EvolDir

June 1, 2015

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.

—— / ——

Conferences

ArizonaStateU EvolMedicine Jun5

Submit abstracts by June 5th for a day-long symposium on “What complex systems theory offers to evolutionary medicine” as a part of the Conference on Complex Systems the first meeting in the USA for the European Conferences on Complex Systems (ECCS) .

http://www.ccs2015.org/ Limited travel support is available.

WHAT COMPLEX SYSTEMS THEORY OFFERS TO EVOLUTIONARY MEDICINE

— Symposium Overview —

Applications of evolutionary biology in medicine are growing fast but are only now incorporating advances in the analysis of complex systems. The range of applications is wide. Gene networks are characterized by complexity vastly different from that of designed systems, resulting in both robustness and special vulnerability. Complex networks of positive and negative feedback loops regulate genomic, cellular and physiological systems whose disruption results in disease that can manifest at all these levels. Therapeutic interventions can disrupt these networks in ways that can be useful, but that can also result in additional risks that require understanding in complex systems terms. Within the broader context of medicine, systems of medical care organization evolve and grow as well, creating sudden transitions that can undermine the quality of patient care. We anticipate that the call for abstracts for this symposium should bring proposals from many scientists working on related problems who will, in the course of this symposium, create new connection and collaborations. The talks by those scientists will be integrated with talks by the organizers .

Abstracts are welcome on all topics at the interface of evolution, medicine, and complexity, but we especially seek contributions on topics related to regulation of gene expression, cellular functions, and physiological systems.

– Organizers –

Randolph Nesse, Arizona State University Ken Buetow, Arizona State University Manfred Laubichler, Arizona State University and The Santa Fe Institute Sander Van Der Leeuw, Arizona State University and The Santa Fe Institute

– Confirmed Presenters –

Athena Aktipis, Arizona State University Ken Buetow, Arizona State University Manfred Laubichler, Arizona State University and The Santa Fe Institute Melanie Mitchell, Portland State University and The Santa Fe Institute Randolph Nesse, Arizona State University Sander Van Der Leeuw, Arizona State University and The Santa Fe Institute

Limited travel and lodging support is available from the

Arizona State University Center for Evolution and Medicine

Please send your abstract by June 5th to nesse@asu.edu and submit it online at

http://www.easychair.org/conferences/?conf=CCs15 . Decisions on abstracts and travel funding will be announced in June, 2015.

For questions and queries, please contact Randolph Nesse nesse@asu.edu

Randolph M. Nesse, MD http://randolphnesse.com The ASU Center for Evolution & Medicine http://evmed.asu.edu The International Society for Evolution, Medicine & Public Health http://evolutionarymedicine.org rmnesse@gmail.com

---

Bainbridge Washington ChromosomeEvolution Aug17-20

Interested in Chromosome Evolution? Want to attend a very cool meeting in the beautiful Pacific Northwest? A small meeting, where you can interact with top researchers and dedicated students at talks, meals, and after-hour get-togethers? The AGA President, Katie Peichel, has reserved an intimate retreat, IslandWood, just outside of Seattle, for this year's AGA President's Symposium.

Registration includes all meals, spacious shared lodging is cheap, and we've thrown in a few drinks every evening.

For more information, poster abstract submission, and registration, go to: http://www.theaga.org/program.htm Space is limited for what promises to be a very popular small meeting. REGISTRATION WILL CLOSE ON JUNE 30, or as soon as space is filled, so register early!

SPEAKERS: Mark Kirkpatrick (University of Texas) Wilhelmine Key Lecture

Doris Bachtrog (UC Berkeley) Chromatin and the evolution of dosage compensation

Dan Barbash (Cornell University) Repetitive DNA dynamics and hybrid incompatibilities

Winston Bellott (Whitehead Institute/MIT) Gene survival and gene amplification on vertebrate sex chromosomes

Jim Birchler (University of Missouri) Using the B chromosome of maize to study the remarkable fluidity of centromere function

Heath Blackmon (University of Texas at Arlington) The fragile Y hypothesis - variation in Y chromosome turnover

Justin Blumenstiel (University of Kansas) Caught in the crossfire: Evolution of transposon silencing in the context of off-target effects

Kirsten Bomblies (Harvard University) Evolution of meiosis after whole genome duplication in Arabidopsis arenosa

Anna Drinnenberg (Fred Hutchinson Cancer Research Center) Holocentric chromosomes

Lila Fishman (University of Montana) Female meiotic drive

Jeff Good (University of Montana) Neo-sex chromosome evolution and speciation in beetles

Jun Kitano (National Institute of Genetics) Drivers of sex chromosome-autosome fusions and their roles in speciation

Michael Lampson (University of Pennsylvania) Violation of Mendel's first law: biased chromosome segregation in meiosis

Mia Levine (University of Pennsylvania) Evolution of heterochromatin binding proteins

Harmit Malik (Fred Hutchinson Cancer Research Center) Centromere drive

Karen Miga (UC Santa Cruz) A genomic and epigenomic study of human centromeres

Rachel O'Neill (University of Connecticut) Centromere function and evolution

Galina Petukhova (Uniformed Services University of the Health Sciences) Mechanisms controlling initiation of genetic recombination in mammals

Daven Presgraves (University of Rochester) Sex chromosomes in the Drosophila male germline: speciation and regulation

Jeremy Searle (Cornell University) Chromosomal hybrid zones and speciation in mice and shrews

Beatriz Vicoso (Institute of Science and Technology Austria) Testing evolutionary hypotheses on the surprisingly diverse sex-chromosomes of flies

Anjanette Bakerâ Managing Editor, Journal of Heredity http://jhered.oxfordjournals.org/ Manager,â American Genetic Association

http://www.theaga.org/â 2030 SE Marine Science Dr Newport, OR 97366 https://www.facebook.com/AmericanGeneticAssociation evoldir@evol.biology.mcmaster.ca

Biddeford Maine EvolGenomics YoungInvest Jul12-17

We will select five "young investigators" to speak in the session: "Young Investigator Presentations: Advances in Ecological and Evolutionary Genomics" at the Gordon Research Conference on Ecological and Evolutionary Genomics (12-17 July 2015 in Biddeford Maine). "Young investigators" include assistant professors, postdocs, and graduate students. We will begin selecting speakers from registered participants on 25 May, 2015. As you can see at the EEG GRC conference website (http://www.grc.org/programs.aspx?id=13135), this is shaping up to be an excellent meeting.

If you would like to be considered to speak during the session you will need to apply at the and submit a poster abstract. Also at that time send a message to Mike Herman through this link (http://www.grc.org/chairs.aspx?meeting=13135), indicating that you are interested in being considered as a young investigator speaker. Once you are approved to attend the meeting, you will need to register to be considered as a speaker, as we select young investigators from registered attendees only. This requires you to pay your registration, so please do so only if you want to come to the meeting, whether or not you are selected as a speaker. Selected speakers will have their registration costs covered, which will be done as a reimbursement after the meeting. Please direct any questions to the co-Chairs via the GRC Conference website.

Hope to see you at the meeting.

Jack Werren & Mike Herman

John (Jack) Werren Nathaniel & Helen Wisch Professor of Biology University of Rochester Rochester, NY 14627 Email: jack.werren@rochester.edu Web: http://www.werrenlab.org/ "Werren, Jack" <werr@mail.rochester.edu>

BiologicalStation UMichigan MolluscConservation Aug28-31

The 81st annual meeting of the American Malacological Society (AMS) will take place from August 28-31, 2015 at the University of Michigan Biological Station in Pellston, Michigan. The program includes a keynote speaker, symposia and special sessions, contributed talks and posters, an auction to earn funds to support student research, Welcome Reception, Banquet and opportunities for field excursions.

Much more additional information about AMS 2015 and links to register and submit abstracts can be found at the meeting website (bit.ly/AMS2015).

Deadline for early registration: May 31, 2015

Deadline for abstract submission: June 15, 2015

Symposia and special sessions: Early Career Malacologists, Conservation of Molluscs, Great Lakes Malacology, Invasives, Larval Biology of Molluscs, Phylogeny, Pacific Island Land Snails and Marine Molluscs. Open sessions are also available for presentations outside of these themes.

Keynote speaker: Alison Sweeney (University of Pennsylvania)

Please visit the meeting website (bit.ly/AMS2015) to learn more about AMS 2015.

If you have any questions about the meeting, please email Tom Duda (tfduda@umich.edu).

Tom Duda <tfduda@umich.edu>

CapeTown PlantDiversity Jul20-22

Plant Diversity in the Greater Cape Floristic Rregion: From Genomes to Biomes

A symposium bringing together researchers interested in understanding plant diversity in the GCFR. Organized by the Dimensions of Biodiversity South Africa Research Group

Location: SANBI, Kirstenbosch, Cape Town, South Africa. Dates: 20 - 22 July Registration: Free (but required)

A poster session and workshops (on the 22bd) are also planned. See website for details.

Website: http://plasticity.uconn.edu/symposium-south-africa-2015/ Feel free to contact us at: zadimensions@gmail.com

Carl Schlichting

Carl Schlichting Professor and Head Dept. of Ecology & Evolutionary Biology 860-486-4056

"Schlichting, Carl" <schlicht@uconn.edu>

EcologicalSocietyofAmerica UsingDataintheClassroom Aug9

Join us at ESA 2015 to kick off an online network that will be focused on testing hands-on, data-driven modules in the undergraduate classroom. Funding is available to support participants' attendance at ESA.

Dates & Location: Sunday, August 9 from 9AM-4:30PM at the Ecological Society of America Annual Meeting in Baltimore, Maryland.

Description: DryadLab is seeking faculty to field test classroom modules during the Fall of 2015. DryadLab is an educational extension of the Dryad Digital Repository, which contains freely available research data from thousands of published scientific papers. DryadLab provides open, high-quality, hands-on, data-driven educational modules suitable for use in undergraduate classrooms, developed by the authors of the original publications in collaboration with experienced educators.

DryadLab is joining forces with the Quantitative Undergraduate Biology Education Synthesis (QUBES) project to provide support for field testers via an online network that will facilitate the sharing of resources and expertise. The network will run from 20 July 2015 to 20 November 2015 and will be hosted online at https://qubeshub.org/ . Prior to the ESA kick-off meeting, participants will have the opportunity to review materials for four DryadLab modules:

1. Introduction to Extinction and Extinction Bias
2. Survivorship in the Natural World
3. A Walk Through the Woods: Data Analysis of Structural Adaptations in Wood
4. The Beetle Affair

Module descriptions are available at: https://qubeshub.org/groups/dryadlabnetwork/dryadlab_module_descriptions During the one-day kick-off, participants will develop a plan for integrating the DryadLab modules into their existing course curriculum. After the in-person meeting, network participants will continue to interact online to refine the modules for their classroom, discuss various implementation challenges, and define strategies to overcome these challenges. Participants will implement these modules in their classroom during the fall and share their experiences with each other.

This mentoring network is most relevant for faculty with an interest in learning how to use real data in the classroom. A total of 14 participants will be selected. To qualify, participants must be willing to incorporate at least 2 modules into their course this fall. Participants must also be able to commit ~1 hour per week to online discussions. Additional time outside of these discussions will also be required for independent work on adapting and reviewing modules. DryadLab is able to provide the following support to participants for the one-day meeting at ESA: Regular ESA member early bird registration, 2 nights hotel, flight costs under $500, and lunch on Saturday.

To apply, please go to: http://goo.gl/forms/Fs5KD97X4E. Application deadline is June 5th. Accepted applicants will be notified by June 15th.

QUESTIONS? Live online Q&A sessions will be held on May 19th, 10-11AM EST, and May 20, 1-2PM EST, at https://quebeshub.org/groups/dryadlabnetwork/q_and_a. Questions can also be directed via email to Samantha Swauger, the DryadLab project manager, at samswauger@gmail.com.

"Hale, Alison Nicole" <anm116@pitt.edu>

ExeterU EvolutionPlantPests Jul12-14

Early bird registration for the British Ecological Society Symposium The Ecology and Evolution of Emerging Plant Pests and Pathogens closes on 31st May.

Symposium will run 12-14 July at Penryn Campus, Exeter University, Cornwall, UK.

Please register here http://www.britishecologicalsociety.org/pests Thank you.

"Bebber, Dan" <D.Bebber@exeter.ac.uk>

IguassuFalls PlantEvolution Oct25-30 2

Dear Colleagues,

The 11th International Plant Molecular Biology meeting will take place this year at Iguassu Falls from October 25th - 30th. Several talks and sessions will address key issues on plant evolution. The scientific program is very exciting and top questions in the field will be addressed.

Visit the website at < http://www.ipmb2015.org/index.php >. Registration is open with reduced price until June 30th. Abstracts are accepted until July 31st.

With our best regards,

Marie-Anne

On behalf of the Bilateral Organizing Committee and IPMB Board

Rita Ulloa (INGEBI, Argentina), Marie-Anne Van Sluys (Universidade de Sao Paulo, Brazil) Fernando Carrari (INTA, Argentina), Marcio C. Silva-Filho (Universidade de Sao Paulo - Brazil)

mavsluys@usp.br

KansasStateU ArhtropodGenomics Jun17-19 Deadline

--*-*-* Ninth Annual Arthropod Genomics Symposium*-*-*-*-*-

June 17 to 19, 2015

Kansas State University

Manhattan, Kansas

Symposium Website: www.ksu.edu/agc HOTEL ROOMS: Deadline to reserve within the room block is Wednesday, May 20. A block of rooms has been reserved at the

Holiday Inn Manhattan at the Campus < http://www.ihg.com/holidayinn/hotels/us/en/manhattan/manhi/hoteldetail >.

RESIDENCE HALL LODGING: The reservation system is now online and ready to accept your reservation!!! Please reserve your room before May 20, 2015. Rooms will be available in Moore Hall on the Kansas State University campus for the nights of June 16 - 20 at the rate of $35/night for a single room; $27/night for a double room. Detailed information regarding the dormitory guest housing can be found at: http://housing.k-state.edu/guest-housing/guest/index.html . To reserve a room, visit: https://apps2.housing.k-state.edu/guest/step1.php. In the box asking you to "Please specify any special housing arrangements, comments, or questions,"please enter: Arthropod Genomics Symposium.

ABSTRACT DEADLINES

Wednesday, May 20 - If you DO wish to present a poster during the Symposium.

Wednesday, May 20 - If you DO wish your abstract to be considered for a poster presentation at the IGTRCN pre-meeting workshop.

(March 9 was the deadline for abstracts to be considered for oral presentations at the symposium.)

REGISTRATION DEADLINES

Please register online at the Symposium website,

www.k-state.edu/agc < http://www.k-state.edu/agc/-symposium_level/index.html >!

June 5 is the deadline for general registration.

SPEAKERS (Presentation titles are on the Speaker page of the website.)

Keynote Speaker: David A. O'Brochta, Institute for Bioscience and Biotechnology Research & Department of Entomology, University of Maryland College Park

Featured Speakers:

+Michelle Cilia, USDA-ARS, Boyce Thompson Institute for Plant Research, Cornell University, USA

+Martin J. Donnelly, Liverpool School of Tropical Medicine and the Wellcome Trust Sanger Institute, UK

+Rosemary G. Gillespie, University of California, Berkeley, USA

+Sijun Liu, Iowa State University, USA

+Frank Lyko, German Cancer Research Center, Heidelberg, Germany

+Duane McKenna, University of Memphis, USA

+Armin P. Moczek, Indiana University, USA

+Amanda J. Moehring, Western University, Ontario, Canada

+Daniel E. Neafsey, Broad Institute of MIT and Harvard University, USA

+Greg Ragland, Kansas State University, USA

+Anne-Nathalie Volkoff, INRA (UMR1333), Montpellier 1 University, France

The symposium focuses on new insights gleaned from analyzing arthropod genomes and is designed for scientists interested in genomic studies of Arthropods, both model organisms and those of agricultural or health relevance. The program will include platform presentations, welcome reception, Genome Train Workshop, Annotation Café, and arthropod genomics-related poster sessions. A few poster abstract submissions will be selected for platform presentations. Postdoctoral, graduate, and undergraduate students are also encouraged to attend. Sessions conclude Friday evening, followed by an optional evening at Konza Prairie with dinner and live music by the

Red State Blues Band < http://-www.redstatebluesband.com/ >.

--*-*-* Pre-Symposium Workshop *-*-*-*-*-

INSECT GENETIC TECHNOLOGY workshop

June 17, 2015 (Wednesday morning and afternoon)

Robust protocols to manipulate genes and genomes have not yet been developed for most insects other than Drosophila melanogaster, and this shortfall is limiting research progress in many aspects of arthropod genomics. The NSF-RCN on Insect Genetic Technologies (IGTRCN: 2014-2019; igtrcn.org) seeks to remedy this problem by facilitating the communication of best practice and new techniques among arthropod genomicists.

This IGTRCN-sponsored workshop will comprise (1) talks that showcase the latest genetic technologies, (2) discussion sessions for exchange of ideas and solutions for effective insect genetic engineering, and (3) posters. Proposals from the workshop will be integrated into the IGTRCN program of hands-on practical workshops, fellowships, and the IGTRCN KnowledgeBase. Early-career researchers are particularly encouraged to present their research at this workshop. A limited number of travel grants to attend the workshop are available for early stage investigators. Application deadline was March 9. For more information on poster abstract and travel grant submission for the workshop, go to

— / —

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

---

Marseilles 19thEvolBiology AcceptedAbstracts

Dear all the list of the first accepted abstracts for the

EBM 19 is available : http://sites.univ-provence.fr/evol-cgr/ www.aeeb.fr The dead line is June 30

all the best Pierre

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

Norwich UK 2015GalaxyCommunity Jul4-8

The 2015 Galaxy Community Conference (GCC2015, http://gcc2015.tsl.ac.uk/) is being held at the Sainsbury Lab in Norwich, United Kingdom, 4-8 July. GCC2015 is an opportunity to meet with 200+ others working at the forefront data-intensive biomedical research. The 2015 edition of GCC includes more than ever before (http://gcc2015.tsl.ac.uk/programme/):

- Coding and Data Wrangling Hackathons (and a colocated BioJS Hackathon too) - Two days of training offering 18 sessions on 15 topics in up to 5 parallel tracks, covering topics ranging from analysis to administration to tool development. - A two day meeting featuring accepted talks, poster presentations, keynote talks, vendor exhibits, lightning talks, birds-of-a-feather meetups, and plenty of networking.

Early registration is now open (but closes Friday, 22 May, *which is this Friday)*. Registering early saves you 40%. Registering now ensures you'll get a spot in the hackathon and training sessions of your choice.

Finally, there are also many other events going on before and after GCC2015, and GCC itself ends right before ISMB / ECCB starts in Dublin. See https://wiki.galaxyproject.org/News/NearGCC2015 for a complete list.

Hope to see you in Norwich!

Dave Clements, on behalf of the GCC2015 Organising Committee

– http://galaxyproject.org/ http://getgalaxy.org/ http://usegalaxy.org/ https://wiki.galaxyproject.org/ clementsgalaxy@gmail.com

---

Porto Portugal Ichthyology Sep7-11

This may be of interest - note impending abstract deadline Please distribute within your department

ABSTRACT SUBMISSION DEADLINE: 30TH APRIL 2015

Dear colleagues,

As you already know the XV European Congress of Ichthyology, organized by the Interdisciplinary Centre of Marine and Environmental Research, will take place from the 7th to 11th September 2015 in Porto Portugal. This is an international congress promoted by the European Ichthyological Societythat has been held on a three-year cycle since 1973. Recent meetings have been able to attract around 250-300 researchers from around the world. The congress will focus on fish as a subject of research in several biological sciences. The scientific program will include sessions following four main topics: I) Phylogeny, systematic and genetics; II) Ecology, conservation and invasive species; III) Life cycles, migration and connectivity; and IV) Physiology, behaviour and toxicology. Two special symposia have also been organized: V) Otoliths as a powerful tool to study fishes; and VI) Mediterranean fish biodiversity.

The congress will be organized with parallel oral sessions and poster exhibitions. The congress will include several invited plenary lectures made by world renowned fish researchers: Drs. Jeffrey Leis (Australia), Joana Robalo (Portugal), Kenneth Able (USA), Marino Vachhi (Italy), Miguel Pineda(Spain), Neil Metcalfe (UK), Rui Oliveira (Portugal) and Steven Campana (Canada).

The abstract submission deadline is fast approaching on the 30th of April 2015. It is mandatory to register first to access the on-line submission form. However, you do not need to pay until the early and late registration dates on the 15th and 30th of June 2015, respectively. The registration feeshave been kept low to attract as much as possible early career researchers (250 euro) and graduate students (150 euro). Members of the EIS have a 20% discount. Students will also have the opportunity to compete for awards for best oral and poster presentations.

The congress will be held at the Hotel HF Ipanema Park, a 5 stars hotel. A complete buffet lunch, including water, juices and wines, is available in the conference hotel for 15 euro per day, but to a limited number of persons. However, within short walking distance (less than 5 minutes) you have other light and inexpensive options, such as a Japanese restaurant, a Pizzeria and a few snack-bars.

Please also check out the organized social program. We have schedule events for each conference day for both participants and accompanying persons. Some of them are free, but you will need to book them through the online registration.

In 2014 Porto was elected the best European destination by European citizens (www.europeanbestdestinations.com/top/europe-best-destinations-2014/), and I am sure that you will be delighted with the city, people and food (and of course Port wine). Our international airport is served by several regular and low-cost airlines companies. But train and car are other options. Bookings for accommodation with special prices for other HF Hotels are also now open. Some low-cost accommodations are now also available on the webpage. We strongly recommend "Casa Diocesana Seminário do Vilar" with single and double rooms ranging from 25 to 39 euro per day with breakfast included. September is still part of the summer season for tourism in Porto so try to reserve your accommodation in advance. If you need any help, feel free to contact us.

Further, and regularly, updated information can be found at the congress webpage (www.ciimar.up.pt/-ecixv). Please follow our latest news onFacebook (www.facebook.com/ECIXV) and Twitter (www.twitter.com/ECI_XV).

We would greatly appreciate if you kindly forward this information to your colleagues and students in your University, Institute and/or national and international networks. Please also accept our apologies for cross-postings.

We hope to see you in Porto in early September.

On behalf of the Organizing Committee Prof. Alberto Teodorico Correia, ECIXV Chair

Dr Lukas Rüber | Naturhistorisches Museum der Burgergemeinde Bern | Bernastrasse 15 | 3005 Bern | Switzerland phone: +41 (0)31 350 72 82 | email: lukas.ruber@nmbe.ch

XV European Congress of Ichthyology, 7-11 September 2015, Porto, Portugal www.ciimar.up.pt/ecixv Lukas Ruber <lukas.ruber@nmbe.ch>

Poznan Poland Evolution Sep24-26

Conference: Poznan_Poland.Evolution

We are pleased to announce third edition of the Polish Evolutionary Conference (PEC III) which will take place in PoznaÅ on 24-26 September 2015 at the Faculty of Biology, Adam Mickiewicz University. The official language of the conference is English.

Plenary talks:

Eva Jablonka, Tel Aviv University "The evolutionary implications of epigenetic inheritance"

GraÅ¼yna JasieÅska, Jagiellonian University "An evolutionary view on women's biology and health"

Jochen Wolf, Uppsala University "Speciation genomics in natural populations"

Ryszard Korona, Jagiellonian University "Genetic dominance and epistasis as buffers against natural selection: insights form experimental analyses of the yeast model".

