prize Committee for this year is chaired by Grazyna Jasienska, and its members are James Bull and Antonis Rokas. Papers by committee members, their students and lab group members are not eligible, and articles by their co-authors or close associates are subject to special conditions. The winner will be invited to present a talk at the meeting of the International Society for Evolution and Medicine.

The firm deadline for nominations is March 31. Nomination instructions at the link.

https://evolutionarymedicine.org/funding-and-awards/-gil-omenn-prize/ Randolph Nesse <nesse@asu.edu>

Avian Plasma Progesterone levels

Dear All,

If you have used Enzo Life Sciences ELISA progesterone kits (product # ADI-900-011 or ADI-901-011) for avian plasma, could you please contact me? Compared to the published results of other enzyme immunoassays, I was surprised by the values returned after analyzing avian plasma samples for progesterone, even when plasma levels were diluted. I have had difficulty finding any published results in the literature using this exact ELISA kit and Enzo has not been able to assist me in this. Any help that you would be able to provide would be greatly appreciated.

Thank you, Misha

– Misha Blizard Ph.D. Candidate Ecology & Evolution University of Chicago blizard@uchicago.edu

misha.blizard@gmail.com

BloodCapillaries For DNA Extraction

Dear all,

I am looking for the best solution to efficiently collect blood from birds in the field (following venipuncture) for DNA extraction and subsequent Illumina sequencing. Glass capillaries in my experience are the most efficient means of collecting (as opposed to double-capped plastic capillary tubes, which tend to have lower capillary forces and leave back a lots of blood on the bird). However, I have trouble finding glass capillaries coated with EDTA rather than heparin.

1) Does anybody know a company producing EDTA-coated glass capillaries? 2) Does anybody have experience with Illumina sequencing from blood collected in heparinized tubes? (as heparin is supposed to inhibit e.g. PCR) 3) Any other tips about how to most efficiently collect blood following venipuncture?

Any help or comment would be highly appreciated.

Thanks a lot & best wishes, Reto

– RETO BURRI Department of Population Ecology, Institute of Ecology Friedrich Schiller University Jena Dornburger Strasse 159 D-07743 Jena, Germany Tel. +49 (0)176 272 155 08

// https://scholar.google.de/citations?user=xqB6K7kAAAAJ&hl=en // https://publons.com/author/420923/reto-burri#profile // https://twitter.com/Reto_Burri Reto Burri <reto.burri@uni-jena.de>

Cairns Australia VolFieldAssist FairyWrens

Avian volunteer field assistant - Lovely fairy-wrens, Australia

We are looking for one field assistant to help monitor a colour-banded population of Lovely fairy-wrens in Cairns, Queensland, Australia, for a research project on female ornamentation from University of Melbourne.

Time period: From August 25th to 25th September. Starting/ending date can be adjusted but needs to be around this time. Assistant is expected to stay a full month.

Location: Cairns region, Queensland, Australia. We will be based in Cairns city but travel to several sites in the area.

The applicant will have the opportunity to enjoy the unique wildlife of North Queensland and leisure time to visit Cairns, the Great Barrier Reef or the world heritage rainforests.

Duties: Censusing of colour-banded birds, searching for and monitoring nests, banding nestlings, behavioural observations while following birds, assisting in behavioural experiments and target mist-netting. After fieldwork video/photo analysis, data entry and other computer activities will occur. Working days are long, with early starts, six days a week.

Qualifications: Experience resighting colour-banded birds, following birds in dense canopy, nest-searching, bird handling skills, mist-netting, banding and behavioural observations. Must also be early riser, physically fit, able to work in extreme weather conditions (hot, humid, and occasional tropical rain), maintain a positive attitude and enjoy shared living conditions. Good knowledge of English is a must. Applicant must be able to work independently and have great hearing and vision. Enthusiasm, self-motivation, organisation, and a strong work ethic are a requisite.

Compensation: Free onsite accommodation is provided, but assistants cover travel to Cairns and their own food costs. The project will reimburse up to AUD$750 for the month towards receipted food and travel expenses (including airfare) to Cairns.

For more information contact: Ana Leitao (anamvleitao@gmail.com). To apply, please email a letter outlining previous relevant field research experience, availability and a CV including names and contact information for 3 referees.

anamvleitao@gmail.com

Caymans YouPay MarineConservationFieldAssist

To Whom This May Concern on EvoDir,

Please circulate this announcement to anyone whom you feel would be interested in The Central Caribbean Marine Institutes (CCMI) new Reef Research Experience during the summer of 2017. Apologies for any cross-postings.