Registration and abstract submission: http://-www.pec2015.pl Early bird deadline: 15th June

Organizing Commitee Jacek Radwan Izabela Makalowska Tomasz Osiejuk

j.w.radwan@gmail.com

StAndrews DataScience Jul6

Dear Evoldir,

The 2015 Summer of V's series of meetings at the University of St Andrews, Scotland, covers the Four V's of Data Science - Veracity, Variety, Velocity and Volume. Meetings are explicitly aimed at all Faculties of the University, including evolutionary biologists. Everyone is very welcome to attend one, all or any number of meetings, whether you are based at St Andrews or elsewhere. Attendance is free.

Meetings begin with a buffet lunch, then a talk from a prestigious invited speaker, followed by contributions from local researchers.

The next meeting is on Monday 6th July, 12:30-4 PM.

The programme includes:

o Professor PETER CHRISTEN, Australian National University (https://researchers.anu.edu.au/researchers/christen-pj), "Advanced record linkage methods: scalability, classification, and privacy".

o Dr AILEEN FYFE, School of History, University of St Andrews.

o Dr LEN THOMAS, Centre for Research into Ecological and Environmental Modeling and School of Mathematics and Statistics, University of St Andrews.

There will also be a discussion panel.

For registration and further details, please see:

http://www.idir.st-andrews.ac.uk/vs This IDIR Summer of V's meeting is scheduled to fit with the International Environmental 'Omics Synthesis Conference (IEOS2015), also at St Andrews. Attendees are welcome to attend one or both meetings. IEOS2015 requires separate registration (http://environmentalomics.org/ieos2015).

We look forward to seeing you on 6th July.

Thank you,

Summer of V's Organising Committee -

Dr Daniel Barker db60@st-andrews.ac.uk, Professor Aaron Quigley aquigley@st-andrews.ac.uk, Professor Simon Dobson Simon.Dobson@st-andrews.ac.uk

http://www.idir.st-andrews.ac.uk/vs The University of St Andrews is a charity registered in Scotland : No SC013532

"db60@st-andrews.ac.uk" <db60@st-andrews.ac.uk>

Stockholm MammalBiol Aug16-22 AbstractDeadline 15May

Dear everyone,

This is a reminder that the deadline for abstract submission expires on the 15th of May.

Please submit your abstract for a talk or poster here: http://www.zoologi.su.se/ecm7/abstract_submit.php The 7th European Congress of Mammalogy will be held in Stockholm, Sweden, between 17-21 August 2015. Visit the conference website to find out more about the conference as well as to register (registration is open until the 15th of June): www.zoologi.su.se/ecm7 The conference will cover a broad range of topics in mammal biology, including Species Interactions, Population Genetics, Conservation Biology and Ecology & Landscapes.

List of Plenary & Keynote speakers: David Macdonald, University of Oxford Heikki Henttonen, Finnish Forest Research Institute Anjali Goswami, University College London Xavier Lambin, University of Aberdeen Jennifer Leonard, Doñana Biological Station Tim Clutton-Brock, University of Cambridge Henrik Andrén, Swedish University of Agricultural Sciences Mike Bruford, Cardiff University Ian Barnes, Natural History Museum London Bodil Elmhagen, Stockholm University Kjell Danell, Swedish University of Agricultural Sciences Nigel Yoccoz, Tromso University Greger Larson, Oxford University Urs Breitenmoser, Bern University Selina Brace, Natural History Museum London Arild Landa, Norwegian Institute for Nature Research

The aim of the European Congresses of Mammalogy is to foster communication between researchers working on issues of mammalian biology in the European arena, as well as providing a venue for the broad dissemination of European mammal research. The relaxed and friendly atmosphere of these congresses provides an excellent opportunity to hear the latest developments in various fields of mammalogy, to share research experience and expertise, and to develop new and closer contacts with colleagues from different countries.

Facebook: https://www.facebook.com/ecm7stockholm Twitter: https://twitter.com/ECMSthlm2015 Instagram: https://instagram.com/ecmsthlm2015/ Love.Dalen@nrm.se

---

Stockholm MammalBiol Aug16-22 LastChance Abstracts

Dear everyone,

There is room for a small number of additional talks in each session at the 7th European Congress of Mammalogy. We have therefore extended the abstract deadline until June 1st.

You can send in your abstracts at: www.zoologi.su.se/ecm7/abstract_submit.php Please don't forget to also register after you have submitted your abstract. Registration can be done here (and is open until June 15th): www.zoologi.su.se/ecm7/registration.php —–

DETAILED INFORMATION:

The 7th European Congress of Mammalogy will be held in Stockholm, Sweden, between 17-21 August 2015. Visit the conference website to find out more about the conference as well as to register (registration is open until the 15th of June): www.zoologi.su.se/ecm7 The conference will cover a broad range of topics in mammal biology, including Species Interactions, Population Genetics, Conservation Biology and Ecology & Landscapes.

List of Plenary & Keynote speakers: §David Macdonald, University of Oxford §Heikki Henttonen, Finnish Forest Research Institute §Anjali Goswami, University College London §Xavier Lambin, University of Aberdeen §Jennifer Leonard, Doñana Biological Station §Tim Clutton-Brock, University of Cambridge §Henrik Andrén, Swedish University of Agricultural Sciences §Mike Bruford, Cardiff University §Ian Barnes, Natural History Museum London §Bodil Elmhagen, Stockholm University §Kjell Danell, Swedish University of Agricultural Sciences §Nigel Yoccoz, Tromso University §Greger Larson, Oxford University §Urs Breitenmoser, Bern University §Selina Brace, Natural History Museum London §Arild Landa, Norwegian Institute for Nature Research

The aim of the European Congresses of Mammalogy is to foster communication between researchers working on issues of mammalian biology in the European arena, as well as providing a venue for the broad dissemination of European mammal research. The relaxed and friendly atmosphere of these congresses provides an excellent opportunity to hear the latest developments in various fields of mammalogy, to share research experience and expertise, and to develop new and closer contacts with colleagues from different countries.

Facebook: https://www.facebook.com/ecm7stockholm Twitter: https://twitter.com/ECMSthlm2015 Instagram: https://instagram.com/ecmsthlm2015/ "Love.Dalen@nrm.se" <Love.Dalen@nrm.se>

Switzerland GenomeEvolution MicrobsPathogens Sep1

ZHAW symposium 2015: "Life in Numbers 2: Genomics and Evolution of Microbial Pathogens"

Date: 1 September 2015 Place: Wädenswil (Zürich lake), Switzerland Organizers: Maria Anisimova and Theo Smits

Summary:

With > 28'000 microbial genomes sequenced today, a broader range of researchers can step into NGS genomics without the prior knowledge of the complexity involved. This one-day conference is organised in two sections: "Genomics in practice" and "Evolutionary genomics"; with the aim to promote the dialogue between the community of microbiologists interested in genome analyses and their practical applications (e.g., in medicine or agriculture) and the community of bioinformatics method developers. During this conference the microbiology community will be able to bring their practical problems to the attention of method developers, prompting the exchange of ideas and leading to new methodologies and applications. The conference will facilitate the translation of academic results in pathogen genomics and bioinformatics to solving practical problems in microbiology.

The conference is in line with the current strategy of ZHAW to expand applied genomics and bioinformatics research and its visibility in this field. The event will take place during the joint ZHAW-SIB summer school GEMP2015 (on a similar topic), and its participants will also attend the conference and will benefit from the invited talks and research discussions.

Program and registration: http://2015.lifeinnumbers.ch/ "Anisimova Maria (anis)" <anis@zhaw.ch>

Tours France EukaryoticGenomes Jul8-10 reminder

Analysis and Annotation of DNA Repeats and Dark Matter in Eukaryotic Genomes < http://www.lestudium-ias.com/#%21analysis-and-annotation-of-dna-repe/c412 >

Dear Colleagues,

LE STUDIUM, Loire Valley Institute for Advanced Studies, would like to remind you that the *Analysis and Annotation of DNA Repeats and Dark Matter in Eykaryotic Genomes Conference* - is open for registration.Click here to access the conference page and announcement < http://www.lestudium-ias.com/#%21analysis-and-annotation-of-dna-repe/c412 >. *Don't miss the early bird registration rate and date of June 1st, 2015!*

The Analysis and Annotation of DNA Repeats and Dark Matter in Eykaryotic Genomes Conference aims to shine light on current and emerging research trends for genomes classification by providing a platform for discussion with a peloton of internationally acknowledged leaders.

Note this conference is the premiere event of the year for researchers to meet, discuss and share ideas on genic repeats and genomes classification! International leaders in the genomic research will gather to discuss, learn and share ideas on a number of areas. Please note there are also opportunities for poster sessions. For more information and to discover the full list of speakers please visit the conference page < http://www.lestudium-ias.com/-#%21analysis-and-annotation-of-dna-repe/c412 >.

This one-off conference is organised with Dr Yves Bigot, Research Director (CNRS - INRA Centre Val de Loire, France) and Dr Peter Arensburger (California State Polytechnic University, Pomona - USA). It offers a unique opportunity to meet like-minded researchers, build new collaborations and enjoy the famous local gastronomy and scenery of the Loire Valley region!

We look forward to welcoming you to Tours, Loire Valley, France in next July 2015 and invite you not to miss the *June 1st, 2015* *early bird registration deadline*. The conference is open to a hundred participants (academics, post-doctorants, students and R&D scientists, enterprises).

Sincerely,

On behalf of the scientific committee,

Nicola Fazzalari Scientific Director

More infos : http://www.lestudium-ias.com Facebook < https://www.facebook.com/pages/LE-STUDIUM-Loire-Valley-Institute-for-Advanced-Studies/316225335183948?fref=ts >

Website < http://lestudium-ias.com >

Email <contact@lestudium-ias.fr>

Sophie Gabillet <sophie.gabillet@lestudium-ias.fr>

Turkey EcolEvolutionaryBiol Aug6-7 DeadlineExt

The abstract submission deadline for the 2nd Ecology and Evolutionary Biology Symposium Turkey 2015 (August 6-7, Ankara) has been extended to May 31st.

Please find more information at http://-eebst2015.bio.metu.edu.tr We invite talks and poster presentations in all areas of evolutionary biology and ecology. All presentations will be in English and we heartily welcome international participation.

This year's keynote speakers are: - Resit Akcakaya (Stony Brook U.), - Sergey Gavrilets (U. Tennessee), - Rasmus Nielsen (U. California, Berkeley), and - Daniel Simberloff (U. Tennessee).

A Cappadocia Tour will be organized following the meeting, for those interested.

We look forward to seeing you in Ankara!

On behalf of the Organizing Committee

Aysegul Birand (birand@metu.edu.tr) and Mehmet Somel (somel.mehmet@googlemail.com)

Mehmet Somel <somel.mehmet@googlemail.com>

UBrno PlantGenetics Sep7-10

Mendel Museum of Masaryk University would like to invite you to the conference Research in plant genetics (From Mendel's peas to the present) which will be take place 7th september - 10th september 2015 in Mendel Museum of Masaryk University in Brno, Czech Republic.

Conference webside: http://www.mendelgenius.com/-en/the-conferences/research-in-plant-genetics-from-mendels-peas-to-the-present Sections/Topics: Mendel's factors today >From Mendel to population genomics Where is the message? - Genome structure Non-Mendelian genetics Reproduction without sex >From genes to phenotypes The impact. Plant breeding and agriculture

Invited/keynote speakers: Ueli Grossniklaus, University of Zurich, Swiss Edward Buckler, Cornell University, USA Peter van Dijk, KeyGene, Netherlands Catherine Rameau, INRA, Versaille, France Jonathan Wendel, Iowa State University, USA Dani Zamir, Hebrew University, Jerusalem, Israel Burstin J., INRA Dijon, France Ellis N., CGIAR, India Varshney R., ICRISAT, India

Important dates: Registration deadline: 30th April 2015 Abstract submission deadline: 30th April 2015

Registration and Call for Papers: Through attached registration form or webside http://-www.mendelgenius.com/en/the-conferences/research-in-plant-genetics-from-mendels-peas-to-the-present Contact: Mendel Museum of Masaryk University Mendlovo nám. 1a 603 00 Brno Czech Republic e-mail:

info@mendelmuseum.muni.cz phone: 00420 549 496 669 www.mendelmuseum.muni.cz www.mendelgenius.com We are looking forward to see you in Brno, Czech Republic!

“Wendel, Jonathan F [EEOBS]” <jfw@iastate.edu>

UCalifornia Berkeley EvoDevo Aug5-9

PanAm EVODEVO ÂV UC Berkeley 5-9 August 2015

[http://www.evodevopanam.org/meetings–events.html] COME ONE, COME ALL! EvoDevo2015 is coming together as the most exciting evodevo event of the year. If you have already registered and submitted your abstract, THANK YOU! We received over 200 submissions. The organizing committee will be selecting abstracts for oral presentations and you will be notified in the next couple of weeks.

THEREÂÂS SOMETHING FOR EVERYONE: Invited talks and the Contributed Sessions are selected to ensure taxonomic diversity and to include a wide variety of innovative tools and techniques for studying evodevo, demonstrating the international nature of the field and highlighting the exciting breath and depth of studies encompassed by the field of Evolutionary Developmental Biology.

[http://www.evodevopanam.org/invited-plenary-speakers.html] PRESENT YOUR LATEST FINDINGS: While abstract submission for oral presentations is closed, we are accepting abstracts for poster presentations and registrations until July 22nd, 2015.

PICTURES ARE WORTH A THOUSAND WORDS!!! THE POSTER SESSION will extend the entire duration of the meeting, and will include large blocks of time (outdoors, with sunshine, food and drink!) for presenters to interact with the community surrounding their latest data. Use this forum to engage in direct conversation with your fellow scientists: students, postdocs and faculty will be presenting their latest data in the form of creative posters and interactive displays.

DO NOT MISS the opportunity to be part of this historic event. Register now for the first biennial meeting of the PanAmerican Society for Evolutionary Developmental Biology!

5-9 August

Berkeley, California

_

Chelsea D. Specht, PhD Associate Professor; Departments of Plant and Microbial Biology & Integrative Biology Curator of Monocots; University and Jepson Herbaria University of California, Berkeley 111 Koshland Hall, MC 3102 Berkeley, CA 94720 510.642.5601

cdspecht@berkeley.edu http://spechtlab.berkeley.edu/ Chelsea Specht <cdspecht@berkeley.edu>

UGottingen EcoGenetics Aug31-Sep4 Deadline

Dear colleagues,

From August 31st to September 4th, 2015, the University of Göttingen will host the 45th Annual Meeting of the Ecological Society of Germany, Austria and Switzerland. The meeting will take place in Göttingen, Germany.

There will be the “Ecological Genetics and Epigenetics in the Omics Era” session among other sessions at this meeting. Those who are willing to participate, either with a talk or a poster, are very welcome to submit their abstracts. Deadline for early registration fee and abstract submission was extended till May 31^st. There will be also several attractive excursions and pre-meeting workshops.

See the conference organizers website for details on deadlines, fees and registration/abstract submission procedures:

http://www.gfoe-2015.de http://www.gfoe-2015.de/-index.php?cat=deadlines http://www.gfoe-2015.de/-index.php?cat=registration The conference homepage also includes instructions on how to prepare your oral presentation or poster. Feel free to contact me if you have any questions or comments regarding the ecological genetics and epigenetics session. We are looking forward to having your abstract submissions and to meeting you in Göttingen this summer!

Thank you for your consideration,

Prof. Dr. Konstantin (Kostya) V. Krutovsky

Department of Forest Genetics and Forest Tree Breeding

Büsgen-Institute

University of Göttingen

Büsgenweg 2

D-37077 Göttingen

Germany

E-mail: kkrutov@gwdg.de

http://www.uni-goettingen.de/en/414626.html +49-(551)-393-35-37 (off.)

+49-(551)-39-83-67 (fax)

"Krutovsky, Konstantin" <konstantin.krutovsky@forst.uni-goettingen.de>

UMichigan SSB Standalone Meeting May20-22

The deadline for registration for the Society of Systematic Biologists (and iEvoBio) meeting at the University of Michigan is *May 1st* Please see the website (http://ssb2015standalone.weebly.com/) for details about the program, workshops, and registration. We hope to see you there!

dewitt832@gmail.com

UStAndrews Omics Jul6-8

THIRD INTERNATIONAL ENVIRONMENTAL 'OMICS SYNTHESIS CONFERENCE

important updates **postgrads submitting abstracts entitled to full registration bursary (first-come-first-serve)** **talk abstracts due 29 May, poster abstracts due 6 June**

University of St Andrews 6-8 July 2015

http://environmentalomics.org/ieos2015/ ABSTRACTS AND REGISTRATION

ABSTRACT (TALK) DEADLINE: 29 May 2015 (extended from 25 May) REGISTRATION DEADLINE: 6 June 2015

The aim of this conference is to bring together researchers and organisations from a range of disciplines with shared interests in the development of new approaches for data handling, generation and analysis in environmental omics. Science areas of interest include bioinformatics, DNA-barcoding, genomics, metagenomics, metabarcoding, transcriptomics, proteomics, metabolomics, epigenetics, evolutionary and ecological omics, phylogenetics, study of ancient DNA and anthropology, new tools, resources and training, and beyond as applied to the study of the natural environmental and environmentally relevant organisms and systems. It is our hope is that the resulting interaction and exchange of ideas will lead to novel approaches, new collaborations and the consolidation of a wider integrated environmental omics community.

EOS and this conference is supported by Natural Environmental Research Council (NERC) through its Mathematics and Informatics for Environmental Omics Data Synthesis programme and the UK Science and Technology Facilities Council (STFC) Global Challenges programme.

Professor Thomas R. Meagher School of Biology, Sir Harold Mitchell Building University of St Andrews St Andrews KY16 9TH UK +44(0)1334 463364 office +44(0)7793356889 mobile +44(0)1334 463366 fax http://www.st-andrews.ac.uk/profile/trm3 Thomas Meagher <trm3@st-andrews.ac.uk>

UStirling PhDEvolBiol Sep8-12 Deadline

The deadline to register for the 21st European Meeting for PhD Students in Evolutionary Biology is fast approaching! Last registration day is May 31st, 2015.

To register, please visit the following link: http://www.epay.ed.ac.uk/browse/extra_info.asp?compid=3D1&modid=3D2&deptid=24&ca tid&prodid86&searchresults=1

For more information on the conference please visit our website: http://empseb21.bio.ed.ac.uk We look forward to seeing you in Stirling in September!

R.E.Butterfield@sms.ed.ac.uk

Vairao Portugal Genomics Jun15-19

Genomics Week @ CIBIO-InBIO

June 15-19, 2015 | CIBIO-InBIO, Vairao, Portugal

>From June 15 to 19, CIBIO-InBIO will host a Genomics Week, taking place at VairÃÂ£o Campus. The programme for this week includes:

- on June 15-17, the advanced course Ãâ¬*ÅGenotypingbySequencing*(*GBS*) : *principles*, *approachesandapplicationsÃâ*¬ï?‘1$_{\overline{2}}$ [Registration required]; and

- on June 18-19, a Genomics Seminar [No registration required].

ADVANCED COURSE GENOTYPING BY SEQUENCING (GBS): PRINCIPLES, APPROACHES AND APPLICATIONS

June 15-17, 2015 | Room 2 - VairÃÂ£o Campus

This course aims to give attendees a broad overview of Genotyping-by-Sequencing (GBS), including the principles of how data are obtained by the various different approaches, and their advantages and disadvantages. There will be a question and answer session to help determine the right approach for different study systems or special cases, such as degraded DNA. There will also be practical data-analysis sessions, where attendees will be guided through example data processing with various analysis tools.

INTENDED AUDIENCE

The course will be open to a maximum number of 20 participants.

Priority will be given to:

I. 1st year PhD students attending the BIODIV Doctoral Programme;

II. Other BIODIV PhD students;

III. PhD students attending other courses;

IV. Other candidates.

REGISTRATION

Registration deadline: June 4, 2015

GENOMICS SEMINAR

June 18-19, 2015 | Auditorium - VairÃÂ£o Campus

During this two-day seminar, five major topics in genomics research will be covered:

1. Environmental Genomics;

2. Phylogenomics;

3. Conservation/Population Genomics;

4. AgriGenomics;

One Health Genomics.

Participation in this seminar is free and the number of attendees is limited to the capacity of the auditorium.

To know more about this event, please visit CIBIO-InBIOÃâ¬*âswebsite*[*http* : *//cibio.up.pt/-conferences/details/genomics − week − at − cibio − inbio*].*References*

1. divulgacao@cibio.up.pt 2. http://cibio.up.pt/ 3. https://www.facebook.com/cibio.inbio CIBIO DivulgaçÃ£o

Vairao Portugal SocotraConservation Sep11-1

14th Annual General Meeting of the FoS and Symposium on“Conservation of the Natural and Cultural Heritage of Socotra”

September 11-13, 2015 @ CIBIO-InBIO, Vairao, Portugal

The Annual General Meeting of the Friends of Soqotra (FoS) is a great opportunity to meet other FoS members and fellow-travellers, to discuss the latest results of scientific research on the Soqotra Archipelago, to learn about ongoing projects, and to share information about FoS activities over the last year. Both members and non-members are very welcome to participate in the meetings.

Between 2001 and 2014 the AGM has been held in different European countries. The 13th Annual General Meeting of FoS and Symposium entitled “Biodiversity and Culture of Socotra” was held on 19 - 21 September 2014 in Rome, Italy.

In 2015 the 14th Annual General Meeting of the FoS and Symposium entitled “Conservation of the Natural and Cultural Heritage of Socotra” will take place on September 11-13 in Portugal hosted by CIBIO-InBIO’s CONGEN [http://cibio.up.pt/research-groups-1/details/congen] group. A discussion workshop relating current pressures to the heritage of Socotra and elaboration of a response plan will also take place during this meeting.

IMPORTANT DATES

Abstract submission deadline: June 30, 2015

Abstract acceptance / Early registration deadline: July 30, 2015

Further information about this event can be found here: http://cibio.up.pt/conferences/details/annual-general-meeting-of-the-fos#prettyPhoto . CIBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos/ InBIO Laboratório Associado, Universidade do Porto Campus Agrário de Vairão Rua Padre Armando Quintas 4485-661 Vairão Portugal

t: +351 252 660 411 Ext. 285 f: +351 252 661 780

e: divulgacao@cibio.up.pt w: http://cibio.up.pt f: https://www.facebook.com/cibio.inbio CIBIO Divulgação

---

Vairco Portugal SocotraConservation Sep11-13

14th Annual General Meeting of the FoS and Symposium on"Conservation of the Natural and Cultural Heritage of Socotra"

September 11-13, 2015 @ CIBIO-InBIO, Vairão, Portugal

The Annual General Meeting of the Friends of Soqotra (FoS) is a great opportunity to meet other FoS members and fellow-travellers, to discuss the latest results of scientific research on the Soqotra Archipelago, to learn about ongoing projects, and to share information about FoS activities over the last year. Both members and non-members are very welcome to participate in the meetings.

Between 2001 and 2014 the AGM has been held in different European countries. The 13th Annual General Meeting of FoS and Symposium entitled "Biodiversity and Culture of Socotra" was held on 19 - 21 September 2014 in Rome, Italy.

In 2015 the 14th Annual General Meeting of the FoS and Symposium entitled "Conservation of the Natural and Cultural Heritage of Socotra" will take place on September 11-13 in Portugal hosted by CIBIO-InBIO's CONGEN [http://cibio.up.pt/research-groups-1/details/congen] group. A discussion workshop relating current pressures to the heritage of Socotra and elaboration of a response plan will also take place during this meeting.