CCMI is a US 501 C3 nonprofit organization, a UK charity (#1104009) and a Cayman Islands charity located on Little Cayman, Cayman Islands. As a remote tropical research, conservation, and education institution; we are aware of the discussions concerning internships, courses, experiences, etc. which are currently going on between all the list serves and welcome any professionally stated questions or comments regarding the cost or validity of research conducted during our programme.

~~~~~

The Central Caribbean Marine Institute - Little Cayman Research Station (CCMI - LCRC)

NEW Reef Research Experience (RRE) - Coral Reef Research and Spatial Ecology

APPLICATION DEADLINE MAY 1^ST, 2017

DO YOU WANT TO CONTRIBUTE TO CORAL CONSERVATION RESEARCH?

The CCMI - LCRC in the Cayman Islands is recruiting 15 junior research assistants for an exciting new coral reef and spatial ecology research experience for a two-week period during the summer of 2017. Junior Research Assistants (JRA's) will work alongside CCMI scientists to focus on answering exciting questions regarding two specific projects:

Project 1: Fish Herbivory and Productivity

This project is funded with the help of the Darwin Initiative, a UK government grant scheme that helps to protect biodiversity and the natural environment in developing countries and UK overseas territories. Junior research assistants will help assist with the expansion of our knowledge regarding the population dynamics of key herbivore species (such as parrotfishes and urchins) in the waters surrounding Little Cayman. Data collection regarding competition in the spatial ecology between reef fishes, algae, and stony corals will contribute to developing a biodiversity action plan for the Cayman Islands.

Project 2: Coral Reef Resilience and Restoration

This project is part of our Long-term Assessment and Monitoring Program (LAMP) funded by various organizations throughout the last 10 years. Junior research assistants will assist with monitoring the health of outplanted Acropora cervicornis colonies at 10 different restoration sites around Little Cayman, across various parameters such as: bleaching, disease, predation, and fragmentation. Junior research assistants will also be conducting benthic habitat surveys as part of our Coral Reef Resilience and Restoration Research program, where you will learn how to analyze data using a new program called CoralNET. CoralNet is a free platform developed by the University of California at Santa Barbara which utilizes artificial intelligence to analyze the composition of marine benthic communities. Data collected from this research will contribute to developing a restoration plan which will assist with the identification of optimal restoration sites around the Cayman Islands.

LENGTH OF PROGRAMME:

Session 1: July 14^th - 28^th, 2017

Session 2: August 16^th - 30^th, 2017 (If session 1 fills)

PROGRAMME OBJECTIVES:

- Establish a Cayman Islands CoralNet database of marine benthic communities

- Enrich our existing database of fish populations, stony coral cover, and algae density

- Create a Cayman Islands web-based field guide of key herbivores species

- Determine localized extinction risks of endangered corals by mapping coral restoration sites and assessing coral -health at our LAMP sites

EXPERIENCE YOU WILL GAIN: Minimum of 15 + research dives (weather permitting)

- Knowledge of coral reef ecology; including Caribbean coral, algae, and fish identification workshops

- Skills in underwater field research methods

- Working directly with endangered coral species (specifically Acropora cervicornis and Acropora palmata)

- Instruction on creating an experimental design, data collection, and data analysis

- Analyzing coral reef images using image analysis software (CoralNet, ArcGIS, and AgiSoft) to construct photo-mosaics and underwater maps to aid in habitat restoration techniques

*CCMI will issue a Certificate of Completion of 80 hours in Coral Reef Research and Spatial Ecology at the completion of the reef research experience.

REQUIREMENTS:

We seek a to fill 15 junior research assistant positions over a 14-day period during the summer of 2017. Requirements include:

- 18+ years of age

- Open Water Diver with at least 20 logged dives (Advanced certification or higher preferred)

- Insured through DAN

- Current enrollment in an undergraduate programme with a focus in Marine Science, Biology, Environmental Science or a related field (or a recent graduate)

- Must be physically fit to work long days in the sun and on the water

— / —

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

DukeU SummerInternshipOpportunity

Duke University: AEOP summer internships - Biomechanics of Ultrafast Movements

The Patek Lab in the Biology Department at Duke University is recruiting one undergraduate student researcher through the US Army Educational Outreach Program (AEOP) during the summer of 2017. The student will participate in projects examining fast, impulsive movements of animals in the natural environment. The focal systems for the project are trap-jaw ants. Responsibilities of the student researchers may include collecting study organisms from local habitats, obtaining high-speed videos of animals, analyzing high-speed videos using computer software, performing statistical analyses and scientific writing. The details of responsibilities and tasks will be determined based on mutual interests of the students and the mentors. There are also possibilities for the students to develop individual projects under our mentorship.

We are looking for motivated, reliable students who are excited about having first-hand research experience at the intersection of biology and physics. Skills to perform the above-mentioned tasks are not required. We especially value students who are curious, hard-working and have an open mind about the possibilities of basic, scientific research. For more information about The Patek Lab, please visit our website: www.thepateklab.org DEADLINE: March 12, 2017, 11:59 pm. All applicants must submit two letters of recommendation, transcripts and must have maintained a cumulative GPA of at least 3.2 in their coursework. Applicants must also include a brief essay that explains their interest in this research and how it relates to their future goals.

TO APPLY: Please click the link below, and then: - Select "Apply" at the bottom of the page - Fill out the forms - At "Please select your 1st preference of URAP location," please select "BDUN53 Duke University"

Application link, through the Undergraduate Research Apprenticeship Program (URAP): http://www.cvent.com/events/2017-undergraduate-research-apprenticeship-program-urap-/event-summary-ccf8d39466294c8391d60121495cfcdf.aspx Chi-Yun Kuo Postdoctoral Associate Patek Lab, Duke University Personal website < https://www.chiyunkuo.com/ > https://pateklab.biology.duke.edu 919-613-0994

Chi-Yun Kuo <chi.yun.kuo@duke.edu>

DukeU SummerInternshipOpportunity 2

DukeUniversity: AEOP summer internships - Biomechanics of Ultrafast Movements

ThePatek Lab in the Biology Department at Duke University is recruiting one undergraduate student researcher through the US Army Educational Outreach Program (AEOP) during the summer of 2017. The student will participate in projects examining fast, impulsive movements of animals in the natural environment. The focal systems for the project are trap-jaw ants. Responsibilities of the student researchers may include collecting study organisms from local habitats, obtaining high-speed videos of animals, analyzing high-speed videos using computer software, performing statistical analyses and scientific writing. The details of responsibilities and tasks will be determined based on mutual interests of the students and the mentors. There are also possibilities for the students to develop individual projects under our mentorship.

Weare looking for motivated, reliable students who are excited about having first-hand research experience at the intersection of biology and physics. Skills to perform the above-mentioned tasks are not required. We especially value students who are curious, hard-working and have an open mind about the possibilities of basic, scientific research. For more information about The Patek Lab, please visit our website: www.thepateklab.org DEADLINE:March 12, 2017, 11:59 pm. All applicants must submit two letters of recommendation, transcripts and must have maintained a cumulative GPA of at least 3.2 in their coursework. Applicants must also include a brief essay that explains their interest in this research and how it relates to their future goals.

TOAPPLY: Please click the link below through the Undergraduate Research Apprenticeship Program (URAP): http://www.cvent.com/events/2017-undergraduate-research-apprenticeship-program-urap-/event-summary-ccf8d39466294c8391d60121495cfcdf.aspx - Select "Apply" at the bottom of the page - Fill out the forms - At "Please select your 1st preference of URAP location," please select “BDUN53 Duke University”

NOTE:The project description from the Army Research Office website was incorrect and has now been fixed. It should read:

“ImpulsiveBiological Performance in the Natural Environment”: Student will focus on impulsive performance in the natural environment. Applicants will need to have taken introductory biology and physics (mechanics). They must have an interest in working outdoors and with live animals.“

chi.yun.kuo@duke.edu

ESEB SpecialTopicsNetworks CallDeadlineMar31

REMINDER - ESEB SPECIAL TOPICS NETWORKS 2017

DEADLINE for proposals: 31 MARCH 2017

ESEB Special Topic Networks - Call for proposals

Small symposia, workshops and courses in various formats can perform functions complementary to those of the ESEB Congresses, allowing more focused interactions within specialist areas, forging new links between previously separate areas or fostering interdisciplinary and innovative ideas that merge specialized fields. One-off events can be valuable but the returns for connected series of events can be even greater. Therefore, ESEB invites proposals for Special Topic Networks (STNs) that will support dynamic and flexible series of small meetings and/or other networking opportunities in focused and currently active research areas.

Each STN will be funded for up to 6 years (subject to review after 2 and 4 years of operation) with an annual budget of up to 10 000 Euros. Two STNs were initiated in 2016 (see http://eseb.org/prizes-funding/-special-topic-networks/), two will be initiated in 2017 and then further STNs will be initiated every other year. The format of these STNs is up to their organisers and innovative ideas are encouraged. All fields of evolutionary biology are eligible. Applicants should provide a proposal with the following components:

1) a description of the research area to be targeted, showing why it is timely to address it in this way and outlining the expected benefits to the field from the STN (max. 1000 words), 2) a plan for the first two years of operation of the STN and an outline of activities over the remaining years (max. 500 words), 3) the names and affiliations of the proposed organisers, with brief (max. one page) CVs, and 4) a budget, with brief justification, for the STN activities proposed for the first two years.

Applicants should also identify an institution that is prepared to open an account in which the funds can be deposited and managed by the applicants. ?Overheads? will not be paid to this institution but reasonable direct administrative costs will be eligible. Funding for each 2-year block will be subject to approval by the STN Committee, established by Council, following receipt of a report of activities in the preceding 2 years. The institution managing funds will be asked to provide a certified statement of expenditure to accompany the report. The principal criterion for renewal will be evidence that the funding provided had been used to further interaction in the topic area.

Applications should be sent to the ESEB office email (office@eseb.org) as PDF files by 31 MARCH 2017. Proposals will be assessed by an independent STN Review Panel appointed by the STN Committee following the closing date and ensuring no conflict of interest by panel members. The STN Review Panel will make funding recommendations to Council. The result will be announced after the next Council meeting, at latest on 31 August 2017.

The principal criterion for selection of an STN will be its focus on an active area of research within the scope of evolutionary biology. Preference might be given to STNs that propose new connections between sub-disciplines or that focus on the resolution of current controversies. A score for this criterion based on part (1) of the application will account for 50% of the overall panel score. It is primarily for the proposers to demonstrate the need for an STN, the potential for it to stimulate progress and the activities that will enable the network to be effective. A typical STN might organise one small discussion meeting per year but it might also organise training events and its members might work together to generate resources or publications. Interaction among members might be fostered, between meetings, using social media, online discussion forums or similar. A score for the effective and innovative nature of the plans laid out in part (2) of the proposal will account for 25% of the overall panel score. The final 25% of the score will be based on the budget and adherence to the following guidelines:

1. A proposal should be supported by at least three ESEB members (membership in date on the closing date for applications), from at least two and typically three countries and taking gender issues into account, who commit to organising the STN for its duration (or

to finding appropriate replacements if forced to step down). A member should support no more than one proposal in a given application round and organisers of current STNs should not be proposers of new STNs. 2. STNs should organise at least one meeting in the non-Congress year following its inception and one in its final non-Congress year. Complementing these meetings with an innovative range of other activities is strongly encouraged. 3. STNs should consider offering a contribution to the ESEB Congress in

— / —

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

---

MaxPlanckInst Seewiesen 2Vol SexualSelectionParrots

MaxPlanckInst_Seewiesen. SexualSelectionParrotsVolunteers

Where: Tenerife, Spain When: beginning of June until end of August 2017 What: Volunteer field assistants - Parrot sexual selection

The Department of Behavioural Ecology and Evolutionary Genetics at the Max Planck Institute for Ornithology in Seewiesen, Bayern, Germany (see http://www.orn.mpg.de/2622/Department_Kempenaers), is seeking 2 volunteers to start working beginning of June and until the end of August 2017.

The volunteers will assist in the collection of courtship displays and egg-laying data. This work would be part of a project that aims to understand sexual selection in parrots of the world. The work will be done with captive animals that are held in the facilities of the Loro Parque Fundacion, located in Tenerife, Spain.

Work will include: . recording courtship displays . following up reproduction (sexual displays, mating, and egg laying) . maintenance of electronic equipment . setting up experimental equipment . data collection, entry, and management Successful candidates should have some experience with video-recording equipment. Experience with monitoring animals is desirable. Applicants should also be highly motivated and well organised, with capabilities of working both in a group and independently. Work will be 5-6 days per week. The working language at the Institute is English, so good knowledge of the language is required. A basic working knowledge of the Spanish language would be advantageous. Eligibility is restricted to EU students. The Max Planck Institute for Ornithology employs a dynamic, dedicated, and international group of researchers who are focused on exploring the fields of evolution, ecology, genetics, and neurobiology.

Benefits will include accommodation and flight ticket to Tenerife.

Please apply (including your CV and cover letter) via email to lcarballo@orn.mpg.de. Deadline: 05 May 2017 or until the positions are filled.

Luisana Carballo Department of Behavioural Ecology and Evolutionary Genetics Max-Planck-Institute for Ornithology Eberhard-Gwinner-Straße, House 8 82319 Seewiesen Germany

"L. Carballo" <lcarballo@orn.mpg.de>

Melbourne VolFieldAssist Mistnetting

We are looking for a volunteer field assistant to help with research on sexual selection and seasonal colour change in superb fairy-wrens (Australia). We need an experienced mist-netter, who is organised, respectful of animals and enjoys being outdoors. The work involves mistnetting for superb fairy-wrens (banding, blood samples, photography and spectral measurements) and behavioural observations of free-living birds. Work will be conducted from May-July and September-October 2017, in an open woodland approximately 1 hour east of Melbourne CBD. Our field site provides many opportunities to see unique Australian wildlife, including kangaroos, wallabys and echidnas. The park has diverse range of native birds, such as crested shrike-tits, sacred kingfishers, spotted pardalotes and red-browed finches. Food, accommodation and local travel expenses are compensated (to be discussed with the applicant). For more information please contact Alex McQueen: alex.mcqueen@monash.edu

"alexandra.mcqueen@monash.edu" <alexandra.mcqueen@monash.edu>

PacBio Competition BombardierBeetle

PacBio World's Most Interesting Genome competition to dispel the myths of intelligent design.

I am writing for your support and vote to help us win PacBio's World's Most Interesting Genome contest. My team aims to unravel the mysteries of the explosive bombardier beetle (Brachinus elongatulus), a species that repels predators with rapid-fire, precisely-aimed explosive discharges of a toxic chemical mix at over 100Â°C, earning them lead roles in media and culture. Yet the genomic basis of this extraordinary ability remains a mystery and bombardiers are currently being used as prototypes of "intelligent design."

We propose sequencing the genome of the bombardier beetle to generate a resource and model system for insect chemical biosynthesis, fill a major gap in our knowledge of the tree of life (>40,000 species!), and provide an unparalleled opportunity to advance understanding of biodiversity and evolutionary biology among the general public. Although their explosive delivery is well-documented, both scientifically and in the popular media (the combined view count for the top the five bombardier beetle YouTube videos is over 3 million!), the genetic basis, evolutionary history, and biosynthesis of defensive chemistry in bombardiers remain poorly understood. The first bombardier genome will allow us to understand the genetic basis of bombardier chemical production, solving a long-standing evolutionary puzzle.

Help Us Sequence The Explosive Bombardier Beetle Genome.

Tanya Renner (San Diego State University) and team's proposal to sequence the bombardier beetle's genome has been selected as one of 5 finalists to undergo a popular vote for the world's most interesting genome.

More than 200 proposals were submitted to the PacBio 2017 Plant and Animal SMRT Grant Program. The final winner is selected by popular vote. We need your VOTE on the PacBio website to help us win this competition: https://goo.gl/xv2lUH You can vote today and everyday through April 5th. You can use up to 3 email addresses to vote per day.

Learn more about our research and watch the bombardier beetle's CHEMICAL CANNON in action on this website: https://youtu.be/BWwgLS5tK80 Thank you for supporting Team Explosive Bombardier Beetle! Tanya #SeqtheBeetle

Tanya Renner, Ph.D.

Assistant Professor San Diego State University Department of Biology North Life Sciences 230 5500 Campanile Dr.

San Diego, CA 92182-4614 trenner@mail.sdsu.edu www.tanyarenner.org Tanya Renner <trenner@mail.sdsu.edu>

PacBio Competition Dingo

I'm writing to see if you could help me with a rather fun competition I'm trying to win. An aim of the project is to look at genes involved in unconscious selection (wolf to dingo) as comparted to artificial selection (dingo ancestor to domestic dogs)

Below is a brief from the University.

A proposal by Bill Ballard in Sydney to study the DNA of a two year old dingo called Sandy Maliki has been announced as one of five finalists in the World's Most Interesting Genome competition.

More than 200 international entries were received for the Pacific Biosciences SMRT Grant, which provides services worth about $20,000 to sequence the complete genome of a particularly fascinating or important plant or animal.

The general public will decide the winner and we need evolutionary biologists to vote on the competition website: http://www.pacb.com/smrt-science/smrt-grant/pag2017/dancing-dingoes/ Sandy's progress can be followed on theDancing with DingoesFacebook page:https://www.facebook.com/DancingwithDingoes/. And on utubehttps://www.youtube.com/watch?v=-FdhF6qwXNao A Sydney Morning Herald report can be found at: http://www.smh.com.au/technology/-sci-tech/unsw-dingo-dna-study-could-be-the-first-test-of-darwins-challenging-theory-20170315-guysi0.html Thanks

Bill

BABS/ UNSW Sydney Australia

Meet Sandy and share the page

VOTE NOW

w.ballard@unsw.edu.au

PacBio Competition PinkPigeon

Dear Members,

The endangered pink pigeon (Nesoenas mayeri) needs your vote in the Pacific Biosciences competition.

The pink pigeon is an endangered species that declined to less than 20 individuals in the 1970's and increased to near 400 individuals currently. Although this is a conservation success story, the pink pigeon is still endangered, threatened by invasive pathogens, and suffering from inbreeding depression.

We (University of East Anglia, Earlham Institute and our collaborators) hope to implement a genetic rescue approach to help the species recover, in particular to develop resistance to the pathogen Trichomona gallinae, which kills over 60% of young. Transcriptome sequencing using Iso-Seq would enable us to identify candidate genes that contribute to resistance so that we can begin screening the captive population for these alleles.

Your vote for the pink pigeon will help us identify the genes associated to resistance, which will help us to better inform captive breeding programmes to safeguard this important genetic variation and enable genetic supplementation of the wild population in the future. This research will also contribute to our understanding of the evolution of the avian genome and the evolution of immune gene regions.

Please vote at: bit.ly/seqthepigeon You can also tweets us at : #seqthepigeon

Thank you very much, Best wishes,

Camilla Ryan, Dr Matt Clark, Professor Cock Van Oosterhout

(If anyone would like further information please contact Camilla at camilla.ryan@earlham.ac.uk)

Camilla_ryan@hotmail.com

PacBio Competition SeaSlug

Dear colleagues,

We need your voice! 3 times a day! 3 weeks long!

Why?

Elysia timida is a brilliant sea slug. It incorporates chloroplasts (the energy-converting organelles inside the cells of plants) from its food algae and lets them continue photosynthesis, almost like a plant! The starch that the chloroplasts produce in the slug allows it to survive during longer periods of starvation.

To better understand how the slug does this, we would like to analyze the genome of Elysia timida, and have submitted a proposal to an international competition organized by PacBio (http://www.pacb.com). The winners get their proposed genome sequenced (with PacBio's latest SMRT technology) and assembled.

Our proposal has been selected by a group of experts from more than 200 project ideas. Now we have to compete against four other finalists.

That is why we need your vote!

How can you help us?

If you think that Elysia timida is an exciting animal and want to know why it has these special abilities, please go to the following website and vote for us:

http://www.pacb.com/smrt-science/smrt-grant/-pag2017/solar-powered-slug/ How does the election work?

Votes are counted daily for three weeks from 15^th March until 5^th April. So you can vote for us every day! And best of all, you can even vote for us three times each day if you use three different e-mail addresses (the name can stay the same). The proposal with the most votes will be the winner.

Learn more and watch this brief video about our project: https://youtu.be/UA7YdtayqlQ We hope for your vote(s)! Thank you for your help!

Your Elysia timida (E.T.) Team

#SeqtheSlug

Carola Greve, Ph. D. Zoological Research Museum Alexander Koenig Adenauerallee 160 53113 Bonn Germany email: c.greve@leibniz-zfmk.de phone (office):

++49 (0)228-9122-242

Greve Carola <C.Greve@leibniz-zfmk.de>

Phyloseminar FordDoolittle March28

Next on http://phyloseminar.org/ ...

Darwinizing Gaia W. Ford Doolittle Dalhousie University Tuesday, March 28, 2017, 10:00 AM PDT

Talks in this series have largely focused on population genetic and phylogenetic methods for reconstructing micro- and macroevolutionary patterns consequent from microevolutionary processes. When natural selection is invoked, it is generally assumed to operate through the differential reproduction of favored variants among populations of physical entities, be they genes, cells, organisms or (rarely) species. The Gaia hypothesis of James Lovelock, co-developed and vigorously promoted by Lynn Margulis in the 1970s, has been very popular with the lay public. But most mainstream Darwinists scorned and still do not accept the notion. They cannot imagine global biospheric stability being selected for at any of the above levels, and do not see the Earth's biosphere as part of a population of comparable global entities engaged in reproductive competition. Most philosophers of biology would similarly argue that any global homeostatic systems (if they exist) can be only "fortuitous byproducts" of lower-level selection. I will suggest that we look at the biogeochemical cycles and other homeostatic processes that might confer stability– rather than the individual organisms or "species" (mostly microbial) that implement them– as the relevant units of selection. By thus focusing our attentions on the "song", not the "singers," a Darwinized Gaia might be developed. Our understanding of evolution by natural selection would however need to be stretched to accommodate differential persistence, and our definition of reproduction would need to be reworked.

Frederick "Erick" Matsen, Associate Member Fred Hutchinson Cancer Research Center http://matsen.fredhutch.org/ ematsen@gmail.com

Phyloseminar MartaCasanellas Apr26

Next talk on http://phyloseminar.org/ :

Phylogenetic invariants: what are they and why should we care Marta Casanellas Rius Universitat Politècnica de Catalunya Wednesday, April 26, 2017, 10:00 AM PDT

It has been now thirty years since the introduction of phylogenetic invariants by Lake, Cavender, and Felsenstein. However, the use of phylogenetic invariants as a method of phylogenetic reconstruction has been in a dormant state for about 20 years; quoting J. Felsenstein in his 2004 book "invariants are worth attention, not for what they do for us now, but what they might lead to in the future".

During the last decade many efforts have been made by mathematicians to completely understand the structure and use of phylogenetic invariants. This has led to the characterization of different types of invariants for many different models: from the most simple Jukes-Cantor model to the general Markov model, and even mixtures of them and the coalescent. Most importantly, this has produced new and efficient methods of phylogenetic reconstruction for complex models. The use of invariants has also been used in model selection and has been crucial in proving the identifiability of parameters for certain models.

In this talk we shall introduce phylogenetic invariants, explain the main ideas that underlie the methods of phylogenetic reconstruction based on invariants and discuss the advantages and drawbacks of them.

– Frederick "Erick" Matsen, Associate Member Fred Hutchinson Cancer Research Center http://matsen.fredhutch.org/ Erick Matsen <ematsen@gmail.com>

PossibleGrants ForScienceExchange

Hi evoldir listers,

I'm excited to share with you that I have been selected as one of 78 international female scientists to take part in the second edition of Homeward Bound (http://homewardboundprojects.com.au/), a 10-year global collaboration of women working together to communicate climate science and gender equity on the world stage. I'm the only representative of Venezuela and the Caribbean in the program.

The Program covers 60% of the cost of my participation, and I need to raise the remaining funds (US$ 16,000). Raising funds from within Venezuela is a real challenge for me, since the currency exchange control established in 2003 by the government seriously limits Venezuelans to obtain any kind of foreign currency.

I'm writing to the list in order to ask information about grants or scholarships I could apply to get funds for my participation in this initiative.

Also, I will really appreciate if people could share my crowdfunding campaign in their social media. https://www.chuffed.org/project/adrianahumanes).

Thanks in advance!

Cheers

Adriana Humanes

– www.adrianahumanes.com https://www.researchgate.net/profile/Adriana_Humanes 0414-0221895

Adriana Humanes <adrihumanes@gmail.com>

Pyrenees VolFieldAssist PlantSpeciation

Nick Barton's group at the Institute of Science and Technology (IST) Austria requires volunteers to assist with field work on plant speciation in the Pyrenees (Spain) this coming summer (late May - early August).

The project: We are studying the evolutionary dynamics underlying species diversification in the genus Antirrhinum (snapdragons). A major focus of this research involves field work on natural hybrid zones between two subspecies with different flower colours. Most of the field work is contributing to a long-term pedigree project aimed at establishing a direct link from genotype to phenotype to fitness. With 20,000 samples collected over six generations (so far), this provides an exciting and powerful system to examine many outstanding questions in speciation and quantitative genetics in wild populations. We are seeking volunteers to assist with the field work, which involves working in teams mapping the location of individual plants (GPS), tagging and sampling them for leaves and flowers, measuring quantitative traits, phenotyping them for flower pigmentation and processing material for later DNA extraction. There may also be opportunities to be involved in other projects we are doing on plant-pollinator interactions, pollen fertility and community ecology surveys. Most of the work is outdoors, however we do spend some time indoors processing samples. The work is highly team orientated, typically in groups of 2-3 in the field and larger groups processing samples back at the research station. This is a great opportunity for anybody looking to obtain experience in field work relating to evolutionary biology, plant ecology and plant-animal interactions. You will also be part of a large multidisciplinary team including researchers from IST Austria (Vienna), John Innes Centre (Norwich, UK) and the University of Toulouse.

The field site is located near Ripoll in a beautiful part of the Pyrenees of North Eastern Spain (Catalonia). We stay in comfortable apartments overlooking a picturesque valley, with close access to hiking trails and small villages. All food, accommodation and travel (within Europe) are covered. However, we cannot offer any further stipend.

For these positions we are looking for hard working and enthusiastic biology students with a strong interest in working outdoors with plants. You must be meticulous with recording data and also be comfortable working as part of a team. Experience with field-based projects and plants is preferred but not essential.

We require assistance between late May and late July. Depending on the year and the plants, we may extend our time into August. Length of stay is flexible but a minimum stay of 3 weeks is required.

Please send any questions to the email address below. How to apply? By the closing date of April 7th, please send a statement of your background, CV, why you are interested and the length of time you would be available via email to maria.clara.melo@ist.ac.at

Best regards,

Dr. Maria Clara Melo Hurtado Postdoctoral Researcher mmelohur@ist.ac.at Barton Group IST Austria Am Campus 1 Klosterneuburg 3400

Maria Clara MELO HURTADO <maria.clara.melo@ist.ac.at>

RohlfMorphometricsMedal CallForNominations

2017 CALL FOR NOMINATIONS

The Rohlf Medal

The Rohlf Medal was established in 2006 by the family and friends of F. James Rohlf to mark his 70th birthday. He has been a longtime Stony Brook University faculty member and is currently Emeritus Distinguished Professor in the Department of Ecology and Evolution, and Research Professor in the Department of Anthropology.

Recipients of the Rohlf Medal will be recognized for excellence in their body of work on the development of new morphometric methods or for their applications in the biomedical or biological sciences, including evolutionary biology, population biology, physical anthropology, developmental biology, neurobiology, computer sciences and medicine. The term 'morphometrics' is intended to include high-dimensional pattern analyses of biological shape, especially those that analyze shape in a comprehensive way, or of covariation of shape with other variables. The award can recognize advances in the mathematical or statistical theory underlying morphometric methods, new software that implements or visualizes new methods, or specific new biological findings that rely crucially on contemporary morphometric methods and represent major advances.

Candidates for the Rohlf Medal may be self-nominated or nominated by others. They must possess a Ph.D. degree or the equivalent.

The winning candidate must agree to attend the award ceremony in person in order to accept the Rohlf Medal and then deliver the award lecture.

Nomination packages should include, (1) a description of the body of work (not to exceed two pages) on which the candidacy is based, (2) reprints of no more than three relevant papers and/or software products, (3) a curriculum vitae, and (4) three letters of support.

Nominating packages should be uploaded to the Rohlf Medal website (http://life.bio.sunysb.edu/ee/-rohlf_medal/apply.html) and received by 5 pm, EST, 15 July 2017 to be assured of full consideration.

The successful candidate will receive the Rohlf Medal and a cash prize at Stony Brook University, planned for October 24th, 2017. She or he will deliver a lecture that is appropriate for a broad audience, ranging from the exact sciences to the humanities, concerning the morphometric methodology, software, or findings for which the Rohlf Medal was awarded.

Benedikt Hallgrimsson <bhallgri@ucalgary.ca>

SocStudyEvol GradStudentCouncil

The Society for the Study of Evolution is looking for three students to join the 2018 cohort of the Graduate Student Advisory Council. The GSAC represents student interests to SSE Council and facilitates interaction among students and between students and mentors. Brief applications are due April 15. Please see the website (http://www.evolutionsociety.org/index.php?module=-content&type=user&func=view&pid=44) or email GSAC@evolutionsociety.org for more information.

"kobie003@umn.edu" <kobie003@umn.edu>

Software NextGeneration RAxML Released

Dear Community,

We have released next generation RAxML, a total redesign of RAxML that should be better, faster, more stable, and more scalable.

The code is available here:

https://github.com/amkozlov/raxml-ng/releases/-tag/0.1.0 and you can find pre-compiled binaries here:

https://github.com/amkozlov/raxml-ng/releases/-download/0.1.0/raxml-ng_v0.1.0b_linux_x86_64.zip
Alexis

– Alexandros (Alexis) Stamatakis

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

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

SSB Grad Student Research Grant

The Society of Systematic Biologists (SSB) Graduate Student Research Awards assist students in the initiation (first two years) of their systematics projects and in the collection of preliminary data to pursue additional sources of support (e.g., Doctoral Dissertation Improvement Grants from the National Science Foundation) or enhance dissertation research (e.g., by visiting additional field collection sites or museums). Awards will range between $1000 - $2000 and approximately 15 awards will be made.

APPLICATION DEADLINE: All application materials are due on April 30, 2017 by 11:59 Eastern Standard Time.

** HOW TO APPLY **

Submit all materials via the SSB website: http://www.systbio.org/graduate-student-research-awards.html The application materials required are:

+ a curriculum vitae

+ brief research proposal including objectives, methods, significance, and schedule

+ budget ($2,000 limit) and budget justification

+ two letters of recommendation.

Please see the SSB website for further details about the aplication materials.

** ELIGIBILITY **

Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications. Previous awardees may not re-apply, but previous applicants who were not selected for funding are encouraged to re-apply.

Systematics is interpreted broadly to include questions below and above the species level, molecular and morphological approaches, and issues of pattern and process. Funding is not limited to any particular aspect of research, but rather is available for field, museum/herbarium, and/or laboratory work.

** CONTACT **

If you have any questions, please contact the Chair of the SSB Awards Committee (Dr. Tracy Heath: ssb.awards.director@gmail.com).

ssb.awards.director@gmail.com

Sweden VolFieldAssit AvianEvolEcol MayJune

Volunteer field assistant/internship in avian evolutionary ecology

PERIOD: 1.5-30.6.2017 LOCATION: Gotland, Sweden

PROJECT Maternal effects play a key role in shaping offspring development and are a source of phenotypic variation. Understanding the proximate mechanisms underlying maternal effects is crucial. I am looking for a volunteer field assistant/intern to a collaborative project on the role of maternal (egg) hormones shaping offspring development and fitness in the collared flycatcher (Ficedula albicollis). The work will be conducted in May and June in a nest-box population on the island of Gotland, Sweden. It is also possible to make part of the data collection into an intern project.

DUTIES The field assistant/intern will be conducting nest-box monitoring and capturing, ringing and measuring chicks/ adult collared flycatchers, together with the rest of the team (international). Potentially also blood-sampling. The field work will include long days (sometimes in bad weather) and work during weekends, thus the candidate needs to be prepared for that.

QUALIFICATIONS Suitable candidates should be hardworking, independent and organized, possess good communication skills and fluent English. Candidates should have a valid driving lisence. Experience in field work with birds, and bird handling/ringing is a definite asset.

WE OFFER We will train the volunteer/student for the fieldwork and bird handling. Travel costs (from Europe) and costs of accommodation (room shared with another assistant/student) will be covered. The candidate will join an enthusiastic team of researchers and students (French, Finnish, Taiwanese). The study populations are located on the beautiful island of Gotland!

If you are interested, please contact me asap and include your CV and a short motivation letter.

Suvi Ruuskanen (suvi.ruuskanen@utu.fi), Section of Ecology, Department of Biology, 20014 University of Turku.

Suvi Ruuskanen, researcher, Academy research fellow Section of Ecology Department of Biology 20014 University of Turku, FINLAND

Mobile +358503256547

Suvi Ruuskanen <skruus@utu.fi>

ULausanne SIBVirtualSeminar LaurentExcoffier TODAY

Dear all,

Please find here a gentle reminder regarding today's speaker, Laurent Excoffier. Please note that the seminar's title has now changed to:

Demographic inference from NGS data: Application to humans and chimpanzees

This seminar will take place in Lausanne, but as always will be broadcast here: https://collab.switch.ch/-sib-cbss/ Looking forward to seeing you there live or on remote.

Best wishes, Diana

"Diana.Marek@sib.swiss" <Diana.Marek@sib.swiss>

ULausanne SIBVirtualSeminar LExcoffier Mar29

Dear all,

We are pleased to announce the next speaker at the SIB Swiss Institute of Bioinformatics Virtual Computational Biology Seminar Series:

Laurent Excoffier, Institute of Ecology and Evolution, Department of Biology, University of Bern & SIB Genomic insights into the settlement of Australia by modern humans Wednesday 29 March 2017 at 16:00 - Genopode Auditorium A - UNIL campus

The seminar will be broadcast live for those unable to attend it physically (https://collab.switch.ch/sib-cbss/). For more information about these seminars as well as the upcoming speakers list and previous screencasts, please visit the SIB virtual seminar series webpage: http://-www.sib.swiss/training/virtual-seminars-series Important: If you want to remain informed about our upcoming seminars, please subscribe to the dedicated mailing list:http://lists.isb-sib.ch/mailman/listinfo/sib-virtual-seminars Looking forward to seeing you all there.

Best regards, Diana Marek

– *Diana Marek, PhD *Vital-IT - Training & Outreach * **SIB | Swiss Institute of Bioinformatics* Quartier Sorge - BÃ'timent Genopode - CH 1015 Lausanne - Switzerland t +41 21 692 40 77 - f +41 21 692 40 65 New email: Diana.Marek@sib.swiss www.vital-it.ch - www.sib.swiss/training

"Diana.Marek@sib.swiss" <Diana.Marek@sib.swiss>

USaskatchewan 4Interns GroundSquirrel

Internship Description: We are looking for 4 interns interested in taking part in a field ecology project on Columbian ground squirrels. Positions will begin on May 15, 2017 and will finish on Aug 31, 2017. The project investigates the ecology of Columbian ground squirrels. As a member of the study, interns will be involved with monitoring the phenology (when animals emerge from hibernation), reproduction and survival of individuals. Fieldwork will involve live-trapping and handling of animals, radio-telemetry, behavioural observation and assistance with the measurement of physiological (metabolism) traits on free-ranging animals. This is an excellent opportunity to gain training and experience working with a collaborative research team on a long-term study of a wild mammal. Opportunities for independent research projects are also available.

All fieldwork is carried out in the spectacular Rocky Mountains of southwestern Alberta, Canada, home to some of the most majestic wildlife in North America. Interns will have the opportunity to interact with, and learn from, other researchers working with ground squirrels on a diversity of projects in behavioural and population ecology. Additionally, a number of other researchers in the area are studying a range of species, from insects to large mammals.

International applicants: We welcome applications from all individuals. If applicants are not Canadians or permanent residents, there is the opportunity to enter Canada and complete the internship as a Visiting Research Student. To be eligible for this program, you must be an undergraduate student, a graduate student, or be in between degrees (e.g., following graduation from a bachelors degree and looking to pursue graduate school). As part of this program, applicants will be registered at the U of S in a non-credit activity and it is expected that you will gain a demonstrable educational benefit from being involved. We are particularly interested in applicants who wish to use this opportunity to pursue an independent research project. Applicants are eligible for this program for a maximum of 6 months per 12 month period. Application forms and information are available at http://grad.usask.ca/admissions/alternate-applicants/visiting-research-student.php If you are interested in this program, please contact us (contact details below) and we will guide you through the process.

Skills Required: These positions are best suited to applicants with interests in ecology, evolutionary biology, wildlife, field biology, and/or physiological ecology. As evidence of this, applicants must either be enrolled in, or have graduated from, a relevant discipline. Successful applicants will need to be able to cope under these field conditions (including periods of time spent camping), enjoy the outdoors, be up-beat, positive, responsible and work well as a member of a team. Evidence of these abilities (gained, for example, through previous involvement on field projects or extended back-packing trips) is expected.

Terms of Employment: Salary is not provided as part of these positions. Accommodation and food are provided. Volunteers are required to provide for their own travel to Saskatoon, Saskatchewan. Travel between the field station and Saskatoon is provided.

If you wish to apply for one of these posts then please send a CV with a cover letter and contact details for three references (with e-mail addresses), by email to Jeff Lane (contact info below) ASAP. Applications will be evaluated as they are received. To ensure full consideration, please apply right away.

Contact:

Dr. Jeff Lane

jeffrey.lane@usask.ca

Department of Biology

University of Saskatchewan

http://www.lanelab.ca "Lane, Jeffrey" <jeffrey.lane@usask.ca>

US NatlMedalScience CallNominations

Dear Colleagues:

One of the most important and gratifying aspects of participating in the scientific community is the nomination of colleagues for honorary awards in celebration of their exceptional contributions to one of our fields. I am sending this email today to urge you to recognize one of your peers by submitting a nomination for the 2017 National Medal of Science.

This premier award for American scientists and engineers – considered by some as the US equivalent of the Nobel Prize – was established by the 86th Congress in 1959. It is the highest recognition our Nation can bestow for outstanding cumulative contributions to knowledge or sustained, impactful work in the fields of engineering, chemistry, physics, biology, mathematics, and behavioral and social sciences. Conferred by the President of the United States during a ceremony at the White House, the Medal has been awarded to approximately 500 pioneering individuals. The National Science of Medal program is administered by the National Science Foundation (NSF) in conjunction with the Executive Office of the President.

Please nominate colleagues and peers for this prestigious honor who have extraordinarily advanced the scientific enterprise. Nominations and three letters of support must be submitted to NSF by April 7, 2017. If you have any questions, please contact the Program Manager for the National Medal of Science at nms@nsf.gov or by phone at 703-292-8040. For more information, please visit the National Medal of Science website at http://www.nsf.gov/od/nms/medal.jsp . I look forward to celebrating new honorees with you in 2018.

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

France Córdova <director@nsf.gov>

Volunteer TeachingEvolutionInNepal

Dear Sir-

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

We are looking a long term volunteer to serve in rural areas of Nepal to teach primary level students in one of the Government school. The volunteer teacher may choose teach science(including evolution), English, Math or their subject of interest starting from April 1 or later, 2017.

The school has not any other source of funding to support the teacher at the moment. The upcoming teacher may come with their own support(some philantrophic or own). Living cost here is expected to be less than 50 U$$/Month.

You may choose to live in Tamang community (learn their ethnic 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.

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>

PostDocs

ArizonaState PopulationGenetics 91
AustralianNationalU StatQuantGenetics 91
CWilliamMary ButterflyPopGenetics 92
DTUAqua Denmark AnalysisOfEnvironmentalDNA 92
DukeU SpeciationGenomicsBioinformatics 93
HarvardMedSchool DiseaseGenomics 94
IndianaU Bloomington HostSymbiontCoevolution . 95
InstitutPasteur Paris KlebsiellaEvolution 95
IowaStateU 2 MolCytogeneticsBioinformatics 96
LudwigMaximiliansU ButterflySpeciation 96
MaxPlanckInst Ploen Adaptation BiologicalClocks 97
MNHN Paris EvolutionDrosophilaSuzukii 98
Montpellier SelectionDetection 99
NewYorkU EvoDevo 100
NHGRI-NIH Bethesda BioinformaticsEvolGenomics 100
NorthCarolinaStateU ComputationalEvolModeling 101
Omaha Nebraska MadagascarBiodiversityGenomics 102
Paris EvolutionaryAndEnvMarineGenomics 103
Paris EvolutionaryEnvironmentalGenomics 104
RockefellerU EvolutionaryGenomics 105
RoslinInst StaticsticalGenetics 105
SaintLouisU EvolInsectCommunication 105
SmithCollege 2 AmoebaeCiliates 106
SouthAfrica eDNA 107
Tampa Florida ModelingCancerEvolution 107

UAdelaide PhylogeographicsBioinformatics 108
UBirmingham AdaptiveEvolution 109
UCalifornia SanDiego PDF Tech YeastExptEvol . . 109
UCambridge BacterialGenomicEpidemiology 110
UCambridge EvolutionaryNeurobiology 111
UCambridge FloralEvolution 111
UCLondon ExcellenceFellowships 112
UFlorida HumanEvolGeneticsEpigenetcs 112
UHalle EvolutionaryBehaviour 113
UIdaho BiomedicalModeling 114
UKansas DrosophilaComplexTraits 114
ULeiden AntibioticResistance 115
ULeuven PDF0rPhD Bioinformatics 116
UmeaU ProteinEvolution 116
UMinnesota BiologyEducation 116
UNebraska PopulationBiology 117
UOslo DevelopmentalBiologyEvolution 118
UOtago NZ GenomicsParasiticMindControl 119
UQueensland QueenslandUTech MarsupialEvol . . . 119
USheffield Speciation 120
USussex PopGenomics 120
UTennessee Knoxville Phylogenetics 121
UValencia Spain VirusSocialEvolution 122
UVermont EvolutionaryEcologicalGenomics 122

ArizonaState PopulationGenetics

The Jensen Lab at Arizona State University is hiring a postdoc in the area of computational population genetics.

Briefly, research in the lab includes the development of population genetic theory and statistical inference approaches, as well as the analysis of large-scale genomic datasets from both natural and experimental populations. Further information regarding current research themes, as well as recent lab publications, may be found at: http://jjensenlab.org

Applications should include a cover letter briefly describing research interests, a CV, as well as contact information for two references - and should be emailed to jeffrey.d.jensen@asu.edu prior to April 30. Start date is flexible.

Jeffrey D. Jensen Professor Arizona State University School of Life Sciences Center for Evolution & Medicine

“jeffrey.jensen@epfl.ch” <jeffrey.jensen@epfl.ch>

AustralianNationalU StatQuantGenetics

*** Postdoctoral Fellow, Australian National University, Statistical/Quantitative Genetics ***

The ANU-CSIRO Centre for Genomics, Metabolomics and Bioinformatics (CGMB) is seeking up to two associate Postdoctoral fellows (Academic Level A4) to be appointed in the ANU Research School of Finance, Actuarial Studies and Statistics (RSFAS). The CGMB combines cutting-edge technologies and principled data science to catalyse biological advances, with an emphasis on transformational agriculture. RSFAS is the home of statistics at the Australian National University and is comprised of a dynamic team of academics focused on achieving excellence in research and teaching.

Successful candidates will be recent PhD graduates in statistics, bioinformatics, computational biology or a related field looking to further develop their research potential with leading academics. They should have the skills and experience to develop and apply statistical methodology in a biological context. They will be provided time to advance their own research agenda and afforded the opportunity to interact with biologists doing cutting-edge science. The candidate will be expected to contribute to experimental design, data analysis and the preparation of publications. They may also assist in teaching and be involved in externally funded research projects.

The Australian National University (ANU) is a national research university located in Canberra, the capital of Australia. Founded in 1946, it is the only university to have been created by the Parliament of Australia. ANU enrols over 22,500 students, comprised of roughly equal numbers of undergraduates and postgraduates. ANU is ranked 22nd in the world (first in Australia) by the 2016/17 QS World University Rankings.

For more information about this position please contact Eric Stone at eric.stone@anu.edu.au.

Salary package: $68,307 to $86,646 AUD per annum plus 17% superannuation Terms: Fixed Term, 3 years Link: http://jobs.anu.edu.au/cw/en/job/515973/-postdoctoral-fellow Eric A. Stone Professor Director, ANU-CSIRO Centre for Genomics, Metabolomics and

Bioinformatics Research School of Biology; College of Medicine, Biology and Environment Research School of Finance, Actuarial Studies and Statistics; College of Business and Economics

R.N Robertson Building, 46 Sullivans Creek Road The Australian National University Canberra ACT 2601 Australia

E: eric.stone@anu.edu.au

"Eric.Stone@anu.edu.au" <Eric.Stone@anu.edu.au>

CWilliamMary ButterflyPopGenetics

Postdoctoral Fellow: Andrew W. Mellon Postdoctoral Fellow @ The College of William and Mary

The Environmental Science and Policy program at the College of William & Mary seeks applications for a two-year postdoctoral scholar position in Environmental Science sponsored by the Andrew W. Mellon Foundation.

The postdoctoral scholar will research the decline of the monarch butterfly and the common milkweed plant using an interdisciplinary approach with techniques including population genetics, chemical ecology, GIS, and analysis of historical collections. The postdoctoral scholar will teach one upper-level primary literature focused seminar course per academic year and arrange an environmental speaker series in the second year. A PhD in Biology or a closely related discipline is required by the time of appointment, August 10, 2017.

The position offers a competitive salary ($45,000), research and travel funds ($5000/year), and administrative support. The postdoctoral fellow will be mentored by two William & Mary faculty members with research interests in plant ecology and population genetics.

Review of applications begins April 1st, 2017 and will continue until an appointment is made. Start date is August 10th, 2017. To apply, please submit online a letter of application and a curriculum vitae as a single PDF document as well as the names and email address of three references at http://jobs.wm.edu. (Job # F0004L)

The College of William and Mary values diversity and invites applications from underrepresented groups who will enrich the research, teaching, and service missions of the university. The College is an Equal Opportunity/Affirmative Action employer and conducts background checks on applicants for employment.

If you have questions please email:

Joshua Puzey, Assistant Professor of Biology, jrpuzey@wm.edu http://puzeylab.weebly.com Harmony Dalgleish, Assistant Professor of Biology, hjdalgleish@wm.edu http://wmpeople.wm.edu/site/page/-hjdalgleish/home Joshua Puzey <jrpuzey@gmail.com>

DTUAqua Denmark AnalysisOfEnvironmentalDNA

Within the research area "Population Genetics" at The National Institute for Aquatic Resources, DTU Aqua, we offer a 3-year post-doctoral fellowship in the field of environmental DNA analysis.

The fellow will be employed at DTU AquasÂs location in Silkeborg, Jutland, which besides the Population Genetics group also hosts the section for Freshwater Fisheries and Ecology (FFE). The starting time is negotiable, but preferably around 1 June 2017.

The successful candidate will work on a number of funded projects within the topic of environmental DNA from marine organisms. The main focus will be on the application and evaluation of an in situ, underwater automated DNA laboratory; the "ESP" (Environmental Sample Processor), for qPCR (quantitative PCR) based eDNA analysis. The aim is to apply the ESP for improved monitoring and management of a number of species, ranging from rare over invasive to marine ecosystem key species. Another main task will be development, test and application of species specific qPCR assays for monitoring a range of invasive species in Danish harbours.

The population genetics group at DTU Aqua has three senior researchers (one professor, two senior research scientists), one postdoc, three laboratory technicians, PhD and masters students (currently four PhD and one MSc student). Our main research focus is on Fisheries and Conservation Genetics, i.e. to apply molecular genetic tools to solve problems in fisheries science and conservation biology in order to contribute to long term sustainable management of marine resources and biodiversity. Our project portfolio ranges from basic science to projects directly targeted at providing specific management advice, and most projects encompass both basic and applied aspects. In recent years the group's main focus has shifted from genetics to genomics. Thus, most ongoing projects include genomic analysis. The facilities in Silkeborg comprise a fully equipped state of the art genetics laboratory, including DNA lab facilities for manipulating sensitive DNA samples.

The DTU Aqua Silkeborg location currently employs around 35 people including six PhD students. The young researchers work on a diversity of projects related to fish ecology and genetics aiming at fisheries resource management and biodiversity protection. They actively interact through various fora including regular seminars and the local study group in population ecology and genetics.

Qualifications

We invite applications from post doc level researchers with a background in eDNA analysis or related research fields. In particular experience in designing, testing and applying qPCR assays for species specific identification and quantification is will be considered an asset.

As we are in a process to expand the group's competences with respect to genomic analysis, we strongly encourage applicants with previous bioinformatics experience in relation to handling and analysing genomic data. The candidate will be selected based on previous scientific track record and qualifications of relevance to the described projects.

Candidates should have a PhD degree or equivalent.

Further information

For further information please contact the Population Genetics research coordinator, professor Einar Eg Nielsen (een@aqua.dtu.dk), tel +45 3588 3115.

You can read more about DTU Aqua at www.aqua.dtu.dk and more on population genetics

Please do not send applications to Principal Investigator, instead apply online as described below.

Salary and terms of employment

The appointment terms will be based on the collective agreement with the Confederation of Professional Associations. The salary will be agreed upon with the relevant union.

Starting date is negotiable. The position is for 3 years.

Place of work is DTU Aqua in Silkeborg, Denmark.

Application procedure We must have your online application by 25 April 2017.

Please go to the web-site (http://www.aqua.dtu.dk/Om_DTU_Aqua/Ledige_stillinger/job?id=9206cbcd-f1b7-432e-b55d-982528cf1f2f), open the link "apply online" and fill in the application form and attach the following documents:

*A letter motivating the application (cover letter) *Your application *Curriculum vitae with publication list *Diploma *Two letters of recommendation *If applicable, other material that you would like to be included in the evaluation.

Applications and enclosures received after the deadline will not be considered.

All interested candidates irrespective of age, gender, race, disability, religion or ethnic background are encouraged to apply.

The purpose of DTU Aqua is to provide research, advice and education at the highest international level within the sustainable exploitation of living marine and freshwater resources, the biology of aquatic

— / —

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

---

DukeU SpeciationGenomicsBioinformatics

The Yoder Lab at Duke University seeks to hire a senior postdoctoral research scientist interested in the genomics of speciation.

The project is focused on an evolutionary radiation of small nocturnal primates endemic to Madagascar, the mouse lemurs (genus Microcebus). These primates constitute something of a classic "cryptic" species radiation in that they are highly similar morphologically and ecologically, but strongly diverged genetically and geographically. Whereas only two species were recognized in 1992, that number has grown to 25. Research questions focus on understanding the phylogenomic relationships among species, the levels of genomic divergence that separate them, the levels of gene flow (if any) among them, and the underlying genomic signatures that define them and perhaps maintain their species identity. Of particular interest is the question of "what are the forces of selection (sexual and/or natural) that might have driven their diversification and maintain their species identity?"

At present, genomic resources relevant to the project include a high-coverage and near-chromosome level assembly of one species within the radiation (the “gray mouse lemur,” generated in collaboration with the Baylor College of Medicine, Human Genome Sequencing Center), low coverage (~20X) genomes of ten other individuals within the species complex, low coverage (6 - 30X) genomes of ten additional species within the genus, and field samples for another five to ten species. In collaboration with investigators Alison Richard, Laurie Godfrey, and Emilienne Rasoazanabary, we are stewards of a large collection of wild-caught samples (> 200 individuals) of the reddish-gray mouse lemur collected from the Beza Mahafaly Special Reserve a population that may be in the earliest stages of ecological speciation in sympatry. Finally, via the captive collections of the Duke Lemur Center, and in collaboration with investigators at the Brunoy Centre National de la Recerche Scientifique, we have access to biological samples from thousands of individual gray mouse lemurs now living, or preserved, from fifty years of captive management.

The main duties of the researcher will be managing, processing, and analyzing next-generation sequence data, generating high-quality genome assemblies, subsequent population/speciation genomic analysis, database organization, and most importantly, shared intellectual leadership of the project aims and publication of the results. There will be some molecular lab work, though the research will be largely bioinformatic. The ideal candidate will have experience working with genomic and population genetic data, a strong publication record, and ideally, demonstrated grant-writing skills. Moreover, the candidate will be highly organized, mature, enthusiastic, motivated, with plenty of esprit de corps and joie de vivre!

Starting salary will be in the range of $50K - $60K, dependent on skills and experience. The position is guaranteed with seed funds for two years (assuming a successful first-year review), with continuation possible through successful grant acquisition.

To Apply:

Via email, send current CV, publications, and contact information for three to four references to:

Anne D. Yoder, Professor Department of Biology Duke University, Box 90338 BioSci 315 Science Drive Durham, NC 27708 anne.yoder@duke.edu http://yoderlab.org

---

HarvardMedSchool DiseaseGenomics

The Department of Biomedical Informatics (DBMI) at Harvard Medical School and the Farhat Lab are looking for a Postdoctoral Fellow in infectious disease genomics.

Pathogens display a remarkable range of variability in phenotypes relevant to disease including transmissibility, organ tropism, and antibiotic resistance. Elucidating the biological mechanisms for these differences is a fundamental question in the study of infectious diseases and creates new avenues for surveillance, diagnosis and personalized treatment. The heritability of disease phenotypes within pathogen species and their evolution over generations indicates that they should be genetically encoded. As a result, the study of pathogen whole genome sequence (WGS) data is expected to further our understanding of these traits. The Farhat lab was one of the first to use phylogenetic convergence to test for association between genes and the drug resistance phenotype on a genome wide scale, and is continuing in this path for both methodological development and application to large scale datasets.

Responsibilities

The Postdoctoral Fellow will be responsible for developing and applying computational methodologies to identify novel infectious disease genomic markers.

Basic Requirements

We are an interdisciplinary lab. Candidates may have an MD or PhD degree in epidemiology, bioinformatics, computational and evolutionary biology, biostatistics, or a related field. Experience with genomics is a must. The candidate interested in this position must be highly motivated and demonstrate initiative in assigned tasks. Due to funding mechanism requirements this position is restricted to US citizens or permanent residents.

Additional Requirements

Experience in programming R, Python, and/or Perl and statistical analysis or at least an interest in learning these skills will be necessary. The candidate and PI can work together to delineate the fellow’s training needs and develop a program to fulfill this, utilizing the department and university’s wide range of resources.

Terms

The position is available immediately and can be renewed annually.

How to apply

Email applications including curriculum vitae, summary statement of personal objective and research interests, PDFs of the best two papers, and the names and email addresses of three references to mrfarhat@partners.org. Maha R Farhat, MD MSc Assistant Professor of Biomedical Informatics, Harvard Medical School Assistant Physician Pulmonary and Critical Care Medicine, Massachusetts General Hospital scholar.harvard.edu/mahafarhat phone: 617-432-5140 skype: maha.reda.farhat

“Farhat, Maha R.,M.D.” <MRFARHAT@partners.org>

IndianaU Bloomington HostSymbiontCoevolution

Job Title: Postdoctoral Fellow, Biology (Wade Lab) OAA#: 21703-03 Job Summary:

The Wade lab at Indiana University, Bloomington, (http://www.bio.indiana.edu/faculty/directory/profile.php?person=mjwade)seeks a collegial, self-motivated, independent, and intellectually curious individual with a recent Ph.D. in Evolutionary Biology or related field(s). The research emphasis is the intersection of population genetics and the evolution of development in complex systems, with an emphasis on models of dual inheritance for investigating general features of indirect genetic effects and niche construction with applications to cyto-nuclear and host-symbiont co-evolution. The candidate will have the opportunity to enrich the interactions between the laboratory groups of Drs. Michael Wade and Armin Moczek. The position is fully funded by a multi-year grant from the John Templeton Foundation and available for 24 months. Anticipated start date desired is July 1, 2017 but negotiable. Please apply via this link: https://indiana.peopleadmin.com/postings/3769 . “Wade, Michael J.” <mjwade@indiana.edu>

InstitutPasteur Paris KlebsiellaEvolution

Postdoc: Institut Pasteur, Paris - Klebsiella pneumoniae ecology, genomics and molecular pathogenesis

We are looking for a young talented researcher in microbial ecology or molecular pathogenesis to perform the following tasks:

* Sample Klebsiella pneumoniae from diverse sources * Characterize strains by genomics and phenotypic methods * Identify colonization or virulence-associated candidate factors using GWAS * Perform functional studies on the identified candidates

Skills. Experience in molecular biology, reverse genetics and infection/colonization models is a priority. Innovative thinking, work autonomy and good communication skills are important. Population genetics and bioinformatics experience will be appreciated but are not absolutely required as they can be provided by members of the lab.

Environment. The candidate will work in the Brisse group in close interactions with European partners of the SpARK project (coordinated by Ed Feil, Bath U.), and with bioinformaticians and microbiologists of the Brisse group: https://research.pasteur.fr/en/team/group-sylvain-brisse/ Conditions. The position is funded by the French Agence Nationale de la Recherche. The monthly salary will correspond to the standards in France (up to 2300 euro netto / month) and will depend on experience. The contract will be for 24 months. The positions is available from June 1st, 2017, but starting date can be delayed for a few months if the chosen candidate has agenda constraints.

Application: Please send your application as a single pdf to Sylvain Brisse (sbrisse@pasteur.fr) with a detailed CV, a cover letter and recommendation letters. Deadline May 1st, 2017.

Sylvain BRISSE <sylvain.brisse@pasteur.fr>

IowaStateU 2 MolCytogeneticsBioinformatics

PostDoctoral Positions in Turtle Molecular Cytogenetics and Bioinformatics

Postdoctoral positions are available to work in the laboratory of Dr. Nicole Valenzuela at Iowa State University on NSF-funded projects to study the evolution of genomes and dosage compensation in turtles.

These projects combine molecular cytogenetics, bioinformatics, transcriptomics, epigenomics, and phylogenetic analyses. The successful candidates will have the opportunity to contribute to one or more of these areas, leveraging and augmenting turtle genomic resources.

*Project description:

Species with sex chromosomes face the challenge posed by differential gene dosage between XX and XY individuals (or ZZ and ZW) that may lead to disease, suboptimal phenotypes or death. Dosage compensation is a mechanism to equalize the activity of X- or Z-linked genes between sex chromosomes and autosomes, and between males and females. As part of this NSF-funded project we are leveraging the multiple independently-evolved sex chromosome systems found in turtles to study the evolution of dosage compensation.

The growing genomic resources we have developed also allow us to continue studying turtle genome evolution across species with temperature-dependent sex determination (TSD) and those with sex chromosomes (GSD) (a) to decipher the molecular architecture of sex determination, both genetic and epigenetic in an ecologically relevant context, (b) to test models of sex chromosome evolution, (b) to reconstruct the evolution of turtle karyotypes, and (c) to identify proximal links between evolutionary chromosomal break points and transitions in sex determination, among others.

*Position Requirements: The ideal candidates will have a PhD degree and strong background in one or both of the following areas (a) Molecular cytogenetics (BAC/probe FISH, whole chromosome painting, chromosome microdissection or flow sorting). (b) Bioinformatics (genome assembly, comparative genome evolution, transcriptome/methylome analyses).

*Position details: Funding is available for 2 years with annual renewal contingent upon performance. The positions are available at any time starting 1 May 2017 (molecular cytogenetics) and November 2017 (Bioinformatics).

*Application deadline: April 1 2017, or until positions are filled.

*How to apply: For inquiries or to apply please email the following to Dr. Nicole Valenzuela at nvalenzu@iastate.edu : 1. Cover letter describing research interests and experience 2. Current CV 3. Copies of up to two relevant publications if available 4. Applicants should arrange to have three letters of recommendation be sent directly to nvalenzu@iastate.edu.

Iowa State University does not discriminate on the basis of race, color, age, religion, national origin, sexual orientation, gender identity, genetic information, sex, marital status, disability, or status as a U.S. veteran.

Dr. Nicole Valenzuela Associate Professor <nvalenzu@iastate.edu> Department of Ecology, Evolution, and Organismal Biology 251 Bessey Hall Iowa State University Ames, IA 50011, USA Phone: 515-294-1285 URL: http://www.public.iastate.edu/~nvalenzu/

"Valenzuela, M. N [EEOBS]" <nvalenzu@iastate.edu>

LudwigMaximiliansU ButterflySpeciation

Postdoc: Behaviour and speciation in Heliconius butterflies

We invite applications for a postdoctoral research position to study visual mate recognition and speciation in *Heliconius *butterflies with Dr Richard Merrill's research group at Ludwig-Maximilians-Universität, Munich, and in close collaboration with the Smithsonian Tropical Research Institute in Panama. The position is funded by the DFG Emmy Noether program, and is initially available for 2.5 years, with a further 2 years of funding available dependent on progress and interests. The position should start on 1 June 2017 or as soon as possible thereafter.

The project is focused on understanding the genetic basis and evolution of differences in mate recognition between divergent *Heliconius *taxa. *Heliconius* butterflies are well known for their bright warning patterns, which are also used as a mate recognition cue. The genetic basis of the colour pattern cues is now known in fantastic detail; however, we still know relatively little about the genetic basis of the corresponding preference behaviours.

The postdoctoral researcher will be primarily based at the Smithsonian Tropical Research Institute in Panama, working in close collaboration with Dr Owen McMillan's research group. The first major aim of the project is to develop methods to efficiently quantify visual attraction behaviours, using automated video analyses. By combining these methods with genetic crosses and genomic techniques the postdoctoral researcher will then investigate the genetic basis of visual preference behaviours in *Heliconius.*

Both at LMU (http://www.evol.bio.lmu.de) and STRI (http://www.stri.si.edu), the postdoctoral researcher will be part of vibrant international communities of scientists. In addition, the researcher will join a collaborative and driven community of *Heliconius *biologists.

Applicants should have a PhD, completed or completion imminent, in evolutionary biology/genetics, behavioural ecology, or a related field. Experience of behavioural analyses would be desirable. Candidates are expected to work collaboratively, within the group and across the community more generally, and to take an active role in the supervision of students and management of insectaries. Enthusiasm, determination and the capacity to work independently are essential.

Further information can be found at (https://richmerrill.wordpress.com), and questions should be directed to Richard Merrill (r.merrill@zoo.cm.ac.uk). Applications, including a current CV, letter of motivation and names and contact details of two referees should be sent to Richard Merrill (r.merrill@zoo.cm.ac.uk) before the deadline of 21 April 2017.

Richard Merrill <r.merrill@zoo.cam.ac.uk>

MaxPlanckInst Ploen Adaptation BiologicalClocks

Postdoc position - "Evolutionary adaptation and physiology of biological clocks"

Max Planck Institute for Evolutionary Biology, Ploen, Germany

The Max Planck Research Group "Biological Clocks" aims to uncover the yet unknown molecular basis of circalunar clocks, using the intertidal midge Clunio marinus (Diptera) as a model. Clunio times its life cycle to the rhythm of the tides by circalunar and circadian clocks. As the tides differ along the coastline, the clocks of Clunio populations are genetically adapted to the local pattern of the tides. We study these adaptations using a combination of evolutionary genomics and molecular biology, behavioral experiments and ecological fieldwork. We have shown that this approach enables the identification of new clock molecules (Nature 540,6973).

Clunio's circalunar clock can be set by moonlight, as well as mechanical cues and temperature cues associated with the tides. The postdoc will work with Clunio strains that are insensitive to mechanical and moonlight cues and use them to identify the receptors responsible for setting the circalunar clock.

The ideal candidate holds a PhD in Biology with a strong background in neurobiology, behavioral physiology or molecular biology. Experience in receptor physiology, immunohistochemistry, genome editing or cell culture are great assets. The postdoc will participate in the genomic work related to the project. As a central member of the group, the postdoc has good communication and organizational skills and will take part in supervising students. The position will be offered for 2 years with the possibility of extension. Starting date is May 2017 or as soon as possible thereafter.

The Max Planck Institute for Evolutionary Biology (http://www.evolbio.mpg.de/2169/en) offers a stimulating and ambitious international working environment. Excellent infrastructure is available at all levels. The MPI collaborates with the nearby Christian Albrechts University of Kiel (http://www.mnf.uni-kiel.de/en/einrichtung/sektion-biologie-1) and the GEOMAR (http://www.geomar.de/en/). The town of Plon is surrounded by lakes and the Baltic Sea is nearby, offering plenty of opportunity for leisure and outdoor activities. The nearby ports of Kiel and Travemünde provide access to Scandinavia, the closest airport is Hamburg.

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

Applications should include a cover letter describing your motivation to work on this project and your relevant experience, a detailed CV and copies of relevant certificates, and the contact details of three academic referees. Please send the above as a single PDF file to kaiser@evolbio.mpg.de.

Review of applications will start on 21st March 2017 and will continue until the position is filled. Feel free to contact me for further information.

Dr. Tobias Kaiser

Max Planck Research Group “Biological Clocks” Max Planck Institute for Evolutionary Biology August-Thienemann-Str. 2 | 24306 Plon | Germany Phone +49-4522-763-224

http://www.evolbio.mpg.de/biologicalclocks

MNHN Paris EvolutionDrosophilaSuzukii

A two years post doctoral position will open in our lab next fall on the phenotypic and genetic evolution of Drosophila suzukii throughout its recent worldwide invasion. The project will include the phenotyping of various traits, in connection with genetic (molecular and quantitative) and genomic data. Possible lines of research include the role of phenotypic plasticity in the success of the invasion or the evolution of quantitative genetic architecture (G matrices), but the project is open to further elaboration.

Inquiries and applications must be sent to Vincent Debat (debat@mnhn.fr)

Starting date is flexible but should be prior to December 2017. Review of applications starts immediately and will continue until position is filled.

The Project

Although positioned within the framework of the ANR funded grant (see below), the selected candidate will have the opportunity to elaborate his/her own research project.

The project is included in a larger collaborative work on D. suzukii invasion, involving three labs: Paris MNHN (part led by Vincent Debat), LBBE (Lyon, part led by Patricia Gibert) and CBGP (Montpellier, part led by Arnaud Estoup).

The Lab

The recruited postdoc will be based in Paris Museum of Natural History (MNHN) and will work in close collaboration with Vincent Debat (http://www.evomorpho.com/) in the team Evolution et Developpement des variation phenotypiques (http://isyeb.mnhn.fr/annuaire-et-pages-personnelles/pages-personnelles /Nouvelle-traduction-Violaine?lang=en). The lab research focus on the evolution of phenotypes and their variation, using various (insect) models - including butterflies and flies, and a combination of morphometric and molecular approaches.

The Salary

Net salary will me circa 2300 euros/month.

Abstract of the ANR funded project