IMPORTANT DATES

Abstract submission deadline: June 30, 2015

Abstract acceptance / Early registration deadline: July 30, 2015

Further information about this event can be found here: http://cibio.up.pt/conferences/details/annual-general-meeting-of-the-fos#prettyPhoto . CIBIO - Centro de Investigação em Biodiversidade e Recursos Genéticos/ InBIO Laboratório Associado, Universidade do Porto Campus Agrário de Vairão Rua Padre Armando Quintas 4485-661 Vairão Portugal

t: +351 252 660 411 Ext. 285 f: +351 252 661 780

e: divulgacao@cibio.up.pt w: http://cibio.up.pt f: https://www.facebook.com/cibio.inbio CIBIO Divulgação

---

Vienna SMBE2015 Fellowship

Dear colleagues,

Recognizing that the difficult funding situation may have made the attendance of SMBE 2015 in Vienna for some people impossible, the Institute of Population Genetics has made 10 fellowships for SMBE attendance available.

The fellowships entail a free registration to SMBE 2015 and will be awarded on a first come, first served basis with special attention given to the different time zones.

In order to apply, please send a short email with the subject "conference fellowship" to office@smbe2015.at explaining your need for the fellowship and a proof for the recently rejected grant. Please note that travel grants count as well as grants submitted by the advisors.

Conference website: https://smbe2015.univie.ac.at/home/ julia.hosp@gmail.com

Vienna SMBE2015 Jul12-16 Participant limit and news

Hello evoldir community,

we're about to reach our capacity limit for SMBE 2015 (July 12-16) in Vienna, Austria. Register NOW to secure your participation and join us in one of the most beautiful cities at the spectacular Imperial Palace (Hofburg) in the heart of Vienna:

https://smbe2015.univie.ac.at/registration/ A few meeting highlights:

- More than 750 posters on display throughout the entire meeting.

- Five poster sessions

- 27 symposia on cutting edge topics suggested by SMBE members

- An Open Symposium featuring five speakers selected by the Local Organising Committee

- A special symposium on NGS library construction

- Plenary speakers: Doris Bachtrog (UC Berkeley), Joe Felsenstein (Univ. of Washington), Johanna Schmitt (UC Davis) and Diethard Tautz (MPI for Evolutionary Biology)

- a conference app featuring schedule, venue information, restaurant and activity tips from locals, social media resources and more

For more information, please consult the online program listing all talks: http://smbe2015.univie.ac.at/program/program/ All details about registration, accommodation options and travel discounts are available at the conference website: www.smbe2015.at The Local Organising Committee is looking forward to welcome you to Vienna in July!

julia.hosp@gmail.com

GradStudentPositions

BlackHillsStateU IntegrativeGenomics

The Masters in Science in Integrative Genomics program at Black Hills State University (Spearfish, South Dakota) currently has openings for the Fall 2015 semester. This program exposes students to modern techniques and instrumentation in the laboratory and field and prepares students for success in both academic and other biotechnology-related pursuits.

Graduate Research Assistantships (RAs) are awarded to students and provide a competitive stipend plus funding for research. All RAs receive a reduced tuition rate (1/3 of in-state rate) and assist with instruction of undergraduate-level science labs.

Black Hills State University, located in the heart of the northern Black Hills in Spearfish, SD, offers 75 academic programs at the associate, bachelor, and master degree levels. BHSU, which has over 4,000 students, has earned a reputation for transforming lives through innovative, high-quality academic programs and a dynamic learning community. Our location provides a natural laboratory for Integrative Genomics. We are also close to the Deep Underground Science and Engineering Laboratory (DUSEL) at Homestake Mine, allowing for collaboration with other major universities (to study, for example, the meta-genomics of the unique microbial communities found in extreme environments).

Learn more about the community here: www.visitspearfish.com www.youtube.com/watch?v=HTsFzC9vESI www.youtube.com/watch?v=BrRRHz2TRDs Information about M.S. Integrative Genomics program requirements and application process can be found here: www.bhsu.edu/Academics/GraduatePrograms/IntegrativeGenomics/tabid/2164/Default.aspx For further information email: Raeann.Mettler@bhsu.edu

Raeann Mettler

School of Natural Sciences Black Hills State University 1200 University Street Unit 9008 Spearfish, SD 57799-9008

Raeann Mettler <raeann.mettler@bhsu.edu>

MaxPlanckInst Seewiessen EvolutionaryGenetics

PhD Position “Evolutionary Genetics of the Embryo Mortality Puzzle in the Zebra Finch” at the Max Planck Institute for Ornithology

A PhD position is available at the Max Planck Institute for Ornithology (MPIO) in Seewiesen (near Munich, Germany) to study the quantitative and molecular genetics of embryo mortality in zebra finches.

It is one of the most fundamental puzzles in evolutionary biology why many animal species show high rates of reproductive failure despite the fact that natural selection should be acting against this in every single generation. For instance, in humans, it is estimated that two out of three fertilized eggs die before birth, and it is still not understood why such a wasteful system has evolved. The case of the zebra finch also represents such a puzzle, because we see high rates of embryo mortality that cannot be attributed to trivial phenomena like environmental effects or inbreeding. The project will combine the use of various genomic tools and QTL mapping with setting up specific experimental crosses to identify and characterize the genetic factors that lead to embryo mortality. In particular, we will attempt to understand better the evolution of incompatibility-causing loci and of selfish genetic elements.

We seek a highly motivated individual who shares our fascination with this topic and who has a background or strong interest in some of the following fields: evolutionary biology, quantitative genetics, molecular genetics and statistics. A Master’s degree in biology or equivalent is required. The project primarily involves handling of extensive data sets of phenotypic and genetic data (breeding records of egg fates, pedigrees, SNPs, microsatellites, sequence data). Any prior knowledge in using R or Python or any experience in using bioinformatics tools in a Linux environment would be advantageous but can also be acquired at a later stage.

Initial appointment will be for three years with a possible extension for another year subject to research progress. Payment will be through a Max Planck PhD position (13/2 TVöD). We provide a supportive research and learning environment with excellent facilities. Working language is English. The Max Planck Society is an equal opportunity employer and encourages disabled persons to apply. The Society aims at increasing the number of women in fields where they are underrepresented, and therefore encourages them to apply.

Please send your application by June 1st 2015 as a single file to our secretary Carmen Dobus (cdobus@orn.mpg.de). This file should include a concise statement of research interests and work experiences relevant to the project, curriculum vitae and contact details for 2-3 academic references.

For further information about the PhD project please contact Wolfgang Forstmeier (forstmeier@orn.mpg.de).

www.orn.mpg.de/forstmeier Max Planck Institute for Ornithology Eberhard-Gwinner-Str. 82319 Seewiesen, Germany

"Dobus, Carmen" <cdobus@orn.mpg.de>

McGill PopulationGenetics

Graduate and postgraduate positions in mathematical and population genetics

Graduate student and postdoc positions in mathematical and population genetics are available in Simon Gravel's group at McGill University in Montreal, Canada. The project aims at creating mathematical models of historical human migrations, family histories, and high-throughput genomic data. Students will be involved in conceptual methods development, implementation, and applications to exciting datasets. This is a unique opportunity to be involved in work that is relevant and interesting from a mathematical, medical, and historical perspectives.

We welcome applications from qualified candidates from diverse backgrounds, including biology, anthropology, mathematics, physics, and computer science. Programming experience and a demonstrated interest in mathematics, statistics, or related fields is required.

The position offers an exceptional opportunity to develop theoretical and computational ideas and apply them to cutting-edge data in a supportive and thriving research environment.

Applications and queries should be sent to gravellab@gmail.com. Please include a statement of interest (1 page) and a CV with a list of publications, contact information for three references, and a low-resolution scan of official transcripts.

simon.gravel@gmail.com

MemorialU WildlifeEvolution

Ecology and Sociobiology of a Wolf-Ungulate Predator-Prey Game

Start Date: September 2015 (flexibility exists for exceptional candidates) We have a fully funded PhD position for a student interested studying the spatial ecology and sociobiology of predator-prey dynamics with links to population and disease ecology in a wolf-ungulate community.

System: Riding Mountain National Park (RMNP) in Manitoba is among the best-studied large mammal communities in Canada. Peer-reviewed research has been produced from the RMNP system for the last 80 years: from Green (1933) and Banfield (1949) to Paquet (1990s) and our recent work. RMNP is a rich system within which to simultaneously ask fundamental and applied ecological and evolutionary questions. Over the coming years and primarily using GPS collars, this project will see all wolf packs and >80% of the elk monitored in one of RMNPs elk subpopulations, creating a near-perfect spatial and temporal picture of predatory-prey interactions between wolves and their primary prey. Furthermore, the successful applicant will have access to our considerable collection of historical individual- and population-level data on space use and population densities of elk, moose, white-tailed deer and wolves (see our papers for examples). As a result, this project will provide excellent opportunities for both academic and professional advancement. Because it is a PhD-level project, the successful applicant will be expected to develop her or his own ideas and research plan in collaboration with the research team.

In the Wildlife Evolutionary Ecology Lab we feel strongly that novel biological ideas are derived from interacting directly with our study species and system, and the successful applicant will be expected to spend considerable amounts of time in the field, supported by an excellent team of biologists at RMNP. The successful applicant will be required to actively investigate kill- and den-sites and to fly telemetry, while simultaneously working with existing data. At the PhD level, this will require an exceptional applicant who can both be in the field and continue to actively analyze and write throughout their program.

Qualifications: In addition to a MSc that complements this research, applicants should have five main qualities: (1) a passion for ecological and evolutionary theory; (2) an aptitude for and commitment to research in the field V in all seasons; (3) well-developed quantitative skills in GIS, statistical programing in R, and experience or an interest in modeling; (4) a track-record of publishing their research in reputable peer-reviewed journals; (5) and foremost, evidence of collegiality.

Team: This research is part of a larger collaborative program studying predatory-prey dynamics in wolf-ungulate systems in southern Manitoba. As a result the successful applicant will be a part of a research team that includes Parks Canada biologists, Manitoba Fish and Wildlife ecologists, a MSc student in RMNP (start date May 2016), and another PhD student studying wolf-ungulate dynamics in eastern MB. This collaborative opportunity will permit the right applicant to participate in projects and publications in addition to their own core research.

Wildlife Evolutionary Ecology Lab (http://ericvanderwal.weebly.com/): We are a question-driven research group; one of a number of productive and dynamic research groups in ecology, evolution, and animal behavior at MUN. We bridge fundamental and applied questions in evolutionary, behavioral, population, and wildlife ecology, particularly with social ungulates. RMNP has been one of our keystone and must productive research systems and this new program aims to further advance our work on density-dependent resource and space use, social and group dynamics of ungulates now with a finer-scale understanding of the predatory-prey game.

To apply please send a letter of interest, CV, and transcripts (unofficial) to eric.vanderwal@mun.ca. Although the position is fully funded, students will be encouraged to compete for internal and external funding; higher GPAs and a history of publications improves competitiveness. The competition will remain open until the position is filled.

~Eric

Eric Vander Wal | Assistant Professor Department of Biology, Memorial University of Newfoundland

Eric Vander Wal <evanderwal@mun.ca>

Montpellier SelferAdaptation

A fully funded PhD position is currently available in our lab Evolutionary Genomics and POPulation management, UMR AGAP (JoÃ«lle Ronfort and Laurène Gay) and CBGP (Miguel Navascués). The aim of the PhD project is to understand adaptation in selfing organisms, using temporal contrasts (populations sampled through time). The PhD could combine methodological developments together with an experimental approach. Details about the PhD project can be found on https://www.adum.fr/as/ed/voirproposition.pl?print=oui&matricule_prop=8200 We are looking for a PhD student with a Master's degree in ecology and/or evolutionary biology, and with a strong-interest in evolutionary questions. Thorough knowledge and curiosity in population genetics and quantitative genetics are recommended, as well as a strong interest in theoretical developments. The PhD candidate will need to be independent and motivated to investigate experiments, statistical and methodological analyses and to collaborate with the technicians (in the greenhouse, in the field and in the lab). To apply or for further information, please send a cover letter, your CV and the contact information of three referees to laurene.gay@supagro.inra.fr, ronfort@supagro.inra.fr and navascues@supagro.inra.fr.

Summary of the PhD proposal How populations will adapt to the ongoing climate change is becoming a challenging question. This is particularly relevant for predominantly selfing species, because theoretical models predict that selfing increases homozygocity and reduces the effective populationsize, which in return affects the efficiency of selection and can reduce the adaptive potential of populations. In this PhD project, we propose to combine methodological developments with an experimental approach. The experimental approach will aim at testing whether three populations of Medicago truncatula, a predominantly selfing Mediterranean species, have adapted to climate change by shifting their flowering time across the past 25 years. The methodological part intends to developa tool to detect a signature of selection using temporal dataadapted to highly selfing organisms. This tool will be tested using genetic data from the three M. truncacula populations to identify the genetic architecture of the hypothetical change in phenology. More generally, this work will allow making recommendations about the choice of a method to detect signatures of selection when studying time series of genetic data and will suggest solutions to reduce the limitations usually imposed bydeviationsfromthe hypothesis of panmixis.

Further informations about the project: http://www.accaf.inra.fr/en/Actions-and-Projects/adaptation_crops/SELFADAPT http://www.agence-nationale-recherche.fr/en/anr-funded-project/?tx_lwmsuivibilan_pi2[CODE]=ANR-13-ADAP-0011 Further informations about the labs: GEÂ^{2}POP http://umr-agap.cirad.fr/en/scientific-teams/evolutionary-genomics-and-population-management/context-and-challenge CBGP http://www1.montpellier.inra.fr/cbgp/?q=fr/content/pr%C3%A9sentation-du-cbgp The PhD will be co-supervised by JoÃ≪lle Ronfort, Laurène Gay and Miguel Navascués and hosted in the Supagro campus in Montpellier (with team GE2POP). Montpellier is situated in the South of France and benefits from a vibrant scientific community, in particular in the fields of Ecology and Evolution. Feel free to broadcast this PhD offer to any candidate who could be suitable and interested.

Laurène Gay Equipe GEÂ^{2}POP (Evolutionary Genomics and POPulation management) UMR AGAP 1334

INRA Campus SupAgro BÃtiment 21 bureau 218 2 place Pierre Viala 34060 MONTPELLIER Cedex 02 Tél: +33 (0)4 99 61 30 87 Email: Laurene.Gay@supagro.inra.fr https://sites.google.com/site/evolutionarybiologylaurenegay/ Laurene Gay <Laurene.Gay@supagro.inra.fr>

Portugal 12 Biodiversity

TWELVE SCHOLARSHIPS ARE AVAILABLE FOR THE BIODIV PhD PROGRAMME Call 2015-16

The Doctoral Programme in Biodiversity, Genetics and Evolution (BIODIV), invites applications for 12 scholarships for the 2015-16 academic year.

Funded by FCT - Portuguese Foundation for Science and Technology, BIODIV is organized by the two largest Portuguese universities - University of Porto < http://sigarra.up.pt/fcup/en/CUR_GERAL.CUR_VIEW?pv_ano_lectivo=2012&pv_origem=CUR&pv_tipo_cur_sigla=D&pv_curso_id=1012 > and the University of Lisbon < http://www.fc.ul.pt/en/cursos/doutoramento/biodiversidade-genetica-e-evolucao > - in partnership with CIBIO-InBIO < http://cibio.up.pt/cibio.php?lang=en > (Research Center in Biodiversity and Genetic Resources/ Associate Laboratory) and cE3c (Centre for Ecology, Evolution and Environmental Changes).

The PhD Programme offers a variety of specialization options and the opportunity to work with leading scientists in an interdisciplinary research environment.

The call for applications is open between May 8 and June 8, 2015.

Information about the programme and on 'How to apply' is available at BIODIV's website < http://www.biodiv.pt/call-2015-16 > (http://www.biodiv.pt/call-2015-16).

Maria Sant'Ana

E: applications@biodiv.pt

T: + 351 252 660 411 F: + 351 252 661 780

CIBIO Divulgação

Seychelles UGroningen BehavEcol

Behavioural ecology of Seychelles warblers Acrocephalus sechellensis

Scientific background: The Cousin Island population of Seychelles warblers has been the centre of a long-term longitudinal study for over twenty years and is currently being used to answer questions relating to ageing, immunity and the evolution of social behaviour. The island of Cousin (27 ha) is a special reserve that hosts around 320 warblers, which are almost all colour banded.

Project details: We are seeking a motivated and adventurous MSc student to undertake a fieldwork-based project on Cousin Island for a period of three months. As part of ongoing data collection, the student will collect biological samples and behavioural data. Behavioural experiments designed to investigate the effect of predation on incubation behaviour are currently being planned; these can form the basis of the MSc project.

The successful candidate will be an enthusiastic fieldworker who can learn to work independently and is content on a remote island with very basic living conditions. Some kind of field experience with birds is essential, and experience with handling birds is preferable.

This project is a collaboration between researchers at the University of Groningen and the University of East Anglia, UK.

Supervisors: Frank Groenewoud & Jan Komdeur Fieldwork dates: between July V September [2.5 to 3 months; exact dates TBA]

Application deadline: May 31st 2015

Interested candidates can send an email to f.groenewoud@rug.nl or K.Bebbington@uea.ac.uk

Frank Groenewoud <f.groenewoud@rug.nl>

Stockholm InsectTaxonomy BiodiversityInformatics

PHD STUDENT POSITION in INSECT TAXONOMY / BIODIVERSITY INFORMATICS

The position forms part of a group of 15 PhD students now being recruited to the EU-funded Marie Sklodowska-Curie Innovative Training Network BIG4. The core of BIG4 is interdisciplinary, cutting-edge research on the diversity and evolution of the four largest insect orders: Hymenoptera, Diptera, Coleoptera, and Lepidoptera ('Biosystematics, Informatics and Genomics of the 4 big insect groups). The program offers unique opportunities in terms of preparing students for an academic or a business career. The training will include secondment to other European labs in the network, and to small companies in the biotechnology and IT sector. The program also includes network-wide training events, and seeks to build student skills in creativity and innovation.

The position is one of three PhD student positions that will be formally associated with the Department of Zoology at Stockholm University, which will award the PhD degrees. The position will be hosted by Savantic AB (http://savanticab.com), a consultant company specializing in bridging the gap between the research and business worlds. All consultants have a doctoral degree in physics. Specialty areas include image analysis, medical technology and environmental technology. The academic training will be provided by the Ronquist lab at the Swedish Museum of Natural History, which is one of the world leaders in the development of software for computational phylogenomics using Bayesian statistical methods. The lab also has a strong research tradition in insect systematics and evolutionary biology.

The successful candidate for this position will focus on the use of citizen science in accelerating research and discovery in insect systematics. For a suitable group of poorly known insects, we will develop visual identification aids based on advanced image analysis. The aim is to generate interest among citizen scientists in contributing to the systematic research on the chosen group, using a commercially viable app.

We are looking for candidates with a broad background, preferably including studies or training in entomology, genomics, bioinformatics, and programming. We expect that you will be creative and independent while being a good team player. Fluency in spoken and written English is essential. We will pay particular attention to scientific and creative talent and potential.

To be eligible for the position, you need to fill the formal requirements to start a PhD program in biology, broadly construed, and have less than 4 years of research experience counted as time of employment in research since receiving the degree for enrollment in a PhD. You cannot have resided or carried out your main activity (work or study) in Sweden for more than 12 months in the 3-year period immediately prior to the recruitment under the project.

Starting date is August 15, 2015. The position is for four years.

The Swedish Museum of Natural History (NRM) is one of the leading institutions of its kind in Europe. It combines a venerable tradition and unique collections with cutting-edge research in geology, paleontology and biology. The museum is close to Stockholm University, the Royal School of Engineering (KTH) and the Karolinska Institute. The Stockholm Phylogenomics Group (http://phylogenomics.se) engages research groups from all of these institutions. The Department of Bioinformatics and Genetics at NRM is focused on research in computational phylogenetics, population genetics and genomics. We run a DNA sequencing facility and host several national and international infrastructures.

The application should consist of a personal letter, a statement describing research interests and career goals (max 3 pages), a CV, and a transcript of your MSc diploma or equivalent. The application should be sent to Karin Carlsson at Savantic AB (karin@savanticab.com). Applications should be received no later than May 29, 2015.

Fredrik Ronquist Professor, Dept. Bioinformatics and Genetics Swedish Museum of Natural History, Stockholm

email: fredrik.ronquist@nrm.se

Karin Carlsson Savantic AB

email: karin@savanticab.com

Fredrik.Ronquist@nrm.se

UBarcelona KaryotypeEvolution

PhD position in Comparative Genomics at the Universitat Autònoma de Barcelona (Spain)

We are looking for a highly motivated candidate to work on a genomic comparative project.

Our group work chiefly in the fields of comparative genomics and evolution, in particular, we are interested in the mechanisms that are driving karyotype evolution and genomic architecture in mammals. Our research activity is aimed at addressing a whole range of different evolutionary questions through a multidisciplinary approach, combining computational and experimental methods such as available genome databases. The aim of the PhD is to study evolutionary genomic regions in different mammalian species.

The Universitat Autònoma de Barcelona offers excellent research facilities and a stimulating working environment. The project will also involve collaboration with researchers in U.K. Salary is according to the National Science Foundation guidelines. Funding is available for 3-4 years.

Interest in evolutionary biology, molecular biology and cell biology is required. Experience in molecular laboratory techniques, working with NGS data and phylogenetic analysis are all potentially relevant. Applicants must hold a Master's degree or equivalent in biology, molecular biology or related disciplines, with a strong background in bioinformatics. The applicants should also possess excellent written and oral communication abilities.

For further information see please (http://grupsderecerca.uab.cat/evolgenom/) or contact Dr Aurora Ruiz-Herrera directly (aurora.ruizherrera@uab.cat).

Complete application packages, including a CV (with a list of publications, if applicable), a brief (1-page) statement of research interests, and the names and e-mail addresses of two referees should be sent to aurora.ruizherrera@uab.cat

Aurora Ruíz Herrera Moreno <Aurora.RuizHerrera@uab.cat>

UBern 2 Biodiversity

Two PhD positions in biodiversity-ecosystem functioning and multitrophic interactions at the University of Bern

Applications are invited for two, PhD positions working with Prof. Eric Allan, at the University of Bern in Switzerland.

Nitrogen enrichment is a key global change driver in grasslands which impacts ecosystem functioning through a range of direct and indirect effects. The project aims to experimentally disentangle some of these mechanisms, including looking at effects of biodiversity loss alongside changes in plant functional composition and foliar fungal pathogen abundance. We also aim to test the effects of global change on pathogen communities, theories about when pathogens have their largest top down effects on plant communities and to explore the host range of fungal pathogens with further experiments.

The two PhD students will set up, and work on, a large grassland field experiment near the city of Bern. One PhD student will focus more on ecosystem functioning (including quantifying measures of nitrogen and carbon cycling and litter decomposition) and the other on responses and effects of pathogens.

We are seeking highly motivated applicants interested in biodiversity-ecosystem functioning, plant community ecology and multitrophic interactions. Applicants must hold (or shortly complete) a Master degree or equivalent in biology or another relevant discipline, with a good background in ecology. Some previous research experience in ecology and good statistical knowledge are desirable. Strong oral and written communication skills in English are required. The positions will be based at the Institute of Plant Sciences in Bern, which offers a stimulating, international research environment and excellent facilities (www.botany.unibe.ch/planteco). Bern is also a beautiful city with a high quality of life.

Please send your application by email (as a single PDF) to eric.allan@ips.unibe.ch. Applications should include a CV, names and addresses of two references and a one page cover letter outlining your motivation for the position and research interests. Applications will be reviewed from 26th June 2015 until the position is filled. The expected start date is 1st September 2015.

For queries on the application process or more information on these positions, please contact Prof. Eric Allan eric.allan@ips.unibe.ch

Dr. Eric Allan, Institute of Plant Sciences University of Bern Altenbergrain 21 CH-3013 Bern email: eric.allan@ips.unibe.ch phone: +41 31 631 4923 http://www.ips.unibe.ch/content/biodiversity/-index_eng.html http://www.researchgate.net/profile/-Eric_Allan Eric Allan <eric.allan@ips.unibe.ch>

UdeLaRochelle SeabirdPhylogenetics

Dear listers,

A doctoral position is available in our labs to work on the phylogenetics and phylogeography of petrels. A description of the project with information on how to apply is available at https://epante.wordpress.com/-opportunities/ Deadline for applying is currently set to May 25, 2015. Start date for the project is Oct 1st, 2015.

Please email us shall you have any question!

Best regards, Eric Pante & Vincent Bretagnolle

pante.eric@gmail.com

UEastAnglia UGroningen EvolutionSeychellesWarblers

Excellent PhD opportunity

Funded PhD position working on the Evolution of promiscuity in Seychelles warblers

with Profs DS Richardson, J Komdeur and Dr H Dugdale

Joint position at the University of East Anglia and the University of Groningen

Deadline 24 April 2015

For more details, eligibility and how to apply go to

https://www.uea.ac.uk/study/-/investigating-the-evolutionary-forces-underlying-promiscuity-in-the-seychelles-warbler-richardsonds_u15sf- or http://www.findaphd.com/search/-ProjectDetails.aspx?PJID=56962&LID=432 David S Richardson Professor in Evolutionary Ecology and Conservation Centre for Evolution, Ecology and Conservation School of Biological Sciences, UEA, Norwich NR4 7TJ, England e-mail: david.richardson@uea.ac.uk http://biobis.bio.uea.ac.uk/biosql/fac_show.aspx?ID=-325 UK Top 15 (14th in the Guardian University Guide 2015; 15th in the Complete University Guide 2015) UK Top 3 for Student Experience (Times Higher Education Student Experience Survey 2014) World top 1% (Times Higher Education World Rankings 2013-14) World Top 100 (Leiden Ranking 2014)

"David Richardson (BIO)" <David.Richardson@uea.ac.uk>

UExeter 2 PhytoplanktonAdaptationSelection

We have an exciting funded PhD studentship available to research the effects of environmental change on phytoplankton communities with Dr. Etienne Low-Décarie with the co- supervision of Professor Richard Geider in the School of Biological Sciences of the University of Essex

The PhD student will investigate how phytoplankton communities change in response to changes in their environment. Phytoplankton are responsible for half of the biological uptake of CO2 from the atmosphere and are the base of most aquatic food webs. In addition, as they are small and grow rapidly, they are perfect model organisms from which inferences can be made for the response to global change of other primary producers. The project will study both freshwater and marine phytoplankton, including strains that have evolved under different environmental conditions for hundreds of generations.

More about the position is available at: http://-etiennelowdecarie.org/2015/05/14/phytoplankton-faces-the-future-eco-evolutionary-response-of-communities-subject-to-environmental-change/ WHERE: University of Essex WHAT: PhD Studentship: Eco-evolutionary response of phytoplankton communities subject to environmental change

"Low-Decarie, Etienne" <elowde@essex.ac.uk>

We have an exciting funded PhD studentship available to explore the factors that influence the efficiency of selection at different levels of biological organization with Dr. Etienne Low-Décarie and with the co-supervision of Dr Corinne Whitby in the School of Biological Sciences of the University of Essex.

The PhD Student will use artificial selection applied to phytoplankton communities to change a target trait (lipid production/pollutant degradation). The approach will allow the investigation of the importance of biodiversity and initial community composition for the response to selection, the determination of the mechanisms such as dispersal across a meta-community that can maintain diversity during the selection process and the predictability of the change in community composition as a response to selection.

More about the position is available at: http://etiennelowdecarie.org/2015/05/14/industrial-strength-eco-evolution-artificial-selection-of-microbial-communities/ WHERE: University of Essex WHAT: PhD Studentship: Industrial strength eco-evolution: artificial selection of microbial communities

"Low-Decarie, Etienne" <elowde@essex.ac.uk>

UGeneva HumanPopulationGenomics

PhD position in human population genetics/genomics at the University of Geneva, Switzerland

A PhD position in human molecular population genomics/genetics is available at the Laboratory of Anthropology, Genetics and Peopling history (AGP lab) of the University of Geneva (Switzerland). The PhD will be supervised by Dr Estella Poloni and will consist in the analysis of genomic data including markers of genes involved in drug metabolism and their association with phenotypic data generated in parallel for several human population samples. This PhD project is included in a research project supported by the Swiss National Science Foundation (SNF) aims at evidencing which evolutionary mechanisms shaped these genomic regions that are functionally important from the clinical and epidemiological point of view, in a key-region of the peopling history of our species (ua.unige.ch/en/agp/recherche/fns/320030-159669/). We are seeking for a highly motivated candidate with broad interests in anthropology and human evolution, and a strong commitment to research.

Requirements: Master degree in biology or equivalent; good skills in biostatistics and data analysis; deep interest for human evolution, population genomics/genetics, molecular evolution, computer tools, and anthropology in general; willingness to carry out sampling missions in various countries (4 missions, 1st year of PhD); Collaboration and communication abilities Good skills in bioinformatics are an advantage.

Terms of employment: duration is 3 years, provided that the first year is successful (trial period). Starting date is September 1, 2015, and salary is as of SNF scale for a Candoc. Other conditions: the PhD student will participate in the teaching and other activities of the AGP lab.

The AGP lab is hosted by the Department of Genetics and Evolution - Anthropology Unit, at the University of Geneva, Switzerland. It offers a very stimulating environment with several independent researchers, international collaborations and excellent computer resources. The Anthropology Unit is located in the heart of Geneva (Acacias) at walking distance from the other University buildings. English and French are the working languages in the lab. More details about the Anthropology Unit can be found at ua.unige.ch/en/.

Applications should be sent as a single pdf file by email to Dr Estella Poloni (estella.poloni@unige.ch) by June 15, 2015. It should include a motivation letter, a detailed CV, contact information of two referees and a statement of past research in the domain (Master Thesis and others).

Dr Estella "Sim" Poloni Laboratory of Anthropology, Genetics and Peopling history (AGP) Department of Genetics and Evolution (GENEV), Anthropology Unit University of Geneva 12, Rue Gustave-Revilliod 1211 Genève 4, Switzerland Phone +41 (0)22 379 69 77, Fax +41 (0)22 379 31 94 http://ua.unige.ch/fr/personne/estellapoloni/ http://genev.unige.ch/ http://ua.unige.ch/fr/ Estella Poloni <estella.poloni@unige.ch>

UGottingen MolluscEvolution

PhD position for evolutionary-developmental biology of biomineralisation

A PhD-position is available to work with Professor Daniel J. Jackson in the Department of Geobiology, University of Göttingen, Germany. The position will be available from August 1st 2015 (and is limited to 3 years). Salary is in accordance with the German state regulated public service salary scale (50% TV-L bracket 13).

The Jackson group is broadly interested in the molecular processes by which metazoans have evolved the ability to form mineralised body parts. We are currently developing the freshwater snail Lymnaea stagnalis as a model organism with which to address these questions. We are developing a range of modern molecular techniques and have established extensive sequence datasets for this research on Lymnaea. With these modern resources it is envisaged that the PhD candidate would marry the wealth of histological knowledge of shell molluscan formation that exists in the classical literature with insights mined from our modern resources. The position would therefore be well suited to an individual with some molecular biology skills and/or familiarity with the analysis of large computational datasets such as RNASeq and whole genome data.

Candidates should hold a master degree with a major in either evolution, developmental biology, molecular biology, or a related field. In addition to their academic qualifications, candidates should have excellent communication and team-working skills, be committed to the topic and to working in a dedicated, interdisciplinary research environment. The working language of the group is English, and applicants from abroad are encouraged to apply.

The University of Göttingen seeks to increase the participation of women in areas in which they are currently under represented and therefore explicitly urges women to apply. Disabled persons with equivalent aptitude will be favoured.

Applications, in English, must include:

1. A full academic CV including a list of all published or unpublished academic work. 2. A 1-2 page summary outlining the candidate's motivation for applying for this particular position. 3. A letter of reference from 1 former supervisor (Diploma or Masters).

Please send your electronic application directly to djackso"at"uni-goettingen.de. The application deadline is 1st July, 2015. Applications will be deleted after five months.

"Jackson, Daniel" <djackso@gwdg.de>

UGuelph DaphniaMutationRate

A position for an MSc student is available starting in September 2015.

Supervisor: Teresa Crease, Department of Integrative Biology, University of Guelph (http://www.uoguelph.ca/~creaslab).

Co-supervisor: Melania Cristescu, Department of Biology, McGill University (http://biology.mcgill.ca/faculty/cristescu).

The primary goals of this research project are to determine the impact of heavy metal contamination on rates of mutation and recombination in ribosomal DNA (rDNA) and transposon activity in Daphnia mutation accumulation lines.

The mutation lines have been maintained with and without exposure to copper and nickel for about 100 generations. The student will use next-generation sequencing and qPCR to assay sequence variation and copy number in the rDNA of a subset of lines from each treatment. Transposon display will be used to assay transposon copy number. The results will be compared to the results of fitness assays conducted on the lines as part of a related project.

This project is part of the NSERC CREATE Training Program in Aquatic Ecosystem Health: Integrative Approaches for Studying Multiple Stressors (ERASMUS). More information about ERASUMS can be found at http://www1.uwindsor.ca/erasmus-create . Students in the ERASMUS training program benefit from unique opportunities that involve exposure to multidisciplinary training through workshops, exchanges with participating institutions and/or internships with industrial and governmental partners.

More information about the MSc program at Guelph can be found at http://www.uoguelph.ca/ib/grad/graduate.shtml Students who are interested in this position should send an email to Teresa Crease (tcrease@uoguelph.ca). Please include a short CV and the names and contact information of at least 2 faculty who could act as referees. Although all interested applicants are encouraged to inquire about the position, preference will be given to applicants who are citizens or permanent residents of Canada.

Teresa Crease, MSc, PhD Associate Dean, Graduate

Studies Professor, Department of Integrative Biology University of Guelph 50 Stone Road East, Guelph, ON N1G 2W1

phone: 519-824-4120 x52723 FAX: 519-767-1656 email: tcrease@uoguelph.ca

"tcrease@uoguelph.ca" <tcrease@uoguelph.ca>

UNewBrunswick SaintJohn BassAdaptation

MSc. Position in Ecological Genomics at University of New Brunswick Saint John: Striped Bass Adaptation (Fall 2015 or Winter 2016)

A position is available for a Masters of Science student to participate in an integrated Striped Bass genomics research program. The student will use ecologically divergent populations and full-genome re-sequencing to determine the genetic basis of adaptation. The student will be part of a lab of a new Canada Research Chair in Aquatic Molecular Ecology and Ecological Genomics at the University of New Brunswick in Saint John.

Funding is available for a stipend or top-up bonus for students with funding. The student will use state-of-the-art laboratory equipment, including robotics, to streamline repetitive tasks and will have priority access to a high-powered computer with 1.5 TB of RAM for bioinformatics. The lab is located at the Canadian Rivers Institute (www.canadianriversinstitute.ca).

Suitable candidates will have a solid quantitative background with experience in genetics and genomics lab work and/or bioinformatics. Candidates must have a positive attitude and willingness to work with a team. Experience in programing with R, Python or Perl computer languages is a plus.

The position will begin in the fall term of 2015 or winter of 2016. Submit a Cover Letter, CV, contact information for three references and unofficial transcripts that include course names to Dr. Scott Pavey (scottapavey@gmail.com). Application packages will be accepted until the position is filled.

Scott Pavey <scottapavey@gmail.com>

UNordland SeagrassMetagenomics

PhD fellowship in Seagrass metagenomics

A three-year PhD fellowship in Seagrass metagenomics is available at the University of Nordland, Faculty of Biosciences and Aquaculture (BodÃ, Norway)

Faculty of Biosciences and Aquaculture (FBA) For more information, see The Faculty's website: www.uin.no/en/fba About the PhD fellowship

FBA is currently inviting applications for a three-year PhD fellowship affiliated with the Strategic Research Group Marine Ecology. The successful candidate will join the marine molecular ecology research unit. The proposed PhD research focuses on the community of microorganisms that live in and on seagrasses - the seagrass "microbiome".

The proposed project combines metagenomics and metatranscriptomics of natural and experimental populations of seagrasses to investigate the ecological and evolutionary role of the seagrass-microbes interaction. It will contribute to understanding fundamental questions about seagrass ecology, evolution and function. Microbiomes diversity is expected to have important ecological effects and such knowledge is essential to assess ecological responses to environmental changes.

Qualifications and requirements

The candidate should hold a Master of Science degree (or equivalent) in Biology in one of the following fields: - Molecular Ecology - Genomics - Microbial Ecology - Marin ecology

Experience with molecular biology methods is required. Experience with bioinformatics, metagenomics and/or seagrass ecology will be advantageous for the position.

The grades at the qualifying MS examination needs to be C or better (ECTS scale from A-E, A being the best grade). Good communication skills in English, both oral and written, are required. International applicants need to document proficiency in English equivalent to the Norwegian Higher Education Entrance Qualification. English proficiency should be certified by internationally recognized examination/test such as TOEFEL, IELTS, APIEL or similar.

The position requires a highly motivated and systematic candidate capable of working independently and in teams.

The successful candidate will join the PhD programme in Aquatic Biosciences at the University of Nordland and is expected to complete a doctorate within the three-year project period. The candidate should fulfill the admission requirements of the aforementioned PhD programme at the Faculty of Biosciences and Aquaculture, and participate in the training components stipulated in regulations of the PhD program. Application for admission to the programme must be submitted within three months after taking up the position. For admission requirements and regulations, see our web page.

Salary and Working Conditions The salary for PhD candidates is set at wage level 50 in the Norwegian State Salary Scale (approximately NOK 427 700 per year). As an employee at the University of Nordland you become a member of the Norwegian Public Service Pension Fund and you will also get access to other social benefits. A statutory amount to the Norwegian Public Service Pension Fund will automatically be deducted from the salary.

The successful person must abide by the laws, agreements and directives that apply to the position at any time.

According to the employment policy of the institution, our staff should reflect the population in general. We encourage candidates with minority background to apply for the position. The University practices moderate allocation according to sex quotas in accordance with the Basic Agreement for the Civil Service.

Contact Information

For further information, prospective applicants can direct their questions to professor Galice Hoarau (gah@uin.no). For questions related to the application process, please contact office manager Irene Stork Wisth (Irene.Stork.Wisth@uin.no), phone +47 755 17 442).

Application

Applicants for the position are requested to send an application in which the motivation for applying is clearly stated, a complete CV (education, scientific publications as well as work experience) and certified copies of educational certificates. Other relevant qualifications should also be documented.

All documents must be uploaded as attachments to the electronic application form. http://www.jobbnorge.no/-ledige-stillinger/stilling/114094/phd-fellowship-in-seagrass-metagenomics Application deadline: 3 June, 2015. It is the applicant's responsibility to submit complete documentation within the application deadline

Ref.nr. 30029072

Jobbnorge-ID: 114094, SÃknadsfrist: 03.06.2015

"Galice.Guillaume.Hoarau@uin.no" <Galice.Guillaume.Hoarau@uin.no>

UParis SexEvolution

PhD position at Universit Paris 13, Laboratorie dEthologie Exprimentale et Compare E.A. 4443, France

Evolutionary transition between hermaphroditism and separate sexes

Application deadline: 25 May 2015

Sex is a central topic in biology and it is often associated to male and female genders. But why males and females are so common in animals? And if there has been some selective advantage in evolving male and female genders, why is hermaphroditism almost ubiquitous among animal taxa and why are there more than 65000 species of hermaphroditic species in animals? Have males and females evolved from hermaphrodites or vice versa? Whereas other questions in the evolution of sex have been the focus of theoretical and empirical research in animals (e.g., sexual selection, the transition between sexual and asexual reproduction, etc.), the transition between hermaphroditism and separate sexes has been rarely explored and we are left with many unsolved questions. This PhD project plan to meet this goal using polychaete worms of the genus Ophryotrocha as biological models and testing the role of hermaphrodite behavioral traits (such as reciprocity and plastic sex allocation) and gonochoric behavioral traits (such as gender specialization) in stabilizing hermaphroditism and/or favoring the transition towards separate sexes.

The project requires doing behavioral experiments where worms are exposed to different conditions (e.g., density and/or mate competition) and/or used in choice tests; data on their mating behavior and mate preferences as well as measures of their reproductive investment will be analysed. Most experiments require working at the stereomicroscope.

Bibliographic references

Lorenzi M.C., Sella G. 2013. In between breeding systems: Neither dioecy nor androdioecy explains sexual polymorphism in functionally dioecious worms. Integrative and Comparative Biology 53:689-700.

Weeks S.C. 2012. The role of androdioecy and gynodioecy in mediating evolutionary transitions between dioecy and hermaphroditism in the animalia. Evolution 66:3670-86.

The language in the lab will be French and English. The position is funded for 3 years and will start on Oct 1st 2015.

Applications for this position should be sent to Prof. Dr. M. Cristina Lorenzi (cristina.lorenzi@leec.univ.paris13.fr) by May 25, 2015, including: letter of interest, CV, proposed research plan and recommendation letters from previous supervisors.Applicants are encouraged to make an informal enquiry beforehand by contacting Prof. Dr. M. Cristina Lorenzi via email ASAP. For further information about the Laboratoire dEthologie Exprimentale et Compare see http://leec.univ-paris13.fr Maria Cristina Lorenzi

LEEC-Laboratoire d'Ethologie Experimentale et Comparee Universite Paris 13, Sorbonne Paris Cite 99 avenue J.-B. Clement 93430 Villetaneuse, France Phone: +33(0)149403196 Email: cristina.lorenzi@leec.univ-paris13.fr

Dept. Life Sciences and Systems Biology Via Accademia Albertina 13, 10123 Torino, Italy Phone: +39 011 670 4512 E-mail: cristina.lorenzi@unito.it

Maria Cristina Lorenzi <cristina.lorenzi@unito.it>

UPlymouth TradeOffEvolution

"The evolution of trade-offs in mating behaviour and physiology" University of Plymouth, UK School of Biological Sciences Applications are invited for a three-year PhD studentship, fully funded for EU/UK students. The studentship will start on October 1st 2015.

Supervisors: Dr Michael Thom (University of Plymouth) Dr Mark Briffa (Plymouth) Prof. Calvin Dytham (University of York) Prof. Helen White-Cooper (University of Cardiff)

Summary: For male animals, successful reproduction involves a number of key processes including mate searching, courtship, copulation, and sperm competition. Many of these are energetically expensive, time-consuming, or otherwise incompatible and as a result males are unlikely to be able to maximise performance in all of them simultaneously. How males value the different processes will depend on both physical and social environment, with males expected to plastically adjust their relative investment in each to maximise their reproductive success under prevailing conditions. Using the model species Drosophila melanogaster, this project will explore how these different components of the male reproductive process are traded off under simultaneous variation in biotic (e.g. population density, sex ratio) and abiotic (e.g. nutritional composition, food distribution) conditions. The student will be based at Plymouth, but will conduct histological work on the rate and fidelity of spermatogenesis with Prof. Helen White-Cooper at Cardiff. In addition to the empirical studies on behaviour and sperm production, the student will have the opportunity to learn the programming language C++, and will use this to develop an agent-based model exploring the evolution of ecological plasticity in mating behaviour and physiology - this will be overseen by Prof. Calvin Dytham at York.

If you wish to discuss this project further informally, please contact Dr Thom on michael.thom@plymouth.ac.uk.

See https://www.plymouth.ac.uk/student-life/your-studies/the-graduate-school/phd-studentship-in-biological-sciences for further details

michael.thom@plymouth.ac.uk

UPortsmouth FloralEvolution

A PhD position at the School of Biological Science at the University of Portsmouth (UK)

Supervisor: Rocio Perez-Barrales and W. Scott Armbruster

Project title: Pollination competition and facilitation as ecological driver of floral diversity and evolution in Mediterranean Linum (Linaceae)

Most plants in communities tent to interact indirectly by sharing pollinators, and these interactions can bring positive or negative effects to plant fitness. At community level, most of the research has focused on whether sharing pollinators is beneficial or costly for plants. This is surprising because the sign and net effect of the interaction is context dependent. For example, adjustments in flowering phenology of species can support the pollinator community during the entire blooming season and increase the residence time of pollinators. In contrast, co-flowering species can compete for the pollinator service, and the strength of these negative interactions may be a density dependent process in a spatially explicit context. All these processes are not mutually exclusive, and they vary temporally and spatially; in the longer term, they can structure species composition and combinations of different floral traits. This PhD project will (i) evaluate how facilitation and competition for pollinator service can structure plant communities by looking at (ii) rates of intra-specific pollen flow and inter-specific pollen flow to (iii) quantify the selective value of these complex interactions as drivers of floral evolution, speciation and differentiation of traits directly linked with female and male fitness.

The research will be conducted in Mediterranean communities of flax species (Linum, Linaceae) in Spain, where often several species coflower and share pollinators.

We are looking for enthusiastic, independent and dynamic candidates with strong interest in plant-animal interactions. Candidates must have a good Master's degree, or good degree in Biology or Environmental Biology, with a background in Plant Population Biology, Ecology and Evolution. The candidate should be familiar with the package R for data analysis of ecological and molecular data, and flexible to work in a team and independently. It is expected that (s)he will be an active part of preparation of grant proposal and manuscripts. The candidate will gain skills both in the field and the lab. The fieldwork will be conducted in Spain, and it would be beneficial for the candidate to speak Spanish. The lab work and greenhouse experiments will be conducted in the facilities of The University of Portsmouth.

In addition the candidate will have access to the Graduate School Development Programme and Department Postgraduate Researcher Training, and will join the Biodiversity and Evolution research team at the School of Biological Science.