The number of worldwide problems related to invasive species, which are largely due to human activities (development of international trade and intercontinental transportation), has strongly increased in the last decades. Invasive species are generally considered as having a negative effect both on economy (crop damage and health problems) and environment (loss of biodiversity). Managing and controlling invasive species requires an understanding of the ecological and evolutionary processes that underlie invasions. On a more academic side, biological invasions represent “natural experiments” for evolutionary biologists and are thus ideal to study the genetic bases of adaptation. In this project, we will investigate the evolutionary processes at play during a biological invasion with a particular focus on the mechanisms of adaptation. We will also infer the evolutionary potential in this species, so as to make short-term and longer-term predictions with respect to adaptation. This project will be carried on an Asian drosophila species (Drosophila suzukii, aka the Spotted Wing Drosophila) that has recently invaded both Europe and North America. Unlike most Drosophilids D. suzukii uses a sclerotized ovipositor to lay eggs in unripe fruits causing dramatic losses to the fruit industry, with a yearly cost estimate exceeding one billion euros worldwide. The rapid dissemination of D. suzukii in North America and Europe demonstrates its remarkable ability to adapt or acclimate to new environments. We propose to: (1) quantify phenotypic variation among and within populations, using quantitative genetics and reaction norms; (2) investigate the associated molecular variation using genomics and transcriptomics approaches; (3) combine phenotypic and molecular approaches to better investigate the traits associated with the invasion success, study the relative importance of natural selection and genetic drift on phenotypic differentiation between native and invasive populations, and to analyze the role of transposable elements in adaptation; (4) investigate how phenotypic plasticity, micro-evolution and symbionts contribute to the capacity of D. suzukii to feed on many different crop species and therefore switch hosts within a year. The strength of this project lies in several points: i) the complementarity of the approaches (molecular and phenotypic), ii) the skills of the partners on both the methods/technics (including the development of new inferential methods of general interest for the statistical analysis of populational pangenomics data) as well as the concepts that will be used, iii) the good knowledge of the biological model that has been the subject of several publications of the partners, iv) our collection of population samples from all around the world that has allowed to obtain valuable and original results on the routes of invasion of this species, v) an existing collaborative network with various socio-economic partners that will allow a rapid and efficient transfer of knowledge.

– Vincent Debat

— / —

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

---

Montpellier SelectionDetection

Post-doc position: Detection of selection from temporal population genomic data

We seek a post-doctoral researcher to work in a project on statistical population genomics. One of the goals of population genetics is understanding the biological processes (migration, selection, etc.) that influence the genetic diversity of populations. To this end, model-based statistical inference is often used to characterize these forces from genetic data. Of particular interest are data of genetic diversity taken at several time points, which allow to track genetic changes through time and are more informative about the processes acting on the population. The amount and nature of the genetic data have changed with the advent of high throughput sequencing technologies. Thus, new statistical approaches are required to analyse population genomic data. The post-doc will evaluate the use of random forests on the approximate Bayesian computation framework for tackling the analysis of population genomic data. The objective of the project will be to provide a statistical framework to co-estimate demography and selection from time-series population genomic data. The methods developed will be applied to one or more data sets from organisms of agronomic interest (e.g. agricultural pest Drosophila suzukii, wild crop relative Medicago truncatula or poplar rust fungus Melampsora larici-populina; data already available).

The ideal candidate will have a PhD in population genetics with an interest in statistics and computing or, alternatively, a PhD in statistics with a strong interest in biology and genetics. Programming skills are required, at the very least with R, but ideally with other languages (such as C or Python). Experience with simulation-based work or approximate Bayesian computation is recommended. The candidate should have good skills in written and spoken English to be able to communicate the results of his/her work.

The postdoc will be based at the CBGP laboratory (Montpellier, France) working under the supervision of Miguel Navascués (population geneticist at the INRA) in collaboration with Jean-Michel Marin (professor of statistics at the University of Montpellier). The postdoc will work in an interdisciplinary environment within a group of researchers working on the development of statistical methods for the analysis of population genetic data. Montpellier is one of the main research poles in France in evolutionary and computational biology. It is a medium-size city in the south of France, with an animated student life and near natural sites on the Mediterranean coast and the Cevennes mountains National Park.

Miguel Navascués: http://www6.montpellier.inra.fr/cbgp_eng/Staff/Permanent-staff/Miguel-Navascues Jean-Michel Marin: http://www.math.univ-montp2.fr/~marin/ CBGP lab and research group: http://www6.montpellier.inra.fr/cbgp_eng/Research/Thematic-groups/Statistical-and-evolutionary-population-genomics Computational Biology Institute: http://www.ibc-montpellier.fr/ Starting date: ideally August-September 2017

Location: Montpellier (France)

Duration: 18 months

Salary: determined by the official standard of the University of Montpellier, depends on experience (around 2000 euro /month net)

Conditions for eligibility: The candidate must hold a PhD degree obtained in the last 6 years. The PhD degree must NOT have been obtained working in a lab belonging to the LabEx AGRO, CEMEB or NUMEV from Montpellier. The candidate must not have worked as a post-doc in France more than 1 year in the last 3 years. We encourage interested candidates who do not fulfil all these conditions to apply, although they might only be selected if no eligible candidate is found .

Application: Send a CV, a motivation letter and contact information of two references to Miguel Navascués (miguel.navascues@inra.fr) and Jean-Michel Marin (jean-michel.marin@umontpellier.fr). Informal enquires are welcome.

– Miguel NAVASCUÃS

!! NEW EMAIL ADDRESS !!

UMR CBGP, INRA Centre de Biologie pour la Gestion des Populations 755 avenue du campus Agropolis CS30016 34988 Montferrier-sur-Lez cedex (France)

phone: +33499623370 fax: +33499623345 e-mail: miguel.navascues AT inra.fr web (personal): http://sites.google.com/site/navascuesresearch/ web (team):

— / —

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

---

NewYorkU EvoDevo

POSTDOC POSITION Genome Regulatory Network of Sexual Dimorphism: Development and Evolution

A postdoctoral position is available in the laboratory of Prof. David Fitch at New York University (Greenwich Village, New York City) to study how morphogenesis is regulated to occur in the appropriate time, place and sex in males of Caenorhabditis elegans and related nematodes. Sexual dimorphism of tail tip morphogenesis has evolved convergently in several lineages of nematodes related to C. elegans and offers a powerful genetic/genomic system for dissecting this process at a very fine scale. One goal is to use genomic-level (e.g. ChIP-seq) and single-cell transcriptomics methodologies already established in the lab to delineate gene expression dynamics of male tail morphogenesis in C. elegans and related species. From these data, we would like to infer the architecture of the genetic regulatory network (GRN) controlling this process and eventually reconstruct its evolution in convergent lineages. Ultimately, such data are required for addressing if and how GRN architecture canalizes evolutionary change, as well as for understanding how sexual dimorphism originates.

The Fitch lab is a part of the Biology Department at NYU, and has access to a full range of facilities for the project, including access to a genomics/bioinformatics core facility, high-resolution microscopy, laser microdissection, the NYU Rhabditid Collection (over 150 different species of nematodes related to C. elegans), culture facilities, and standard molecular biology and genetics facilities. The postdoc will join a community of other C. elegans biologists, enjoying access to their collective wisdom and resources. The department and school also maintain excellent mentoring programs for postdocs, who have multiple opportunities for participating in the vibrant academic environment of NYU and the city in which it resides.

Funding is currently available for a two-year period, with the opportunity to be extended into subsequent years. Prior experience in C. elegans genetics and molecular biology is preferred. Knowledge regarding bioinformatics analyses and tools is advantageous. Applications will be reviewed on a rolling basis until the position is filled. Please send CV and contact information for at least two people who can serve as references to: david.fitch@nyu.edu

"df3@nyu.edu" <df3@nyu.edu>

NHGRI-NIH Bethesda BioinformaticsEvolGenomics

Computationaland Statistical Genomics Branch NationalHuman Genome Research Institute NationalInstitutes of Health

PostdoctoralFellowship in Bioinformatics and Evolutionary Genomics

Apostdoctoral training position is currently available in the Computational and Statistical Genomics Branch (CSGB) of the National Human Genome Research Institute (NHGRI). The position is located in the laboratory of Andy Baxevanis, Ph.D., whose research group uses comparative genomics approaches to better-understand the molecular innovations that drove the surge of diversity in early animal evolution. The overarching theme of Dr. Baxevanis' research program is focused on how non-traditional animal models can be used to convey critical insights into human disease research, in line with the NIH Intramural Research Program's renewed emphasis on developing new animal models for the study of basic biology.

Withthis translational context in mind, Dr. Baxevanis' group is currently leading an international effort to sequence two cnidarian species: Hydractinia echinata and Hydractinia symbiolongicarpus. The regenerative abilities of these colonial hydrozoans make them excellent models for the study of key questions related to pluripotency, allorecognition, and stem cell biology, work that will be significantly advanced by the availability of high-quality whole-genome sequencing data from these organisms. In addition, and in collaboration with colleagues at the Whitney Marine Laboratory of the University of Florida, the group is also now focusing on polychaete species that show particular promise for advancing our understanding of regeneration and early developmental processes. The successful applicant will have the opportunity to develop and apply bioinformatic approaches to these and other large-scale genomic data sets, focusing on the evolution of specific protein families, with an emphasis on examining their putative roles in disease causation.

Candidatesshould have or be close to obtaining a Ph.D. or equivalent degree in bioinformatics, computational biology, computer science, molecular biology, or a closely related field. Candidates with a background in evolutionary biology are particularly encouraged to apply. Programming skills and experience in the application of computational methods to genomic data are highly desirable. Applicants must possess good communication skills and be fluent in both spoken and written English. The ability to learn how to use new software and quickly become expert in its use, critical thinking, problem-solving abilities, and the ability to work semi-independently are required.

TheNIH Intramural Research Program is on the Bethesda, Maryland campus and offers a wide array of training opportunities for scientists early in their careers. The funding for this position is stable and offers the trainee wide latitude in the design and pursuit of their research project. The successful candidate will have access to NHGRI's established and robust bioinformatics infrastructure, as well as a 'Top 500' high-performance computing resource made available through NIH's Center for Information Technology (CIT).

Interestedapplicants should submit a curriculum vitae, a detailed letter of interest, and the names of three potential references to Dr. Baxevanis at andy@mail.nih.gov.

Formore information on CSGB and NHGRI's Intramural Research Program, please see http://genome.gov/DIR/ . DHHSand NIH are Equal Opportunity Employers and encourage applications from women and minorities.

andy@mail.nih.gov

NorthCarolinaStateU ComputationalEvolModeling

Postdoc position - "High-performance computational tools for evolutionary sequence analyses"

North Carolina State University, Department of Biological Sciences, Raleigh NC.

A post-doctoral position is available to work with Prof. Michela Becchi and Gavin Conant at NC State University. The successful applicant will be part of a collaborative research project on the use of new computing hardware platforms and algorithms for large-scale genomic analyses. She or he will conduct research either developing algorithms on such platforms or using tools from computational collaborators to study the question of whether increasing volumes of genomic data, coupled to improved computing hardware, can resolve long-standing problems in functional genomics involving finding regulatory elements and resolving orthology relationships. Computing platforms under consideration includes: GPUs, FPGAs, Micron's Automata Processor and Intel Phi coprocessor devices.

The candidate must hold a Ph.D. or equivalent doctorate (e.g., M.D., D.V.M., Sc.D.) in appropriate field awarded no more than five (5) years from initial date of postdoctoral appointment and must be able to program in c, c++ or Fortran and have a working knowledge of bioinformatics and computational genomics. Knowledge of parallel programming or string matching algorithms is strongly preferred.

The successful applicant will be located on the main campus of NC State University, close to downtown Raleigh. Collaborative opportunities include NCSU's Bioinformatics Research Center (https://brc.ncsu.edu), its Genetics program (https://genetics.sciences.ncsu.edu), its Department of Electrical and Computer Engineering (https://www.ece.ncsu.edu/) and the Triangle Center for Evolutionary Medicine (formerly NESCENT; https://www.nescent.org).

Full details of the position and formal application instructions are available at https://jobs.ncsu.edu/postings/82212 . Review of applications will begin on March 10th and continue until the position is filled.

Informal inquires may be directed to Gavin Conant: gconant@ncsu.edu

Gavin Conant Associate Professor Department of Biological Sciences 356 Ricks Hall North Carolina State University Raleigh NC 27695

email: gconant@ncsu.edu web: www4.ncsu.edu/~gconant

"gconant@ncsu.edu" <gconant@ncsu.edu>

Omaha Nebraska MadagascarBiodiversityGenomics

Postdoctoral Fellow - Madagascar Biodiversity Genomics

Job Description:

Omaha's Henry Doorly Zoo & Aquarium Department of Conservation Genetics (OHDZA-CG) based in Omaha, Nebraska, is seeking a post-doctoral researcher with interest/expertise in the generation and analysis of next-generation sequencing data of lemurs, tortoises, and other taxa from Madagascar.

Duties:

The successful applicant will be proficient in the construction genomic libraries and in solution hybridization methodologies for high throughput sequencing as well as all relevant analysis of large datasets, and manage next-generation sequence workflows. This individual will be responsible for development, implementation, and support of software applications related to variant detection and interpretation from high-throughput experiments involving multiple species of lemurs, tortoises, and taxa from Madagascar. Assembly of whole genomes is in-progress, but will likely require additional analysis pertinent to specific research projects. Interested candidates should be highly motivated, organized, independent, and have extensive experience with molecular genomics and bioinformatics, and be able to efficiently write and revise manuscripts. Travel to Madagascar to support the field programs of OHDZA-CG is required for a minimum of five week intervals twice a year.

Basic Qualifications:

Applicants should hold a PhD in bioinformatics, computer science, molecular genomics or related field and have more than one year of experience in high-throughput genome sequence analysis. Applicants should be experienced at software related to next generation sequencing data and be able to manipulate genomic data for phylogenetics and phylogeography. Our group's focus is large-scale sequencing for phylogenetics, phylogeography and evolutionary studies of lemurs, tortoises and other taxa from Madagascar. Thus, previous experience in genome assemblies, annotation and analysis of a variety of next generation sequencing (NGS) pipelines is preferable. The ideal candidate will be independent, highly motivated, productive, and able to work effectively in a team with members from a variety of diverse backgrounds with outstanding written and verbal communication skills. The successful applicant must be interested in interdisciplinary science and field research and have a solid publication record that illustrates ability to conduct novel, independent research.

Preferred Qualifications

Candidates should have 3+ years of experience in molecular biology, genetics, or bioinformatics. The position requires proficiency in programming (perl or python) and bash scripting using Linux operating systems. Applicants are also expected to be familiar with bioinformatics tools, be able to implement complex computational pipelines, incorporate genomics databases and have extensive and creditable laboratory experience with constructing genomic libraries. The applicant will need to work closely with two full time technicians to manage NGS lab work, as well as with a full time bioinformatician. While in Madagascar the applicant will work with a variety of Malagasy graduate students, and is expected to assist with the progression of a variety of projects, and assist with completion of their degrees and peer-reviewed manuscripts. Based on all these above duties requires a candidate with excellent interpersonal skills, and the ability to train and teach both national and international audiences is necessary. The candidate must also be able to jump between a variety of projects, based on needs of the research group.

Must be legally entitled to work in the USA. Visa sponsorship is not available.

Appointment:

The selected candidate will be based primarily at OHDZA-CG, but the individual will be required to travel and conduct field work with the projects under the management of the Madagascar Biodiversity Partnership, NGO (www.madagascarpartnership.org). Salary/benefits are based on OHDZA-CG's salary/benefits structure, and are commensurate with experience. The initial appointment is for duration of two-years, but is renewable for an additional two years based on performance. The position will begin approximately mid-August 2017.

Application:

Applicants should send curriculum vitae, a statement of research interests and career goals, a few publications, and the names and addresses of three academic and professional references to:

Dr. Edward E. Louis, Jr.

Director of the Department of Conservation Genetics

Center for Conservation and Research

Omaha's Henry Doorly Zoo & Aquarium

3701 South 10^th Street, Omaha, NE 68107 USA

Email: genetics@omahazoo.com

Review of applications will begin immediately upon receipt.

Genetics Department <genetics@omahazoo.com>

Paris EvolutionaryAndEnvMarineGenomics

Postdoc Position in Evolutionary and Environmental Marine Genomics: Large scale metatranscriptomics of eukaryote plankton ecology and evolution in the Global Ocean .

We invite applications for a 2 years postdoctoral fellowship to analyze large scale metagenomics and metatranscriptomics eukaryotic data from the Tara Oceans and Tara Oceans Polar Circle expeditions.

PROJECT: Plankton communities are composed of viruses, bacteria, protists and multicellular eukaryotes that all together perform biological and geochemical processes important for global earth and climate regulations. The Tara Oceans and Tara Oceans Polar Circle expeditions have systematically sampled marine plankton at hundred sites of the world's oceans, covering the entire ecosystem diversity from viruses and prokaryotes to eukaryotes, and generating the largest standardized eco-morpho-metaomics dataset available (> 40 Terabases), including over 1,000 virus-, prokaryote-, and eukaryote-enriched metagenomes and metatranscriptomes, as well as 4 billion eukaryotic and prokaryotic metabarcodes from 3,000 size-fractionated plankton communities worldwide. This dataset covering global geographic and taxonomic scales represents a unique opportunity to explore the boundaries of a planetary ecosystem at the interface between oceanography, biodiversity, ecology, and evolution. The selected candidate will investigate and compare meta-transcriptomics and meta-genomics data at the organismal level to explore responses to population and environmental changes in the whole set of sampled locations.

CANDIDATE: The successful candidate should have a PhD in the fields of bioinformatics or environmental genomics. The following expertises would be favored: i) extensive first-hand experience in computational analysis of biological sequences (particularly: population genetics, meta-omics mining), ii) proficiency in statistical methods using R, or iii) demonstrated script programming skills in *NIX environments (Perl, python, shell etc.) as well as familiarity with the use of compute farms. Knowledge of numerical ecology approaches and/or oceanography will be very favorably considered.

APPLICATION: Applications and informal queries should be addressed to Eric Pelletier (eric.pelletier@genoscope.fr). Interested candidates should send their CV with a publications list, and a cover letter describing their research interests and motivation. Candidates should also arrange for at least two referees to e-mail recommendation letters directly to Eric Pelletier <eric.pelletier@genoscope.fr>. Review of applications will begin on March 1st, 2017 and applications will continue to be accepted until the position is filled.

CONTRACT AND ENVIRONMENT: The position will start at the earliest possible date, taking into account that drafting the work contract usually takes at least 8 weeks. The salary will be 2,700~3,000 euro , based on the CEA salary grid, and depends on qualifications and experience. The position is based at Genoscope near Paris and will involve close national and international collaboration in particular with other partner institutions of the Tara Oceans consortia. The selected candidate will work in a team of 10 people in the Laboratory of Eukaryotic Genomics led by Patrick Wincker.

REFERENCES:

https://www.embl.de/tara-oceans Guidi, L. et al. Plankton networks driving carbon export in the oligotrophic ocean. Nature 532, 465-470, doi:10.1038/nature16942 (2016).

Roux, S. et al. Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. Nature, doi:10.1038/nature19366 (2016).

De Vargas, C. et al. Eukaryotic plankton diversity in the sunlit ocean. Science. May 2;348(6237) doi: 10.1126/science.1261605. (2015)

Brum, JR. et al. Patterns and ecological drivers of ocean viral communities. Science. May2;348(6237) doi: 10.1126/science.aah6502. (2015)

Sunagawa, S. et al. Structure and function of the global

ocean microbiome. Science. May 22;348(6237) doi: 10.1126/science.1261359. (2015)

Villar, E. et al. Environmental characteristics of Agulhas rings affect interocean plankton transport. Science May 22; doi: 10.1126/science.1261447.(2015)

– Dr Eric Pelletier | CEA / Genoscope Environmental (Meta)Genomics | CNRS UMR-8030 Tel: (33) 0 160 872 519 | CP 5706 91057 Evry cedex - France

---

Paris EvolutionaryEnvironmentalGenomics

*Postdoc Position in Evolutionary and Environmental Genomics: Investigating the plankton ecology and evolution in the Arctic Ocean in relation to adjacent ecosystems. *

We invite applications for a 2 years postdoctoral fellowship to analyze plankton ecology through data mining of environmental genomics datasets from the expeditions /Tara/ Oceans and /Tara/ Oceans Polar Circle.

PROJECT: Plankton communities are composed of viruses, bacteria, protists and multicellular eukaryotes that all together perform biological and geochemical processes important for global earth and climate regulations.The /Tara/ Oceans and /Tara/ Oceans Polar Circle expeditions have systematically sampled marine plankton at hundred sites of the world's oceans, covering the entire ecosystem diversity from viruses and prokaryotes to eukaryotes [1]. The /Tara /Oceans//project has generated the largest standardized eco-morpho-metaomics dataset available (>40 Terabases), including over 1,000 virus-, prokaryote-, and eukaryote-enriched metagenomes and metatranscriptomes, as well as 4 billion eukaryotic and prokaryotic metabarcodes from 3,000 size-fractionated plankton communities worldwide. This dataset covering global geographic and taxonomic scales represents a unique opportunity to explore the boundaries of a planetary ecosystem at the interface between oceanography, biodiversity, ecology, and evolution.

Following the first /Tara/ Oceans global analyses published in Science and Nature in 2015 and 2016[2], the selected candidate will investigate and compare genomics data from two distinct environments, the temperate and Arctic Oceans which are connected through North Atlantic. In collaboration with other researchers, the candidate will address the question of the impact of the physical connectivity between the Atlantic basin and the Arctic basin on the ecology, genetic and evolution of organisms.

CANDIDATE: The successful candidate should have a PhD in the fields of bioinformatics or environmental genomics. The following expertises would be favored: i) extensive first-hand experience in computational analysis of biological sequences (particularly: similarity searching, phylogeny, variant identification, population genetics, meta-omics mining), ii) proficiency in statistical methods using R, or iii) demonstrated script programming skills in *NIX environments (Perl, python, bash etc.) as well as familiarity with the use of compute farms. Knowledge of numerical ecology approaches and/or oceanography will be very favorably considered.

APPLICATION: Applications and informal queries should be addressed to Olivier Jaillon (< ojaillon@genoscope.cns.fr <mailto:ojaillon@genoscope.cns.fr>>). Interested candidates should send their CV with a publications list, and a cover letter describing their research interests and motivation. Candidates should also arrange for at least two referees to e-mail recommendation letters directly to.

Review of applications will begin on March 1st, 2017 and applications will continue to be accepted until the position is filled.

CONTRACT AND ENVIRONMENT: The position will start at the earliest possible date, taking into account that drafting the work contract usually takes at least 8 weeks. The salary will be based on the CEA salary grid and depends on qualifications and experience. The position is based at Genoscope near Paris and will involve close national and international collaboration in particular with the Stazione Zoologica of Naples and with other partner institutions of the /Tara/ Oceans consortia. The selected candidate will work in a team of 10 people in the Laboratory of Eukaryotic Genomics (Lage) led by Patrick Wincker.

REFERENCES: [1] https://www.embl.de/tara-oceans[2] Guidi, L. et al. Plankton networks driving carbon export in the oligotrophic ocean. Nature 532, 465-470, doi:10.1038/nature16942 (2016). Biard, T. et al. In situ imaging reveals the biomass of giant protists in the global ocean. Nature 532, 504-507, doi:10.1038/nature17652 (2016). Roux, S. et al. Ecogenomics and potential biogeochemical impacts of globally abundant ocean viruses. Nature, doi:10.1038/nature19366 (2016). De Vargas, C. et al. Eukaryotic plankton diversity in the sunlit ocean. Science. May 2;348(6237) doi: 10.1126/science.1261605. (2015)

Brum, JR. et al. Patterns and ecological drivers of ocean viral communities. Science. May2;348(6237) doi: 10.1126/science.aah6502. (2015)

Sunagawa, S. et al. Structure and function of the global ocean microbiome. Science. May 22;348(6237) doi: 10.1126/science.1261359. (2015)

Villar, E. et al. Environmental characteristics of Agulhas rings affect interocean plankton transport. Science May 22; doi: 10.1126/science.1261447.(2015)

Olivier Jaillon <ojaillon@genoscope.cns.fr>

RockefellerU EvolutionaryGenomics

A postdoctoral researcher position is available in the Laboratory of Evolutionary Genetics and Genomics (PI: Li Zhao) at the Rockefeller University. The project will involve genomic and transcriptomic experiments and analysis to understand the evolution and molecular genetics of newly evolved genes. The ideal candidate for the position will have a strong background in computational biology, evolutionary genomics, as well as interests in functional genetics and population genetics. A background with Drosophila or human evolutionary biology is highly desirable.

The Laboratory of Evolutionary Genetics is a newly established lab at the Rockefeller University located in the Upper East Side of Manhattan in New York City. We work on a number of projects on genome evolution, gene evolution, gene function, and genetic basis of local adaptation. Rockefeller University supports a vibrant research community in insect and human genetics and creates a multidisciplinary research atmosphere for studying fundamental biological questions. Candidates who have strong background in Drosophila functional genetics and behavior are also encouraged to contact Li Zhao for possible opportunities.

Applications will be accepted until the position is filled. The anticipated start date for this appointment is summer 2017. To apply, please send your CV, a statement of your research background and interests, and contact information for three references to Li Zhao at lzhao@rockefeller.edu.

Best regards,

Li Zhao

Li Zhao, Ph.D. Assistant Professor and Head of Laboratory Laboratory of Evolutionary Genetics and Genomics Rockefeller University 1230 York Ave, New York, NY 10065

"lzhao@rockefeller.edu" <lzhao@rockefeller.edu>

RoslinInst StaticsticalGenetics

Dear All,

We have available an exciting post to develop, implement and apply statistical methods for the analysis of binary phenotypes for someone with strong statistical and programming background.

Further details can be found at https://www.vacancies.ed.ac.uk/pls/corehrrecruit/erq_search_package.search_form?p_company=5&p_internal_external=E# . The vacancy reference is 039228. Please, address informal inquires to me (albert.tenesa@ed.ac.uk). Best wishes, Albert

TENESA Albert <Albert.Tenesa@ed.ac.uk>

SaintLouisU EvolInsectCommunication

The Fowler-Finn Lab at Saint Louis University is seeking applicants for a postdoctoral scholar to lead a dynamic research team in an NSF-funded project investigating thermal effects on reproductive performance and sexual communication in natural populations of treehoppers (Hemiptera: Membracidae). This project implements a function-valued approach to characterize plasticity in thermally-sensitive reproductive traits, and classic quantitative genetics to measure genetic variation across a latitudinal gradient. There is also an outreach component to the project that capitalizes on the ability of the bizarre and beautiful vibrational songs of treehoppers to capture the imagination of the public. There will be opportunities for the postdoc to develop related projects, and the postdoctoral scholar is encouraged to interact and collaborate with other members of the Evolution, Ecology, and Behavior community in the Saint Louis area.

The successful candidate will have (i) a Ph.D. in Evolutionary Biology (or related field), (ii) demonstrated expertise in behavioral experimentation, (iii) excellent organizational skills, strong work ethic, and desire to collaborate with and lead a team, (iv) a strong record of written and oral communication in English, and (v) commitment to supporting diversity and outreach education in STEM. Additional valuable skills and experience include: familiarity with classic quantitative genetics, statistical analysis of complex phenotypic data, strong interest in mentorship of students, and a general attitude of having fun while working hard in the lab! The initial appointment will be made for one year, with an additional 1-2 years contingent on satisfactory progress. Start date: spring 2017 or until filled. To apply, please email the following materials to (Kasey Fowler-Finn) with the email subject “Postdoc_Treehoppers”: (1) cover letter with research experience, training and qualifications for the position as described in this advertisement, (2) up-to-date CV, and (3) names of three mentors/colleagues from whom you can request letters of support. For best consideration, please apply by February March 31, 2017.

Saint Louis University is an Affirmative Action/Equal Opportunity Employer (AA/EOE), and encourages nominations of and applications from women and minorities.

Kasey Fowler-Finn, Ph.D. Assistant Professor Department of Biology Saint Louis University http://bio.slu.edu/fowlerfinn/ Kasey Fowler-Finn <fowlerfinn@slu.edu>

SmithCollege 2 AmoebaeCiliates

The Katz lab < http://www.science.smith.edu/katz-lab/research/ > is recruiting two full-time postdoctoral research fellows to work on testate amoebae and ciliates.

The first position— < http://apply.interfolio.com/41040 >combines microscopy and molecular tools to explore the diversity of testate amoebae in New England bogs and fens. The aims of this project include characterizing the diversity of testate amoebae morphospecies and communities in low pH bogs and fens, and collecting transcriptomic data from testate amoebae. The ideal candidate will: be a productive researcher with interests in biodiversity and phylogenomics of microorganisms; have experience identifying and isolating diverse amoebae; and have knowledge of bioinformatic and/or phylogenetic tools. Excellence in communication and an interest in collaborating with graduate and undergraduate students in the laboratory are essential. Ph.D. in Biological Sciences or related field required by time of appointment.

The second position < http://apply.interfolio.com/-41036 > focuses on using single cell ’omics’ to characterize genomes of ciliates isolated from various freshwater and marine habitats. The goals of the project are to assess intraspecific variation in both somatic macronuclei and germline micronuclei from diverse ciliates. The ideal candidate will: be a productive researcher with interests in phylogenomics of microorganisms, including analyzing complex genomic data; have experience identifying and isolating diverse ciliates; have knowledge of bioinformatic tools, and ideally have familiarity with python or a comparable computer language. Excellence in communication and an interest in collaborating with graduate and undergraduate students in the laboratory are essential. Ph.D. in Biological Sciences or related field required by time of appointment. In both cases, the position will begin on or after July 2017, and the initial appointment is for one year, with the possibility of extending for additional years. Applications must be submitted through interfolio to be considered (http://apply.interfolio.com/-41040 ,http://apply.interfolio.com/41036), though potential applicants can contact Laura <mailto:lkatz@smith.edu> with any questions. Please submit applications through interfolio with a letter of application, C.V., a statement of research interests, three representative publications, and the names and contact information of three references. Review of applications will begin April 1, 2017.

Diversifying the student body, faculty, administration, staff, and curriculum is crucial to the mission of and vision for the College. Smith is committed to providing access and reasonable accommodation in the application process for individuals with disabilities and encourage applicants to request any needed accommodation(s). The college values and is committed to a host of diverse populations and cultures, including, but not limited to, those based on ability, age, ethnicity, gender, gender identity, national origin, race, religion, sexual orientation, and veteran status.

Smith College is an EO/AA/Vet/Disability Employer. Women, underrepresented racial groups, veterans and individuals with disabilities are encouraged to apply.

Laura A Katz <lkatz@smith.edu>

SouthAfrica eDNA

We are looking for a postdoctoral fellow to work on eDNA of marine and estuarine communities in South Africa, in particular characterising the communities associated with seagrass meadows. This is part of a National Research Foundation funded project on eDNA, hosted in the lab of Prof. Sophie von der Heyden (www.vonderheydenlab.com), in collaboration with the Molecular Ecology and Fisheries Genetics Lab at Bangor University (http://mefgl.bangor.ac.uk/staff/si.php). The primary focus of this research project is to use an environmental DNA metabarcoding approach to characterise known and hidden genetic diversity in a variety of marine ecosystems in South Africa, to not only allow comparison between sites, but to 1. assess this methodology as a tool for monitoring change in African marine ecosystems and 2. utilise seascape genetic approaches to help disentangle the biological drivers of community structuring.

Applicants must have evidence of working with eDNA, including the necessary skills for the collection of samples, isolation of DNA, subsequent PCRs and relevant bioinformatics skills. A proven track record of publications in international journals is a must. Ideally, the candidate would be familiar with southern African marine systems, but this is not essential. This is an exciting opportunity for someone looking to work in one of the most biodiverse and beautiful parts of the world as the project will cover much of the ˜3600km of coastline that South African has to offer. Good people skills are a must, as this project also supports postgraduate students.

The tenure of the postdoc would be for two years (starting date negotiable) or longer, depending on the availability of funds. The successful candidate will need to apply to the University of Stellenbosch Postdoctoral Fellowship scheme (details available from PI von der Heyden) and also apply to the Claude Leon Foundation for postdoctoral support (http://www.leonfoundation.co.za/-postdoctoral.htm). The vdH lab is housed in the Department of Botany and Zoology at the University of Stellenbosch. This university is one of the top-ranked in the southern Hemisphere, with strong undergraduate and postgraduate training and research. Stellenbosch is a historical, safe and vibrant community surrounded by magnificent mountains, close to the sea. Find out more at www.sun.ac.za. To apply or to find out more about the projects, please contact Prof. Sophie von der Heyden (svdh@sun.ac.za) with a comprehensive CV, detailing your research background and publication record and a short statement on your expertise with eDNA, by the 24th March.

"Von der Heyden, S, Prof <svdh@sun.ac.za>" <svdh@sun.ac.za>

Tampa Florida ModelingCancerEvolution

Link: http://scholar.harvard.edu/files/paltrock/-files/altrocklab_postdocposition_march2017.pdf
Text: Postdoctoral Position in Mathematical Oncology/Computational Biology The Evolutionary Dynamics lab, headed by Dr. Philipp Altrock at the Department of Integrated Mathematical Oncology, Moffitt Cancer Center and Research Institute, in Tampa, Florida, is seeking to fill a postdoctoral position. Moffitt is the only Florida cancer center to receive the National Cancer Institute designation for its scientific excellence and offers unique opportunities for interdisciplinary collaborations at the forefront of finding new cancer cures.

Candidates ideally hold a PhD in mathematics, computer science or physics and have a strong interest in cancer biology and medicine.

Applicants from other areas with a quantitative background in biology or medicine are also encouraged to apply. Applicants should clearly state their desire to work in close collaboration with experimental and clinical oncologists, as well as their experience in mathematical or computational modeling, data analysis and visualization, and scientific writing. Please send a cover letter including a brief research statement, a CV, and a publication list highlighting individual contributions. Send all in one pdf document to philipp.altrock@moffitt.org, and have three letters of recommendation sent independently. The position is posted until filled.

The lab focuses on mathematical and statistical models that elucidate the role of selective forces acting in homeostatic tissues and growing tumors. Our goals are to better understand onset and epidemiology of cancers, as well as cell phenotypic and tissue environmental features in somatic and cancer evolution. To achieve these goals, data from novel experiments at Moffitt and Harvard Medical School will be used.

In addition, publically available datasets are evaluated and incorporated in the modeling process. We are particularly interested in blood disease in which cell interact with the microenvironment and the immune system.

The Department of Integrated Mathematical Oncology (IMO) consists of 7 internationally renowned cancer researchers and mathematical modelers.

The focus of all IMO research groups is to apply physical, mathematical and mechanical principles to cancer biology to decipher first order principles of tumor growth that can be exploited for novel cancer treatments. Moffitt Cancer Center and Research Institute, in Tampa, is Florida's largest cancer center, located on the campus of the University of South Florida, near beautiful beaches in the Gulf of Mexico.

Dr. Philipp M. Altrock Assistant Member Moffitt Cancer Center, Tampa, FL scholar.harvard.edu/paltrock philipp.altrock@moffitt.org Please consider the environment before printing this email.

"Altrock, Philipp M" <Philipp.Altrock@moffitt.org>

UAdelaide PhylogeographicsBioinformatics

PostdoctoralResearcher Position at the Australian Centre for Ancient DNA, The University of Adelaide

Keywords:Phylogenetics, Bioinformatics, Molecular Evolution, Population Genetics, Ancient DNA.

Two(2) post-doctoral position are available at the Australian Centre for Ancient DNA (ACAD; adelaide.edu.au/acad) for 1-year (extendable). Highly independent and motivated researchers with strong phylogenetics, statistical genetics and bioinformatics are invited to apply. The successful candidates will work under the supervision of Prof Alan Cooper, and will have the opportunity to work on ACAD's wide range of high-profile projects (ACAD's publications; adelaide.edu.au/acad/publications/). We are currently conducting a range of projects investigating molecular evolution, and phylogeographics of a number of organisms including dental microbiome, large mammals, and humans. The successful applicant will lead a program to develop and integrate analytical methods and pipelines for the analysis of large ancient genomic datasets, and co-supervise a group of postgraduate students in collaboration with local, and overseas colleagues and the University's School of Mathematical Sciences.

TheUniversity of Adelaide is one of Australia's leading Group of Eight, research-intensive universities and is consistently ranked among the top 1% of universities in the world. Established in 1874, it is Australia's third oldest university with a particularly strong reputation for scientific research. The Faculty of Sciences is one of five faculties at the University of Adelaide. As the first university in Australia to grant degrees in science (1882), science has long been at the cornerstone of the institution and this continues today. As a research and education leader in fields such as biomedical sciences, agricultural, environmental and earth sciences, the faculty offers an exciting and innovative work environment. ACAD sits within the Flagship Environment Institute, and is a world reference ancient DNA research centre, regularly publishing in high-impact journals such as Nature and Science. The applicant would be expected to operate at this level.

*To be successful you should have: - A PhD or MSc involving bioinformatics, biostatistics, population genetics, biomedical or ancient DNA research, or other relevant disciplines. - Expertise in UNIX based systems, including scripting in bash and at least one pre-compiled language (preferentially Python), data analytics language (R and/or Matlab) (as well as proficiency in working on Linux clusters and databases. - Demonstrated knowledge and experience with Next Generation Sequencing and genomics datasets, including filtering/processing large datasets, multivariate statistical analysis, developing analytical methods and pipelines, and performing population genetics analyses. - Demonstrated ability to publish in scientific journals, and present research at international conferences. - Excellent written and oral communication skills with the ability to liaise, collaborate and interact with a wide range of national and international scientific researchers.

*Salary: Level A $78,525 - $84,291 per annum, and up to 9.5% Superannuation applies.

Thisis a great opportunity to study abroad (for international candidates) as Adelaide is a vibrant cosmopolitan city with a Mediterranean climate guaranteeing a great lifestyle. Interested applicants are encouraged to send a resume, a cover letter and a list with full contact details of three referees to Prof Alan Cooper (alan.cooper@adelaide.edu.au), and Dr. Yassine Souilmi (yassine.souilmi@adelaide.edu.au).

yassine.souilmi@adelaide.edu.au

UBirmingham AdaptiveEvolution

dear community, * *

*A 30-month postdoc position**is open at the University of Birmingham in the Environmental Genomics Group**for an evolutionary biologist. *

the live link to the application on the University webpage is the following: https://atsv7.wcn.co.uk/search_engine/jobs.cgi?amN vZGU9MTYy MTM5MSZ2 dF90ZW1w bGF0ZT03 Njcmb3du ZXI9NTAzM jUyMSZvd2 5lcnR5cG U9ZmFpci ZicmFuZF 9pZD0wJn ZhY2Zpcm0 udmFjdGl0 bGU9NTY3 NDMmcG9z dGluZ19j b2RlPTEx NyZyZXFza Wc9MTQ4ND U4NjM4My 04NDEzMD RhNjNiMm Q5MDU5YT JmNzQxOGI wOTY5ZTRl ZTI2YzBi OTNj=&jc ode21 391&vt_t emplate=7 67&owner= 5032521& ownertyp eúir&b rand_id= 0&vacfirm .vactitle V743&p osting_c ode7& reqsig=1 484586383 -841304a6 3b2d9059 a2f7418b 0969e4ee 26c0b93c

Job description

One 30-month postdoctoral research fellowship in Experimental Evolutionary Ecology and Omics is available within the School of Biosciences in the Environmental Genomics Group at the University of Birmingham, UK.

"Cracking the Code of Adaptive Evolution" (dCODE) is a multidisciplinary collaboration among seven investigators at the University of Birmingham who form a vibrant research community to advance the field of environmental omics. We pursue foundational science using natural populations of the ecologically relevant model species Daphnia. This project seeks to discover the relative contributions of phenotypic plasticity, the epigenome, and of molecular evolution to the process of adaptation, by experimenting on an historical Daphnia population that is "resurrected" from dormancy spanning 100 years of evolution.

The candidate will contribute to the planned research by (1) designing and conducting experiments to assess fitness changes leading to species persistence in presence of anthropogenic stress; (2) performing advanced statistical analyses to summarize fitness responses at species level; (3) linking fitness responses at species level with ecosystem services. Ability to code in R or similar software is required. The ideal candidate will: (i) understand theoretical underpinnings of evolutionary theories; (ii) have proven experience in conducting and analyzing experiments in the field of evolutionary ecology; (iii) have prior knowledge on how to link biodiversity and genetic diversity to ecosystem functioning and services; (iv) have prior experience with working in a multidisciplinary context.

The successful candidate will be responsible for all aspects related to laboratory experiments using Daphnia.

Applicants must hold a PhD-degree with substantial experience in experimental evolution design and analysis, statistics and biostatistics. Ability to perform ecological modeling and in combining experimental and omics data will be considered an advantage.

thanks, Luisa Orsini

–

Dr Luisa Orsini Lecturer in BioSystems and Environmental Change Fellow of the Higher Education Academy Environmental Genomics Group, School of Biosciences, University of Birmingham Birmingham, B15 2TT, United Kingdom T: +44 (0)121 4145894 F: +44 (0)121 414 5925 Email: l.orsini[at]bham.ac.uk

https://lorsini5.wixsite.com/luisaorsini http://www.birmingham.ac.uk/schools/biosciences/staff/profile.aspx?ReferenceId=63090&Name=dr-luisa-orsini https://www.researchgate.net/profile/Luisa_Orsini "Luisa Orsini (School of Biosciences)" <l.orsini@bham.ac.uk>

UCalifornia SanDiego PDF Tech YeastExptEvol

Postdoc and technician positions available to work on experimental evolution of gene drives in yeast

Gene drives are technology that will potentially transform our capacity to eliminate diseases like malaria, extricate invasive species, and combat hunger. The newest iteration of this technology incorporates CRISPER/Cas9 into genetic elements that can transfer from one copy of a chromosome to others. This property allows the elements to defy Mendelian inheritance and to drive through a population. As they drive, the elements can carry beneficial genes, such malarial resistance alleles in mosquito populations. While gene drives are powerful molecular tools, there are a number of unknowns about their evolution and the evolutionary pressures they impose on the genomes they are introduced to. Will the elements evolve loss of function mutations or others that cause unintended transfers, will the drives impose selection on their host genomes to coevolve, and will drive-induced mutagenesis alter the target genome's evolutionary trajectory? Sergey Kryazhimskiy and Justin Meyer's labs at UC San Diego will begin to answer these questions using experimental evolution of Saccharomyces cerevisiae. This project will be part of a larger active genetics initiative at UCSD and the creation of the Tata Institute for Genetics and Society on campus and in India. Two positions are available, a postdoc and technician, that will begin in June of 2017. Please e-mail Justin, jrmeyer@ucsd.edu with your cv and short cover letter if you're interested in joining this important and groundbreaking work. Ideal candidates will have experience with yeast genetic engineering, genomics, and evolutionary theory.

Justin Meyer Asst Prof, Biology, U.C. San Diego http://labs.biology.ucsd.edu/meyer Justin Meyer <jrmeyer@ucsd.edu>

UCambridge BacterialGenomicEpidemiology

University of Cambridge. The funds for this post are available until 23 April 2020 in the first instance.

http://www.jobs.cam.ac.uk/job/13109/ Applications are invited for a Research Assistant/Research Associate position in bacterial genomic epidemiology to start from 1 May 2017 or as soon as possible after this date, funded by the Medical Research Council through a Joint Programming Initiative on Antimicrobial Resistance international consortium project aiming to understand the transmission of antimicrobial resistance (AMR) at the genome, bacterium, national and international levels. This research is highly topical and relevant to both human and animal health. The work will be conducted within a One Health framework, consistent with research recommended by several international policy reviews, including the Food and Agriculture Organization, the World Organisation for Animal Health, and the World Health Organization.

The focus of the research is on extended-spectrum cephalosporin (ESC) resistance in Enterobacteriaceae, comparing bacteria, host populations (humans and domestic animals) and countries. Collaborators providing data are from Canada, France and Germany. A suite of quantitative approaches will be used, including epidemiological, phylodynamic and bioinformatics methods, analysing whole genome sequences. This post will be based in Cambridge led by Dr Alison Mather and Professor James Wood, with opportunities to visit the other consortium partners.

Applicants will have a PhD (or have submitted a PhD) in epidemiology, computational biology or a related quantitative discipline, and experience working with next generation sequencing data. Desirable skills will be experience in mathematical modelling and programming skills in Unix, python and R. The candidate must value teamwork and collaboration, be able to work independently, and have excellent communication and interpersonal skills.

Some of the main duties will include:

Selection of isolates for whole genome sequencing (WGS) from bacterial collections held by collaborators

Epidemiological analysis of bacterial collections

Analysis of WGS data to assess transmission and evolution of bacteria and AMR

A full detailed description of the key responsibilities is available in the further particulars file.

Where a PhD award is pending (e.g, the thesis has been submitted but has not yet been examined), an appointment will be made as a Research Assistant and amended to Research Associate when the PhD is awarded.

For informal enquires please contact: Natalie Wills nw366@cam.ac.uk

To submit an application for this vacancy, please visit the vacancy pages on the following website: http://www.jobs.cam.ac.uk/ Further particulars for the role and information about the Department www.vet.cam.ac.uk . Fixed-term: The funds for this post are available until 23 April 2020 in the first instance.

To apply online for this vacancy, please click on the 'Apply' button below. This will route you to the University's Web Recruitment System, where you will need to register an account (if you have not already) and log in before completing the online application form.

Please ensure that you upload your Curriculum Vitae (CV) and a covering letter in the Upload section of the online application. If you upload any additional documents which have not been requested, we will not be able to consider these as part of your application

Closing date: 17 April 2017

Interviews will be held on 5 May 2017

Please quote reference PP11624 on your application and in any correspondence about this vacancy.

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

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

lucy.weinert@googlemail.com

UCambridge EvolutionaryNeurobiology

Postdoc in brain evolution in butterflies

We invite applications for postdoctoral Research Associate position in the Department of Zoology in Central Cambridge on Downing Street with Dr Stephen Montgomery's research group. It is funded for up to 12 month and should start on 1 June 2017 or as soon as possible thereafter.

The PDRA will study the cellular basis of evolved differences in mushroom body size across Heliconius butterflies and their closest relatives. We have recently confirmed previous reports that Heliconius have evolved massively expanded mushroom bodies (see Montgomery et al. 2016 J. Comp. Neurol. 524 (9):1747-1769; and Merrill et al. 2015 J. Evol. Biol. 28(8): 1417-1438 for a wider review of Heliconius behaviour), providing a novel case study for investigating the causes and consequences of volumetric expansion of 'higher order' brain regions.

We are interested in understanding the cellular basis of mushroom body expansion by investigating how the number of neurons and synaptic complexes co-evolve with size, and by testing the hypothesis that mushroom body expansion co-evolves with changes in input to the mushroom bodies from other brain regions.

The successful applicant should have a Ph.D., completed or completion imminent, in comparative neurobiology, evolutionary biology cell/developmental biology or a related field, and a strong interest in brain and behavioural evolution. Candidates should have a good collaborative spirit, and can expect a high degree of support and assistance from the PI. Enthusiasm, determination and the capacity to work independently are also essential.

Fixed-term: The funds for this post are available for up to 12 months.

Further details about the post can be found here: http://www.jobs.cam.ac.uk/job/13015/ Departmental webpage: http://www.zoo.cam.ac.uk/directory/-stephen-montgomery Personal webpage: http:/-/www.shmontgomery.co.uk Stephen Montgomery <shm37@cam.ac.uk>

UCambridge FloralEvolution

Deadline: 26 March

A position is open for a NERC-funded postdoctoral research associate based within the Department of Plant Sciences at the University of Cambridge, and supervised by Professor Beverley Glover in collaboration with Professor Allan Ellis (University of Stellenbosch).

The appointee will investigate the ecological, population genetic and molecular developmental processes that generate and maintain floral variation and lead to incipient speciation in the South African daisy Gorteria diffusa. In this project we aim to understand how morphological variation within a species is produced genetically, how variation is affected by natural selection resulting from ecological context, and how such variation is maintained when varieties meet. We are particularly focused on the insect-mimicking spots found on the ray florets of Gorteria diffusa.

The primary objectives of this project are:

1. To describe the evolutionary patterns underpinning morphologically distinct populations by character mapping floral traits and the genes underlying them onto our established phylogeny of the system.

2. To determine the ecological causes of intraspecific variation in targeted floral traits through field studies including reciprocal transplant experiments and analyses of ecological context.

3. To determine the evolutionary processes maintaining intraspecific floral variation by investigating barriers to hybridization.

4. To determine the molecular developmental pathways that allow floral variation to evolve, using comparative transcriptomic approaches to identify genetic regulators of petal spots.

We are looking for a highly motivated post-doctoral scientist to work in this area. The successful candidate must be able to demonstrate a strong background in the evolution and development of flowering plants, including a PhD in a relevant area. Experience with molecular genetic, systematic and developmental techniques will be necessary, along with prior experience of ecological techniques.

The appointee will be expected to carry out field work in South Africa over at least two austral springs. For further information contact Professor Beverley Glover (bjg26@cam.ac.uk).

For more information and to apply go to: http://www.plantsci.cam.ac.uk/jobs/pd11523 "bjg26@hermes.cam.ac.uk" <bjg26@hermes.cam.ac.uk>

UCLondon ExcellenceFellowships

UCL Excellence Fellowships Department of Genetics, Evolution, and Environment University College London

UCL's Department of Genetics, Evolution and Environment (GEE) is a world class department with a broad research portfolio. We are currently recruiting promising early-career researchers via UCL's Excellence Fellowship programme. We aim to expand our current strengths by encouraging applications from outstanding applicants in the main research areas within the department:

- Comparative 'omics' and deep evolutionary analysis (new Centre for Life's Origins and Evolution, contact Prof. Max Telford, m.telford@ucl.ac.uk) - Research at the interface between biodiversity and environmental change (Centre for Biodiversity and Environmental Research, contact Prof. Georgina Mace, g.mace@ucl.ac.uk) - Statistical and computational biology (R.A. Fisher Centre for Computational Biology, contact Prof. Ziheng Yang, z.yang@ucl.ac.uk) - Genetics of health and disease (UCL Genetics Institute, contact Prof. François Balloux, f.balloux@ucl.ac.uk) - Biology of ageing (Institute for Healthy Ageing, contact Prof. Linda Partridge, l.partridge@ucl.ac.uk)

The UCL Excellence Fellowship scheme is run by the School of Life and Medical Sciences and is open to the full range of disciplines in basic and applied life sciences. The fellowship offers salary and research funding, as well as generous funding supplements for individuals transferring existing, externally funded fellowships to UCL. Excellence Fellows who are not already holding awards are expected to apply to externally funded schemes, including ERC, Royal Society, NERC, BBSRC, and Wellcome Trust. This requires that Excellence Fellowship applicants are eligible and competitive for these awards. For more information on the Excellence scheme and application process, see http://www.ucl.ac.uk/slms/research/excellence-fellowship/ Candidates are required to identify a sponsor in GEE by contacting a relevant member of staff. Please identify a sponsor and contact Prof. Anjali Goswami (a.goswami@ucl.ac.uk) and Dr Max Reuter (m.reuter@ucl.ac.uk), who are in charge of fellowship support for GEE, to notify us of your interest in applying by April 7, 2017. GEE runs a pre-selection to identify candidates for departmental support. Preliminary applications, including a one-page proposal, full CV and the name of the sponsor, should be submitted for internal review by April 25, 2017. Documents should be sent to Prof. Anjali Goswami and Dr Max Reuter. They can also provide assistance with identifying a potential sponsor if contacted in advance of the deadline. Based on the preliminary applications, a shortlist of applicants will be selected for departmental support and invited to submit a full application by the scheme deadline of May 10, 2017.

The Department has had great success supporting fellowship applicants from initial application to securing subsequent permanent employment within UCL. You can find more information about the department and its research centres and institutes at http://www.ucl.ac.uk/gee . A note for non-UK applicants: Fellowships allow early- and mid-career scientists to concentrate on their work unhindered by teaching and administrative loads. They are an integral part of the UK academic system and are a typical route towards permanent academic positions. Schemes covering salary and research expenses from a range of funding agencies are open to non-UK applicants. Please see http://www.ucl.ac.uk/gee/fellowships for more details.

"Goswami, Anjali" <a.goswami@ucl.ac.uk>

UFlorida HumanEvolGeneticsEpigenetcs

Post-doctoral position in Human Evolutionary Genetics and Epigenetics, Laboratory of Connie Mulligan, Department of Anthropology, University of Florida, Gainesville, FL, USA

Post-doctoral position to work on two ongoing NSF and internally funded projects: 1) Investigation of an epigenetic mechanism to mediate the effects of maternal stress on maternal and infant health in the Democratic Republic of Congo (DRC). We are testing for associations between maternal stress exposures, newborn health outcomes and changes in DNA methylation and gene expression in mothers and their infants. More broadly, we are interested in the idea that mechanisms may have evolved to allow the genome to respond to psychosocial stressors, specifically behavior and complex phenotypes may be shaped by early life experiences that alter gene expression through epigenetic alterations. Samples and data have already been collected and research is funded by a newly awarded NSF grant. See http://www.tandfonline.com/doi/pdf/-10.4161/epi.21180 and http://onlinelibrary.wiley.com/-doi/10.1111/cdev.12487/epdf .2) Investigation of genetic, epigenetic, and biological signatures of war trauma exposures and impact of a program intervention in Syrian refugees. This is a collaboration with Catherine Panter-Brick (Anthropology, Yale University) and Rana Dajani (Hashemite University, Jordan) to integrate genetic and epigenetic analyses into an ongoing study to measure the health effects of a program intervention to reduce psychosocial stress in Syrian refugees. Genetic variants are assayed to predict the impact of past stress exposures and the effects of the program intervention on self-reported mental health. Epigenetic variants will be tested as possible mediators of the effect of stress on mental health outcomes. See project website at http://www.elrha.org/map-location/-yale-psychosocial-call2/. In addition, samples are currently being collected for an intergenerational study to investigate the epigenetic impacts in offspring of war-exposed mothers and grandmothers. The bigger question is to determine if environmentally-induced methylation changes are heritable across two generations in humans.

Qualifications: A PhD, good publication record, and strong background in the generation of genetic data (microarray, gene expression, NGS, SNP detection) and data analysis (gene association analysis, regression analysis, genetic ancestry estimation, linkage analysis, etc) are essential. A background in evolutionary genetics and experience with methylation data (Illumina chips, pyrosequencing, etc), RNA sequence/gene expression array data and/or additional computational or bioinformatics experience (e.g. computer programming, simulation analysis, etc) is a plus. Candidates who speak French or Swahili are encouraged to apply. In addition to the projects listed above, there are excellent opportunities for the successful candidate to develop new lines of research as well as productive collaborations outside the lab.

The University of Florida is a leading research institution with a university-wide commitment to genetics research. The Department of Anthropology (www.anthro.ufl.edu) has 30 full-time faculty with diverse interests and is one of the top rated programs in the country (6th among public institutions, 11th overall). The University of Florida Genetics Institute (www.ufgi.ufl.edu) is an inter-college institute with a dedicated research building intended to enhance opportunities for collaboration. Gainesville is located in north central Florida (away from the hurricanes!), with average temperatures ranging from 45F to 90F. Beaches on the gulf and Atlantic coast are ~ 1Â½ hours away.

To apply: via email, send a CV, statement of research interests, and names and contact information for three references. Applications and inquiries should be addressed to Connie Mulligan at cmulligan@ufl.edu.

Review of materials will begin March 31 and will continue until the position is filled. Start date is flexible and the successful candidate can begin as early as May, 2017. Salary is commensurate with experience. Position may be extended for a total of three years. Informal inquiries prior to submitting a formal application are welcome. AA/EOE.

"Connie J. Mulligan" <cmulligan@ad.ufl.edu>

UHalle EvolutionaryBehaviour

Postdoctoral Research Scholar in Behaviour at University of Halle, Germany

An experienced research scientist/assistant/associate professor with an emphasis on behaviour (e.g. behavioural ecology, sociobiology) is sought for a full-time position to join the Paxton lab at the University of Halle, Germany. Broad research themes of the group are host-parasite interactions, pollination, conservation biology and social evolution:

http://www.zoologie.uni-halle.de/allgemeine_zoologie/-research/ The group's taxonomic focus is on insects, particularly bees, it draws heavily on molecular genetics, and research infrastructure is excellent. We seek a highly motivated individual with strong quantitative skills who can work independently to develop a research program complementary to one or more of the group's themes and contribute to teaching behaviour at undergraduate and postgraduate levels within general zoology. Halle is a delightful, historic city of a quarter million people with a large, research-intensive university situated 260 km southwest of Berlin and 40 km from Leipzig. You will be a member of a supportive and dynamic group that interacts closely within and outside the university, including with the UFZ-Helmholtz Environmental Research Center at Halle-Leipzig:

http://www.ufz.de/ and with the recently established DFG-funded biodiversity center iDIV: http://-

www.idiv.de/ a collaboration of the universities of Halle, Leipzig and Jena.

Applicants must hold a university doctoral degree in biology or a related discipline and address current topics in behaviour (e.g. behavioural ecology, sociobiology). Applicants should have a proven track record in publishing high quality scientific papers. Experience in writing grant applications and past success in attracting research funding is of advantage. The working language of the group is English, though knowledge of German is essential for teaching purposes. The position is fixed term, initially for 3 years, commencing 1 August 2017 or as soon as possible thereafter, with the possibility of extension for a further 3 years. The salary is currently at the German standard postdoctoral rate (TV-L 13, 100%). The University of Halle is an equal opportunity employer. Further details of the position can be obtained from Robert Paxton (email below), to whom applications should be emailed as a single pdf file, to include (i) a letter of motivation, (ii) cv, (iii) list of publications, (iv) list of externally acquired funds, (v) a single page on research achievements and future plans, (vi) a single page on experiences and approaches to teaching, and (vii) contact details of three referees, by 15 May 2017. Interviews are scheduled for the end of June 2017.

Prof. Robert Paxton, General Zoology/Institute of Biology, Uni. Halle, Hoher Weg 8, D-06120 Halle/Saale, Germany. Tel.: +49-345-5526500; Email: robert.paxton [at] zoologie.uni-halle.de

Robert Paxton <robert.paxton@zoologie.uni-halle.de>

UIdaho BiomedicalModeling

The NIH-funded Center for Modeling Complex Interactions (CMCI) at the University of Idaho (UI) is an intellectual, cultural, and physical environment to foster synergy in interdisciplinary biomedical research. The focal point of CMCI is the Collaboratorium, a space and a culture for collaborative modeling. It brings together faculty and students from both the empirical and modeling realms with postdoctoral scientists who reside in the Collaboratorium and devote full-time effort to collaborative modeling. We currently have openings in the Collaboratorium for two postdoctoral fellows interested in biomedical modeling.

CMCI fellows are knowledgeable modelers who are creative, collaborative, and strong communicators. They engage in interdisciplinary research, working with both experimentalists and other modelers, and take leadership roles on research direction, manuscript preparation, offering workshops to the UI research community, and presenting research at national and international scientific meetings.

CMCI interfaces with several strong research programs at UI including bioinformatics, computational biology, evolutionary biology, microbiome ecology, infectious disease, and movement science. Fellows will have opportunities to collaborate across campus on these and other areas of biomedical research.

For more information about CMCI, visit http://www.cmciuidaho.org/. To apply submit: 1) a letter of application addressing the criteria outlined above; 2) a CV; 3) contact information for three individuals who can provide recommendations; and 4) PDFs of up to three publications to cmci@uidaho.edu. Use COLLABORATIVE POSTDOC APPLICATION as the subject line. Review of applications will begin in mid-March and will continue until all positions are filled.

“mmattoon@uidaho.edu” <mmattoon@uidaho.edu>

UKansas DrosophilaComplexTraits

A postdoc position is available in my lab at KU to work on any of a number of evolutionary genomics projects that use flies to understand and dissect complex trait variation. Projects emphasize the Drosophila Synthetic Population Resource (DSPR) that my lab is developing. The formal announcement, and links to the institutional employment website are provided below. I'll be at the fly meeting in San Diego in a few days if anyone would like to talk more about the position. Feel free to email me with any questions. Stuart Macdonald (sjmac@ku.edu)

The Macdonald lab at the University of Kansas seeks a postdoctoral researcher with interests in the genetics of complex trait variation. The Macdonald group uses a range of molecular, genetic, and genomic technologies to dissect the genetic basis of complex phenotypic variation using Drosophila as a model system. We are also leading the development of the Drosophila Synthetic Population Resource (DSPR, FlyRILs.org) in collaboration with Tony Long's group at UC Irvine. As part of the DSPR project we are generating large sets of phenotyping data, and various large-scale, tissue-specific RNAseq and ATACseq datasets. A principal goal is to combine these data to dissect trait variation to the level of causative polymorphisms, and ultimately validate via CRISPR/Cas9 editing. The breadth and depth of the data we are collecting allows for a range of questions to be addressed, allowing the successful candidate to position themselves as an independent investigator. The position is funded through a multi-year NIH grant and has an anticipated start date of 1 July 2017 (although this is negotiable).

Required qualifications include a PhD in evolution/genetics/bioinformatics (or a related field), and a first-author publication that shows your ability to initiate and execute a research project. Prior experience with Drosophila, with big data analysis, and with genome editing would all be useful, but are not required.

For a complete announcement and to apply online, go to https://employment.ku.edu/staff/8359BR Please direct any questions about the position to Stuart Macdonald (sjmac@ku.edu).

A complete online application includes the following materials: A CV, a cover letter outlining relevant experience, research interests and accomplishments, and contact information (phone/email/address) for three referees. Initial review of applications begins 1 May 2017 and will continue until the position is filled.

The University of Kansas prohibits discrimination on the basis of race, color, ethnicity, religion, sex, national origin, age, ancestry, disability, status as a veteran, sexual orientation, marital status, parental status, gender identity, gender expression, genetic information and retaliation in the University's programs and activities. Access to information regarding equal opportunity and diversity worksite posters is available at http://www.humanresources.ku.edu/policies_procedures/category_details/index.aspx?category=8 or you may contact 785-864-4946 or employ@ku.edu for alternate access options. Any inquiries regarding the non-discrimination policies should be directed to: Executive Director of the Office of Institutional Opportunity and Access, IOA@ku.edu, 1246 W. Campus Road, Room 153A, Lawrence, KS, 66045, (785)864-6414, 711 TTY.

Dr. Stuart J. Macdonald Department of Molecular Biosciences 4043 Haworth Hall 1200 Sunnyside Avenue University of Kansas Lawrence KS 66045

office: 785-864-5362 lab: 785-864-5777 fax: 785-864-5321 email: sjmac@ku.edu web: FlyRILs.org

"sjmac@ku.edu" <sjmac@ku.edu>

ULeiden AntibioticResistance

3-year Postdoc, Evolution of Antibiotic Resistance Institute of Biology, Leiden University, The Netherlands

A 3-year Postdoc position is available in my lab at the University of Leiden in The Netherlands. This JPI-AMR (Joint Programming Initiative on Antimicrobial Resistance) funded project will study the structure, causes and consequences of collateral sensitivity (CS) networks for antibiotic resistance in Streptococcus pneumoniae. The project is part of an international collaboration between experimentalists and theoreticians, with labs in Norway (Pal Johnsen and Pia Abel zur Weisch), Sweden (Dan Andersson) and Denmark (Niels Frimodt-Moller).

Collateral sensitivity between a pair of antibiotics occurs when a mutation causing resistance to one antibiotic increases susceptibility to another. Across multiple antibiotics, CS networks define how resistance mutations for any given drug influences the response of a bacterial strain to exposure to a suite of alternative agents. By understanding these responses at a phenotypic and mechanistic level, CS networks can be used to make rational and informed decisions about drug choice and dosage that can suppress the emergence and spread of de novo resistance, and also potentially arrest the transmission of pre-existing resistance in clinical isolates.

The postdoc will identify CS networks for both chromosomal and horizontally acquired resistance for Streptococcus pneumoniae, a gram-positive pathogen responsible for more than 1 million deaths in children annually, and seek to answer the following questions: 1) Can the spread of strains with pre-existing antibiotic resistance be suppressed via CS-based therapy; 2) do CS networks vary as a function of genetic background; 3) Is CS in laboratory isolates informative of CS in clinical isolates; and 4) What is the interplay between S. pneumoniae transformation and CS?

Interested applicants should have experience in microbiology, microbial evolution and molecular genetics and a strong interest in antibiotic resistance. Bioinformatics experience and design of methods and analysis for high-throughput screening is also desirable.

Written applications, including a motivation letter, a CV and the names of three references, will be reviewed until the position is filled.

Informal enquiries can be addressed to: Daniel

Rozen, Tel: +31 (0)71 527 7990, Email: d.e.rozen@biology.leidenuniv.nl

"Rozen, D.E." <d.e.rozen@biology.leidenuniv.nl>

ULeuven PDF0rPhD Bioinformatics

Postdoc or Ph.D bioinformatics: Single molecule sequencing

The Laboratory for Cytogenetics and Genome research at the Center for Human Genetics is looking for a:

Postdoc or Ph.D bioinformatics: Single molecule sequencing

The Laboratory for Cytogenetics and Genome research at the Center for Human Genetics develops tools for genome analyses. Currently, we are implementing PacBio single molecule sequencing for de novo genome assemblies and we are exploring the use of PacBio sequencing for haplotyping.

Website unit < http://gbiomed.kuleuven.be/apps/cme/index.html?en >:

Project * Implementation and development of bioinformatics tools to enable genome wide haplotyping from single molecule sequencing data. * Combining short and long read sequencing technologies to improve genome wide de novo assemblies. * Involvement in targeted haplotype reconstruction. * Participation in structural variation detection. * Gene discovery based on structural variation analysis.

Profile * You have a masters/doctoral degree in bioinformatics or biology but with strong bioinformatics skills. * You have experience with massive parallel sequencing data analysis and genomics. * You can work independently. * You have a proven scientific track record and have strong scientific interests.

Offer * A job of three (Postdoctoral researcher) or four years (Ph.D researcher). * A position in an international environment, a vibrant work atmosphere and in modern facilities. The KU Leuven (University of Leuven) is located in the city of Leuven, a historic, dynamic and lively city located in the heart of Europe.

Interested? For more information please contact Prof. dr. Joris Vermeesch, tel.: +3216345941, mail: joris.vermeesch@kuleuven.be You can apply for this job no later than April 16, 2017 via the