Application should be sent before the 4th June on line at http://www.port.ac.uk/postgraduate-research/-funding/phd-geography-earth-and-environmental/-, but please contact me before applying at rocio.barrales@port.ac.uk

Rocio Perez-Barrales

Lecturer in Evolutionary Biology

School of Biological Sciences

University of Portsmouth

Rocio Perez-Barrales <ropeba@us.es>

USouthampton WildlifeConservation

MRes Wildlife Conservation

Applications are currently open for the University of Southamptons MRes in Wildlife Conservation, run on collaboration with conservation organisation Marwell Wildlife, making it a unique programme. Please let your current final year undergraduate students know about the course, we are interested in students with an ecological, environmental science or geography background. More information about the course is available here http://www.southampton.ac.uk/wildlifeconservation and also here http://www.findamasters.com/search/-masters-degree.aspx?course=3D28163 Best wishes,

Judith

Dr Judith Lock Centre for Biological Sciences, Life Sciences B85, University of Southampton, Southampton SO17 1BJ Tel: 02380594312 Twitter: @Judith_Lock MRes Wildlife Conservation, Joint Programme Manager http://www.southampton.ac.uk/wildlifeconservation "Lock J.E." <J.E.Lock@soton.ac.uk>

UZurich PlantSystematicsEvolution

Two PhD positions in systematic botany / phylogenetics at the University of Zurich

Project description: the selected student will work with Dr. Colin Hughes. http://www.systbot.uzh.ch/-Personen/ProfessorenundDozenten/ColinHughes.html on a research project entitled Global Legume diversity patterns: macroevolutionary and ecological processes shaping biodiversity, funded by the Swiss National Science Foundation in the Institute of Systematic Botany at the University of Zurich. http://www.systbot.uzh.ch/-index=5Fen.html We are interested in how diversity evolves and understanding the processes and factors that determine the spatial distribution of life on Earth. Using comparative approaches and one of the most evolutionary successful families of flowering plants, the legumes (Leguminosae = Fabaceae), as a study system, we are addressing a set of inter-related questions about global plant diversity patterns. We are making use of recent developments in comparative phylogenomics and global-scale species distribution modelling to quantify phylogenetic turnover and the ecological factors underlying patterns of diversity across large-scale ecological gradients.

The PhD projects will focus on specific legume clades, and especially subfamily Mimosoideae, a pantropical clade spanning all lowland tropical biomes and potentially involve fieldwork, laboratory work to generate DNA sequence data using NGS, herbarium specimen database work, and phylogenetic/ macroevolutionary analysis. This will build on foundations - genomic data, development of NGS approaches, taxonomic knowledge and research material - already established in Zurich.

The Institute of Systematic Botany in Zurich offers excellent research facilities and a stimulating working environment for graduate students in plant systematics and evolution. The project will also involve collaboration with legume researchers in Brasil, the Netherlands, U.K., U.S.A. and Canada. Salary is according to the Swiss National Science Foundation guidelines. Funding, including for laboratory and field work, is available for 3 years. Â Requirements: Applicants should hold a Masters degree in systematics, biodiversity or evolutionary biology. Experience in molecular laboratory techniques, working with NGS data, phylogenetic analysis, macroevolutionary analysis, fieldwork and GIS are all potentially relevant. Excellent knowledge of English, written and oral, is essential. How to apply: Send the following documents by email AS A SINGLE PDF FILE to Dr. Colin Hughes, colin.hughes@systbot.uzh.ch:Â i) a two-page application letter describing your research interests, outlining why you think working on mimosoid legumes is interesting, why are you interested in a Ph.D. position in systematic botany and your career goals; ii) your CV, including a list of publications (if applicable); iii) a copy of your undergraduate and graduate academic record; iv) names and contact details of at least two referees selected from your academic advisors.

Deadline for applications: Applications will be screened from May 25th 2015 onwards until the positions are filled.

Starting date: Sept/Oct 2015.

colin.hughes@systbot.uzh.ch

Yale-NUS Singapore Evolution

Ph.D. Scholarships in Tropical Ecology, Evolution, and Biodiversity. Yale-NUS College, Singapore

Deadlines for application: May 15 (entrance in January 2016) or November 15 (entrance in August 2016). If interested in January entrance, deadline can be extended.

Yale-NUS College, the first liberal arts college in Singapore, has Ph.D. scholarships available for students interested in pursuing a doctoral degree in the Life Sciences. Doctoral degrees are awarded through the Department of Biological Sciences, National University of Singapore. Faculty listed below are interested in recruiting students for academic year 2015/2016 or 2016/2017

- Phyloinformatics and spider evolution (William H. Piel; william.piel@yale- nus.edu.sg)

- Conservation ecology and amphibian biodiversity (Jennifer Sheridan; jasheridan@yale-nus.edu.sg)

- Evolution of development of butterfly wing patterns (Antónia Monteiro; antonia.monteiro@nus.edu.sg)

- Evolution of stalk-eyed flies (Philip Johns; philip.johns@yale- nus.edu.sg)

- Evolution, photonics, and material science of organismal structural colors (Vinod Saranathan, vinodkumar.saranathan@aya.yale.edu)

- Functional ecology and restoration of tropical forests (Michiel van Breugel, michiel.vanbreugel@yale-nus.edu.sg)

If interested in pursuing PhD research in these general areas please contact respective faculty (https://www.yale-nus.edu.sg/about/faculty/) and visit the web page of the Department of Biological Sciences, National University of Singapore to learn more about the graduate program:

http://www.dbs.nus.edu.sg/education/graduates_prospective/index.html antonia.monteiro@yale.edu

Jobs

DukeU LabTech PrimateBehaviour

An Associate in Research/Laboratory Research Analyst position available, starting immediately, in the Tung lab at Duke University. The Tung lab studies the relationship between behavior, the social environment, and genetics and genomics, with a focus on nonhuman primate populations. We combine detailed phenotypic and demographic information with modern genomic data sets on gene regulation and epigenetics. Current projects focus on the gene regulatory mechanisms linking social adversity and health in rhesus macaques, the epigenetic signature of early life ecological and social adversity, and the genomic and phenotypic consequences of hybridization in wild baboons. Duties will include performance of basic molecular biology laboratory techniques, including DNA and RNA sample extraction and sample preparation for high-throughput sequencing, and responsibility for day-to-day logistics, including purchasing, shipping and receiving, and working with trainees in the lab.

Important skills/traits include: aseptic technique, molecular techniques, attention to detail, ability to work independently, careful record keeping.

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

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

For more information about the lab and our work, see: http://www.tung-lab.org/ If interested, email resume, including contact information for two references, to Amanda Shaver, *aos7@duke.edu*

Duke University is an Equal Opportunity/Affirmative Action/ADA Employer committed to providing employment opportunity without regard to an individuals age, color, disability, genetic information, gender, gender identity, national origin, race, religion, sexual orientation, or veteran status.

Jenny Tung Assistant Professor Department of Evolutionary Anthropology and Duke Population Research Institute

Amanda Shaver <amandaoshaver@gmail.com>

EcoHealthAlliance ResAssist DiseaseDynamics

Job Title: Research Assistant

EcoHealthAlliance seeks an organized, self-motivated research assistant for our programs on emerging disease ecology, evolution, and modeling. The research assistant will assist senior research scientists on our USAID-funded PREDICT and NIH-funded projects examine the dynamics of pathogen transmission within and among wildlife populations, livestock, and humans; as well as the risk of spillover, patterns of infection, cophylogenetic and phylogenetic relationships, and phylodynamics of emerging zoonotic diseases. The candidate should be self-motivated and proactive.

Description and Responsibilities

Reporting to senior research scientists this position will: - Work on modeling and other projects that broadly integrate evolutionary, ecological, and biodiversity data into emerging disease and zoonotic disease models. - Liaise with scientists to generate hypotheses and to assist with development of models and plan avenues of scientific investigation - Provide modeling and analytical support to EcoHealth Alliance scientists - Participate in and/or coordinate science and other meetings - Assist in project management and provide administrative support for project managers - Lead administration of grant proposals and reporting including contracting, coordinating invoicing, payments, and reports - Assist with finances, reimbursements, and expense coding - Take minutes and generate draft agendas for meetings - Assist with grant and manuscript writing - Have responsibility for some grant management and program coordination

Qualifications - Minimum of B.S./B.A. in: Biology, Ecology, Evolutionary Biology, Public Health, or related field in the life sciences; Master's degree preferred - Strong quantitative analytical skills - Experience with basic statistical analyses, particularly using R - Previous experience writing grants and with grant administration - Ability to conduct literature reviews, data collation and cleaning, and exploratory data analyses - Excellent oral and written communication skills - Publications in peer-reviewed scientific journals - Proven ability to work independently - A strong sense of team spirit and diplomacy - Previous experience in public health or infectious diseases - Cultural sensitivity - Fluency in English - Experience with phylogenetic and evolutionary analyses is a strong plus. Particularly, phylogenetic tools in R (e.g. ape, picante, geiger, etc.); software for building phylogenetic trees (including Geneious, and other programs for alignment and building likelihood and Bayesian trees); and molecular evolution (esp. BEAST)

EcoHealth Alliance offers a competitive salary and a comprehensive benefit package including health, dental, and vision coverage, and a 403(b) pension plan. EcoHealth alliance is an equal opportunity employer. For further information about EcoHealth Alliance, please visit our website: www.ecohealthalliance.org How to Apply: Send an email a single attachment labeled with your first and last name only ('first last.pdf') in PDF format containing with (a) a cover letter, (b) CV, and (c) three references to jobs@ecohealthalliance.org with "EHA RA SPRING 2015" in the subject line. Emails without the subject line or with multiple attachments will not be received. No formal text is required within the body of your email, since emails will not be evaluated. All inquires will receive an automatic response confirming receipt. Applicants will be evaluated and only appropriate candidates will be contacted. Thank you for your interest in EcoHealth Alliance!

Aleksei Chmura <chmura@ecohealthalliance.org>

INRA nearParis 2yr ComputationalBiol

The INRA laboratory UMR 1290 Bioger (Thiverval-Grignon, France) has a two-year open position for a research engineer in genomics and bioinformatics in the team EGIP (Evolution and Genomics of Plant Pathogen Interactions).

Position: We are seeking a motivated applicant interested in providing computational and bio-informatics expertise to different fungal genomics projects developed in the team (Illumina sequencing data handling, de novo genome assembly, polymorphism detection, genome annotation, transcriptomics). The applicant will work as a member of a multidisciplinary team with evolutionary biologists, geneticists, and plant pathologists with skills in bioinformatics and fungal genome analysis. Genome annotation will be performed in close collaboration with the JGI-DOE Mycocosm project. The contract may include a stay at the JGI office in Walnut Creek near San Francisco, CA, USA.

Required qualifications: Master in biology or computer science; bioinformatics experience or working knowledge of bioinformatics tools; good understanding of Linux and solid programming experience; good practice of scientific English. Please send a CV and letter(s) of recommendation to Dr Marc-Henri Lebrun (marc-henri.lebrun@versailles.inra.fr). The position is open and review of applications will continue until the position is filled.

BIOGER is located on the ground of the AgroParisTech School for Engineers in Agriculture at Thiverval-Grignon. The Campus is located in the country side South-West of Paris, close to a railway station easily connected to Gare Montparnasse (http://www6.versailles-grignon.inra.fr/bioger).

"anne.genissel@versailles.inra.fr"

InstitutPasteur Paris 2 ComparativeGenomics

Permanent positions in comparative genomics and evolutionary bioinformatics at Pasteur Institute (Paris)

Announcement below has been diffused on evoldir recently. Two of these positions will be attached to the research teams of Eduardo Rocha (comparative genomics, molecular evolution, microbiology, http://tinyurl.com/-ok257jy) and Olivier Gascuel (evolutionary bioinformatics, phylogenetics, molecular evolution, epidemiology, viruses, www.lirmm.fr/gascuel). If interested, apply on https://c3bi.pasteur.fr/hub-available-positions/ before May 15 and contact these PIs.

—–

Ten permanent positions in Bioinformatics and Biostatistics at Institut Pasteur (Paris)

The new direction of Institut Pasteur has defined bioinformatics and systems biology as strategic priorities. A "Center for Bioinformatics, Biostatistics and Integrative Biology" has been recently created on the Parisian Campus. The objective of this center is to federate and strengthen capacities in bioinformatics in different yet complementary research areas developed within the Institute, such as genomics of hosts and pathogens, biology of infection, evolutionary genetics, population genetics, structural biology or health biology.

In this framework, Institut Pasteur proposes 10 permanent positions in bio-informatics and biostatistics for 2015. People will be affiliated to the new center and to the Hub of bioinformatics and biostatistics and will be supervised by the director of the Center. They may be assigned for most of their time to research units and / or platforms to work on different projects while being close to the data and experimental biology.

To apply and know more on these positions: https://-c3bi.pasteur.fr/hub-available-positions/ Dead line May 15.

Olivier Gascuel <gascuel@lirmm.fr>

NewcastleU WildlifeManagement

Newcastle University has a vacancy for a senior lecturer in Ecology and Wildlife management to complement current research groups in this area. This could, for example, be a molecular ecologist, either in plants or animals, to broaden skills and opportunities in our area.

The deadline is 22nd May. For further information: https://www15.i-grasp.com/fe/tpl_newcastle02.asp?s=-4A515F4E5A565B1A&jobid=57364,8654124823&key=-90786486&c=482587021387&pagestamp=-dblkliofuempkfyivh Best wishes, Kirsten

Dr Kirsten Wolff Reader in Evolutionary Genetics Newcastle University, School of Biology Devonshire Building 5th floor Newcastle NE1 7RU, UK Phone: 0191 2084852 (internally 84852) email: kirsten.wolff@ncl.ac.uk www.staff.ncl.ac.uk/kirsten.wolff/ http://-research.ncl.ac.uk/tiliageneticsresearch/ Kirsten Wolff <kirsten.wolff@newcastle.ac.uk>

Portugal FieldAssist MammalEvolution

Paid field research assistant position available in a project on ecology of freshwater semiaquatic mammals' (mostly Iberian desman and otter) in Northern Portugal.

Work will start very shortly (mid-end of May 2015), there will be a break during August, and will begin again in September and possibly October, with the possibility that it will continue for the next year/s.

Autonomy, fluent Portuguese speaking, car driving license (and possibly experience in 4x4 car driving), and adaptability to difficult field working conditions are required. Statistics and GIS knowledge (and possibly programming skills!) would be an advantage.

Salary (35 euro per day) and accommodation (and probably food) will be provided.

The candidate will mainly assist with data collection and compilation, and report writing, but opportunities to participate as co-author in scientific papers could arise.

Interested candidates: please send me a private email (lorenzo.quaglietta@gmail.com) with your CV, picture, short (no more than 300 words) motivation letter, 1-2 references.

Please note: ONLY selected candidates will be contacted and a Skype meeting will be scheduled for an interview.

Lorenzo

Lorenzo Quaglietta

Post-Doc at EDP Chair in Biodiversity http://maerua.iict.pt/applecol/ Applied Population and Community Ecology Research Group at CIBIO (Research Center in Biodiversity and Genetics Resources - Porto University)

Jardim Botânico Tropical - IICT (Tropical Scientific Research Institute) Tv. Conde da Ribeira, 9 - 1300-142 Lisboa, Portugal

Phone +351 213616340 ext. 307 Mobile+351964416826 Fax +351 213631460 Skype MartinLUTRAking

Lorenzo Quaglietta <lontrenzo@gmail.com>

SeniorEditor FuncEcology

The journal /Functional Ecology/ is seeking a Senior Editor to strengthen and complement the current editorial team and to continue raising the Journal's profile worldwide. The Journal's Senior Editors are supported by an international board of Associate Editors and dedicated editorial office personnel. The Senior Editors work together to determine Journal strategy and to increase the reputation and quality of the Journal, in addition to making decisions on submitted manuscripts. Further details about the Journal and its current editorial team can be found on the journal website www.functionalecology.org . Applications are welcome from leading scientists from any field who could contribute to the Journal's development in topical and developing areas, but we particularly seek applications from ecologists (including evolutionary ecologists) with expertise in the areas of animal physiology or plant-animal interactions and who are enthusiastic about increasing the journals online profile through the use of social media and/or multimedia (e.g. interviewing authors in podcasts, coordinating production of videos highlighting author contributions). Applications from those who could help increase the geographic or gender diversity of the board would be welcome.

Editors must be highly motivated, decisive, and be outstanding communicators that are expected to act with probity. They must have an excellent understanding of their own field of ecology, as well as the wider discipline; have experience of refereeing and the editing processes; a commitment to maintaining the high editorial standards of the journal; and an interest in ongoing developments within academic publishing. This post is a part-time three-year contract (current salary c. Â£5,900 per annum) located at the holder's host university or organisation. Some additional support is available to facilitate attendance at meetings with other BES journal editors and to act as ambassadors for the journal at relevant conferences.

Please see the *full job description* here: http://www.britishecologicalsociety.org/wp-content/uploads/Publ_FE_Advert-for-FE-editor_April-2015.pdf. The post can be discussed further with the Executive Editor, Professor Chuck Fox (cfox@uky.edu).

To apply, please send your CV and a letter stating what you have to offer to the Journal and how you would contribute to developing it over the next three years to Andrea Baier, Senior Managing Editor: andrea@britishecologicalsociety.org.

Interviews will take place on Wednesday 17th June 2015.

– Dr. Charles W. Fox Professor and Director of Graduate Studies Department of Entomology University of Kentucky Lexington, KY 40546-0091 phone: 859-257-7474 e-mail: cfox@uky.edu web: www.uky.edu/~cfox Charles Fox <cfox@uky.edu>

Singapore 4 ComputationalBiol

Research Fellow (Bioinformatics and Computational Biology)

Four talented and highly motivated postdoctoral fellows are wanted to join the Singapore Center on Environmental Life Sciences Engineering in the laboratory for Genomics and Meta'omics, headed by Prof. Stephan C. Schuster. The group operates a substantial DNA sequencing and computing facility that includes high-throughput and single molecule sequencing.

Contracts are initially awarded for 2 years, but can potentially be expanded to 5 years.

Our work focuses on analyzing information from large scale data sets (e.g., whole genome sequencing, RNA-seq, metagenomics, meta-transcritpomics etc.).

We aim to generate reference genomes for environmental and model systems, conduct cohort and population genetic studies, as well as characterize functional differences via transcriptome analysis.

We are particularly interested in candidates with research interests and experiences in:

* Genome assembly * Comparative Genomics * Population Genomics * Metagenomics * Transcriptomics

Educational Requirements

Doctoral degree in human genetics, quantitative genetics, bioinformatics, population genetics, microbiology, computational biology, or other fields with strong quantitative skills are required.

Required Experience

* PhD required in one of the following: bioinformatics, biostatistics, computer science (with some complementary background in molecular biology/genetics), statistics or genetics (with significant computational expertise) * Highly analytical, critical thinker and highly meticulous in work * Experience in working with next generation sequencing data and related analysis tools and workflows * Strong knowledge of Unix/Linux operating system * Considerable programming/scripting skills in R, Perl, Java, Python, C/C++ * Familiarity with parallel computing environments (Linux clusters, SunGridEngine, etc) * Experience in development of algorithms/machine learning/statistical models for bioinformatics * Excellent verbal and written communication skills in English

Desired experience and skills

* Demonstrated skills in effective data visualization * Familiarity with genome informatics concepts (e.g. software tools, file formats, and workflows involved in next-generation sequencing)

To apply:

Interested applicants should submit curriculum vitae, a detailed letter of interest, and the names of three potential referees too SCELSE-HR@ntu.edu.sg. Please indicate 'Research Fellow (Bioinformatics & Computational Biology)' in the subject line.

http://www.scelse.sg/careers/research.html Hie Lim Kim Ph.D. | Senior Research Fellow | SCELSE | Nanyang Technological University 60 Nanyang Drive, SBS-B3N-27, Singapore 637551 Tel: (65) 6908-3375 | Email: HLKIM@ntu.edu.sg

"Kim Hie Lim (Dr)" <HLKIM@ntu.edu.sg>

SouthAfrica StripedMouseProject manager

1 position as research manager

1 position as station manager

starting 1st July / August 2015 or 1st January 2016 at the striped mouse project in South Africa, for 1-3 years

We are looking for an extremely motivated and independent biology student with a master's degree to join the striped mouse project for a minimum of 1 and a maximum of 3 years as either a research or as a station manager. Somebody who would like to gain experience in field work and scientific management. We will appoint two people, one for July 2015 and one for January 2016. Managers get free accommodation at the station, and R4500/month to cover their daily costs. Travel costs can be refunded by up to an additional R 12 000 / year. Both managers will work closely together and share responsibilities. However, each will have specific main duties, but should also be able to deal with all other duties (for example when the other manager is on leave, or when a new manager has to be trained).

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

You must be hard-working, highly motivated, able to work independently, good in communicating with people, able to supervise others, and not afraid of snakes. You should love to live at a remote place in nature, without regular internet and cell-phone reception. Most importantly, you are fascinated by nature and science!

Shared duties

- Trapping
- Observing
- Radio-tracking, putting radio-collars on
- Blood sampling

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

Primary duties research manager / secondary duties station manager

Data:

- Weekly data entry
- Weekly data check
- Monthly data backup
- Monthly data report

Training and supervision of field assistants

Training of students and postdocs

Support for students and postdocs

Management of transmitters

Management of field and laboratory supplies

Primary duties station manager / secondary duties research manager

Technical support research station:

- Water system incl. sewage system
- Solar system
- Gas bottles replacement
- House and furniture

Running of the respirometry laboratory

Management of the captive colony

Management of the research station car

Management of bank account and cash box

Management of research station supplies

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

Compensation:

§Free accommodation.

* A monthly compensation of R 4 500, which is sufficient to pay all costs of living (approx. 3500/month). * For travel costs, R12 000 per year can be refunded, but proof (receipts) must be presented for this. This refund is only payable after 12, 18. 24 ..months and can be transferred to a bank account overseas (so you get it in Euro or USD). * You will become a honorary researcher at the University of the Witwatersrand in the group of Prof. N. Pillay. * Scientific co-authorship or even becoming a first author will be possible if the manager contributes to the success of projects by not only collecting data the majority of data, but also by data analysis and writing of the manuscript.

Responsibilities:

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

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

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

How to apply? Please send a CV, a letter of motivation and the names and contact information of at least two scientists available for reference. The letter of motivation should state for which of the two positions you apply for (or that you apply for any of the two), why you think you are the perfect candidate for this, and when you could start. Application deadline: There is no deadline, but applications will be reviewed until a suitable candidate is found.

— / —

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

---

TexasAMU LecturerCurator

Dear All,

The Department of Wildlife and Fisheries Sciences Department at Texas A&M University is seeking to fill a position for a lecturer/staff curator (aka, collections manager). The position is temporary one-year, with possibility of continuance. Teaching responsibilities are 45% (approximately 2 classes per semester) and curatorial responsibilities are 50%. Curatorial duties will primarily take place in the mammal collection. Minimum qualifications include a PhD, evidence of teaching, and at least 2 years of experience in specimen-based mammalogy.

Please see the announcement below for additional information. If you have any questions, please direct them to Jessica Light at jlight2@tamu.edu.

Many thanks, Jessica

Texas A&M University

Department of Wildlife and Fisheries Sciences

*Lecturer *

**

Job Announcement:

The Department of Wildlife and Fisheries Sciences, one of the largest in the nation, seeks to fill the following position: Lecturer (with Mammal curation responsibilities (Temporary, One-year appointment with possibility for continuance)).

Responsibilities:

/_Teaching_/__45%__

Teaching responsibilities include two undergraduate courses per semester. These courses include Animal Behavior (WFSC 422/632), Ecology and Society (WFSC 420/630), Wildlife and Fisheries Conservation (WFSC 304), and Urban Wildlife and Fisheries (WFSC 405).Other undergraduate courses as assigned.

/__/

/_Curatorial _/50%__

Primary responsibilities include daily management, development, and providing support and use of the Collection of Mammals and Genetic Resources in the Biodiversity Research and Teaching Collections (BRTC, formerly the TCWC; http://brtc.tamu.edu/). Responsibilities may also include minimal management of the Collection of Birds.The incumbent will participate in all aspects of collection management, including maintaining and organizing collections, specimen preparation, cataloguing, and maintaining and disseminating computerized specimen databases.Further duties include processing specimen loans, accommodating visiting scientists, and supervising student workers and volunteers.The incumbent will also take an active role in writing collections enhancement proposals and annual reports, and will be responsible for maintaining all permits relevant to the collections.