Online application tool: http://www.kuleuven.be/eapplyingforjobs/light/54118024 Job description: http://gbiomed.kuleuven.be/apps/cme/jobdetail.html?job_id=223 Gregory Maes, Ph.D. University of Leuven (KU Leuven) Laboratory for Cytogenetics and Genome Research Centre for Human Genetics | Genomics Core O&N I Herestraat 49 - box 602 UZ Leuven B-3000 Leuven Belgium Phone: +32 (0)16 37 25 22 E-mail: gregory.maes@kuleuven.be

Gregory Maes <gregory.maes@kuleuven.be>

UmeaU ProteinEvolution

There is a post doc position available in the lab of Vasili Hauryliuk, MIMS Nordic EMBL, Umea University, Sweden:

http://www.ucmr.umu.se/images/postdoc2017/Hauryliuk.pdf http://www.mims.umu.se/groups/vasili-hauryliuk.html The project is on small alarmone ((p)ppGpp) syntetase enzymes in bacteria, and their recently discovered regulation by RNA (Beljantseva et al. PNAS, in press). These enzymes are important for many aspects of bacterial physiology, and response to stress including antibiotic challenges. The project is open ended, and can be either wet lab based, or computer based (including comparative genomics and phylogenetics). Bioinformatic investigations would be co-supervised by me (http://www.molbiol.umu.se/english/research/researchers/gemma-atkinson/).

Contact: vasili.hauryliuk@umu.se

Please spread the word!

Best wishes,

Gemma C. Atkinson

Umea Centre for Microbial Research (UCMR)

Department of Molecular Biology

Umea University, Sweden

Gemma Atkinson <gemma.atkinson@umu.se>

UMinnesota BiologyEducation

Postdoctoral Associate - University of Minnesota

The Cotner lab seeks a post-doc for 1-2 years (or more, pending funding). Duties include:ÃCollaborating with Andamio Games (https://www.andamiogames.com/), Biology Teaching and Learning (BTL), and Center for Educational Innovation (CEI) faculty and staff at the University of Minnesota; teaching in the non-majors course series; and researching one or more of the following: STEM equity, STEM games in a k-12 setting, and course-based undergraduate research experiences for non-majors. The selected candidate will: serve as the scientific consultant on a Phase II ÃSerious STEM GamesÃ project (NSF funded), to develop educational games centered on metabolism; teach Biology 1003 in Spring 2018 (department funded), and conduct Biology Education Research aligned with personal and PI goals (PI funded).Ã

Essential Qualifications: PhD in the natural sciences; documentation of evidence-based teaching; interest in the above topics

Preferred Qualifications: ÃPeer-reviewed publications in both the natural sciences and discipline-based education research

I'd love this individual to start in May, but can be flexible. I'll begin reviewing applicationsÃMarch 20.

Lab website: https://cbs.umn.edu/cotner-lab Job posting: https://cbs.umn.edu/academics/departments/btl/hiring/cotner-postdoc-associate Applicants canÃapplyÃby: 1) VisitingÃhttp://www1.umn.edu/ohr/employment/ 2) Clicking on the tab in the center of the page that corresponds to their situation 3) Searching Job ID# 316032

Cissy Ballen, PhD Postdoctoral Associate Dept. of Biology Teaching and Learning College of Biological Sciences University of Minnesota 3-154 Molecular & Cellular Biology 420 Washington Avenue SE Minneapolis, MN 55455 *P *607 279 2625 | *E* balle027@umn.edu

Cissy Ballen <balle027@umn.edu>

UNebraska PopulationBiology

UNebraska-Population Biology Post-doc

POPULATION BIOLOGY POSTDOCTORAL RESEARCH FELLOWSHIP

THE UNIVERSITY OF NEBRASKA-LINCOLN is seeking applications for a 2-year postdoctoral position in the Population Biology Program of Excellence. The goal of the Population Biology-POE Postdoctoral Fellowship is to stimulate synergistic interactions between faculty and postdoctoral scholars interested in the broad area of Population Biology. We are seeking applications from recent PhDs who show promise of conducting cutting edge research related to, and expanding upon, faculty research areas in the Ecology, Evolution & Behavior (EEB) section in the School of Biological Sciences (http://biosci.unl.edu/research-specializations). The POE also seeks to identify potential postdoctoral fellows who will enhance graduate education, serve as a model for graduate students in career development, and promote interactions among faculty at UNL. Qualified candidates are required to submit a single, coherent 2-year research proposal to be completed under the guidance of a faculty member in the Ecology, Evolution & Behavior (EEB) section in the School of Biological Sciences. The position does not include research funds so the extent of contributions from the faculty sponsor should be addressed in the proposal. While in residence, the postdoctoral fellow will be expected to lead a seminar, symposium or outreach project that will appeal to Population Biologists across campus. Applications must include a CV, a 1-page description of previous or current research and a 2- 3 page description of proposed research. Additional proposal guidelines and suggestions should be obtained from the proposed faculty sponsor. In addition, the applicant must arrange for two recommendation letters from non-UNL faculty, and one from the UNL faculty sponsor (a total of 3 letters) to be emailed to the address below. The expected salary will be $45,000 per year with a start date of August 1, 2017. Priority will be given to applicants who have completed their degree and are new to UNL. Research descriptions for past and current POE postdoctoral fellows can be viewed at http://biosci.unl.edu/population-biology/ Application materials should be emailed to: Dr. Johannes Knops at: jknops2@unl.edu. The subject line should read "Population Biology Post-doc application". Applications should be received by May 1, 2017. We anticipate notifying the successful applicant by June 1, 2017, with a starting date of August 1 or later in 2017. We strongly encourage applications from women and members of minority groups. The University of Nebraska is committed to a pluralistic campus community through affirmative action, equal opportunity, work-life balance, and dual careers. We assure responsible accommodation under the Americans with Disabilities Act.

Diana Pilson

Associate Dean for Academic Programs

College of Arts and Sciences

1223 Oldfather Hall

University of Nebraska

402-472-2891

School of Biological Sciences

408 Manter Hall

Manter Hall

402-472-2347

Diana Pilson <dpilson@unl.edu>

UOslo DevelopmentalBiologyEvolution

Researcher in Developmental Biology and Evolution A three year position as Researcher in Developmental Biology and Evolution is available at CEES, Department of Biosciences. The researcher will be part of the MOLBAR project (The molecular basis of postzygotic hybridization barriers in plants) lead by Professor Anne Brysting and Professor Paul Grini, where the main goal is to elucidate the molecular basis of postzygotic hybridization barriers in plants. The candidate will work in close collaboration with the PIs and the rest of the international project team, which includes molecular-, developmental- and evolutionary biologists, representing a diverse array of expertise ranging from phenotypic developmental analysis and the epigenetics of genomic imprinting to molecular systematics and speciation theory. The position will be affiliated to the Centre for Ecological and Evolutionary Synthesis (CEES) and Section for Genetics and Evolutionary Biology (EVOGENE) at the Department of Biosciences, University of Oslo. The appointment is for a period of three years. The Research Council of Norway finances the project. The candidate should be able to fill the position by the project start 01.08.2017 (given funding from the RCN).

Location The University of Oslo is Norway's oldest and highest rated institution of research and education with 28 000 students and 7000 employees. Its broad range of academic disciplines and internationally esteemed research communities make UiO an important contributor to society. The Centre for Ecological and Evolutionary Synthesis (CEES) is a Centre of Excellence (CoE) based at the Department of Biosciences, University of Oslo. CEES combines a broad spectrum of disciplines (population biology, genomics, statistics, mathematical modelling) to foster the concept of ecology as a driving force of evolution via selective processes, with a corresponding influence of evolutionary changes on ecology. CEES has over 160 members (Professors (20), postdocs/researchers (45), PhDs (25), Master's students (25) and technical and administrative staff) and many guest researchers. The members represent 30 nationalities and constitute a vibrant and creative research environment. CEES coordinate several international networks. The budget = 150 million NOK (about 50 externally funded research projects). CEES is chaired by Professor Nils Chr. Stenseth.

Project description The evolution of reproductive isolation is a classic problem in evolutionary biology. Plant species are typically isolated by different pre- and postzygotic barriers in potentially complex interactions. Much progress has been made in characterizing individual components of reproductive isolation but still the evolutionary forces responsible for development of postzygotic barriers are virtually unknown. The aim of the MOLBAR project is to elucidate the molecular and phenotypic basis of postzygotic hybridization barriers. Our approach is unique as it integrates detailed observation of embryo and endosperm development in hybrid seeds with identification of genes and mechanisms responsible for the barrier. To test our hypotheses, we will cross species within two Brassicaceae genera (Arabidopsis and Draba), look for similar patterns of aberrant seed development and relate these to underlying imprinting programs and gene networks. As part of the experimental setup, we will 1) characterize seed developmental phenotypes of postzygotic barriers in crosses between different species, different ploidy levels and cryptic species; 2) characterize maternal and paternal expression patterns in hybrid seeds using mRNA-seq; 3) determine imprinting status of selected candidate genes; and 4) integrate the results to improve our common knowledge on one of the core issues in evolution - the underlying causes of the evolution of reproduction barriers, and thus speciation.

Requirements The Faculty of Mathematics and Natural Sciences has a strategic ambition of being a leading research faculty. The candidates for research fellowships will be selected in accordance with this, and expected to be in the upper segment of their class with respect to academic credentials. The main purpose of research fellowships is to qualify researchers to work in top academic positions within their disciplines. Applicants must hold a PhD-degree in Biology (or other corresponding education equivalent to a Norwegian doctoral degree) and additionally have post-doctoral or researcher experience. In particular, research experience in both molecular plant developmental biology and plant evolution will be preferred. The ideal candidate must have hands on experience working with different species and ploidies within the Draba or Arabidopsis genera, experimental experience in genetic and phenotypic analyses of plant reproduction, and experience with the analysis of genomic imprinting. We are seeking a highly motivated, enthusiastic and hard-working

— / —

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

UOtago NZ GenomicsParasiticMindControl

Postdoctoral Opportunity

Parasitic Puppeteers - How do They Pull the Strings? We are currently seeking an outstanding postdoctoral researcher with interests in genetics, evolution and parasitology to spearhead a new project to investigate the molecular mechanisms through which parasitic worms alter the behaviour of their insect hosts.

The position is funded by a grant from the Royal Society Marsden Fund and is available with an immediate start through to 29/2/2020.

Project Description: Parasites can have profound effects on the animal hosts they invade, manipulating host biology with exquisite precision to enhance host-to-host transmission. One of the most extraordinary of these host manipulations is the water-seeking behaviour that some nematodes and hairworms induce in their hosts so that the worms might exit the host and reproduce. The process is the stuff of science fiction; the worm hijacks the host's central nervous system forcing it to seek water. Once water is found the adult worm, often many times the size of the host, emerges, sacrificing the host. This amazing alteration in behaviour is induced by parasitic worms spanning two phyla (Nematoda and Nematomorpha) and is observed in a variety of arthropod hosts, notably crickets, weta, earwigs, and sandhoppers, leading us to hypothesise that a common and conserved mechanism is being utilised by the parasites to induce this behaviour in their hosts. Here we propose to couple field and laboratory studies of two phylogenetically distinct hosts and their parasites, with powerful genomic and bioinformatic comparisons to elucidate the trigger and genetic cascade through which these parasitic puppeteers elicit this highly conserved, yet astonishing behavioural response.

The project emerges from a new Marsden Grant headed by Professor Neil Gemmell (Anatomy) in collaboration with Professor Robert Poulin (Zoology) and will be based in the Gemmell laboratory at the University of Otago.

The Ideal Candidate: will possess experience in molecular genetics/genomics, evolutionary biology and bioinformatics. Knowledge of NGS approaches and analyses is essential, while past work in comparative genomics and an interest in parasitology and neurobiology may be helpful. The successful candidate will be motivated and organised, with a demonstrated capacity to master the broad skill set necessary for the successful completion of a research project. They will be collegial and able to work alongside a wide variety of people. In addition they will have a strong commitment to research excellence with a track record of high research productivity based on international, peer-reviewed publications commensurate for their career stage.

How to Apply: Interested applicants are encouraged to make informal enquiries to Professor Neil Gemmell. Please send your Curriculum Vitae, a sample of your best scientific work and the names of three referees with a covering letter to:

Professor Neil J. Gemmell e-mail: neil.gemmell@otago.ac.nz

Formal Applications must be made at: https://otago.taleo.net/careersection/2/jobdetail.ftl?lang=en&job=1700616 Salary Level and Range: Postdoctoral Fellow (NZ$74,896)

Reference Number: 1700616

Closing Date: 21 April 2017

Neil Gemmell <neil.gemmell@otago.ac.nz>

UQueensland QueenslandUTech MarsupialEvol

The Weisbecker lab at the University of Queensland and the Phillips lab at the Queensland University of Technology are looking for a postdoctoral researcher to support the Australian Research Council Discovery Grant “A new molecular/morphological view of animal evolution based on marsupials”. The primary purpose of this work is to develop novel methods for integrating molecular/phylogenetic and shape data, to refine our understanding of marsupial evolution and uncover mechanisms underpinning biodiversity variation in animals.

Applicants should possess qualifications in either evolution, genetics, bioinformatics or an equivalent combination of qualifications and experience in a similar field. They should have a proven research track record in computational phylogenetics and/or inference of morphological evolution (particulary in the field of 3D geometric morphometrics) in an animal clade, with demonstrated experience with computation in either R or BEAST/MrBayes. Applicants should also have well-developed written and oral communication skills and a demonstrated track record in publishing presenting at conferences.

For the full advert and to apply, please use the following link: http://jobs.uq.edu.au/caw/en/job/500211/-postdoctoral-research-fellow . For further information, contact Vera Weisbecker (v.weisbecker@uq.edu.au)

Dr Vera Weisbecker Lecturer University of Queensland School of Biological Sciences Goddard Building 8 St. Lucia 4072 Australia Ph.: +61 7 336 57071 UQ ALLY :: Supporting the diversity of sexuality and gender identity at UQ.

www.weisbeckerlab.com.au

USheffield Speciation

The Post-doctoral Research Associate will work with Professor Roger Butlin and Dr Anja Westram to advance a NERC-funded project on the routes to speciation in the coastal gastropod, Littorina saxatilis. The project is focused on the roles of divergent selection and incompatibility in speciation and requires a mix of skills including molecular ecology laboratory techniques, analysis of next generation sequence and genotype data, phenotypic (including behavioural) observations and field sampling with the help of collaborators. You will be expected to have a strong commitment to research in evolutionary genetics and a special interest in processes of speciation.

You should hold a PhD (or equivalent experience) in evolutionary genetics and have experience of research in evolutionary genetics. Experience in the handling of sequence and/ or expression data and experience of constructing bioinformatics pipelines is desirable.

The position is available from 1 May 2017, or as soon as possible thereafter, until 30 September 2019

For further details, and to apply, go to www.shef.ac.uk/-jobs - position reference UOS015526, closing date 30 March 2017

For more information, email r.k.butlin@shef.ac.uk or a.westram@shef.ac.uk

– Roger K Butlin

Professor of Evolutionary Biology Guest Professor Animal and Plant Sciences Centre for Marine Evolutionary Biology The University of Sheffield Department of Marine Sciences Western Bank University of Gothenburg Sheffield S10 2TN Gothenburg UK Sweden

r.k.butlin@shef.ac.uk

+44(0)114 2220097

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

USussex PopGenomics

Postdoctoral position in population genomics of balancing selection

University of Sussex EBE group, School of Life Sciences Falmer, Brighton, UK

Full time, Fixed term for up to 3.5 years Closing date for applications: 10 April 2017

Description The Fraser lab is looking for a postdoc with experience in population genomic analysis to work on a project investigating balancing selection in the Trinidadian guppy. Accounting for high genetic diversity in ecologically-important traits is a fundamental problem in evolutionary biology. Recent work implicates an advantage to rare types as a critical factor maintaining variation in the Trinidadian guppy, but we have little understanding of how this process actually unfolds in the wild. Using natural populations, laboratory lines, and closely related species, we will use whole-genome DNA sequencing to identify genes that show signatures of balancing selection and are linked to highly polymorphic traits.

The main duties of the postdoctoral researcher will be processing and analyzing next generation sequence data, including quality control, mapping reads, calling SNPs, and population genetic analysis. There will be some molecular lab work (constructing genomic libraries) and potentially field work in Trinidad. The ideal candidate should have experience working with genomic data and population genetics, and have enthusiasm for evolutionary based questions.

The post is part of a larger funded NERC-NSF grant on Ecological Genomics of Adaptive Polymorphisms led by Bonnie Fraser, Kim Hughes (Florida State University), David Houle (Florida State University), Helen Rodd (University of Toronto), and Deborah Charlesworth (University of Edinburgh).

The School of Life Sciences at Sussex is at the forefront of research in the biological sciences in the UK, coming in the top 10 in the REF 2014.The School is committed to equality and valuing diversity, and currently holds an Athena SWAN Silver Award. Applications are particularly welcomed from women and black and minority ethnic candidates, who are under-represented in academic posts in science and engineering at Sussex. The School of Life Sciences welcomes applications to academic posts from candidates who wish to work part-time or as job-sharers. The University offers various schemes < http://www.sussex.ac.uk/humanresources/-personnel/familyfriendlypolicies > to provide real benefits to parents.

The University of Sussex is located just outside the city of Brighton and approximately 20 minutes to Gatwick Airport and a one hour commute to London (by train). Brighton is a lively and diverse city known for its famous seafront and is closely located to the South Downs National Park and stunning white chalk cliffs of the south coast.

Further information on research in the Fraser lab can be found here: http://www.sussex.ac.uk/-lifesci/fraserlab/index Further information on the research in the EBE group at Sussex can be found here: http://www.sussex.ac.uk/lifesci/ebe/-research To apply, please follow the instructions found: http://www.sussex.ac.uk/about/jobs/-postdoctoral-researcher-1811 .Informal inquires can be made to Bonnie Fraser b.fraser@sussex.ac.uk.

Bonnie Fraser <B.Fraser@sussex.ac.uk>

UTennessee Knoxville Phylogenetics

I am currently seeking two postdocs for NSF-funded work in my lab. One will work on developing and deploying new methods to compute and distribute chronograms, and the other will work on approximate Bayesian computation methods for comparative methods of univariate and multivariate traits. My lab is based in Knoxville, TN, an area rich in natural beauty, computational resources, and affordability. However, working remotely is possible for candidates with the demonstrated ability to do so successfully. Out of 12 postdocs I have mentored directly through my lab or as one of their National Institute for Mathematical and Biological Synthesis (NIMBioS) mentors, seven have chosen to go onto tenure track faculty positions, two are working in health research positions, and three are currently postdocs. I strive to create a welcoming and diverse environment. Research in the lab ranges from empirical work on plant diversification to quantitative trait evolution models to models of protein evolution. For more information on the positions, please go to http://-brianomeara.info/lab/postdoc/ .

Applications should be emailed to bomeara@utk.edu and should include 1) A cover letter (include expected completion date of PhD, if appropriate, as well as relevant skills) 2) A CV 3) A short research statement 4) Contact information for two references 5) Link(s) to repositories with examples of code you have written or attachments including such code.

Please feel free to contact me with questions before formally applying.

More information about the research:

The DateLife project is to allow easier communication and creation of chronograms. It has an R package and website so far (both alpha-quality at the moment). The comparative method project extends TreEvo, an approximate Bayesian computation method for trait evolution. http://brianomeara.info/lab/postdoc/ has links to the relevant grants and software for both.

Experience in programming is strongly preferred; experience in R is desired, but not required. If in doubt, apply: please do not self-select yourself out from what might be a mutually beneficial position.

Review of applications will continue until filled (start dates are flexible). Presubmission inquiries are encouraged.

All qualified applicants will receive equal consideration for employment and admissions without regard to race, color, national origin, religion, sex, pregnancy, marital status, sexual orientation, gender identity, age, physical or mental disability, or covered veteran status.

Eligibility and other terms and conditions of employment benefits at The University of Tennessee are governed by laws and regulations of the State of Tennessee, and this non-discrimination statement is intended to be consistent with those laws and regulations.

In accordance with the requirements of Title VI of the Civil Rights Act of 1964, Title IX of the Education Amendments of 1972, Section 504 of the Rehabilitation Act of 1973, and the Americans with Disabilities Act of 1990, The University of Tennessee affirmatively states that it does not discriminate on the basis of race, sex, or disability in its education programs and activities, and this policy extends to employment by the University.

Inquiries and charges of violation of Title VI (race, color, national origin), Title IX (sex), Section 504 (disability), ADA (disability), Age Discrimination in Employment Act (age), sexualorientation, or veteran status should be directed to the Office of Equity and Diversity (OED), 1840 Melrose Avenue, Knoxville, TN 37996-3560, telephone (865) 974-2498 (V/TTY available) or 974-2440. Requests for accommodation of a disability should be directed to the ADA Coordinator at the Office of Equity and Diversity.

Brian O'Meara, http://www.brianomeara.info Associate Professor, Dept. of Ecology & Evolutionary Biology, UT Knoxville Associate Head, Dept. of Ecology & Evolutionary Biology, UT Knoxville Associate Director for Postdoctoral Activities, National Institute for Mathematical & Biological Synthesis (NIMBioS) Communication Director, Society of Systematic Biologists

omeara.brian@gmail.com

UValencia Spain VirusSocialEvolution

Two 2-3 year postdoc contracts are available at the laboratory of Rafael Sanjuán (University of Valencia, Spain).

Starting date: flexible (mid 2017 to early 2018).

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

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

Funding: ERC Consolidator Grant, 2017-2022.

Goal: understand how multi-virion infectious units determine social-like interactions in viruses (cooperation versus conflict). We will use vesicular stomatitis virus and/or enteroviruses and/or baculoviruses as model systems.

Candidates should have a background in virology and molecular/cell biology.

ERC project summary:

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

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

Rafael Sanjuan <rafael.sanjuan@uv.es>

UVermont EvolutionaryEcologicalGenomics

Postdoctoral Position: Genomics of Adaptation in Copepods

The Pespeni Lab in the Department of Biology at the

University of Vermont is looking to hire a postdoctoral fellow in evolutionary and ecological genomics using copepods in the genus Acartia as a model. The successful candidate will join an NSF-funded collaborative team focused on revealing potential genetic and epigenetic mechanisms of adaptation to elevated temperature and CO2 in a warm-adapted and a cold-adapted copepod species. Full-factorial multi-generation selection experiments are running in the lab of PI Hans Dam, with Co-PIs Hannes Baumann and Michael Finiguerra, at the University of Connecticut. PI Pespeni and Co-PIs are looking for applicants with expertise and interest in genomics and evolutionary biology to participate in this exciting research.

Required qualifications: Ph.D. by the time of start date in one of the following fields: evolutionary biology, genomics, population genetics, zooplankton ecology, and marine biology. Excellent communication and organizational skills.

Preferred qualifications: - Experience generating, analyzing, and/or integrating large datasets â euro “ whole genome sequencing, transcriptome sequencing, bisulfite sequencing (or similar). - Experience with selection experiments. - Strong quantitative, statistical, and computational skills. Fluency in Python or Perl, and R. - Strong written and oral communication skills.

Ideal applicants will be creative, highly motivated, and enthusiastic! They will be able to work independently and as part of a collaborative team. The fellow can expect to be a part of a supportive research environment, have the opportunity to mentor students, and work closely with the PI.

Initial appointment will be for one year, with the possibility of extension for one or two additional years, contingent on performance and funding. The salary will be commensurate with experience. Start date is preferably June 2017, but flexible.

To apply, e-mail a single PDF including a cover letter, a CV, and the names and contact information of three references to Dr. Pespeni (mpespeni@uvm.edu), with the subject line as ”Postdoctoral application <your name>“. Review of applications will begin in the beginning of April and continue until a suitable candidate is identified. Informal inquiries prior to application are welcome.

Burlington is a hip, little city surrounded by the lakes and mountains of northern Vermont. The area thrives on local food, international culture, and outdoor activities year-round.

– Melissa Pespeni, Ph.D. Assistant Professor University of Vermont Department of Biology Marsh Life Sciences, Rm 326A 109 Carrigan Drive Burlington, Vermont 05405 802-656-0628 <(802)%20656-0628>

Lab website: *http://blog.uvm.edu/mpespeni/* ”mpespeni@uvm.edu“ <mpespeni@uvm.edu>

WorkshopsCourses

Arolla Switzerland EvoDevo Jul18-21 124
Berlin AdvancedPython Nov13-17 125
Berlin DataAnalysisInHighThroughputBiology May29-Jun2 2 126
Berlin EvolutionInCognition Jul15-19 127
Berlin GenomicDatavizWithR Sep11-15 128
Berlin Metabarcoding Apr3-7 3 129
Berlin PythonForBiologists Oct2-6 130
Boston PlantStructureFunction Jul30-Aug12 131
Canada ColdSpringHarb Bioinformatics Summer2017 132
CatalinaIsland GenomicsWorkshops Aug11-23 133
HinxtonUK GeneticAnalysis Jul19-25 133
Leipzig ModellingBiodiversity Sep3-15 134

MichiganStateU EvolutionaryModeling Jul23-28 . . 134
Naples BringingMathsToLife Jun7-9 134
NewOrleans ArbovirusEvolution May30-31 135
OregonStateU Macroevolution June22-23 136
Portugal 3 cE3c 136
Roscoff EcolEvolutionaryGenomics Jun5-16 137
Seattle StatisticalGenetics Jul10-28 AFewScholarshipsRemain 139
Siegen Germany FishSim AnimationToolchain Oct20-22 139
SwissAlps Sexual Selection Aug28-31 140
Toulouse EvolutionEconomics Jun1-2 140
UK GeneticDataAnalysisUsingR ThibautJombart Oct23-27 141
UK MetaAnalysisInEcologyAndEvolution Jul24-28 142
ULeicester 2 DNAseqRNAseqAnalysis May 143
ULeicester 2 NGSanalysis May 143
UPadova ProteinInteractions Apr10-13 143
Wales ModellingUsingR Apr24-28 PartialScholarships 144
WoodsHole MolecularEvolution Jul20-30 145
Zurich PolygenicAdaptationCourse Aug28-Sep1 . . 146

Arolla Switzerland EvoDevo Jul18-21

"Early-environment effects: Towards integrating theoretical and empirical approaches"

Workshop, 18-21 July 2017, Arolla, Switzerland

Organizer: Barbara Taborsky

A workshop of the CUSO 'Doctoral Program in Ecology and Evolution' (DPEE)

There is ample evidence that the environment organisms experience during early development can shape their phenotype for lifetime, and that these early environment effects can even be transmitted across generations. In the past two decades the field of early environment effects was dominated by empirical research. Recently an exciting body of theoretical work has started to emerge modelling how direct environmental, epigenetic and genetic information shapes the phenotypes of developing organisms. Although, opposite to other areas in biology, this novel theory is developed in close exchange with empiricists, phenotypic development is still modelled at a high level of abstraction ignoring the architecture of the physical substrate of development. This workshop shall focus on effects of early experience on phenotypic development in general, and the development of animal behaviour in particular. It will bring together researchers of function and mechanisms of early environment effects with theoreticians modelling these effects. Invited speakers will give lectures about their field of expertise (behavioural ecology, cognition, psychology, theory and molecular brain mechanisms) followed by joint discussions with the participants in small working groups. Questions discussed will involve, among others, which kind of theory is required to aid the conceptual development of future empirical research and, in turn, which kind of data are needed to enhance the development of more predictive theory. Further we will ask how to integrate molecular, neurological and psychological mechanisms in theoretical models. A final discussion will collect the ideas of all participants on these questions.

Invited Speakers

- Victoria Braithwaite, Penn State University, USA

- Sinead English, University of Cambridge, UK

- Tim Fawcett, University of Exeter, UK

- Bram Kuijper, University of Exeter, UK

- Olof Leimar, University of Stockholm, SE

- Suvi Ruuskanen, University of Turku, FIN

- Carmen Sandi, Ãcole Polytechnique Federale Lausanne (EPFL), CH

The workshop takes place at the Grand-H0tel 'Kurhaus' in a breathtaking scenery amidst some of the finest mountain peaks of Switzerland. The venue is situated above the picturesque mountain village of Arolla, at 2100 m sea level in the very heart of the Swiss high alps. We can host about 40 participants (including invited speakers).

For more details on the program, the location, and attendance see http://behav.zoology.unibe.ch/-index.php?pp=56&p=196 For further information please contact barbara.taborsky@iee.unibe.ch

"barbara.taborsky@iee.unibe.ch"
<barbara.taborsky@iee.unibe.ch>

Berlin AdvancedPython Nov13-17

Advanced Python for biologists

13-17 November 2017, Berlin (Germany)

https://www.physalia-courses.org/courses/course12/ Instructor: Dr. Martin Jones (founder, Python for Biologists)

http://www.physalia-courses.org/instructors/t1/ Registration deadline: 20th October 2017

Overview

Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. This workshop is aimed at people who already have a basic knowledge of Python and are interested in using the language to tackle larger problems. In it, we will look in detail at the parts of the language which are particularly useful in scientific programming, and at the tools Python offers for making development faster and easier. The workshop will use examples and exercises drawn from various aspects of bioinformatics work. After completing the workshop, students should be in a position to (1) take advantage of the advanced language features in their own programs and (2) use appropriate tools when developing software programs.

Who should attend

This workshop is aimed at researchers and technical workers with a background in biology and a basic knowledge of Python. The Advanced course is aimed at people who want to develop bigger or more complicated programs in Python, or to learn more about the language, or to explore different approaches (object-oriented, functional) to programming. The material covered is very general purpose and can be applied to any kind of problem.

Requirements

Students should have enough biological/bioinformatics background to appreciate the examples and exercise problems (i.e. they should know what a protein accession number, BLAST report, and FASTA sequence is). They should also have basic Python experience (the Introduction to Python for Biologists course will fulfil these requirements). Students should be familiar with the use of lists, loops, functions and conditions in Python and have written at least a few small programs from scratch.

Session content

Monday 13th - Classes from 09:30 to 17:30

Session 1: Data structures in Python

In this session we will briefly recap Python's basic data structures, before looking at a couple of new data types tuples and sets and discussing where each should be used. We will then see how we can combine these basic types to make more complex data structures for solving specific problems. We'll finish our discussion by looking at specialized data types that are found in the Python core library. This session will also be our first introduction to benchmarking as we talk about the relative performance of different data types. In the practical session we'll learn how to parse an input file into a complex data structure which we can then use to rapidly query the data. Core concepts introduced: tuples, sets, higher-order data structures, default dicts, Counters, big-O notation.

Session 2: Recursion and trees

In this session we will cover two very closely related concepts: trees (i.e. the various ways that we can store hierarchical data) and recursive functions (the best way to operate on treelike data). As recursion is inherently confusing, we'll start with a gentle introduction using biological examples before moving on to consider a number of core tree algorithms concerning parents, children, and common ancestors. In the practical session we'll look in detail at one particular way of identifying the last common ancestor of a group of nodes, which will give us an opportunity to explore the role of recursion. Core concepts introduced: nested lists, storing hierarchical data, recursive functions, relationship between recursion and iteration.

Tuesday 14th - Classes from 09:30 to 17:30

Session 3: Classes and objects

In this session we will introduce the core concepts of object-oriented programming, and see how the data types that we use all the time in Python are actually examples of classes. We'll take a very simple example and use it to examine how we can construct our own classes, moving from an imperative style of programming to an object-oriented style. As we do so, we'll discuss where and when object-orientation is a good idea. In the practical we will practise writing classes to solve simple biological problems and familiarize ourselves with the division of code into library and client that object-oriented programming demands. Core concepts introduced: classes, instances, methods vs. functions, self, constructors, magic methods.

Session 4: Object-oriented programming

Following on from the previous session, we will go over some advanced ideas that are common to most object-oriented programming languages. For each idea we'll discuss the basic concept, the scenarios in which it's

— / —

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

---

Berlin DataAnalysisInHighThroughputBiology May29-Jun2
2

Dear all,

We have still a few places available for the "Data analysis in high throughput biology https://www.physalia-courses.org/courses/course3/ " workshop, which will run from the 29th of May to the 2nd of June 2017 in Berlin, Germany (https://www.physalia-courses.org/courses/course3/).

Registration deadline: April 24th, 2017

Instructor: Dr. January Weiner (Max Planck Institute for Infection Biology; https://www.physalia-courses.org/instructors/t14/).

Course overview

High throughput (HT) techniques such as transcriptomics or metabolomics are of great significance in many areas of biology. With the standard techniques becoming more affordable and new techniques being introduced all the time, the amount of data sets generated is staggering. However, statistical and computational analysis of HT data sets present many challenges. In this course, the students will gain the ability to independently process and analyse HT data sets, select the appropriate tools, functionally interpret the results as well as learn the paradigms of computational biology and statistics which will allow them to efficiently communicate with computational biologists.

Intended audience

In general, the course is aimed at biologists who would like to take their data analysis in their own hands. While an aptitude for computational work is necessary, the main goal of the course is the application of biological and statistical knowledge to HT sets with as little effort as necessary.

* basic computer skills (a rudimentary knowledge of programming principles in any language is recommended, but not mandatory) * basic understanding of statistics * basic understanding of molecular techniques for generating high throughput data

The students should be comfortable with using a computer and have at least a rudimentary understanding of computer programming. However, no specific skills are necessary; the students will learn basic R programming in this course.

Basic skills in statistics are necessary. The students should understand the concepts of statistical hypothesis testing and p-values. However, an in-depth introduction to these concepts will also be provided.

Target student skills