**

/_Other Duties as Assigned_/5%

**

Qualifications:

Minimum qualifications include a PhD in an appropriate biological science, evidence of teaching experience (at or above the level of graduate teaching assistant), and at least 2 years experience in specimen-based mammalogy with curatorial experience, specimen preparation (including skeletal and tissue preparations of museum study skins), and database management.

**

*About the Department: *As an administrative unit of the College of Agriculture and Life Sciences, Texas AgriLife Research, and Texas AgriLife Extension within The Texas A&M University System, the Department of Wildlife and Fisheries Sciences has a diverse and dynamic mission with over 35 faculty and staff members engaged in teaching, research, and extension at several locations throughout the state, nation, and world.

//

/Biodiversity Research and Teaching Collections /(BRTC)/./The collections within the BRTC serve as historical evidence of the distribution of wildlife in Texas, and provide valuable ecological and life history information for an array of vertebrate species. The collections serve as the repository for more than one million specimens with ancillary preparations, genetic samples, and associated data. Collections at BRTC are used in the research of Texas A&M faculty, graduate students, and scientists worldwide, as well as for extensive undergraduate teaching of natural history, conservation and wildlife management courses.

For more information about the Department of Wildlife and Fisheries Sciences at Texas A&M University, please visit http://wfsc.tamu.edu/ **

*Application Process: *

Submit electronically a single PDF file comprising a CV and contact information for three references to Dr. Gary Voelker, Search Committee Chair, Department of Wildlife and Fisheries Sciences, gvoelker@tamu.edu. Inquiries can be directed to Dr. Voelker or to Dr. Jessica Light, Assistant Professor and Curator of Mammals (jlight2@tamu.edu).Review of applications will begin on May 15, 2015. Applicants may address their ability to contribute to the universitys diversity plan(_http://diversity.tamu.edu/Documents/DiversityPlan.pdf_).

The Texas A&M University System is an Equal Opportunity Employercommitted to building a diverse faculty, staff, and student body reflecting the population and educational needs of Texas and the Nation.

Jessica E. Light

— / —

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

UGeorgia ResTech SexChromosomeEvol

The laboratory of Michael White in the Department of Genetics at the University of Georgia is seeking applicants for a research technician to help explore the mechanisms driving the evolution of sex chromosomes in the threespine stickleback fish. The successful candidate will have the opportunity to work on a number of exciting evolutionary genomics projects using a combination of molecular and bioinformatic techniques. This a great opportunity to help set up a new laboratory from the ground up and is ideal for recent biology graduates who are seeking additional research experience.

Duties and responsibilities: -Maintain a small fish facility. -Assist with lab research projects. -Purchase, inventory, and organize lab supplies. -Participate in lab meetings. -Help train new lab members.

Qualifications: -Bachelors degree in biology or a related field. -Experience with general molecular biology techniques. -Proficiency with computers and Microsoft Excel. -Highly organized and detail-oriented.

Preferred Qualifications: -Experience with bioinformatics.

Interested candidates should apply at https://www.ugajobsearch.com/applicants/jsp/shared/Welcome_css.jsp using the job posting number: 20150988.

Please include a cover letter explaining qualifications and interest in the position, a CV, and contact information for three references.

Any questions can be sent to: whitem@uga.edu.

Michael A. White Assistant Professor Department of Genetics University of Georgia Athens, GA

"whitem@uga.edu" <whitem@uga.edu>

UNewBrunswick StJohn EvolutionaryMarineBiol

Academic Employment Opportunity Department of Biology: Faculty of Science, Applied Science & Engineering UNB Saint John

Competition #: #15-05 Closing Date: Review of applications will begin on June 15, 2015 and continue until the position is filled.

Details The Department of Biology at the University of New Brunswick Saint John invites applications for a tenure-track appointment at the Assistant Professor level, beginning on either September 1, 2015 or January 1, 2016, depending on the availability of the candidate. The position is subject to final budgetary approval.

The successful candidate will be a Marine Biologist whose research interests complement the current strengths within the Department. The candidate will offer undergraduate courses in Marine Sciences, and teach in our Marine Semester at the Huntsman Marine Science Centre in St. Andrews, NB. UNB Saint John has a strong commitment to teaching and a demonstrated excellence in teaching will be an asset. Qualifications include a PhD degree and clear evidence of research ability as the successful candidate will be expected to establish an externally funded research program and be involved in the supervision of BSc (Honours) and graduate (MSc and PhD) students. The Department welcomes applications from Evolutionary Biologists that meet these qualifications. The Department of Biology offers 4-year BSc programs in Marine Biology, Biology, Environmental Biology, and Biology-Psychology. It has fifteen faculty members with research expertise in marine biology, ecology, evolution, physiology, aquaculture, environmental biology, ecotoxicology, botany, microbiology, natural products chemistry, geology, and biodiversity. For more information, visit the Departmental website: http://www.unb.ca/saintjohn/sase/dept/biology/index.html . Applicants are requested to submit electronically (preferably a single PDF) a current curriculum vitae, the names and addresses (including e-mail and telephone number) of three referees, a statement of teaching philosophy and research interests, and up to three reprints of recent publications to:

Dr. Remy Rochette, Chair of Biology Email: sjbiol@unb.ca

Review of applications will begin on June 15, 2015 and continue until the position is filled. All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. Applicants should indicate current citizenship status.

THE UNIVERSITY OF NEW BRUNSWICK IS COMMITTED TO THE PRINCIPLE OF EMPLOYMENT EQUITY

Remy

Remy Rochette <rochette@unb.ca>

UPorto 3yr Biodiversity

INVITED CHAIR IN BIODIVERSITY REN - BIODIVERSITY

Applications are open for an Invited Research Chair in Biodiversity to be hosted by CIBIO-InBIO (https://cibio.up.pt/) - Research Centre In Biodiversity and Genetic Resources-Research Network in Biodiversity and Evolutionary Biology, and by the University of Porto (http://sigarra.up.pt/up/en/WEB_PAGE.INICIAL), sponsored by REN (http://www.ren.pt/?culture=en-GB) - Redes Energéticas Nacionais and FCT (http://www.fct.pt/index.phtml.en) - Portuguese Foundation for Science and Technology.

CIBIO-InBIO is a young and highly dynamic research centre located near Porto, in Northern Portugal, which conducts world-class research in the fields of biodiversity and evolution. The Centre offers great opportunities for multidisciplinary research and hosts 18 research groups, which include over 160 PhD level researchers, and over 100 MSc and PhD students, from many different countries. The Centre has state of the art ecology and molecular laboratories and conducts research projects at a global scale. Besides CIBIO-InBIO, the University of Porto hosts several top-level research centres in the fields of environmental and life sciences, providing multiple opportunities for collaborative projects. CIBIO-InBIO offers a vibrant, multicultural and enthusiastic working atmosphere. In addition, the Northern region of Portugal provides rich cultural and outdoor activities and Porto is a world-heritage city and the capital of Port wine.

We seek a talented and outstanding scientist to conduct innovative research in the field of biodiversity, focusing particularly on the impact of the activities of REN. The successful candidate will have a background in biology and biodiversity, with at least five years of postdoctoral experience and a strong research record, including a significant list of relevant publications in peer reviewed journals, supervision of MSc and PhD students, and demonstrated ability to attract external research funding. S/he is expected to develop a top-level and independent research program, to establish solid collaborations, attract national and international funding, and contribute to graduate and undergraduate teaching.

The Invited Chair will be supported partly by REN and partly by FCT and will have an initial duration of three years. The contract is equivalent to the position of Full Professor/Coordinating Researcher (gross annual salary ca. euro 65.000) and will be complemented with research money to cover costs with personnel, equipment and fieldwork.

Applications for this position will include a detailed CV, a research statement and a motivation letter, as well as the email contact of three referees. Applications will be reviewed immediately and will be open until the position is filled. There is no obligation to hire any of the candidates.

Applications should be sent to diretor@cibio.up.pt. We aim to ensure that no applicant receives less favorable consideration on the grounds of gender, marital status, age, nationality, ethnic origin or religious belief.

Applications are open from the 21st of April to the 21st of May 2015.

The selected applicant is expected to start in June 1st, 2015.

Informal enquiries can be made to diretor@cibio.up.pt.

Click here (http://www.eracareers.pt/opportunities/index.aspx?task=global&jobId=59953) to see the advert in eracareers.

Maria JoÃ£o GuimarÃ£es Fonseca CIBIO - Centro de InvestigaçÃ£o em Biodiversidade e Recursos Genéticos/ InBIO Laboratório Associado, Universidade do Porto Campus Agrário de VairÃ£o Rua Padre Armando Quintas 4485-661 VairÃ£o Portugal

t: +351 252 660 411 Ext. 285 f: +351 252 661 780

e: divulgacao@cibio.up.pt w: http://cibio.up.pt f: https://www.facebook.com/cibio.inbio CIBIO DivulgaçÃ£o

Uppsala Sweden Bioinformatician BILS

BIOINFORMATICIAN WITH FOCUS ON GENOME ANNOTATION

Full time permanent position. The position is available as soon as possible. 6 months trial period.

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 makes Uppsala University one of Sweden's most exciting work places. Uppsala University has 45.000 students, 6,800 employees and a turnover of SEK 6,300 million.

Bioinformatics Infrastructure for Life Sciences (BILS; http://bils.se) is furthering life science research in Sweden by providing support in the field of bioinformatics. Over 45 experts are currently employed at multiple sites in Sweden, supporting projects in a wide array of areas such as genomics, transcriptomics, proteomics, metabolomics, statistics, and more. BILS is working closely together with SciLifeLab (http://www.scilifelab.se), a national resource that facilitates research in molecular biosciences by providing access to advanced technologies and technical know-how. Through recent acquisitions, SciLifeLab is now the third largest sequencing center in Europe. The large amount of resources available makes Sweden one of the best countries in the world to perform life science research, and together with talented Swedish researchers this has placed Sweden at the forefront of fields such as comparative genomics and genome evolution.

BILS is now looking for a new member to the genome assembly and annotation team to work with in particular annotation of eukaryote genomes. The team is placed at Uppsala University in the creative environment of the SciLifeLab Uppsala node "The Hub" where more than 20 bioinformaticians as well as core facilities and many different research groups are interacting. The team is working in close collaboration with Swedish research groups to supply genome assemblies and genome annotations of a high international standard.

Job description: We are looking for an expert with a strong background in NGS bioinformatics and an interest in genome annotation. The work will involve helping Swedish genome annotation projects with anything from providing guidance in the setup and running of annotation projects to completely running the whole annotation process for the customer. The projects will differ in complexity from quick-running jobs of a few days to longer projects of several months and can focus on any type of organism, but mostly eukaryotes. A familiarity with scripting and automation of procedures in a Linux environment is of importance, as the work also will involve the maintenance and improvement of existing pipelines and methods.

Qualifications: We seek a candidate with a PhD in bioinformatics, molecular biology, computer science or any related field with a strong competence in genome annotation or a related field such as transcriptomics. Experience from large eukaryote genome projects is valued highly. Proficiency in one or more scripting languages (e.g. Perl, Python, Ruby) is a necessity, with experience in Ensembl-API or Ensembl-Hive considered extra beneficial. The ability to drive projects and work in a collaborative, yet service-minded environment is a must. Excellent communication skills in both written and spoken English are required, since the candidate will collaborate with scientists of very different backgrounds. Emphasis will be placed on personal suitability for the position.

Information: For questions regarding BILS, please check out our website at http://www.bils.se or contact the director of BILS, Bengt Persson (bengt.persson@bils.se). For questions regarding the position, please send an E-mail to Henrik Lantz (henrik.lantz@imbim.uu.se).

You are welcome to submit your application no later than June 1, 2015, UFV-PA 2015/1037. Use the link below to access the application form.We decline offers of recruitment and advertising help. We only accept the application the way described in the advertisement.

http://www.uu.se/en/about-uu/join-us/details/?positionId=3D65233 henrik.lantz@imbim.uu.se

USouthampton EvolutionaryBiology

Dear Evoldir,

We are currently hiring a Lecturer or Associate Professor in Ecology/Evolutionary Biology at the University of Southampton. Please pass on the following to anyone who may be interested in applying. Best wishes, Mark

Lecturer or Associate Professor in Ecology/Evolutionary Biology (Ref:560215BJ) https://jobs.soton.ac.uk/-

Vacancy.aspx?ref=560215BJ Lecturer or Associate Professor in Ecology or Evolutionary Biology

We wish to appoint an outstanding academic, whose research fits within the broad theme of Ecology or Evolutionary Biology. An appointment would be preferred in behavioural ecology, conservation or evolutionary biology, but we welcome strong candidates from fields that would complement existing research strengths in spatial ecology, population genetics, biodiversity, ecosystem functioning and services, adaptations to environmental change.

For either level of appointment it is necessary that you have an established track record of research and are well positioned to attract RCUK, EU or charity funding. At Lecturer level, we expect the appointed person to obtain external grant income within 2 years. For appointment at Associate Professor level, we expect the appointed person to have experience of gaining external funding.

You will be expected to contribute fully to our Biology, Zoology, and Ecology undergraduate BSc and MSci programmes, as well as being able to teach on our postgraduate programmes in Biology, and Wildlife Conservation. We would also encourage applicants who are able to develop and teach field courses. It is especially important that you show enthusiasm and potential to teach innovatively across a wide range of disciplines.

You will join the Centre for Biological Sciences, which is at the hub of interdisciplinary initiatives through its engagement with the Institute for Life Sciences (IfLS, http://www.southampton.ac.uk/ifls). You will be encouraged to pursue collaborative multidisciplinary research with other groups across the university, especially within the Faculty of Natural and Environmental Sciences (Ocean & Earth Science, Chemistry).

You should demonstrate:

evidence of distinction in research through high-quality publications;

ability or potential to obtain peer-reviewed funding in your research area;

ability or potential for undergraduate and postgraduate teaching, thereby contributing to the programmes run by Biological Sciences;

Potential applicants who wish to discuss this post are welcome to contact Professor Keith Jones (Head of Biological Sciences, K.T.Jones@soton.ac.uk).

Interviews are likely to take place in June or July 2015.

Dr. Mark A. Chapman M.Chapman@soton.ac.uk +44 (0)2380 594396

Co-ordinator - Centre for Underutilised Crops http://www.southampton.ac.uk/cuc/ [twitter2]@CUCsoton

Centre for Biological Sciences University of Southampton Life Sciences Building 85 Highfield Campus Southampton SO17 1BJ

"Chapman M." <M.Chapman@soton.ac.uk>

WesternAustralia Fieldassist FairyWrens

WesternAustralia.Fieldassist.FairyWrens

I am looking for a field assistant to help monitor a population of red-winged fairy-wrens in south-west Australia from 1 October 2015 to ~21 January 2016 as part of an on-going study on cooperation and competition. The study is based at Smithbrook Nature Reserve in one of the 35 biodiversity hotspots of the world!

Duties include searching for nests, monitoring colour-ringed birds, behavioural observations, mist netting and data entry. Working days are long, start early and consist of lots of hiking through dense forest with occasional encounters with venomous snakes. Applicants must be physically fit and have outstanding hearing and vision, be able to work independently, get along well with others in remote field setting and tolerate hot weather conditions. Enthusiasm, self-motivation, and a strong work ethic are a must.

Required qualifications: experience in monitoring colour-ringed birds, nest-searching, mist netting and current drivers licence. Field assistant will get an allowance of AU$7000 for total period. Onsite accommodation is provided, but candidate must pay their own flight to Perth, Australia. Candidate must be Australian citizen or eligible for appropriate visa e.g. subclass 417, 600 or 601.

To apply, please email a letter outlining previous relevant field research experience, and a resume including names and contact information for 3 referees to Lyanne Brouwer (lyanne.brouwer at anu.edu.au). Applicants will be considered as they apply until the position is filled.

Lyanne Brouwer <Lyanne.Brouwer@anu.edu.au>

WheatonCollege TemporaryPartTime TeachingEvolution

Job Notice

VISITING ASSISTANT PROFESSOR/INSTRUCTOR (Academic Year 2016) - The Biology Department at Wheaton College is seeking applicants for a temporary part time Visiting Assistant Professor to teach a 200 level genetics course with a laboratory (3 hrs lecture and 3 hrs lab/wk, roughly 24 undergraduates) for the Fall 2015 and Spring 2016 academic semesters, as well as a 300 level course without a lab in an area of expertise in either semester. There is the possibility of extending this position to a second year pending approval of funds. Completion or near completion of Ph.D. required. To apply, please go to https://jobs.wheatoncollege.edu, or send your CV, cover letter detailing teaching experience, and two letters of recommendation to Dr. S. Shawn McCafferty, Chair, Biology Department, Wheaton College, Norton, MA 02766 or smccaffe@wheatonma.edu. Additional information about the course, dates, and times are available upon request. The deadline for application is 01 July 2015 or until position is filled.

Wheaton College is an independent selective liberal arts college with ca. 1,600 undergraduates. Wheaton College seeks educational excellence through diversity and strongly encourages applications from women and men from minority groups. Wheaton College is an affirmative action / equal opportunity employer.

Information about the Biology Department may be found at http:// wheatoncollege.edu/biology/.

S. Shawn McCafferty Associate Professor Chair - Biology Department Coordinator Bioinformatics Major

Rm 2133, Mars Center for Science and Technology Wheaton College Norton, MA 02766-2322

Email: smccaffe@wheatonma.edu Phone: 508-286-5642 FAX: 508-286-8278

“S. Shawn McCafferty” <smccaffe@wheatonma.edu>

Other

AnimalExpt Petition

Dear EvolDir community,

We all do science and we know that our work is important for finding out new things that continosly change and shape human society. More discoveries lead to more insight. Animal experimentation has undoubtedly become a heavily critisised discipline but also here a lot of progress has been made. Both in the results emerging from the research, but also in avoiding animal experiments. However, there are experiments that cannot be avoided, and these have high priority in some research lines. It is good to lead a lively discussion about the need about each animal experiment, but somtimes these discussions go too far. In short, we have seen a case of an esteemed neuroscience researcher (Nikos Logothetis) with a research agenda on non-human primate brains has been thretened to such an extent as to annouce to drop his research altogether. If you like, please read a longer version here: http://www.cin.uni-tuebingen.de/-sign-open-letter.php . It is an open letter in support of this type of research, which you can sign if you like.

Thanks for your consideration.

Robert

ASN Awards RegionalMeetings

Deadline Reminder - May 10th

ASN Awards for Support of Regional Meetings in Ecology, Evolution and Behavior

The American Society of Naturalists solicits proposals from organizers of regional meetings in the fields of ecology, evolution and behavior. The purpose of these small awards is to promote increased participation in regional meetings that fall along the research interests supported by the ASN and to use this support as a way of recruiting new membership to ASN. The awards typically provide subsidized registration for ASN members at these regional meetings. Organizers of regional meetings should submit a one-page proposal describing the research focus of the meeting for which funds are requested as well as details of the meeting such as anticipated number of participants, meeting venue and dates. Please also include a brief budget justifying the amount requested. We anticipate funding 3-5 awards and award amounts are usually between $1000-$1500.

Please send proposals to the ASN Regional Society Liaison Committee Chair Renee Duckworth at rad3@email.arizona.edu by May 10th.

rad3@email.arizona.edu

Brazil Visa

Hey U.S. people going to Brazil for Evolution 2015: DO YOUR VISA NOW. IT'S A HUGE PAIN, at least for those of us that haven't been to Brazil before. And it will take POSSIBLY 15 BUSINESS DAYS PLUS MAILING TIME ETC.

Before too much griping, note that the aforementioned pain exists only because the U.S. does the same thing to Brazilians. So it won't be easier until there is some mutual agreement reached between the governments.

Since I blew half the day figuring it out, I will post the list of documents and basic procedure below. Of course you are responsible for your own decisions and I might have something wrong, I am not a lawyer, yadda yadda.

GOAL: US citizens need a tourist visa for Brazil. They need approval stamped ON THEIR PASSPORT before they leave the U.S.

TIME: The Atlanta Consulate says processing time is 15 business days (!). In other words, DO IT NOW.

REQUIRED DOCUMENTS, which you will mail to the closest Brazilian consulate in the U.S. (unless you make an appointment at a consulate in person)

===1. U.S. passport. Yes, you will MAIL your precious passport to the consulate, they will stamp it and mail it back. No, this isn't tremendously clear in the instructions. The passport must:

1a. be signed (make sure you sign it) 1b. have at least 6 months left on it from the time you enter Brazil 1c. have at least 2 blank pages 1d. You should scan / copy / iPhone photo your passport for backup before you mail it off

2. Plane tickets with ticket numbers for entry and exiting Brazil.

3. The invitation letter from the Evolution 2015 meeting, which you can get as a PDF after you register, by logging into http://evolution2015.org/ 4. A recent

passport-type photo with a neutral expression. No glare, so take your glasses off. I got two at Walgreens for $12.

5. Fill out the online visa application, then print it out, then (a) glue on the passport photo, (b) sign it, and (c) also hand-write Contact Person and their phone number handwritten.

The online application asks for a bunch of information including:

- passport number etc. - hotel. The conference hotel is:

Casa Grande Hotel Resort & Spa Telefone (Phone #): 55 13 3389-4000 Av Miguel Stéfano, 1001 - CEP: 11440-530. Enseada Guarujá/SP - Brasil Tel.: (55 13) 3389.4000. Fax.: (55 13) 3389.4023 www.casagrandehotel.com.br/en/ hotel@casagrandehotel.com.br

(notes: SP = the state of SÃ£o Paulo; CEP is I think the equivalent of zip code)

6. Recent bank statement showing "sufficient funds" to be a tourist. Your guess is as good as mine what that means, I am just printing out my checking account statement showing I have slightly more than $0.

7. You have to pay US$160.00, *not* with a check, but *only* with a U.S. Postal Service Money Order made out to "Consulate of Brasil". Make sure to write your name on the money order. http://atlanta.itamaraty.gov.br/en-us/payment_options.xml Note: The U.S. Post Office ONLY takes ATM/Debit, or cash, for Money Orders. No credit cards, no checks.

8. I am throwing in my hotel reservation and the extra passport photo because, why the heck not.

9. Pre-stamped, pre-addressed return envelope, with USPS tracking number. At the Post Office I got USPS Priority Mail each way, this comes with tracking numbers and $50 insurance., about $7 each way.

Take the above stack of documents to the Post Office, and mail them to the local consulate with a USPS tracking number.

=== INSTRUCTIONS PAGES – the relevant info is spread over many pages. The best pages seem to be those *for the specific consulate that serves your region*, since there are differences between consulates.

I recommend printing out all of these pages, reading them, and taking them to the Post Office in case questions come up. The most important thing is the address of the consulate. These were for the Atlanta, GA consulate, yours might be different and might have different instructions:

===http://atlanta.itamaraty.gov.br/en-us/visas.xml http://atlanta.itamaraty.gov.br/en-us/how_to_apply_%28in_person,_by_mail,_by_third_party%29.xml http://atlanta.itamaraty.gov.br/en-us/frequently_asked_questions.xml http://atlanta.itamaraty.gov.br/en-us/basic_information_for_all_types_of_visa.xml http://atlanta.itamaraty.gov.br/en-us/tourist_visa.xml

— / —

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

---

ESEB equal opportunities committee

Â We are seeking Evolutionary Biologists for the newly founded equal opportunities committee of the ESEB.

Why an equal opportunities committee? The representation of women in academia remains low in most fields in science and engineering, despite near equal gender ratios at graduation. The problem is often phrased as the "Leaky Pipeline" problem, which describes the attrition of women from science at various stages along the academic career trajectory. Among the many contributing factors are unconscious biases that we have about the ability of men and women to perform a given scientific task.

For example, a recent study found that fewer women give invited talks at the ESEB congress than might be expected. As a consequence, ESEB audiences are exposed to fewer top quality female speakers than are available, which reinforces gender stereotypes. Furthermore, ESEB student members experience fewer female role models than they could; this may demotivate young women to pursue an academic career in our field. Similar problems exist for other underrepresented groups (for example, ethnicities).

The ESEB Equal Opportunities committee will target these and similar problems.

Our aims are to: 1) to ensure equal opportunities in all activities and facets of ESEB 2) to increase awareness of the problem of underrepresented groups 3) to produce "best practice guidelines" for both ESEB as a society, the congress, and the journal 4) to monitor status and progress of underrepresented groups in our society and field

The committee has a budget and an important task of committee members is to review applications and decide how to best spend our budget. The committee members will also work on guidelines and on monitoring.

We are hoping to create a diverse committee with people who can bring diverse points of view and experience. If you have experience with improving participation of underrepresented groups, you are especially welcome to apply.

If you are interested to bring yourself in and work forward to these goals as a committee member, please send an email with a very brief description of how you would like to help to

julia.schroeder@gmail.com and pspennings@gmail.com

Deadline is 20.05.2015

If you are interested to apply for money to improve participation of underrepresented groups, we'd be interested to hear from you too, although we need to form a committee before we post a formal call for proposals.

Best wishes, Julia Schroeder and Pleuni Pennings

Julia Schroeder

Group Leader Evolutionary Biology Max Planck Institute for Ornithology Seewiesen, Germany +49 1721838836

Julia Schroeder <julia.schroeder@gmail.com>

Evol Biol series topics

Now in its eight year, *The Year in Evolutionary Biology* reviews series (2014 < http://onlinelibrary.wiley.com/doi/10.1111/nyas.2014.1320.issue-1/issuetoc >, 2013 < http://onlinelibrary.wiley.com/doi/10.1111/nyas.2013.1289.issue-1/issuetoc >, 2012 < http://onlinelibrary.wiley.com/doi/10.1111/nyas.2012.1256.issue-1/issuetoc >, 2010, < http://onlinelibrary.wiley.com/doi/10.1111/nyas.2010.1206.issue-1/issuetoc > 2009 < http://onlinelibrary.wiley.com/doi/10.1111/nyas.2009.1168.issue-1/issuetoc >, 2008 < http://onlinelibrary.wiley.com/doi/10.1196/nyas.2008.1133.issue-1/issuetoc >) is open for presubmission inquiries for scholarly reviews in all areas of evolutionary biology.Published in /Annals of the New York Academy of Sciences/, *The Year in Evolutionary Biology* series is edited by Charles Fox and Timothy Mousseau, with input from an international Editorial Board < http://onlinelibrary.wiley.com/doi/10.1111/nyas.12505/pdf >.

Previously published reviews have included Hidden Reaction Norms, Cryptic Genetic Variation, and Evolvability < http://onlinelibrary.wiley.com/doi/10.1196/annals.1438.010/abstract > (2008, with 98 citations); The Covariance between Genetic and Environmental Influences across Ecological Gradients < http://onlinelibrary.wiley.com/doi/10.1111/j.1749-6632.2009.04575.x/abstract >(2009, with 121 citations); Global change and the evolution of phenotypic plasticity in plants < http://onlinelibrary.wiley.com/doi/10.1111/j.1749-6632.2010.05704.x/abstract >(2010, with 99 citations); Genome and gene duplications and gene expression divergence: a view from plants < http://onlinelibrary.wiley.com/doi/10.1111/j.1749-6632.2011.06384.x/abstract >(2012, with 44 citations); An integrative view of phylogenetic comparative methods: connections to population genetics, community ecology, and paleobiology < http://onlinelibrary.wiley.com/doi/10.1111/nyas.12157/abstract > (2013, with 31 citations)

If you would like to contribute to an upcoming volume, please submit a cover letter (maximum 1000 words) summarizing the topic, goals, and theme of a proposed review. Please also include a list of 10-15 primary research articles published in the past 5 years that highlight the timeliness and empirical foundation of the proposed article.Proposals should be *submitted by May 30, 2015 for consideration for inclusion in the 2016 volume*.

Submission should be made to Douglas Braaten dbraaten@nyas.org

Dr. Charles W. Fox Professor and Director of Graduate Studies Department of Entomology University of Kentucky Lexington, KY 40546-0091 phone: 859-257-7474 e-mail: cfox@uky.edu web: www.uky.edu/~cfox

Evolution print copies

Free to New Owner: Back-run of print journal - EVOLUTION

I have a nearly complete run of print issues of the journal EVOLUTION. This starts with Volume 1 and continues through Vol. 69, #2, Feb. 2015. Volumes 1 - 27 are bound. There may be a few gaps of individual issues. Mostly in excellent condition. These are free to whomever is interested and willing to pay the costs of boxing and shipping these. Thank you for your interest.

Donald M. Waller dmwaller@wisc.edu

Dept. of Botany (608) 263-2042 232 Birge Hall FAX: 608-262-7509 430 Lincoln Drive University of Wisconsin Madison, WI 53706 USA

Don Waller <dmwaller@wisc.edu>

FuturePhy Phylogenetics Conferences Workshops

Announcement: FuturePhy Conferences and Workshops on Phylogenetics

FuturePhy is an NSF-sponsored, three-year program of conferences, workshops and hackathons on the Tree of Life. The project aims to promote novel, integrative data analyses and visualization, interdisciplinary syntheses of phylogenetic sciences, and cross-cutting uses of phylogenetics to develop and address new research questions and applications.

The first phase of this mission is critical: to bring together a broad community of people from diverse backgrounds who are active in phylogenetics research, who use the tree of life in research or education, who will benefit in applied or practical ways from a comprehensive tree of life, or who come from a background that offers new perspectives on defining, addressing or transcending key challenges in phylogenetics.

Help accelerate progress in all aspects of phylogenetics research by joining FuturePhy today. Diverse opportunities will be available to attend FuturePhy sessions in person or virtually, and to link FuturePhy to existing projects and initiatives.

We invite you to participate in the project in several ways:

1. Register on http://futurephy.org < http://l.facebook.com/l.php?u=-http%3A%2F%2Ffuturephy.org%2F&h=-WAQEDO1IB&enc=AZMRzVR3o0P0GMrpWbi6cTCpga0PvTciH_KfD00wsQQbVspl7NgXCtjBErtKuHoCvmHyRIKfw0-p_d96GApQxYW3PXyxSInDIp6hOQYIgz5iURRFDlXsQG84wD-Xmf6TnTpg4TIgraYTL5oBYyy5QdHPvmv9v_KhDj_l4sEdP3bbmg&s=1 > Scientists from all aspects of the phylogenetic sciences, educators, members of the tree-using community, and others interested in phylogenetics are welcome.

2. Contribute to the discussion forum on http://futurephy.org < http://l.facebook.com/-l.php?u=http%3A%2F%2Ffuturephy.org%2F&h=-yAQH7gdp8&enc=AZOsa6W8Xb77W6pAQH8vGI2OmifA51b2vNLHw
2Vw6n4BIfKI0ORxSpJvM5oHo9UWsCqR5ZwHctcCDLZexf2RkOx1Y-
VrAIjGxYwwSoc9mRNbu5mdulweJ_RHCqJjxc61GG539F_u2aX_awvR
1 > This is the best way to log your interest and contribute ideas.

3. See our main themes, comment on them and take the survey to rank them: https://www.surveymonkey.com/-s/8CWXMRF < https://www.facebook.com/l.php?u=-https%3A%2F%2Fwww.surveymonkey.com%2Fs%2F8CWXMRF&h=
pAQFb_xuq&enc=AZNbsPCzgTRHKJuhIpztQktXAzXIcZJ8Lt2jjemN
UfgONaGlbCdADEkMmcXcO0fRMF1m050l8CP-ZCvnLr9DAsW4lM3NQ-BKhAv5lJY0ppri204pCA6PGo3XqakNtOqcV8gN7405PNd7vA&s=1 >

4. Email contact@futurephy.org with ideas or comments

5. Tweet to the FuturePhy community: @FuturePhy

6. Comment in the FuturePhy thread on http://phylobabble.org < http://l.facebook.com/-l.php?u=http%3A%2F%2Fphylobabble.org%2F&h=-xAQEyYPJ6&enc=AZOGdov1wg_Y8pQTO8OEnQHrAK7-Y5AwtHVNl17V6xxYPMkgaUcS-_jihfpr_xJP4rYXi22UljASHytBUTQlk2dOfu1ORznXY6PIUH4400VV-DsGnqU8HoYPG5u5HWW6nWeIs-2CbF6cZxYThOF82OQ1IFkc2UEzgG71IptVfooamQ&s=1 >

– Mark W. Westneat Professor, Department of Organismal Biology and Anatomy University of Chicago 1027 E. 57th Street, Chicago IL 60637 (773) 702-2412 Lab Web site: http://westneatlab.uchicago.edu email: mwestneat@uchicago.edu

Research Associate, Field Museum of Natural History mwestneat@fieldmuseum.org <mwestneat@uchicago.edu>

Mark Westneat <mwestneat@uchicago.edu>

Math in Biology

Dear EvolDir users:

I'm a doctoral candidate in Mathematics Education at the University of Texas, Austin, conducting a study on biologists use of math to identify the main mathematical and statistical tools currently used in the field. The results of the study would help to inform the graduate and undergraduate curriculum in Biology and MathematicsXas well as the curriculum of related training programs outside of academiaXso that they would better align to student needs at their future workplace.

The first part of the study consists of an online survey designed for biologists (from the areas of ecology, evolution, and behavior and developmental biology) that was piloted by faculty members and students at UT Austin, and has an average completion time of 9 minutes. I am emailing to ask for your participation in the survey.

I can offer no compensation but I would be happy to share the results of the study, and make you eligible to win one of four $25 Amazon gift cardsXI know is not really not much, I am limited to a very small budget. The online survey is completely anonymous; you will just need to click on the link below to take it.

https://utexas.qualtrics.com/SE/?SID=SV_3sAsOBtAhu4R8BD Thank you so much for taking the time to consider my request, and please let me know if you have any further questions.

Pablo Duran Doctoral candidate in Mathematics Education The University of Texas at Austin

Pablo Duran <pduran@utexas.edu>

Microsatellite DataSets

Hi everyone,

For a meta-analysis, we are looking for microsatellite (SSR) datasets from plants sampled in North-America. If you have such data available -either published or unpublished- are you willing to share it with us?

Many thanks in advance,

Patrick Meirmans

Patrick Meirmans Institute for Biodiversity and Ecosystem Dynamics (IBED) University of Amsterdam Postal address: P.O. Box 94248, 1090GE Amsterdam Visiting address: Science Park 904, room C4.165, 1098XH Amsterdam Tel: +31 20 5258424

p.g.meirmans@uva.nl http://www.patrickmeirmans.com/software Patrick Meirmans <p.g.meirmans@uva.nl>

MiSeqDatasets desired

Looking for multiplexed MiSeq datasets in diploid plants for bioinformatics pipeline testing

We are looking for multiplexed MiSeq datasets in population samples of diploid plants, particularly for those landscape genetics studies, to test our bioinformatics pipeline for SNP discovery and sample genotyping in natural populations, and wondering if someone has published such datasets or is willing to share with us such dataset for pipeline testing. So far we are unable to find such datasets by searching with google.

If you do, please help us by contacting Dr. Yong-Bi Fu (yong-bi.fu@agr.gc.ca). Thank you for your attention.

Yong-Bi Fu, Ph.D., Research Scientist Plant Gene Resources of Canada Agriculture and Agri-Food Canada / Government of Canada 107 Science Place, Saskatoon, SK S7N 0X2 Canada E-mail Address: yong-bi.fu@agr.gc.ca / Tel: 306-385-9298 / Fax: 306-385-9489 http://pgrc3.agr.ca/staff/fu_e.html Les Ressources Phytogenetiques du Canada Agriculture et Agroalimentaire Canada / Gouvernement du Canada 107 Science Place, Saskatoon, SK S7N 0X2 Canada E-mail Address: yong-bi.fu@agr.gc.ca / Tel: 306-385-9298 / Fax: 306-385-9489 http://pgrc3.agr.ca/staff/fu_e.html "Fu, Yong-Bi" <Yong-Bi.Fu@AGR.GC.CA>

NESCent 2015 VideoContest Deadline

DEADLINE APPROACHING! NESCent/HHMI/SSE 2015 Evolution Film Festival/Video Contest

Scientists and science educators of all stripes - students, postdocs, faculty, and full- or part-time science communicators - are invited to enter the Fifth Annual Evolution Video Competition, sponsored by the National Evolutionary Synthesis Center (NESCent), the Howard Hughes Medical Institute (HHMI), and the Society for the Study of Evolution (SSE). To enter, please submit a video that explains a fun fact, key concept, compelling question, or exciting area of evolution research in THREE MINUTES OR LESS.

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

The finalists will be screened at the 2015 Evolution meeting in Guarujá, Brazil. (You do not need to attend the conference in order to enter a video.)

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

The deadline to submit your video(s) is SUNDAY, MAY 31st, 2015 (11:00 PM, EST).

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

Jory P. Weintraub, PhD Assistant Director, Education & Outreach National Evolutionary Synthesis Center (NESCent) 2024 West Main St., Suite A200, Durham, NC 27705 Phone: 919.668.4578 Fax: 919.668.9198 Email: jory@nescent.org Skype: jory.weintraub

"Weintraub, Jory P" <lviscrst@live.unc.edu>

Phylobabble org Website

The phylobabble.org web site is a discussion forum for phylogenetic theory and applications. The primary goal of this forum is to discuss best practice and new developments in phylogenetics. Although we do have a Troubleshooting4 < http://phylobabble.org/category/-troubleshooting > category for getting feedback on analyses, this is not a help site for running phylogenetics programs.

We are just getting started, and we hope to become a great place to chat about phylogenetics for researchers and the broader community of students and science-interested citizens. Thank you and don't hesitate to ping Erick < http://matsen.fhcrc.org/members.html > or tweet to us < https://twitter.com/phylobabble > if you have any questions or comments.

"Foley, Brian Thomas" <btf@lanl.gov>

Seewiesen Germany VolLabAssistant AvianSenescence

Volunteer laboratory assistant position

The Evolutionary Biology Group at the Max Planck Institute for Ornithology in Seewiesen, Germany is offering one laboratory assistant position to prepare and analysis samples for the study of reproductive senescence in house sparrows. Desired period: July - October 2015. You will learn or improve your skills in: microscopy, cell analysis, and data management. Candidates should enjoy independent laboratory work, and have a strong work ethic. Experience in cell biology and basic microscopy is desired. The working language at the Institute is English, so good English is a must. A small grant will be offered to high quality applicants, and application is competitive. The Max Planck Institute for Ornithology employs a dedicated and international group of researchers who are focused on exploring the fields of evolution, ecology, genetics, and neurobiology. Review of applications will start immediately until the position is filled. To apply, please email your CV and name and addresses of at least one person who could give you a reference to agirndt@orn.mpg.de

Antje Girndt, PhD Student https://www.orn.mpg.de/-218867/Research-Group-Schroeder Eberhard-Gwinner Str. 11 Max Planck Institute for Ornithology 82319 Seewiesen, Germany desk +49(0)8157 932370 fax +49(0)8157 932344

Antje Girndt <agirndt@orn.mpg.de>

Software DAMBE update

Dear All,

I have just uploaded a new version of DAMBE. The main news is that (distance-based method + pairwise alignment) performs much better than (maximum likelihood method + multiple alignment) based on extensive sequence simulations of amino acid, codon and nucleotide sequences of increasing sequence divergence. The difference in performance disappears only when sequences are easily aligned or when sequences experienced full substitution saturation (when no method can recover any true tree or subtrees). The function for (distance-based method + pairwise alignment) can be accessed by clicking 'Phylogenetics|Distance-based methods|Phylogenetics with pairwise alignment'.

If you wish to compare the performance by doing simulation yourself, here are the associated functions:

1. Do sequence simulation with indels, and save the resulting unaligned sequences into a FASTA file (The indels introduced in simulation leads to different sequence lengths. Make sure that some sequences will not accumulate so many deletions that only a few AA, codon or nucleotides are left). If you take a tree with 24 OTUs and simulate 100 sets, then the FASTA file will be

>S1 Sequence... >S2 Sequence... ... S20 Sequence... >S1 Sequence... >S2 Sequence... ... S20 Sequence... ...

2. To use DAMBE to reconstruct 100 trees from these 100 sets of sequences, start DAMBE and click 'File|Open file with multiple datasets' to read in the file (You will be asked to enter "Number of sequences per set" and you should enter 24 if there are 24 OTUs per set of data. This is needed because FASTA files have no internal structure to indicate the beginning and ending of each set of sequences). In the dialogbox on what job to perform, click 'Distance-based phylogenetics' and click 'Run'. In the following dialog boxes, just keep default values.

3. To analyze the sequences by ML method, e.g., (PROML and DNAML in PHYLIP), you can use DAMBE to do batch alignment and then save to PHYLIP format. That is, you click 'File|Open file with multiple datasets' to read in the file and enter the number OTUs (e.g., 24). In the dialog box on what job to perform, click 'Align multiple sets of sequences'. You may use either the built-in alignment tool (ClustalW) or use external alignment programs (I often use mafft.bat). Once the sequences are aligned, you may save them to PHYLIP format. If you have simulated 100 sets of AA sequences, then it is better to save the 100 sets of sequences into multiple files and run PROML in a parallel fashion (otherwise it may take months). In DAMBE, once the alignment is done, you will be presented with the option of saving the multiple sets to one file or to multiple files.

4. If, in your simulation of 100 sets of sequences, the simulation program produce 100 separate files, each with 24 sequences, then you click 'File|Read multiple files for batch processing'. The rest is the same.

5. Once you have produced the trees in a file, e.g., outtree from PHYLIP, paste the "true tree" (the tree used in simulation) into the file as the first tree. You need to know which methods recover more true trees/subtrees. Click 'Phylogenetics|Robinson- Foulds analysis on trees'. This will compare the 100 reconstructed tree against the first tree (the true tree).

By the way, DAMBE has a good codon alignment function that align codon sequences with a 64-by-64 score matrix. It is quite good. If you simulate codon sequences, then you should align them by codon instead of by nucleotide because aligning by codon is not only faster (the sequences are three times shorter), but also more accurate.

There are also a number of minor bug fixes in this release.

For those who do not know what DAMBE is: it is a comprehensive software package for data analysis in molecular biology and evolution, freely available at: http://dambe.bio.uottawa.ca/dambe.asp Best Xuhua http://dambe.bio.uottawa.ca http://www.biology.uottawa.ca/bio/professor_details.html?en/31 Xuhua Xia Professor Biology Department University of Ottawa Rm 278 Gendron 30 Marie Curie, Ottawa, Ontario Canada K1N 6N5 Tel: (613) 562-5800 ext 6886

Xuhua Xia <Xuhua.Xia@uottawa.ca>

SSBSymposia for Evolution2016

Call for 2016 SSB Symposia

The Society for Systematic Biologists invites proposals for symposia to be held at the 2016 SSB meeting in Austin, Texas from June 17-21st. The meeting will be held jointly with the American Society of Naturalists (ASN) and the Society for the Study of Evolution (SSE).

Proposals should include (1) a descriptive title, (2) one or two paragraphs explaining the purpose of the symposium and its relevance to systematics, (3) a list of presentations including proposed speakers, their institutions or affiliations, and their presentation titles, and (4) an indication of whether the speakers have been invited and whether they have agreed to participate.

Symposia are restricted to half-day sessions (typically 6 half hour talks). The society is particularly interested in symposia whose topics do not overlap with those from previous meetings, that introduce new ideas or synthesize important concepts, or those that are particularly good examples of the analysis of empirical data. Proposals that unite systematics with other fields are also desirable. We encourage participation from young investigators and others typically under-represented in symposia. Limited funding is available.

The deadline for full consideration is June 23, 2015. Proposals should be emailed (Word or PDF format) to the Program Chairperson, Stacey D. Smith, Stacey.D.Smith@Colorado.edu (Department of Ecology and Evolutionary Biology, University of Colorado, Boulder, CO, 80309-0334). Please use the subject heading: SSB Symposium Proposal.

The program chair will confirm receipt of submitted proposals; please inquire if you do not receive email confirmation. The proposals will be considered by the SSB Council, and the two selected symposia will receive funds to partially defer participant costs.

dewitt832@gmail.com

SymposiumProposals EvolutionMeeting Austin2016

The 2016 annual meeting of the Society for the Study of Evolution is planned for June 17-21, 2016 at the Austin Convention Center in Austin, TX. The SSE Council invites proposals for the two Society-sponsored symposia to be held in conjunction with the meeting. Symposium proposals should include: (1) a synopsis of the symposium theme (about one page); (2) a tentative list of speakers, including institutional affiliations, and topics; (3) a rationale for the symposium explaining why this topic and this group of speakers are particularly appropriate for a Society- sponsored symposium; and (4) a statement that all potential speakers have been contacted and agree to participate in the symposium.

In evaluating proposals, SSE Council seriously considers the diversity of participants as a major qualification. Symposium organizers are expected to take into account gender, seniority, nationality, and other aspects traditionally underrepresented in Society symposia when preparing proposals. In addition, Council will favor those proposals whose topics concern newly emerging fields, fields ripe for syntheses, and fields different from those that have been included in recent Society symposia.

The Council will select two proposals for half-day symposia at the annual meeting in June 2015. All applicants will be notified of the Council's decision in August. The Society provides travel support for organizers and participants in sponsored symposia. Details are available on request. To be assured of full consideration, proposals must be received by midnight Eastern Standard Time on June 16, 2015.

Proposals should be sent by email (bbrodie@virginia.edu) as a single attachment in PDF format (under subject heading: SSE Symposia Proposal). Please expect and request confirmation of receipt of the proposal.

Butch Brodie <bbrodie@virginia.edu>

Teaching Evolution using games

Dear friends,

I am teaching evolutionary biology and I would like to receive suggestions about games to teach evolution.

Maybe there are something envolving variation simulation and selection measurements!

Thanks for any help!

Prof. Dr. J. C. VOLTOLINI Grupo de Pesquisa e Ensino em Biologia da Conservação - ECOTROP Universidade de Taubaté, Departamento de Biologia Taubaté, SP. 12030-010. E-Mail: jcvoltol@uol.com.br * Grupo de pesquisa ECOTROP CNPq: http://dgp.cnpq.br/buscaoperacional/detalhepesq.jsp?pesq=8137155809735635 * Currículo Lattes: http://lattes.cnpq.br/8137155809735635 * Assessoria Estatística: http://assessoria-estatistica.blogspot.com.br/ * Fotos de Cursos e Projetos: http://www.facebook.com/ecotrop VOLTOLINI <jcvoltol@uol.com.br>

Trinidad Interns GuppyEvolution

Research Internships Evolutionary Biology

Research interns are needed to assist in a multidisciplinary, multi-investigator, experimental study of the interactions between ecology and evolution in Trinidad. The research is led by Professor David Reznick at the University of California, Riverside.We seek to integrate multiple biological fields for the study of these interactions in experimental populations of guppies in Trinidad. Duties include assisting in monthly censuses of guppy populations in montane streams. The monthly censuses include long hours in the field and laboratory. Qualifications: We seek interns who are entertaining the possibility of pursing graduate studies in some area of ecology and evolution and who wish to gain some field research experience before entering graduate school.Research will take place in semi-remote areas of Trinidad sometimes under bad weather conditions. Applicants must be able to live and work well with others. Research will involve carrying heavy packs over slippery and steep terrain. Applicants must be in good physical condition and be able to meet the demands of field research under these conditions. Ability to drive a standard transmission vehicle is desirable but not required. Applicants with first-aid/first responder training, skills in automobile maintenance, and construction skills are highly desirable. Please address these skills when applying.