* overview of commonly used high-throughput data types * techniques for data clean-up and preparation for analysis * understanding of computational problems associated with high- throughput data analysis * statistical problems and solutions in analysis of HT data * practical skills in analysis methods of HT data: * basic differential analysis (limma, DESeq, alternative and non- parametric techniques) * set enrichment techniques (GSEA, gene ontologies, metabolic profiling and more) * multivariate approaches to data analysis (PCA / ICA, PLS, multiple correspondance analysis) * basic approaches in machine learning: cross * Communication skills in statistics and computational biology

After the course, the student should be able to prepare, analyse and interpret a HT data set, including multivariate and machine learning techniques.

Teaching format

On each day, the course will consist of four parts:

* Lecture: theoretical introduction to the days focus * Hands-on guide: guided practical session in R where students replicate the analysis performed by the teacher. While the lecture is general, here specific R techniques and R packages are introduced * Guided self-study: students are given excercises and problems to solve and work on them individually under the guidance of the teacher * Individual project work: each student will receive a transcriptomic (RNASeq or microarray) data set to analyse throughout the course * Lecture: wrap-up and side notes; preparation for the following day * Venue

Botanischer Garten und Botanisches Museum (BGBM) Berlin-Dahlem/Freie Universität Berlin, Königin-Luise-Straße 6-8, 14195 Berlin

Course plan

* Day 1: Introduction to statistical reasoning and R o Lecture: "Statistics gone wrong: basics of statistical problems in HT applications" o Hands-on guide: working with R: first steps o Guided self-study: using R for data loading and basic statistical calculations o Individual project work: loading data for the individual project o Lecture: "On the importance of lab books - documentation and organization in computational projects"

* Day 2: Data preparation and basic differential analyses o Lectures: + "Steps in HT data analysis and overview of HT techniques" + "Differential analysis in transcriptomics" o Hands-on guide: documentation with knitr, data pre-processing, QC o Guided self-study: creating self-documenting R code; basic steps in transcriptomic analyses o Individual project work: basic analysis of the individual data sets

— / —

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

---

Berlin EvolutionInCognition Jul15-19

Second call for contribution for the Evolution in Cognition Workshop, deadline in one week.

2nd Evolution in Cognition Workshop to be held as part of the

2017 Genetic and Evolutionary Computation Conference (GECCO-2017) July 15-19, Berlin, Germany

Organized by ACM SIGEVO http://gecco-2017.sigevo.org Webpage: https://sites.google.com/champlain.edu/eic2017/ Submission Deadline: March 31st, 2017

=== Topic =Evolution by natural selection has shaped life over billions of years leading to the emergence of complex organism capable of exceptional cognitive abilities. These natural evolutionary processes have inspired the development of Evolutionary Algorithms (EAs), which are optimization algorithms widely popular due to their efficiency and robustness. Beyond their ability to optimize, EAs have also proven to be creative and efficient at generating innovative solutions to novel problems. The combination of these two abilities makes them a tool of choice for the resolution of complex problems.

There is evidence that the principle of selection on variation is at play in the human brain, as proposed in Changeux's and Edelman's models of Neuronal Darwinism, and more recently properly reformulated in the theory of the Neuronal Replicators. Consequently, the idea of an interaction between evolutionary processes and cognition over physiological time scales has been gaining some traction. Since the development of human cognition requires years of maturation, it can be expected that artificial cognitive agents will also require months if not years of learning and adaptation. It is in this context that the optimizing and creative abilities of EAs could become an ideal framework that complement, aid in understanding, and facilitate the implementation of cognitive processes. Additionally, a better understanding of how evolution can be implemented as part of an artificial cognitive architecture can lead to new insights into cognition in humans and other animals.

The goals of the workshop are to depict the current state of the art of evolution in cognition and to sketch the main challenges and future directions. In particular, we aim at bringing together the different theoretical and empirical approaches that can potentially contribute to the understanding of how evolution and cognition can act together in an algorithmic way in order to solve complex problems. In this workshop we welcome approaches that contribute to an improved understanding of evolution in cognition using robotic agents, in silico computation as well as mathematical models.

Keywords: Evolutionary Computation, Evolution, Cognition, Darwinian Neurodynamics, Neuronal Darwisnism, robotics.

=== Invited speakers =Prof. Eors Szathmary Additional invited speakers will be announced in the near future.

=== Organizers =Prof. Stephane Doncieux, University Pierre and Marie Curie, France Dr. Joshua Auerbach, Champlain College Prof. Richard Duro, Universidade da Coruna, Spain Dr. Harold P. de Vladar, iASK - Institute of Advanced Studies KÃ'szeg, Hungary

=== Submissions and deadlines Âsubmissions: Original: experimental work, position papers as well as overviews of author's recent work are all welcome. These submissions will be included in the proceedings and be presented during the workshop Abstracts submitted as poster to GECCO 2017: the authors of selected abstracts will be given a talk. The abstract won't be included in the proceedings. Hot-of-the-press: authors can submit a recently published work. Selected articles will be given a talk.

Submission: extended abstracts (2-4 pages) and long papers (8 pages) are accepted. They should follow ACM template and should be sent in electronic form (pdf) to eic_ws@isir.upmc.fr:

March, 31st, 2017: Papers Submission Deadline April, 14th, 2017: Notification of Acceptance April, 21th, 2016: Camera-Ready Paper Submission July 15 or 16th, 2017: Workshop

GECCO is sponsored by the Association for Computing Machinery Special Interest Group on Genetic and Evolutionary Computation (SIGEVO). SIG Services: 2 Penn Plaza, Suite 701, New York, NY, 10121, USA, 1-800-342-6626 (USA and Canada) or +212-626-0500 (Global).

Stephane Doncieux, Josh Auerbach, Richard Duro and Harold P. de Vladar

harold.vladar@parmenides-foundation.org

Berlin GenomicDatavizWithR Sep11-15

Workshop title: Genomic Data Visualization and Interpretation (https://www.physalia-courses.org/courses/-course14/)

Course Details:

Topic: Advanced R and bioinformatics applications for visualization and interpretation of genomic data.

Length: 5 days (~ 9.30 AM to 5.30 PM with breaks)

Instructors: Drs. Obi Griffith, Malachi Griffith, Zachary Skidmore (McDonnell Genome Institute; http://-/genome.wustl.edu/people/groups/detail/griffith-lab/)

Anticipated participants: max 30.

Dates: 11th-15th September

Course overview

The advent of rapid and relatively cheap massively parallel sequencing has dramatically increased the availability of genome, transcriptome, and epigenome profiling. Analysis workflows and published best practices are also now available to process raw sequence data into alignments, variant calls, expression estimates, etc., in relatively standardized file formats. Interpretation and visualization of these data, often consisting of thousands to billions of data points, and extracting biological meaning remains a serious challenge. In this workshop we will explore a number of best-in-class visualization tools, and provide working examples that demonstrate important principles of 'omic interpretation strategies.

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 complete individual exercises. After and during each exercise, interpretation of results will be discussed as a group. Computing will be done using a combination of tools installed on the attendees laptop computer and web resources accessed via web browser.

Who should attend

This workshop is aimed at researchers and technical workers who are analyzing some kind of omic data (e.g. WGS, exome, RNA-seq, variant files, etc.). Examples demonstrated in this course will involve primarily human genome/transcriptome data but many of the concepts learned will be applicable to model organisms, metagenomics, simulated data, etc.

Requirements

Attendees should have a background in biology and a basic knowledge of R. We will dedicate one session to a brief R/linux primer. Attendees should have also some familiarity with genomic data. The course will teach relatively advanced usage of R (especially ggplot2 and Bioconductor packages). Attendees should have a working installation of R and RStudio on their laptop.

Example data

Attendees will learn to visualize and interpret results from real human genome data sets generated at the McDonnell Genome Institute at Washington University School of Medicine. These data will be analyzed to determine previously known as well as potentially novel interpretations. Since the example data are not simulated or arbitrarily filtered, interpretation and visualization will be performed in the context of representative levels of sequence error, and other sources of technical and biological noise.

Curriculum

Day 1 Lecture 1: Introduction to Genomic Data Visualization and Interpretation

* Central dogma * Omic technologies and data * Reference files: GTF, BAM, VCF, MAF, BED, etc * Genome

annotation resources, browsers, etc. * Introduction to demonstration data sets

Lab 1: Genome Browsing and Visualization exercises

* IGV o Basics o Creating custom genomes o Sashimi plots * UCSC * Ensembl

Lab 2: Web resources for variant annotation and visualization

* VEP/SnpEff * ProteinPaint * CBioportal * Ensembl BioMart

Day 2

Lecture 2. Introduction to R for Genomic Data Visualization and Interpretation

Lab 3: Intro to R

* Installation * CRAN and Bioconductor * Data types * Reading and writing Data * Data Frames, slicing, and manipulation * Basic control structures * apply() family of functions * Additional resources

Lab 4: Intro to ggplot

* wide vs long format * geom and aes * axis scaling and manipulation * faceting * themes and colours * ggvis * Additional resources

Lab 5: Real world examples using ggplot

* Heatmaps * Regression lines * Survival analysis * circos

Day 3

Lab 6. Popular genomic visualizations with GenVisR

* Waterfall plots * TvTi plots * cnSpec plots * cnView plots * lohSpec plots * genCov plots

Lecture 3: Differential gene expression and pathway analysis

Lab 7: Differential expression analysis

* DEseq2

Day 4

Lab 8: Tools and datasets for pathway analysis

* KEGG * GO * GAGE (R package)

Lab 9: Pathway visualization

* Pathview (R package) * Cytoscape

Lecture 4: Clinical interpretation of variants

Lab 10: Clinical variant interpretations

* Variant identity o HGVS o TransVar o Mutalyzer

— / —

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

---

Berlin Metabarcoding Apr3-7 3

Dear all,

There are the last 2 places left for the "16S rRNA gene Metabarcoding" workshop, 3-7 April 2017 in Berlin (Germany).https://www.physalia-courses.org/courses/course8/ Registration deadline: March 3rd, 2017

Instructor: Dr. Alexandre de Menezes (National University of Ireland Galway) https://www.physalia-courses.org/instructors/t5/ Course overview

The 16s rRNA gene has become the standard marker for prokaryote phylogenetic analysis, and combined with high-throughput sequencing technologies it is widely used to infer the structure and composition of microbial communities. Due to the continuous improvements in sequencing technologies and bioinformatics tools, there is a wide choice of methods for sequencing and analysing 16S rRNA gene assemblies. This workshop is designed to give students the necessary background and practical experience of the strategies for the analysis of the diversity and structure of prokaryote communities, covering i) experimental design and primer choices; ii) wet-lab and library preparation options; iii) sequence quality control and analysis and iv) statistical analysis of microbial community data. The many sequencing and analysis options will be discussed, whereas a more in-depth tutorial using real sequence data will provide an opportunity for the student to practice 16S rRNA sequence analysis from raw sequence files to ecological interpretation. Course material, such as presentation slides and necessary model data, will be provided to the students.

Targeted audience and assumed background

This workshop is intended for students and researchers interested in microbial ecology but who are not yet very familiar with the techniques involved. Choosing the appropriate primers, library preparation kits, sequencing methodologies and bioinformatics pipelines can be quite daunting to the uninitiated. This workshop will allow researchers interested more confidence in their methodology and analyses choices. The target audience include students of animal or plant microbiomes as well as those studying environmental microbial communities. It is assumed that the workshop attendees are interested in performing 16S rRNA metabarcoding using the Illumina MiSeq platform, although other sequencing technologies will be discussed during the workshop.

Knowledge of Linux and R or familiarity with working in the command line will be helpful, but for those new to the area detailed instructions will allow students to follow the workshop. Students will need to have a computer running either on Linux or a Linux virtual machine running on MacOX/Windows computers. Contact the instructor at ademez@gmail.com mailto:ademez@gmail.com if in doubt about computational requirements.

Workshop structure

The workshop will consist of both lectures and practical classes. Background information will be provided to help workshop attendees choose the appropriate experimental design, primers, sequencing library preparation kits and to contextualise the bioinformatics and statistical analysis methods. Practical tutorials will be conducted on a step-by-step basis to guide the student from when receiving data from a sequence provider to obtaining plots and tables describing microbial community diversity, structure and relationships to environmental variables or host data.

Venue

Botanischer Garten und Botanisches Museum (BGBM) Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Straße 6-8, 14195 Berlin.

Session contents

Monday 3rd-Classes from 10:00 to 18:00

Session 1: the 16S rRNA gene

The use of the 16S rRNA gene as a marker for prokaryote phylogenetics will be discussed to introduce the students to the concept of conserved and hypervariable regions. The student will learn about the history of this molecular marker and why it is the choice for prokaryote diversity studies. The primer combinations used to target the different hypervariable regions will be discussed, as well as what is known regarding their advantages and disadvantages. The pros and cons of PCR-based 16S rRNA gene sequencing versus PCR-free shot-gun metagenomics will also be discussed.

This session will also include an overview of current sequencing technologies, and the Illumina MiSeq platform will be contrasted with other sequencing technologies (Ion Torrent, MinIon, PacBio and Moleculo).

Session 2: sequencing experimental design and initial hands-on exercises

Focusing on the MiSeq platform, experimental design considerations will be discussed and topics discussed will include sequence depth, replication, contamination and the use of appropriate controls and mock communities. Other topics that will be taught include: metadata collection, DNA extraction and RNA-cDNA sequencing. Demo sequence data will be used to check that the appropriate tools are installed correctly

— / —

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

---

Berlin PythonForBiologists Oct2-6

Introduction to Python for biologists

2-6 October 2017 in Berlin, Germany (https://www.physalia-courses.org/courses/course2/) Instructor: Dr Martin Jones (founder, Python for biologists: https://www.physalia-courses.org/instructors/t1/)

Application deadline is: September 2nd, 2017

Overview:

Python is a dynamic, readable language that is a popular platform for all types of bioinformatics work, from simple one-off scripts to large, complex software projects. This workshop is aimed at complete beginners and assumes no prior programming experience. It gives an overview of the language with an emphasis on practical problem-solving, using examples and exercises drawn from various aspects of bioinformatics work. After completing the workshop, students should be in a position to (1) apply the skills they have learned to tackling problems in their own research and (2) continue their Python education in a self-directed way. All course materials (including copies of presentations, practical exercises, data files, and example scripts prepared by the instructing team) will be provided electronically to participants.

Intended audience:

This workshop is aimed at all researchers and technical workers with a background in biology who want to learn programming. The syllabus has been planned with complete beginners in mind; people with previous programming experience are welcome to attend as a refresher but may find the pace a bit slow. If in doubt, take a look at the detailed session content below or drop Martin Jones (martin@pythonforbiologists.com) an email.

Teaching format:

The workshop is delivered over ten half-day sessions (see the detailed curriculum below). Each session consists of roughly a one hour lecture followed by two hours of practical exercises, with breaks at the organizer's discretion. There will also be plenty of time for students to discuss their own problems and data.

Assumed background:

Students should have enough biological background to appreciate the examples and exercise problems (i.e. they should know about DNA and protein sequences, what translation is, and what introns and exons are). No previous programming experience or computer skills (beyond the ability to use a text editor) are necessary, but you'll need to have a laptop with Python installed.

Curriculum:

Monday 2nd - From 09:30 to 17:30

Session 1-. Introduction

In this session I introduce the students to Python and explain what we expect them to get out of it and how learning to program can benefit their research. I explain the format of the course and take care of any housekeeping details (like coffee breaks and catering arrangements). I outline the edit-run-fix cycle of software development and talk about how to avoid common text editing errors. In this session, we also check that the computing infrastructure for the rest of the course is in place (e.g. making sure that everybody has an appropriate version of Python installed). Core concepts introduced: source code, text editors, whitespace, syntax and syntax errors, Python versions.

Session 2-Output and text manipulation

In this session students learn to write very simple programs that produce output to the terminal, and in doing so become comfortable with editing and running Python code. This session also introduces many of the technical terms that we'll rely on in future sessions. I run through some examples of tools for working with text and show how they work in the context of biological sequence manipulation. We also cover different types of errors and error messages, and learn how to go about fixing them methodically. Core concepts introduced: terminals, standard output, variables and naming, strings and characters, special characters, output formatting, statements, functions, methods, arguments, comments.

Tuesday 3rd - From 09:30 to 17:30

Session 3-File IO and user interfaces

I introduce this session by talking about the importance of files in bioinformatics pipelines and workflows, and we then explore the Python interfaces for reading from and writing to files. This involves introducing the idea of types and objects, and a bit of discussion about how Python interacts with the operating system. The practical session is spent combining the techniques from session 2 with the file IO tools to create basic file-processing scripts. Core concepts introduced: objects and classes, paths and folders, relationships between variables and values, text and binary files, newlines.

Session 4. Flow control 1 : loops

A discussion of the limitations of the techniques learned in session 3 quickly reveals that flow control is required to write more sophisticated file-processing programs, and I introduce the concept of loops. We look at the way in which Python loops work, and how they can be used in a

— / —

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

---

Boston PlantStructureFunction Jul30-Aug12

microMORPH& Arnold Arboretum Summer Course 2017 - Plant Anatomy: Development, Function, and Evolution

Thistwo-week short course (July 30th - August 12th, 2017) will be taught by experts from around the world as an intense lecture, laboratory, and living collections learning experience. The course will be based at the Weld Hill Research Building at the Arnold Arboretum in Boston (Massachusetts), which offers a state-of-the-art microscopy laboratory for teaching and sits amid the 15,000+ living specimens of more than 2,200 species at the Arnold Arboretum.

Thiscourse will provide a working knowledge of tools and concepts that are central to understanding the anatomical basis for structural and functional diversity. Topics include the anatomy of the primary plant body, anatomy throughout plant development, evolutionary trends in plant anatomy, and the anatomy and diversity of secondary/woody growth. Each day will consist of lecture and laboratory sessions, with ample opportunity to explore the Arnold Arboretum.

Thereare no course fees, and funds are available to help defray costs of participant travel.

CourseInstructors: Pieter Baas (Naturalis Biodiversity Center), Pamela Diggle (University of Connecticut), William (Ned) Friedman (Harvard University), Peter Gasson (Royal Botanic Gardens, Kew), Cynthia Jones (University of Connecticut), Elisabeth Wheeler (North Carolina State University).

ApplicationDeadline: Applications must be submitted by 11:30 pm April 15th, 2017. Application instructions are available on the course website: http://projects.iq.harvard.edu/micromorph/-summer-course-2017 Eligibility:microMORPH summer short courses are open to postdoctoral researchers, graduate students, and undergraduates in their final year of study (who have been admitted to a graduate or professional program for the fall of 2017). Non-US-citizens are welcome to apply (but are responsible for obtaining the appropriate visa to be able to attend the course).

Howto Apply: For full application instructions (including list of required documents) and to submit applications, please visit the microMORPH website (http://-projects.iq.harvard.edu/micromorph).

Questionsor Comments? Contact Becky Povilus at RCN-micromorph@gmail.com, and visit our website at http:/-/projects.iq.harvard.edu/micromorph . PamelaDiggle

Professor Departmentof Ecology and Evolutionary Biology Universityof Connecticut

860-486-4788

pamela.diggle@uconn.edu

Canada ColdSpringHarb Bioinformatics Summer2017

Canadian Bioinformatics Workshops 2017 Series

New for 2017:

* Workshops will be held in Vancouver, Montreal, Quebec City, Cold Spring Harbor, and Toronto * Travel and registration awards to eligible trainees * New workshops in epidemiology, genomic medicine, and the microbiome

The CBW is pleased to be offering the following advanced training opportunities in 2017:

* High-Throughput Biology - From Sequence to Networks: Cold Spring Harbor, NY, March 20 - 26, 2017 * Infectious Disease Genomic Epidemiolgy: Vancouver, May 1 - 3, 2017 (NEW) * Bioinformatics of Genomic Medicine: Toronto, May 10 - 11, 2017 (NEW) * Informatics on High-throughpuut Sequencing Data: Toronto, May 25 - 26, 2017 * Bioinformatics for Cancer Genomics: Toronto, May 29 - June 2, 2017 * Informatics and Statistics for Metabolomics: Toronto, June 6 - 7, 2017 * Introduction to R: Toronto, June 12, 2017 * Exploratory Analysis of Biological Data using R: Toronto, June 13 - 14, 2017 * Epigenomic Data Analysis: Montreal, June 15 - 16, 2017 * Microbiome Summer School: Quebec City, June 19 - 22, 2017 (NEW) * Pathway and Network Analysis of -omics Data: Toronto, June 26 - 28, 2017 * Cloud Computing in Bioinformatics with Big Data: Toronto, July 5 - 6, 2017 * Informatics for RNA-seq Analysis: Toronto, July 10 - 12, 2017 (1 day longer)

For more information on our 2017 workshop series, visit https://bioinformatics.ca/workshops-2017. A link to our new full program poster can be found here: https:/-/goo.gl/a3zi4d Early registration closes April 3, 2017. All award applications are due April 3, 2017. –

Ann Meyer, PhD Manager, Knowledge and Research Exchange

Ontario Institute for Cancer Research

MaRS Centre

661 University Avenue

Suite 510

Toronto, Ontario

Canada M5G 0A3

Email: Ann.Meyer@oicr.on.ca

Phone: 647-260-7925

Cell: 647-295-2612

Toll-free: 1-866-678-6427

Twitter: @OICR_news

www.oicr.on.ca Ann.Meyer@oicr.on.ca

CatalinaIsland GenomicsWorkshops Aug11-23

Hi Colleagues,

This summer we're offering two workshops on the use of high-throughput sequencing to study population genetic variation and community diversity. For more details, see this link or the description that follows.

http://people.oregonstate.edu/˜meyere/workshops.html We aim to train biologists with little or no NGS experience to prepare sequencing libraries and analyze the millions of DNA sequences that result. Participants are expected to provide DNA samples from their own study systems, and we will prepare sequencing libraries together from those samples as well as a shared set of samples for a group project.

Participants will learn to analyze these data using simple command line tools on a high-performance computing cluster. Altogether, we'll cover the process from raw genomic DNA in a tube, to millions of DNA sequences, to biological data on population and/or community diversity.

Registration for these workshops covers room and board (three meals a day, with ample coffee and snacks) during the workshop, and reagents/sequencing such that each participant can sequence and analyze up to 10 of their own samples.

For the 5-day amplicon sequencing workshop (Aug 11-15), registration costs $1,300. For the 9-day 2bRAD genotyping workshop (Aug 15-23), registration costs $1,900. Participants enrolling in both workshops will have the option of participating in a 'bonus' special topics in bioinformatics session and pay a discounted rate of $3,000 for both workshops.

For more information, including information from previous years' workshops, please see the full posting at the following website: http://people.oregonstate.edu/˜meyere/workshops.html To reserve your spot, please contact Demian Willette (demian.willette@lmu.edu), Eli Meyer (eli.meyer@oregonstate.edu), or Carly Kenkel (carly.kenkel@gmail.com) with "Workshops 2017" in the subject line.

Space is limited! To reserve your spot, please confirm your participation no later than May 31st and pay registration fee no later than June 30th.

Thanks, hope to see some of you on Catalina this August!

Eli, Demian, and Carly

Eli Meyer, Oregon State University. eli.meyer@oregonstate.edu

Demian Willette, Loyola Marymount University. demian.willette@lmu.edu Carly Kenkel, University of Southern California. carly.kenkel@gmail.com

Eli Meyer <meyere@oregonstate.edu>

HinxtonUK GeneticAnalysis Jul19-25

GeneticAnalysis of Mendelian and Complex Disorders 19-25 July 2017

Finalapplications and bursary requests are now invited for this popular Wellcome Trust Advanced Course held on the Wellcome Genome Campus, in Hinxton near Cambridge UK. Deadline for applications: 24 March 2017.

Formerlyknown as Human Genome Analysis: Genetic Analysis of Multifactorial Diseases, the 2017 Genetic Analysis of Mendelian and Complex Disorders course is aimed at scientists actively involved in genetic analysis of both rare (Mendelian) and complex human traits. The course provides a broad and comprehensive overview of the statistical methods currently used to map disease susceptibility genes in human populations. The programme includes lecture and practical computer-based sessions and will discuss fundamental issues needed to increase success in gene mapping studies, including: Optimal study design, Power to detect linkage and association, Determining the most appropriate statistical methods and software, Quality control strategies, Interpretation of statistical results and trouble shooting, Basic principles of statistical inference, Hypothesis testing, and Population and quantitative genetics

COURSEINSTRUCTORS: Daniel E. Weeks, University of Pittsburgh, USA. Heather Cordell, Newcastle University, UK, Janet Sinsheimer, University of California, LA, USA. Eric Sobel, University of California, LA, USA, Joe Terwilliger, Columbia University, USA, Simon Heath, Centre Nacional d'Anàlisi GenÃ²mica (CNAG), Barcelona, Spain

2017KEYNOTE SPEAKERS

StephenBurgess, University of Cambridge, UK

NancyCox, Vanderbilt University, USA

DaniellePosthuma, VU University and VU Medical Centre, The Netherlands

ShamilSunyaev, Harvard University, USA

JanetS@mednet.ucla.edu

Leipzig ModellingBiodiversity Sep3-15

iDiv Summer School 2017 "Synthesising and modelling biodiversity data"

3-15 September 2017, Leipzig, Germany Open to PhD students and advanced master's students www.summerschool.idiv.de The German Centre for Integrative Biodiversity Research Halle-Jena-Leipzig (iDiv) invites PhD students to apply to its third summer school taking place from the 3rd to 15th of September 2017 in Leipzig, Germany. The summer school gives 20 young scientists and five local doctoral researchers the opportunity to conduct a biodiversity synthesis project under the tutoring of senior iDiv scientists, aiming at the submission of the work for publication. The programme combines training in synthesis methods, plenary lectures on integrative biodiversity research, hands-on collaborative work in small groups, and networking with biodiversity scientists at iDiv. A varied social programme is organized together with the iDiv doctoral researchers. The lead teacher of the summer school is Nico Eisenhauer, iDiv Professor and head of the research group Experimental Interaction Ecology. Other lecturers and tutors include senior iDiv staff and invited scientists. The summer school invites applications mainly from PhD students working on biodiversity topics, but also applications from advanced masters level students will be considered. A limited number of travel grants are offered to candidates with limited resources. Applications from the developing countries, in particular female applicants, are strongly encouraged.

Application deadline for the course is Tuesday, 2nd of May 2017.

More detailed information on the course can be found online at www.summerschool.idiv.de "ulrike.schmidt@idiv.de" <ulrike.schmidt@idiv.de>

MichiganStateU EvolutionaryModeling Jul23-28

Applications are now open for the 2017 Summer Workshop "Making Meaning through Models: Problem solving in biology" to be held July 23-28 at Michigan State University. More information about the workshop is available here: https://qubeshub.org/groups/-summer2017 or see the attached flier.

Modeling is a key tool in the evolutionary biology tool box, and helping students to develop modeling skills as early in their career allows deeper exploration of evolutionary concepts. At this summer's workshop we will delve into how to engage our students more productively with models and the process of modeling. Join us as we consider how to enhance the skills students need to understand and build models, how to expand upon models already in our curriculum, and ultimately how to enhance student understanding of the nature and process of science with modeling. We will discuss effective pedagogical approaches, share excellent resources, and build community around effective use of models. The intensive week-long workshop is followed by the opportunity to continue to work with colleagues on the QUBESHub through the fall semester to develop and implement new approaches or materials.

The summer workshop is appropriate for two and four year faculty teaching all levels of undergraduate biology, quantitative biology, and life science-oriented mathematics. We encourage future faculty, full and part time faculty and teams of faculty from the same or affiliated institutions to apply. Please share this information with any of your colleagues who might be interested!

– Kristin P. Jenkins, PhD Director

BioQUEST Curriculum Consortium bioquest.org (608) 622.9394

kristin.jenkins@bioquest.org

Naples BringingMathsToLife Jun7-9

3rd Bringing Maths to Life 7-9 June 2017, Naples, Italy

Deadline Extension: BMTL2017 Workshop

Dear Colleague,

We would like to invite you to the 3rd edition of the Bringing Maths to Life Workshop, that will be held in Naples on 7-9 June 2017 (http://www.bmtl.it). NEW: ABSTRACTS SUBMISSION DEADLINE EXTENSION 15th APRIL 2017

The workshop provides an occasion for biologists and mathematicians to join forces in addressing key areas in biology that face demanding mathematical challenges.Discussing existing cases to identify gaps or to share existing solutions should help these disciplines in successfully linking up.

BMTL 2017 workshop, as a melange of different fields, will consist of selected contributions for open discussion to present and confront the most updated results at the interface of mathematics and biology in three main sessions:

1) Data: acquisition, pre-processing and storage of different -omics datasets. The goal of this session is to discuss effective ways of acquiring, processing, and storing data as a starting point for any kind of analysis. Two large-scale projects will be presented within this session. The first project, SardiNIA, recruited over 1.5 million Sardinians across the island to gather enough cases and controls to investigate genetic factors for a wide range of conditions and diseases (see: https://sardinia.nia.nih.gov/). The second, MetaSUB (Metagenomics & Metadesign of Subways & Urban Biomes), includes scientists tracking the microbes in city subways and describe their diffusion on an interactive map (see: http://metasub.org/).

2) Information: data analysis, novel -omics technologies, the application of deep learning to different -omics datasets. The integration of experimental data prior to their analysis requires full understanding of the algorithms that need to be used in order to ensure a correct application in answering biological questions. Case studies of this session are two examples of metagenomics analyses. The first is the analysis of data collected during the Tara Oceans expedition including samples from 210 stations across the world oceans (see: http://taraexpeditions-it.blogspot.it/)). The project is deciphering how the most complex organisms evolved from primordial bacteria and in future it will tell us about the fate of the myriad organisms present today. The second concern the analysis of human gut microbiome.

3) Knowledge: integration of different -omics data, system biology of -omics data. Methods for the integrative analysis of multi-omics data are required to draw a more complete and accurate picture of the dynamics of molecular systems. Unveiling the interactions between diverse types of data allows to fully exploit their information. The keynote lectures of this session will show the integration of genomic, biochemical, and metabolic data under comprehensive mathematical models. This year the workshop will be held in the magnificent Capitolo Hall of St. Domenico Maggiore Convent, one of the most important spaces created during the renovation started by the prior Ruffo (XVII century).

Confirmed speakers include:

Dr. Valeria D'Argenio, University of Naples Federico II, Italy Prof. Antti Honkela, University of Helsinki, Finland Dr. Daniele Iudicone, Zoological Station of Naples A. Dohrn, Italy Dr. Carlo Sidore, Institute of Genetic and Biomedical Research ?C CNR, Italy Prof. Klas I. Udekwu, The Wenner-Gren Institute Stockholm University, Sweden Prof. Hans Westerhoff, University of Amsterdam, Netherlands For more information visit the website http://www.bmtl.it Important dates: Abstract submission & early registration: April 15th, 2017

Scientists are invited to send their contributions. Abstracts should be in English and contain original research results. All abstracts will be peer reviewed by the international scientific board that will decide whether presenting them as a poster or an oral contribution.

Selected papers will be considered for peer-reviewing and publication on a special issue of BMC Bioinformatics.

We hope to meeting you in Naples! Kind regards, The BMTL Organizing Committee Vincenza Colonna, IGB - CNR Mario Guarracino, ICAR - CNR Alessandra Rogato, IBBR - CNR Valeria Zazzu, formerly IGB - CNR

Learn More

www.bmtl.it info@bmtl.it +39 0815515192

Bringing Maths To Life <newsletter@bmtl.it>

NewOrleans ArbovirusEvolution May30-31

Kathy Hanley (New Mexico State University) and Paul Turner (Yale University) invite you to apply for a workshop we are organizing on Evolutionary Causes and Consequences of Arbovirus Emergence (http://ideas.princeton.edu/workshop-for-2017/). The workshop occurs on May 30-31, 2017 in New Orleans, just in advance of the ASM Microbe meeting. This workshop is sponsored by the NSF-funded Research Coordination Network on Infectious Disease Evolution Across Scales (RCN-IDEAS).

Applications to participate are being accepted through April 8, 2017; travel and lodging expenses are covered for accepted applicants. More information on the workshop, as well as the application guidelines, are available here: http://ideas.princeton.edu/workshop-for-2017/ Thanks, and we look forward to seeing your application for the workshop!

Kathy and Paul

Kathy Hanley: khanley@nmsu.edu

Paul Turner: paul.turner@yale.edu

"Turner, Paul" <paul.turner@yale.edu>

OregonStateU Macroevolution June22-23

Short course on the analysis of diversification rates from phylogenies: June 22-23 on the campus of Oregon State University, to coincide with the North American Evolution meetings (SSE/ASN/SSB) in Portland (June 23 - June 27). The workshop is funded in part by the National Science Foundation with additional support from Oregon State University and is co-organized by Dr. Dan Rabosky (University of Michigan) and Dr. Brian Sidlauskas (Oregon State University). Travel awards of up to $500 per person are available to cover participation costs.

Overview: Rates of speciation, extinction, and phenotypic evolution vary widely across the Tree of Life and through time. This workshop will provide theoretical background and a hands-on practicum in the analysis of lineage diversification rates using time-calibrated phylogenetic trees. Topics will include:

Working with phylogenies in R Theoretical foundations of diversification models Developing your intuition for diversification models Using BAMM to study complex patterns of diversification rate variation on phylogenies Testing hypotheses about trait-dependent diversification Assessing the reliability of inferences with BAMM and other methods Visualizing macroevolutionary dynamics on phylogenies Studying diversification rates on phylogenies that include fossils

Course will primarily be taught by Dan Rabosky (University of Michigan) with contributions from several co-instructors. The course will assume basic proficiency with the R programming/statistical environment and some familiarity with command line interfaces. Example datasets will be provided, but participants are encouraged to bring any phylogenetic dataset they wish to analyze (time calibrated phylogenetic trees). A personal laptop is essential.

Workshop participants will arrive in Corvallis (Oregon) any time on Wednesday June 21 and we will depart for Portland on the evening of Friday June 23, such that individuals can attend the Evolution meeting. Shuttles offer easy transport between the Portland Airport and OSU's campus every two hours, and housing is available at several hotels near campus. Details regarding accommodation and transport will be provided to successful applicants.

To apply, please send a CV and a short statement (1-2 paragraphs) detailing your research interests, why you are interested in the course, and your prior experience with R and phylogenetics / comparative methods. Please email your application (or questions) to Dan Rabosky (macroevolution.workshop@gmail.com).

Applications will be accepted until April 2, 2016, but please apply early as spaces are limited. Target audience is graduate students and postdocs but applications from researchers at other career stages are welcome. Preference will be given to students with a clear interest and research focus in phylogenetics & macroevolution.

Dan Rabosky Assistant Professor & Curator of Herpetology Museum of Zoology & Department of Ecology and Evolutionary Biology University of Michigan Ann Arbor, MI 48109-1079 USA

drabosky@umich.edu http://www.raboskylab.org http://www.lsa.umich.edu/ummz/ "drabosky@umich.edu" <drabosky@umich.edu>

Portugal 3 cE3c

Subject: Portugal-cE3c-Course: three advanced courses with deadlines April-May 2017

cE3c - Centre for Ecology, Evolution and Environmental Changes is organizing several Advanced Courses: see below the two courses with closer deadlines.

Additional informations at:

http://ce3c.ciencias.ulisboa.pt/training/?cat=8 Subject: Portugal-cE3c-Course: three advanced courses with deadlines April-early May cE3c - Centre for Ecology, Evolution and Environmental Changes is organizing several Advanced Courses: see below the three courses with closer deadlines.

Additional informations at:

http://ce3c.ciencias.ulisboa.pt/training/?cat=8 Course Nature-Based Design Frameworks organized by Gil Penha-Lopes and Hugo Oliveira | New calendar! May 15h-19th 2017 @ Lisbon, Portugal

Objectives: The course will introduce participants to different Nature-based bodies of knowledge and experience, such as the Biomimicry, Permaculture and Resilience topics. With almost 2 days per topic, the students will get a good feeling of how these topics see, do research and implement effective and sustainable solutions targeting a wide variety of societal, ecological and economic challenges.

Course instructors Gil Penha-Lopes (Invited Assistant Professor at FCUL, Leader of the Subgroup 'Adaptation and Sustainability', CCIAM, cE3c) http://ce3c.ciencias.ulisboa.pt/member/gil-pessanha-penha-lopes and Hugo Oliveira (PhD student, CCIAM, cE3c) http://ce3c.ciencias.ulisboa.pt/member/hugo-ferreira-calado-de-oliveira Intended audience: This five days intensive course will be open to a maximum number of 24 participants, being directed to PhD or MSc students in Biology, Environmental studies, Geography or related areas, and postdocs and other professionals working in related topics. Minimal formation of students: Bachelor in Biology, Geography or related areas.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (BIODIV UL; UP), Biology and Ecology of Global Changes (BEAG UL; UA) and Climate Change and Sustainable Development Policies (UL). For information of fees for other participants see the programme details.

Deadline for applications: April 13th, 2017 Candidates should send a short CV and motivation letter to Gil Penha-Lopes (email gppenha-lopes@fc.ul.pt) and £ngela Antunes (email amantunes@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: gppenha-lopes@fc.ul.pt

Course Natural History Collections and Biodiversity Organized by Maria Judite Alves, Raquel Barata, Cristiane Bastos-Silveira et al. | May 29 - June 2 @ Lisbon, Portugal

Objectives Natural history museums are privileged spaces for seminal research on different subjects of biological sciences such as biodiversity, evolution, ecology, biogeography and taxonomy. This crucial role is due to the fact that they represent biological diversity repositories becoming huge libraries of information on Earth living organisms. The long-term sampling through various decades renders to natural history collections an historic perspective that allows reconstructing a "memory", sometimes secular, of natural patterns and processes. This aspect gains particular relevance nowadays because of the increasing rate of species extinctions and biodiversity decrease.

This course aims to: - evidence the importance of natural history collections for the study of biodiversity. - show new tools and approaches to extract and disseminate biodiversity data from natural history collections - increase awareness of young researchers for the scientific and culture value of Natural History Museums.

Course coordinator Maria Judite Alves (Researcher at the Centre for Ecology, Evolution and Environmental Changes (cE3c), Leader of the Subgroup Animal Biodiversity, Evolution and Systematics, NHS group)

(http://ce3c.ciencias.ulisboa.pt/member/maria-judite-silva-cardoso-alves)

Intended audience This five days intensive course will be open to a maximum number of 16 participants, being directed to PhD or MSc students in Biology, Evolution, Ecology or related areas, and postdocs and other professionals working in related topics.

Minimum formation: Bachelor in Biology or related area. The course is free for 1st year PhD students in the Doctoral programme

— / —

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

---

Roscoff EcolEvolutionaryGenomics Jun5-16

13^th Summer course on marine ecological & evolutionary genomics at the Marine Biological Station of Roscoff

(F)

First announcement

>From June 5th^ - June 16th, 2017

the 13^th Summer Course on Marine Ecological & Evolutionary Genomics - MEEG 2017

takes place at the Station Biologique de Roscoff, Roscoff, France.

Aims:

Genomic knowledge is crucial for understanding the marine environment and for an efficient use of its resources. State of the art NGS methods have revolutionized the field, spawning applications in basic research, biotechnology and resource management. The course will focus on the latest developments in population genomics, including biodiversity, evolution, comparative and functional aspects through lectures, case studies and computer labs. It takes place at the Biological Station, a vibrant research community of 273 scientists and support personnel, located in the old town and fishing port of Roscoff, Brittany, France.

The course includes lectures, tutorials and computer based exercises on the following topics.

- Genomics - next generation sequencing, database searching, basic skills in data handling and bioinformatics

- Population genomics - diversity, structure, connectivity and gene flow, assignment, effective population size, population dynamics, adaptive variation, genotyping by sequencing

- Environmental genomics - environment-genome interactions, ecogenomics and metagenetics

- Functional genomics - genome structure, molecular evolution at the functional level, genomic architecture, functional networks

- Comparative genomics - whole genome comparisons, concatenated phylogenies, genome organization, annotating genomic information, co-evolution

- metagenomics

The course covers all aspects of life in the ocean.

Target group:

PhD students (at least in their second year) and junior postdocs with a solid knowledge in ecological and/or evolutionary genetics.

18 participants will be selected on the following criteria:

1. Relevance of the course for their PhD or post-doc project

2. Background and experience

3. We aim at training people with different research backgrounds; not more than one person per institute will be considered. We implement a gender policy.

The selected persons will be notified by Friday 14^th April and will have to confirm attendance within 7 days. There is a waiting list in case of non-confirmations and cancellations.

Teaching staff :

Nicola Barson, NMBU, No

Sarah Bouchemousse, UniFr, Ch

Jonas Collen, SB-Roscoff, FR

Simon Creer, Univ. Bangor, UK

Yves Desdevises, OO-Banyuls, FR

Erica Leder, Univ. Turku, Fi

Daniel Vaulot, SB-Roscoff

Frederique Viard, SB-Roscoff, FR

Filip Volckaert, Univ. Leuven, BE

Mathias Wegner, AWI-Sylt, GE

Organizing committee

Jonas Collen, SB-Roscoff, FR

Damien Guiffant, SB-Roscoff, FR

Matthias Obst, Univ. Gothenburg, SE

Nic Blouin, Univ. Rhode Island, USA

Nathalie Turque, EMBRC-France, FR

Daniel Vaulot, SB-Roscoff, FR

Filip Volckaert, Univ. Leuven, BE

For information, a flyer and application please check http://meeg2017.sciencesconf.org . Application deadline is April 2 2017.

Filip Volckaert <filip.volckaert@kuleuven.be>

Seattle StatisticalGenetics Jul10-28 AFewScholarshipsRemain

We have awarded scholarships for the 22nd Summer Institute in Statistical Genetics (http://-www.biostat.washington.edu/suminst) to people who applied by March 1.

We expect to be able to award a few more for applications received by April 1, 2017.

thanks

Bruce

bsweir@uw.edu

Bruce Weir <bsweir@uw.edu>

Siegen Germany FishSim AnimationToolchain Oct20-22

Workshop announcement: "Discovering FishSim in 3 days - new software for computer-animated 3D fish stimuli for innovative research in animal behavior"

When? October, 20th - 22nd 2017 Where? University of Siegen, Hölderlinstr. 3, 57076 Siegen, Germany

Application deadline: Friday, 30th June 2017

BACKGROUND Scientists are continuously looking for new methods to improve experimental procedures and to pave new ways to study animal behavior. Nowadays, more and more scientists tend to use various forms of computer animations that assist in research and lead to higher control and standardization during experiments. Computer animations offer various opportunities for specific manipulation of morphology and behavior of a virtually created animal stimulus in a range not possible with live stimulus animals. Furthermore, computer animations serve to implement the 3Rs principle in research by replacing and reducing the use of experimental animals and by refining experimental procedures. Currently, researchers can choose from a conglomeration of software solutions to create and animate 2D and 3D virtual stimuli. Nevertheless, easy-to-use toolchains that are designed for the specific needs of behavioral biologists and that combine all necessary steps, from creation of the stimulus to its presentation, do nearly not exist (but see anyFish; http://swordtail.tamu.edu/anyfish).

Within the scope of the DFG funded Virtual Fish Project at University of Siegen (Germany), we developed the free and open-source "FishSim Animation Toolchain" (FishSim) which combines easy creation, animation and presentation of realistic 3D computer-animated fish stimuli for the use in experiments with live test fish (üller et al. 2016, doi: 10.1093/cz/zow106; Gierszewski et al. 2016, doi: 10.1093/cz/zow108). FishSim was specifically designed for behavioral experiments using common one-choice and two-choice set-ups, as in studies on visual signaling and mate choice. FishSim provides various possibilities to experimentally manipulate morphology and behavior of any number of virtual 3D fish with presentation via monitors. Since FishSim is based on a computer game engine, it offers a unique way for animating 3D fish via real-time input from an external video-game controller.

To introduce FishSim and to assist in the implementation of our toolchain, we would like to welcome you to join a 3-day international workshop for behavioral and evolutionary biologists on "Discovering FishSim in 3 days - new software for computer-animated 3D fish stimuli for innovative research in animal behavior". The workshop will be held at University of Siegen in Siegen, Germany, from October 20-22, 2017, and is organized by Dipl.-Biol. Stefanie Gierszewski (Institute of Biology, University of Siegen), Prof. Dr. Klaudia Witte (Institute of Biology, University of Siegen), Dipl.-Inform. Klaus üller (Institute of Real-Time Learning Systems, University of Siegen) and BSc. Jan-Marco Hütwohl (Institute of Real-Time Learning Systems, University of Siegen).

The goal of this 3-day workshop is to provide detailed information on the free and open-source FishSim Basic and its integrated tools FishCreator, FishSteering and FishPlayer in both theory and practice. DOs and DON'Ts for implementation of FishSim Basic in future research are discussed. Working computers with all software installed will be provided but it is also possible to use personal laptops. Assistance and advice for working with own data will be given.

THE SOFTWARE

Please visit our workshop webpage for more information on the FishSim software: https://-virtualfishproject.wixsite.com/fishsim PRELIINARY PROGRAM Day 1: Friday, October 20th, 2017 Room: TBA 15:00 - 16:00 Registration 16:00 - 16:15 Welcome 16:15 - 17:00 Introducing the "Virtual Fish Project" 17:00 - open end Software installation and updates on personal laptops

Day 2: Saturday, October 21st, 2017 Room: TBA 09:00 - 11:00 Workshop part I 11:00 - 11:30 Coffee break 11:30 - 13:00 Workshop part II 13:00 - 14:00 Lunch 14:00 - 15:00 Guided tour through the laboratories of the Institute of Biology 15:00 - 16:30 Workshop part III 16:30 - 17:00 Coffee break 17:00 - 19:00 Workshop part IV 19:00 - 20:00 Break 20:00 - open end Social event

Day 3: Sunday, October 22nd, 2017 Room: TBA 09:00 - 10:00 Workshop part V (Q&A) 10:00 - 10:30 Coffee break 10:30 - 12:30 Workshop part VI (time for own projects) 12:30 - 13:00 Closing remarks and workshop evaluation 13:00 Official ending

APPLICATION / REGISTRATION Any scientist in the field of fish behavior (asters and PhD students, postdocs, senior scientists) is welcome to register for the workshop. Registration fees (50 euro for students, 70 euro for postdocs and senior researchers) include catering during the workshop as well

— / —

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

SwissAlps Sexual Selection Aug28-31

SIGNIFICANCE OF SEXUAL SELECTION FOR POPULATION FITNESS

WHEN ? 28-31 August 2017

WHERE? Fafleralp, Swiss Alps (CH)

MORE INFOS AND REGISTRATION https://www.cuso.ch/activity/?p=3D1128&uid=3D3366 ORGANIZER Prof. Claus Wedekind, University of Lausanne (CH)

INVITED SPEAKERS Prof. David Berger, University of Uppsala (SE) Prof. Andrew P. Hendry, McGill University (CA) Prof. Hanna Kokko, University of Zürich (CH) Prof. John Pannell, University of Lausanne (CH) Prof. Jacek Radwan, University of Poznan (PL) Prof. Leigh Simmons, University of Western Australia (AU)

DESCRIPTION Sexual selection is expected to promote population fitness by enhancing the reproductive success of individuals of high genetic quality (i.e. of high breeding value for fitness), or by purging the genome of deleterious mutations, e.g. via mate preferences for condition-Â'dependent traits or dominance fights within sexes. The significance of such effects is not sufficiently understood yet. Estimates range from minor importance to the benefits of sexual selection even outweighing the costs of sex. We will discuss the problem in the context of current environmental changes and the potential of rapid evolution.

QUERIES caroline.betto-colliard@unil.ch

"Caroline.Betto-Colliard@unil.ch" <Caroline.Betto-Colliard@unil.ch>

Toulouse EvolutionEconomics Jun1-2

Dear colleagues,

Registration for the *5th Toulouse* *Economics and Biol**ogy **Workshop, **June 01-02*, is now open. *(Registration deadline is April 30th).*

https://www.iast.fr/conference/5th-annual-toulouse-economics-and- biology-workshop-evolution-and-economics-family

Please note the deadline for posters' submission is March 31.

Submissions (abstract + C.V.) should be sent to *econ-bio_poster@iast.fr*

A limited number of travel grants will be available. To apply, please join a cover letter explaining why you are applying for a grant and why you are interested in attending the workshop.

The theme of the workshop this year is *" The Evolution & Economics of the Family"*.

The speakers are:

Robert BROOKS < http://www.bees.unsw.edu.au/rob-brooks >, University of New South Wales

Pierre-André CHIAPPORI < http://www.columbia.edu/~pc2167/ >, Columbia University

Donald COX < https://www2.bc.edu/donald-cox/ >, Boston College

Partha DASGUPTA < http://www.econ.cam.ac.uk/people/crsid.html?crsid=pd10000&group=emeritus >, University of Cambridge

David DE LA CROIX < http://perso.uclouvain.be/david.delacroix/ >, Université Catholique de Louvain

Lena EDLUND < http://www.columbia.edu/~le93/ >, Columbia University

Lee GETTLER < http://anthropology.nd.edu/-faculty-and-staff/faculty-by-alpha/lee-gettler/ > , University of Notre Dame

Hanna KOKKO < http://www.ieu.uzh.ch/en/staff/-member/kokko_hanna.html >, University of Zürich

Ruth MACE < https://www.ucl.ac.uk/anthropology/-people/academic-teaching-staff/ruce-mace > , University College London

Brooke SCELZA < http://www.anthro.ucla.edu/-faculty/brooke-scelza >, UCLA

Brian WOOD < http://anthropology.yale.edu/-people/brian-wood >*, *Yale University

The workshop will take place at the Institute for Advanced Study in Toulouse, Manufacture des Tabacs, 21 Allée de Brienne, 31015 Toulouse, France.

We look forward to welcoming you!

Organizers: Ingela Alger, Jörgen Weibull and Jonathan Stieglitz

Co-organizers: Alice Baniel and Mark Dyble

For any information please contact us at *econ-bio@iast.fr*

Alice Baniel <alice.baniel@gmail.com>

UK GeneticDataAnalysisUsingR ThibautJombart Oct23-27

"Genetic data analysis/exploration using R" (GDAR03)

This course will be delivered by Dr. Thibaut Jombart who authors the adegenet package and Dr. Zhian Kamvar.

This course will run from the 23rd - 27th October at Margam discovery centre in Wales, United Kingdom.

Course Overview: This course provides a comprehensive introduction to exploratory statistical methods used in population genetics and molecular ecology. Participants will become proficient in a range of approaches for uncovering genetic structures from usual genetic data including most genetic markers (e.g. microsatellites, SNPs, AFLP) and genetic sequences (DNA or amino-acid). After covering different types of phylogenetic reconstruction, and basic population genetics tests, a strong emphasis will be put on using factorial methods (e.g. Principal Component Analysis) for investigating genetic diversity. In particular, we will focus on the identification and description of genetic clusters, and on characterising spatial genetic patterns. The last day of the course will be an open problem day, where participants will be able to analyse their own data.

Day 1 Intro to phylogenetic reconstruction. Module 1a: Reconstructing phylogenies from genetic sequence data. Three main approaches covered: distance-based phylogenies; maximum parsimony; and likelihood-based approaches. Module 1b: Short R refresher. Practical 1: Phylogenetic reconstruction using R. Three main approaches plus rooting a tree; assessing/testing for a molecular clock; and bootstrapping. Main packages: ape, phangorn.

Day 2 Intro to multivariate analysis of genetic data Module 2: Key concepts in multivariate analysis. Focus on using factorial methods for genetic data analysis. Practical 2: Basics of multivariate analysis of genetic data in R. Topics include: data handling, population genetic tests of population structure (PCA, PCoA). Main packages: adegenet, ade4, ape.

Day 3 Exploring group diversity Module 3: Approaches to identifying and describing genetic clusters. Topics include: hierarchical clustering, K-means, population-level multivariate analysis (between-group-PCA, DA, DAPC). Practical 3: Applying the approaches covered in morning lecture and emphasising their strengths and weaknesses. Main packages: adegenet, ade4.

Day 4 Spatial genetic structures Module 4: Discussing the origin and significance of spatial genetic patterns, and how to test for them. Practical 4: Visualising and analysing spatial genetic data. Topics: spatial density estimates, Moran/Mantel tests, mapping principal components in PCA, spatial PCA. Main packages: adegenet, adehabitat, ade4.

Day 5 Using R for reproducible science. Module 5: Using R for reproducible science Practical 5: Practical session based on morning lecture Main packages: knitr, Sweave, rmarkdown

If you have any questions please email oliverhooker@prstatistics.com or visit www.prstatistics.com To book online go to http://www.prstatistics.com/-course/genetic-data- analysis-exploration-using-r-gdar03/

Other up-coming courses are as follows

1. ADVANCES IN MULTIVARIATE ANALYSIS OF SPATIAL ECOLOGICAL DATA USING R #MVSP 3rd - 7th April 2017, Scotland, Prof. Pierre Legendre, Dr.

Olivier Gauthier http://www.prstatistics.com/course/advances-in-spatial-analysis-of-multivariate-ecological-data-theory-and-practice-mvsp02/ 2. ADVANCING IN STATISTICAL MODELLING FOR EVOLUTIONARY BIOLOGISTS AND ECOLOGISTS USING R #ADVR 17th - 21st April 2017, Scotland, Dr. Luc Bussiere, Dr. Ane Timenes Laugen http://www.prstatistics.com/course/advancing-statistical-modelling-using-r-advr06/ 3. CODING, DATA MANAGEMENT AND SHINY APPLICATIONS USING RSTUDIO FOR EVOLUTIONARY BIOLOGISTS AND ECOLOGISTS #CDSR 15th - 19th May, Scotland Dr. Aline Quadros http://www.prstatistics.com/course/coding-data-management-and-shiny-applications-using-rstudio-for-evolutionary-biologists-and-ecologists-cdsr01/ 4. GEOMETRIC MORPHOMETRICS USING R #GMMR 5th - 9th June 2017, Scotland, Prof. Dean Adams, Prof. Michael Collyer, Dr. Antigoni Kaliontzopoulou http://www.prstatistics.com/course/geometric-morphometrics-using-r-gmmr01/ 5. MULTIVARIATE ANALYSIS OF SPATIAL ECOLOGICAL DATA #MASE 19th - 23rd June, Canada, Prof. Subhash Lele, Dr. Peter Solymos

— / —

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

---

UK MetaAnalysisInEcologyAndEvolution Jul24-28

“Meta-analysis in ecology, evolution and environmental sciences ”

This course will be delivered by Prof. Julia Koricheva who has co-edited “Handbook of meta-analysis in ecology and evolution” (Princeton University Press, 2013), the first handbook on meta-analysis written specially for ecologists and evolutionary biologists and Prof. Elena Kulinskaya.

http://www.prstatistics.com/course/meta-analysis-in-ecology-evolution-and-environmental-sciences-metr01/ This course will run from 24th - 28th July 2017 at SCENE field station, Loch Lomond, Glasgow

Course only and all inclusive packages are available.

This 5-day course will involve combination of lectures and practical sessions where students will practice conducting meta-analysis using the metafor package in R. In addition, students will conduct their own mini-meta-analyses by working in small groups on an assigned ecological topic with 8-10 primary research papers provided per topic. Students would need to decide on effect size metric to use and inclusion criteria, extract the data from the primary studies, design the extraction spreadsheet, conduct meta-analysis using the metafor package and present their results in the form of a PowerPoint Presentation. After successfully completing this course students should be able to: 1) formulate questions for meta-analysis 2) formulate inclusion criteria for primary studies to be included in the analysis design spreadsheets for data extraction 3) conduct literature search on the topic 4) extract data from published studies 5) conduct meta-analysis using metafor package in R 6) present the results of the meta-analysis

Course content is as follows

DAY 1 -Lectures Types of quantitative research synthesis (vote counting, combining probabilities, meta-analysis) History of meta-analysis and its applications in ecology Types of ecological data and their conversion to effect sizes Question formulation and inclusion criteria Literature search and data extraction -Practical Work in groups: students decide on inclusion criteria and metrics of effect size for their own meta-analysis based on 8-10 studies and begin data extraction

Tuesday DAY 2 -Lecture Combining effect sizes across studies, fixed vs random effects models Practical Using metafor package in R to calculate effect sizes and overall mean effects using fixed and random effect models. -Work in groups: completing data extraction for own meta-analysis and running meta-analysis.

DAY 3 -Lecture Exploring the causes of heterogeneity in effect sizes by meta-regression -Practical Meta-regression analyses using metafor. -Lecture Dealing with non-independence of observations (including phylogeny bias) -Practical Work in groups: testing for moderators, considering sources of non-independence.

DAY 4 -Lecture Publication bias Statistical methods for bias detection -Practical Exploring publication and related biases in metafor -Lecture Dealing with missing data and variable research quality Format of meta-analysis report: good and bad examples, critique of meta-analysis -Practical -Work in groups: testing for bias in own dataset; finalizing analyses; preparing Power Point presentation with results of the analyses

DAY 5 -Morning Student presentations on the results of their analyses + Discussion -Afternoon Individual consultations for students planning to do meta-analysis in their own research projects

Please email any inquiries to oliverhooker@prstatistics.com or visit our website www.prstatistics.com Please feel free to distribute this material anywhere you feel is suitable

Our other courses

1. ADVANCES IN MULTIVARIATE ANALYSIS OF SPATIAL ECOLOGICAL DATA USING R #MVSP 3rd - 7th April 2017, Scotland, Prof. Pierre Legendre, Dr. Olivier Gauthier http://www.prstatistics.com/course/advances-in-spatial-analysis-of-multivariate-ecological-data-theory-and-practice-mvsp02/ 2. ADVANCING IN STATISTICAL MODELLING FOR EVOLUTIONARY BIOLOGISTS AND ECOLOGISTS USING R #ADVR 17th - 21st April 2017, Scotland, Dr. Luc Bussiere, Dr. Ane Timenes Laugen http://www.prstatistics.com/course/advancing-statistical-modelling-using-r-advr06/ 3. CODING, DATA MANAGEMENT AND SHINY APPLICATIONS USING RSTUDIO FOR EVOLUTIONARY BIOLOGISTS AND ECOLOGISTS #CDSR 15th - 19th May, Scotland Dr. Aline Quadros

— / —

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

ULeicester 2 DNAseqRNAseqAnalysis May

One week to registration deadline for the BBASH Next Generation Sequencing workshops at University of Leicester!

For additional information: http://www2.le.ac.uk/colleges/medbiopsych/facilities-and-services/cbs/bbash/training/upcoming DNA-Seq NGS Analysis Workshop Venue: University of Leicester - College Court Conference Centre Date: 2nd, 3rd & 4th May 2017 Time: 9:00am to 5:00pm each day Organizers: Matthew Blades and Chiara Batini Admin support: NGStraining@le.ac.uk Participation: Open application with selection Registration opens: REGISTRATION NOW OPEN (closing date for registration is 5pm 3rd April 2017)

RNA-Seq NGS Analysis Workshop Venue: University of Leicester - College Court Conference Centre Date: 24th, 25th, 26th May 2017 Time: 9:00am to 5:00pm each day Organizers: Matthew Blades and Ben Hunt Admin support: Matt Blades - NGStraining@le.ac.uk Participation: Open application with selection Registration: REGISTRATION NOW OPEN (closing date for registration is 5pm 3rd April 2017)

"Batini, Chiara (Dr.)" <cb334@leicester.ac.uk>

ULeicester 2 NGSanalysis May

BBASH at University of Leicester is pleased to announce that applications for the upcoming training Next Generation Sequencing workshops are now open.

DNA-Seq NGS Analysis Workshop Venue: University of Leicester - College Court Conference Centre Date: 2nd, 3rd & 4th May 2017 Time: 9:00am to 5:00pm each day Organizers: Matthew Blades and Chiara Batini Admin support: NGStraining@le.ac.uk Participation: Open application with selection Registration opens: REGISTRATION NOW OPEN (closing date for registration is 5pm 3rd April 2017)

RNA-Seq NGS Analysis Workshop Venue: University of Leicester - College Court Conference Centre Date: 24th, 25th, 26th May 2017 Time: 9:00am to 5:00pm each day Organizers: Matthew Blades and Ben Hunt Admin support: Matt Blades - NGStraining@le.ac.uk Participation: Open application with selection Registration: REGISTRATION NOW OPEN (closing date for registration is 5pm 3rd April 2017)

For additional information: http://www2.le.ac.uk/colleges/medbiopsych/facilities-and-services/cbs/bbash/training/upcoming "Batini, Chiara (Dr.)" <cb334@leicester.ac.uk>

UPadova ProteinInteractions Apr10-13

ELIXIR-IIB, in collaboration with the University of Padova and RGS-Italy, is pleased to inform you that the applications for the upcoming training course on "Computational approaches to the study of protein interactions and rational drug design" are now open.

IMPORTANT DATES for this Course:

*- Deadline for applications: 31st March 2017 * *- Course date: 10-13 April 2017*

Venue: Campus di Biologia e Biomedicina “Fiore di Botta”, University of Padova, Via del Pescarotto, 8, Padova, IT

Speakers: Prof. Alexandre Bonvin - Faculty of Science, Utrecht University, the Netherlands Dr. Norman Davey - University College Dublin, Dublin, Ireland) Dr. Stefano Forli - Dept. Molecular Biology, The Scripps Research Institute, La Jolla, USA Prof. Stefano Moro - Dept. of Pharmaceutical and Pharmacological Sciences, University of Padova, Padova, Italy

A maximum of 30 candidates will be accepted in the course. Selection will start on March 10th, 2017 and those with an adequate profile will be accepted immediately, especially if they come from other cities and/or countries (to allow them to find reasonably cheap flight tickets).

Course description: This workshop is aimed at students in master degree courses, PhD students and postdoctoral researchers who are working or planning to work in the field of protein interactions from a molecular and structural point of view. In this workshop, participants will familiarize with docking approaches to the study of protein-protein interactions (PPIs) and protein-small molecule interactions. Irreversible binders design using molecular docking and computational methods to rational drug design will be also described, as well as the functional role of the intrinsically disordered proteins.

Should you have any question, do not hesitate to contact the ELIXIR-IIB training coordinator, Dr Allegra Via, at allegra.via@cnr.it or elixi r.ita.training@gmail.com.

Full details at can be found here < https://elixir-iib-training.github.io/website/2017/04/10/protein-interactions-padova.html >.

Best regards,

The ELIXIR-IIB Training Team

Vincenza Colonna, PhD http://www.igb.cnr.it/-popgenlab Consiglio Nazionale delle Ricerche Istituto di Genetica e Biofisica “Adriano Buzzati-Traverso” piano 1, stanza 20 -via Pietro Castellino 111 - 80131 Napoli - IT

tel +39 081 6132 254 - fax +39 081 6132 706 - skype enza.colonna email vincenza.colonna@igb.cnr.it google scholar < http://goo.gl/SzimG0 >

would you like to know about the most amazing project ever? http://www.igb.cnr.it/obilab interested in Life Science and/or Mathematics? visit http://www.bmtl.it/ vincenza colonna <vincenza.colonna@igb.cnr.it>

Wales ModellingUsingR Apr24-28 PartialScholarships

PR STATISTICS ARE PLEASED TO ANNOUNCE THAT THROUGH THEIR FUNDING SCHEME THEY CAN OFFER 5 PART-FUNDED SCHOLARSHIPS FOR OUR UP-COMING COURSE “Advancing in statistical modelling for evolutionary biologists and ecologists using R (ADVR06)”

SCHOLARSHIPS CONTRIBUTE TOWARDS TUITION FEES AND ACCOMMODATION WITH 5 ’ALL INCLUSIVE PLACES’ AVAILABLE AT 450.00 (Fees have been subsidised by 35% from 700.00).

Applications should be sent to oliverhooker@prstatistics.com and contain the following. 1. Full name 2. Institute name 3. PhD subject title or Post doc research questions 4. Do you hold a funded position 5. 150 words why this course would be relevant to your research or how it would help.

Application deadline is Tuesday 4th April 2017

We still have ’normal’ places available for anyone else interested.

Full course details are given below

http://www.prstatistics.com/course/advancing-statistical-modelling-using-r-advr06/ This course will run from 24th - 28th April at Margam Discovery Centre, Wales.

This is an introduction to model selection and simplification, generalised linear models, mixed effects models and non-linear models.

The course is aimed at biologists with a basic to moderate knowledge in R. The course content is designed to bridge the gap between basic R coding and more advanced statistical modelling. This five day course will consist of series of modules, each lasting roughly half a day and comprised of lectures and practicals designed to either build required skills for future modules or to perform a family of analyses that is frequently encountered in the biological literature.

Course content is as follows

Day 1 Course introduction - Techniques for data manipulation, aggregation, and visualisation; introduction to linear regression. Packages: {tidyr}, {dplyr}, {ggplot2}

Day 2 Linear models - Diagnostics, collinearity, scaling, plotting fitted values); fitting and interpreting interaction terms; model selection and simplification; general linear models and ANCOVA. - Packages: {stats}, {car}

Day 3 Generalized linear models - Logistic and Poisson regression; predicting using model objects and visualizing model fits. - Packages: {broom}, {visreg}, {ggplot2}

Day 4 Mixed effects models - Theory and practice of mixed effect models; visualising fixed and random effects. - Packages: {lme4}, {broom}, {ggplot2}, {sjPlot}

Day 5 Fitting nonlinear functions - Polynomial & Mechanistic models; brief introduction to more advanced topics & combining methods (e.g., generalised linear mixed effects, nonlinear mixed effects, and zero-inflated and zero-altered models). - Packages: {nlsTools}. - Afternoon to discuss own data if time permits or visit our website www.prstatistics.com Please feel free to distribute this material anywhere you feel is suitable.

Upcoming courses - email for details oliverhooker@prstatistics.com

ADVANCES IN MULTIVARIATE ANALYSIS OF SPATIAL ECOLOGICAL DATA USING R #MVSP 3rd - 7th April 2017, Scotland, Prof. Pierre Legendre, Dr. Olivier Gauthier http://www.prstatistics.com/course/advances-in-spatial-analysis-of-multivariate-ecological-data-theory-and-practice-mvsp02/ ADVANCING IN STATISTICAL MODELLING FOR EVOLUTIONARY BIOLOGISTS AND ECOLOGISTS USING R #ADVR 17th - 21st April 2017, Scotland, Dr. Luc Bussiere, Dr. Ane Timenes Laugen http://www.prstatistics.com/course/advancing-statistical-modelling-using-r-advr06/ CODING, DATA MANAGEMENT AND SHINY APPLICATIONS USING RSTUDIO FOR EVOLUTIONARY BIOLOGISTS AND ECOLOGISTS #CDSR 15th - 19th May, Scotland Dr. Aline Quadros http://www.prstatistics.com/course/coding-data-management-and-shiny-applications-using-rstudio-for-evolutionary-biologists-and-ecologists-cdsr01/ GEOMETRIC MORPHOMETRICS USING R #GMMR 5th - 9th June 2017, Scotland, Prof. Dean Adams, Prof. Michael Collyer, Dr. Antigoni Kaliontzopoulou http://www.prstatistics.com/course/geometric-morphometrics-using-r-gmmr01/ MULTIVARIATE ANALYSIS OF SPATIAL ECOLOGICAL DATA #MASE 19th - 23rd June, Canada, Prof. Subhash Lele, Dr. Peter Solymos http://www.prstatistics.com/course/multivariate-analysis-of-spatial-ecological-data-using-r-mase01/

— / —

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

---

WoodsHole MolecularEvolution Jul20-30

APPLICATION DEADLINE: April 7, 2017

Convening for its 30th year at the Marine Biological Lab in Woods Hole, MA, the Workshop on Molecular Evolution will be held July 20-30, 2017. The Workshop is the premier program for integrating the methods, theory, and applications of molecular phylogenetics, statistical genetics, molecular evolution, and related disciplines. Students work closely with internationally-recognized scientists, receiving (i) high-level instruction in the principles of molecular evolution and evolutionary genomics, (ii) advanced training in statistical methods best suited to modern datasets, and (iii) hands-on experience with the latest software tools (often from the authors of the programs they are using). The material is delivered via lectures, discussions, and bioinformatic exercises motivated by contemporary topics in molecular evolution. A hallmark of this workshop is the direct interaction between students and field-leading scientists. The workshop serves graduate students, postdocs, and established faculty from around the world seeking to apply the principles of molecular evolution to questions of both basic and applied biological sciences. A priority of this workshop is to foster an environment where students can learn from each other as well from the course faculty.

As the course progresses, participants learn how to use the following software to address questions concerning the origins, maintenance, and function of molecular variation: ASTRAL, BEAST2, BEST, BPP, FASTA, FigTree, GARLI, MIGRATE, MAFFT, MP-EST, RaxML, RevBayes, PAML, PAUP*, Phybase, ipyrad and SVD Quartets. Students will have the opportunity to work with software on their own laptops as well as receive training on how to use the same programs on a high performance computer cluster.

Course instructors include Peter Beerli, Joseph Bielawski, Belinda Chang, Mario dos Reis, Casey Dunn, Deren Eaton, Scott Edwards, Tracy Heath, David Hillis, Mark Holder, John Huelsenbeck, Lacey Knowles, Laura Kubatko, Peter Larsen, Paul Lewis, Emily Jane McTavish, Conor Meehan, Nicholas Meyerson, William

Pearson, David Swofford, David Weisrock, April Wright, and Anne Yoder.

information on the Workshop and a link to the application page are available on the dedicated course website: https://urldefense.proofpoint.com/v2/url?u=3Dhttps-3A__molevol.mbl.edu_index.php_Main-5FPage&d=DwIBAg&c=imBPVzF25OnBgGmVOlcsiEgHoG1i6YHLR0Sj_gZ4adc&r=aUlrl-ZempeNaLRY0gsnZTpP6CecsU48drplVPr1dj0&m=e3dZATSpks5obk9WV_KwbfytIFddaFpDLUSYuGAfrX0&s=HlWyls6tFplb-DCiL4rByDycvIANYFYoV0vYoO8GjhE&e=

The dates for the Workshop are designed to allow students to segue directly into the Strategies and Techniques for Analyzing Microbial Population Structures (STAMPS) course, though please note that applications for STAMPS must be submitted and are evaluated separately from those for the Workshop on Molecular Evolution.

For further information, please contact Workshop co-Directors:

Anne Yoder (anne.yoder@duke.edu) and Joseph Bielawski (j.bielawski@dal.ca)

"adyoder@duke.edu" <adyoder@duke.edu>

Zurich PolygenicAdaptationCourse Aug28-Sep1

A Summer School and a Symposium will take place this summer in Zurich calling for students and scientists keen to learn and discuss about the most recent theory, methods and applications to detect the genomic signal of polygenic adaptation and understanding the role of epistasis in evolution.

The invited speakers include, Prof Nick Barton (IST Austria, Austria) Dr. Jeremy Berg (Columbia University, USA) Prof Ã-rjan Carlborg (Uppsala University, Sweden) Dr. Josephine Daub (University Pompeu Fabra, Barcelona, Spain) Prof. Frederic Guillaume (University of Zurich, Switzerland) Prof. Thomas Hansen (University of Oslo, Norway) Prof Joachim Hermisson (University of Vienna, Austria) Prof Sergey Kryazhimskiy (University of California San Diego, USA) Prof. John Mckay (Colorado State University, USA) Dr. Josh Payne (University of Zurich, Switzerland) Prof. Peter Visscher (Institute for Molecular Bioscience, Queensland, Australia) Prof. Sam Yeaman (University of Calgary, Canada)

For more information visit the event websites: Summer School on "Integrated methods to detect polygenic adaptation from genomic data"

28 Aug - 30 Aug 2017, WSL, Birmensdorf, Switzerland http://www.ieu.uzh.ch/en/teaching/Polygenic-Adaptation.html Symposium on the "Genomics of polygenic adaptation and the role of epistasis in evolution"

31 Aug - 1 Sep 2017, ETH Zentrum, Zurich, Switzerland http://www.evolution.uzh.ch/en/events/symposium.html Informal inquiries may be addressed to Katalin Csillery at katalin.csillery@wsl.ch

Looking forward to seeing you this summer!

The organising committee: Dr Katalin Csillery (ETH Zurich & WSL Birmensdorf) Prof Dr Frederic Guillaume (University of Zurich) Dr Felix Gugerli (WSL Birmensdorf) Dr Christian Rellstab (WSL Birmensdorf) Dr Alejandra Rodriguez-Verdugo (ETH Zurich) Dr. Tony Weingril (University of Zurich) Prof Dr Alex Widmer (ETH Zurich) Dr. Debra Zuppinger-Dingley (University of Zurich)

Katalin Csillery <katalin.csillery@env.ethz.ch>

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.