Interns will be required to spend a minimum of 3-months in Trinidad, with possibility of extension. Starting dates are as early as August 2015. We will cover alltravel and living expenses and provide housing.

Please see our website cnas.ucr.edu/guppy for more information on the project and access to reprints. Our video menu includes a guppy censuses submenu that details the main tasks associated with the internship.

Applicants should send cover letter, CV and the names, phone numbers and e-mail addresses of three or more professional references to David Reznick (gupy@ucr.edu). At least two of the references should be academics.

Andrés López-Sepulcre <lopezsepulcre@gmail.com>

Trinidad VolResAssist EvolutionSociality

Research Assistant: Tropical Fieldwork Trinidad July 2015 A volunteer field assistant is required to help with a field-based project on behaviour in social wasps. This project combines behavioural experiments with next-generation sequencing to understand the molecular mechanisms behind sociality. Fieldwork will be conducted on the island of Trinidad, and will run from July-September. Research involves marking individual wasps, manipulations, conducting censuses, sample collections, and behavioural observations. Research is suited towards those with a keen interest in behavioural ecology, social evolution, and/or entomology. See link below:

http://www.sumnerlab.co.uk/wp-content/uploads/-2014/11/research_assistant_trinidad2015.pdf *Dr Daisy Taylor* Post-doctoral Research Assistant School of Biological Sciences 24 Tyndall Avenue Bristol BS8 1TQ UK daisy.taylor@bristol.ac.uk

DA Taylor <daisy.taylor@bristol.ac.uk>

UBern Fieldassist CichlidResearchZambia

Wanted: Field assistants for field trip to Lake Tanganyika

The Behavioural Ecology Department of the University of Bern provides opportunities to participate in field work in Zambia form late August until end of November 2015. This is a great opportunity to get field experience at a tropical lake and to visit sub-Saharan Africa aside the usual tourist routes.

Project: We study cooperatively breeding, colonial cichlids in Lake Tanganyika. All work will be done by SCUBA diving.

Tasks: Usually there will be 2 dives/day on 6 days/week. Applicants will work independently after a training phase.

Living: We live at a very basic lodge (no electricity, no tap water) located directly at the shore of Lake Tanganyika in the vicinity of the city of Mpulungu, Zambia. Limited computer and internet facilities are available. Meals will be provided by the lodge stuff.

Requirements: Applicants must be in good health and physically fit, as the diving is very demanding. Experience with living in the tropics and under basic conditions without access to the usual amenities of modern life would be advantageous. Interest in behavioural and/or cichlid ecology is a basic requirement. A PADI (or equivalent) diving certificate and some diving experience are required. The successful applicant is expected to stay with us in Zambia for the complete 3 month field season.

Conditions: Travelling and accommodation costs will be covered; costs for food and personal needs are the responsibility of each team member. Consider at least 7 US$ for food expenses/day. Diving equipment will be provided, but mask, fins, wet-suit (7mm+), and diving computer need to be brought by each team member. How to apply: Please send your application (including CV, a brief statement of motivation, diving experience, field work in general, and living in the tropics) per e-mail to dario.josi@iee.unibe.ch or joachim.frommen@iee.unibe.ch. Application deadline is the 05th of June 2015.

dario.josi@iee.unibe.ch

UCalifornia Riverside Internship GuppyEvolution

Research Internships ? Evolutionary Biology

Research interns are needed to assist in a multidisciplinary, multi-investigator, experimental study of the inter actions between ecology and evolution in Trinidad. The research is led by Professor David Reznick at the University of California, Riverside.??We seek to integrate multiple biological fields for the study of these interactions in experimental populations of guppies in Trinidad. Duties include assisting in monthly censuses of guppy populations in montane streams. The monthly censuses include long hours in the field and laboratory.

Qualifications: We seek interns who are entertaining the possibility of pursing graduate studies in some area of e cology and evolution and who wish to gain some field research experience before entering graduate school.??Research will take place in semi-remote areas of Trinidad sometimes under bad weather conditions. Applicants must be able to live and work well with others. Research will involve carrying heavy packs over slippery and steep terrain. Applicants must be in good physical condition and be able to meet the demands of field research under these conditions. Ability to drive a standard transmission vehicle is desirable but not required. Applicants with first-aid/first responder training, skills in automobile maintenance, and construction skills are highly desirable. Please address these skills when applying.

Interns will be required to spend a minimum of 3-months in Trinidad, with possibility of extension. Starting dates are as early as August 2015. We will cover all?travel and living expenses and provide housing.

Please see our website <cnas.ucr.edu/guppy> for more information on the project and access to reprints. Our video menu includes a ?guppy censuses? submenu that details the main tasks associated with the internship.

Applicants should send cover letter, CV and the names, phone numbers and e-mail addresses of three or more professional references to David Reznick (gupy@ucr.edu). At least two of the references should be academics.

David Reznick <david.reznick@ucr.edu>

UExeter 2 PhytoplanktonAdaptationSelectionPhyloseminar GytisDudas Jun10

Next on http://phyloseminar.org/ :

Gytis Dudas (U Edinburgh) Ebola virus epidemiology, transmission, and viral evolution from four months of sequencing in Sierra Leone (Analysis and Methods) Wednesday, June 10, 2015, 9:00 AM PDT

Adding to the work reported in Gire, et al (Science, 2014) which sequenced Ebola viruses from the first three weeks of the epidemic in Sierra Leone, we here present analyses of 150 additional viral genomes sampled from EVD cases at Kenema Government Hospital between the months of June to September 2014. We describe continued evidence for sustained human-to-human transmission with no additional zoonotic events, and preliminary results concerning new lineages from Guinea. We also characterize the epidemiological history of the limited number of exported viruses from the country. We also observe a slowing of the viral substitution rate over the course of the outbreak, consistent with the increased effect of purifying selection as the outbreak continues over time. These findings allow a closer view of viral evolution during its extended time in human populations and provide critical insights into the movement of the virus through the region.

This is the second talk in a pair of talks from collaborators Daniel Park and Gytis Dudas concerning their analysis of Ebola virus sequences.

Frederick “Erick” Matsen, Associate Member Fred Hutchinson Cancer Research Center http://matsen.fredhutch.org/ matsen@fredhutch.org

Warming expt analysis

Hi folks,

As you might (or might not) know, we have for five years now been running a large-scale warming experiment in which we have warmed twelve 5 meter diameter open-top chambers in forest understory at Duke Forest. We have warmed these chambers in a regression design with the warmest chambers as warm as temperatures are predicted to be in the region in 2100 and the coolest chambers at ambient temperatures (We also have no-chamber controls). These are small worlds each of which mimics aspects of futures we might face. This entire set-up is replicated at Harvard Forest. In these chambers we have been studying the response of insects (with a focus on ants) and plants over the last five years. When we built them these chambers were the biggest warming experiment in a forest understory in the world. I don't know if it is still true, but it probably is, if only because chambers of this size are so hard to keep going (especially in the early we felt like Fitzcarraldo dragging a ship through the rainforest) that most people have decided against repeating them elsewhere.

Some basics on the chambers... http://robdunnlab.com/projects/warming-chambers/
I'm writing because on May 25th we are taking the chambers down and doing a final inventory of the response of everything–all the life we can possibly evaluate–to this warming. To varying extents we have considered the phenology of plants in the chambers, many things about ants in the chambers, shifts in composition of invertebrates in the chambers and simple responses of bacterial and fungal assemblages in the chambers. But, we have done all of this delicately, always mindful to not overly disturb the future world we are simulating. Now though that the chambers are coming down we can and will consider roots, plant biomass, the abundance of insect pests, fungal pathogens and much, much, more.

As we do this intensive survey, we are hoping to train as many different eyes, lenses and perspectives on the chambers as possible. If you are potentially interested in studying some aspect of the response of understory forest life to warming, let us know. If you are interested in studying something that can be extracted from soil or litter samples, we may be able to send you material you can work on. If you have something grander in mind (and we love grand things), then we may need more help from you. If interested, send an email to me, copied to MJ Epps (Mj Epps <mycota@gmail.com>). This collaboration might be in the form of bringing a new method to the chambers (looking at microbial processes, for instance) or considering a group of organisms we've somewhat ignored (e.g., fly larvae) or it might be something totally off the wall. Feel free to share this email with likable folks that might be interested.

I'm also delighted to hear creative ideas about visualizing the differences that have emerged over the years of this experiment (hence the inclusion of several artists of various sorts on this email list, if you were wondering why you were copied).

I hope this email finds you well.

Best,

Rob

– Margarita M. López-Uribe Postdoctoral Researcher Department of Entomology North Carolina State University https://sites.google.com/a/cornell.edu/mm-lopez-uribe/ mmlopezu@ncsu.edu

PostDocs

AmherstCollege USA CichlidEvolution

Funding for postdoctoral fellow for 1.5 years (can be extended if funds available) for project on coloration and vision in Neotropical cichlids. Must be SCUBA certified. Start date flexible, but must be available for field-work starting January 2016. Contact Ethan Clotfelter (edclotfelter@amherst.edu) at Amherst College, Massachusetts, USA with questions.

Ethan Clotfelter <edclotfelter@amherst.edu>

ArizonaStateU TeachingEvolMedicine

Postdoctoral Fellow in Evolution & Medicine: Education Resources Development and Online Learning Reference #11183 Full-time

The Center for Evolution & Medicine (CEM) at Arizona State University (ASU) invites applications for a Postdoctoral Fellow in Education Resources Development and Online Learning. Anticipated start date is August 3, 2015. This is a full-time (1.0) benefits-eligible, fiscal year (July 1 - June 30) appointment. Renewal is possible on an annual basis contingent on satisfactory performance, availability of resources, and the needs of the program. For additional information and policies regarding postdoctoral scholars at ASU, please see http://provost.asu.edu/postdoc . The successful candidate will help curate existing online resources in evolutionary medicine, participate in the development and delivery of new innovative evolutionary medicine courses, both in-person and online, and will evaluate and study the impact and effectiveness of these resources and courses. The fellow will help develop a project plan to build courses that will initially be offered to ASU and ASU online students and later to medical personnel all over the world. This is an exciting opportunity to work with an interdisciplinary faculty in a growing field of study to develop, implement, and research innovative curriculum and other resources related to evolution and medicine.

While specific technology expertise is not required, an ideal candidate would demonstrate a strong interest in the applications of technology in higher education, and would have an aptitude for developing and assessing new approaches to learning and how they are best supported by new technologies. This, together with experience in curriculum development and teaching, will allow the Education Resources Fellow to provide disciplinary and pedagogical expertise in creating innovative and rigorously assessed learning experiences. The Fellow may have supervisory responsibilities that include the training and mentoring of staff and/or student interns.

This Postdoctoral Fellows Program is a service and training program designed for early career scientist-teachers who are interested in an academic pathway involving curriculum development, teaching, and educational programming in the interdisciplinary field of Evolutionary Medicine. As a training opportunity fellows will receive mentorship to support their development as educators throughout the duration of the fellowship and have an opportunity to participate in the ASU Science Education Group, the Evidenced-based Teaching Seminar series, as well as the Biology Education Research Lab.

Candidates must have a Ph.D. in anthropology, biology or other natural science or science education field that provides an extensive background in evolutionary biology. Cross-training and experience in education is desirable. Candidates with experience in the following are preferred: developing and assessing education resources; conducting educational research; and using developing digital resources for online and classroom use. The successful candidates will have a commitment to science education, must have outstanding writing and organizational skills, demonstrated capacity for independence and innovation, and the ability to work as part of a team.

Arizona State University is a dynamic, progressive university dedicated to interdisciplinary collaborations, to rethinking university education, and to integrating excellence in both research and teaching.

The Center for Evolution and Medicine at Arizona State University's Tempe campus is a university-wide presidential initiative whose mission is to establish evolutionary biology as an essential basic science for medicine, worldwide. The Center will bring leading scientists to ASU to join existing faculty in research that demonstrates the power of evolutionary biology to address problems in medicine and public health. The new courses and degrees they create will begin to meet the growing demand for such experiences, and will educate a generation of future researchers and health professionals. Many of these experiences will be at ASU, and some will be in conjunction with the new Mayo medical school, but others will be available online open access worldwide, providing the authoritative content that has long been needed to bridge the gap between evolutionary biology and medicine.

To apply, please email a single pdf document containing a letter of application that states your interest in and qualifications for the position, a curriculum vitae, names of three references, and an item of choice that represents your approach to teaching in undergraduate science classroom to evmedsearch@asu.edu. The initial closing date for receipt of complete applications is June 30, 2015; applications will be reviewed weekly thereafter until the search is closed. A background check is required for employment.

— / —

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

---

ArizonaStateU TeachingEvolutionaryMedicine

Postdoctoral Fellow in Evolution & Medicine: Education Resources Development and Online Learning

Reference #11183 Full-time

The Center for Evolution & Medicine (CEM) at Arizona State University (ASU) invites applications for a Postdoctoral Fellow in Education Resources Development and Online Learning. Anticipated start date is August 3, 2015. This is a full-time (1.0) benefits-eligible, fiscal year (July 1 - June 30) appointment. Renewal is possible on an annual basis contingent on satisfactory performance, availability of resources, and the needs of the program. For additional information and policies regarding postdoctoral scholars at ASU, please see http://provost.asu.edu/postdoc . The Center's website is at http://evmed.asu.edu The successful candidate will help curate existing online resources in evolutionary medicine, participate in the development and delivery of new innovative evolutionary medicine courses, both in-person and online, and will evaluate and study the impact and effectiveness of these resources and courses. The fellow will help develop a project plan to build courses that will initially be offered to ASU and ASU online students and later to medical personnel all over the world. This is an exciting opportunity to work with an interdisciplinary faculty in a growing field of study to develop, implement, and research innovative curriculum and other resources related to evolution and medicine.

While specific technology expertise is not required, an ideal candidate would demonstrate a strong interest in the applications of technology in higher education, and would have an aptitude for developing and assessing new approaches to learning and how they are best supported by new technologies. This, together with experience in curriculum development and teaching, will allow the Education Resources Fellow to provide disciplinary and pedagogical expertise in creating innovative and rigorously assessed learning experiences. The Fellow may have supervisory responsibilities that include the training and mentoring of staff and/or student interns.

This Postdoctoral Fellows Program is a service and training program designed for early career scientist-teachers who are interested in an academic pathway involving curriculum development, teaching, and educational programming in the interdisciplinary field of Evolutionary Medicine. As a training opportunity fellows will receive mentorship to support their development as educators throughout the duration of the fellowship and have an opportunity to participate in the ASU Science Education Group, the Evidenced-based Teaching Seminar series, as well as the Biology Education Research Lab.

Candidates must have a Ph.D. in anthropology, biology or other natural science or science education field that provides an extensive background in evolutionary biology. Cross-training and experience in education is desirable. Candidates with experience in the following are preferred: developing and assessing education resources; conducting educational research; and using developing digital resources for online and classroom use. The successful candidates will have a commitment to science education, must have outstanding writing and organizational skills, demonstrated capacity for independence and innovation, and the ability to work as part of a team.

Arizona State University is a dynamic, progressive university dedicated to interdisciplinary collaborations, to rethinking university education, and to integrating excellence in both research and teaching.

The Center for Evolution and Medicine at Arizona State University's Tempe campus is a university-wide presidential initiative whose mission is to establish evolutionary biology as an essential basic science for medicine, worldwide. The Center will bring leading scientists to ASU to join existing faculty in research that demonstrates the power of evolutionary biology to address problems in medicine and public health. The new courses and degrees they create will begin to meet the growing demand for such experiences, and will educate a generation of future researchers and health professionals. Many of these experiences will be at ASU, and some will be in conjunction with the new Mayo medical school, but others will be available online open access worldwide, providing the authoritative content that has long been needed to bridge the gap between evolutionary biology and medicine.

To apply, please email a single pdf document containing a letter of application that states your interest in and qualifications for the position, a curriculum vitae, names of three references, and an item of choice that represents your approach to teaching in undergraduate science classroom to evmedsearch@asu.edu. The initial closing date for receipt of complete applications is June 30, 2015; applications will

— / —

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

AuburnU EvolutionaryPhysiology

Postdoctoral Fellow in Evolutionary Physiology at Auburn University

The Hood lab at Auburn University is looking to hire a post-doctoral scholar to evaluate the role of mitochondria in tradeoffs between reproduction and longevity in the house mouse. A focus of the project will be to evaluate mtDNA mutation rates using high throughput sequencing approaches. A strong background in genomics, physiology, and life history theory and excellent communication, organization, and leadership skills are required. The individual will be expected to assist with training and mentoring graduate students and undergraduates, develop synergistic projects, write grants, and produce first authored papers and contribute to co-authored papers. This is a one-year position with the possibility of renewal pending satisfactory work.

Dr. Wendy Hood operates the laboratory. Information about the lab and abstracts for funded projects can be found at: thehoodlaboratory.com.

Applicants must have a Ph.D. in an appropriate field. The candidate selected for this position must be able to meet eligibility requirements to work in the United States at the time the appointment is scheduled to begin and continue working legally for the proposed term of employment. Women and minorities are strongly encouraged to apply.

This announcement is informal in nature and candidates of interest will be asked to submit a formal application for complete consideration after initial screening.

If interest please send a CV and a statement of interest to Wendy Hood at wrhood@auburn.edu (please note our mail system is limited to 25Mb messages). Receipt of application will be confirmed within 3 days. Review of applications will begin April 20, 2015 and continue until a suitable applicant is found.

Wendy R Hood, PhD Assistant Professor, Auburn University Department of Biological Sciences Auburn, AL 36849 334-844-7437

Email: wrhood@auburn.edu Web: thehoodlaboratory.com

Wendy Hood <wrh0001@auburn.edu>

BathU BacterialGenomics

9 month post doc available in the Feil lab (Bath, UK) to work on whole genome sequence data of S. aureus http://tinyurl.com/nrhnv9c bssef@bath.ac.uk

BrooklynCollege EvolutionaryTheory

I am recruiting a postdoc to join my new research group at Brooklyn College. My work uses computation and theory to explore how complex adaptations evolve.

Potential projects include:

- Extending a model of stochastic gene networks to answer evolutionary questions about plasticity and evolvability.

- Applying math and computation to understand adaptation on fitness landscapes, with applications to evolution experiments.

- Modeling virus life-histories to make predictions about host shifts.

Visit [1]www.jeremydraghi.com for more information about my research.

The ideal candidate would have experience in evolutionary theory, strong writing and programming skills and a record of creative problem-solving. In addition to research, the postdoc will have the opportunities to help develop grant applications, participate in collaborations with experimental labs, and mentor students.

The lab is part of a beautiful campus in the middle of Brooklyn, NYC. As part of the City University of New York, you will have access to an array of seminars and networking opportunities.

Salary is $44,000 plus benefits. Start date is Fall 2015 and candidates should have their Ph.D., or have a firm defense date, by the start of the position. The appointment is for one year with potential for renewal.

Formal applications will begin in September through the Brooklyn College HR office. Inquires about the position can be sent to me at jdraghi (at) gmail (dot) com.

Brooklyn College-CUNY is an equal opportunity/affirmative action employer.

References

1. http://www.jeremydraghi.com/ Jeremy Draghi <jdraghi@gmail.com>

Brussels TropicalTreeEvol

A 2-year postdoctoral position in theoretical population genetics and bioinformatics is available in the team of Dr Olivier Hardy (http://ebe.ulb.ac.be/ebe/Hardy.html) at the Universite Libre de Bruxelles, Belgium . The team is working on the evolution and dynamics of African rainforest plants and its main research topics include comparative phylogeography, population and quantitative genetics, seed and pollen dispersal, species delimitation, and (phylo)diversity patterns of tree communities. Current projects include the acquisition of NGS-based genomic data to conduct high-resolution phylogeographic studies and infer past demographic and evolutionary processes. The postdoc will work on the project Next-generation biodiversity studies deciphering the dynamics of African rain forests, financed by the FNRS, and is expected to develop data analyses methods for comparative phylogeography and species delimitation, to analyze available datasets, and possibly to acquire complementary datasets. Available datasets include in particular (i) SSR or SNP genotypes at large spatial scales in multiple sympatric species, (ii) NGS data for the genome assembly of tree species. The postdoc requires a good background in theoretical population genetics and computer programming / bioinformatics, with experience in coalescence and/or landscape genetics modeling, and/or with genome assembly. Experience with the R language and cluster computing and/or with tropical plants would be beneficial. The research project of the candidate will be flexible and adapted to his/her previous experience.

The candidate will be based in Brussels, will have access to a molecular lab and might realize field missions in Africa. He/she will work in close collaboration with Olivier Hardy and other team members (currently 3 postdocs, 4 PhD students, 1 technician, MSc students). Candidates must have a PhD obtained less than 6 years ago and cannot be of Belgian nationality or be residing in Belgium for more than 2 years (conditions imposed by the grant). Interested candidates should send to Olivier Hardy (ohardy@ulb.ac.be) their CV and a brief letter of motivation stating how their expertise fits with the position, preferably before 10 June 2015. More details about the projects will be provided. The postdoc grant should ideally start this summer (1 July 2015 being ideal).

Olivier Hardy

Olivier Hardy <ohardy@ulb.ac.be>

ClemsonU StrepotococcusEvolution

Vince Richards lab in the Department of Biological Sciences at Clemson University is accepting applications for a post-doctoral position. The post-doc's primary responsibility will be a USDA project investigating genetic population structure and transmission dynamics of the zoonotic pathogen Streptococcus agalactiae . This bacteria is an important pathogen that infects multiple species including humans, livestock, and aquaculture. Towards a better understanding of the evolution and transmission dynamics of S. agalactiae both within and across host species, this project leverages comparative genomic approaches to a global collection of hundreds of S. agalactiae strains isolated from a diverse range of host species. Other responsibilities include contributing to the ongoing research within the laboratory.

The candidate should have a strong publication record, a background in population and evolutionary genetics, experience analyzing next-generation sequence data, and be well versed in Linux/bash. Strong communication and writing skills are essential. The position is available for 1.5 years, with the possibility of extension. Applicants should contact Vince Richards directly at vpricha@clemson.edu. Please provide a cover letter, CV, PDFs of representative publications, and contact information for three references.

Clemson University is ranked 20th among national public universities by U.S. News & World Report and is located on Lake Hartwell near the Blue Ridge mountains in beautiful Upstate South Carolina.

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

Duke-NUS Singapore VirusEvolution

Applications are invited for a Research Fellow (postdoctoral) position in Vijaykishna Dhanasekarans research group at Duke-NUS Graduate Medical School, Singapore to work in the area of infectious disease evolution and epidemiology making use of the latest technology in sequencing and computational biology. More details on the job description, requirements and application procedure can be found here https://www.duke-nus.edu.sg/about/careers/-appointments/vacanciesresearch-fellow-code-oreidvd vijay.dhanasekaran@duke-nus.edu.sg

FredHutch ImmuneRepertoireDynamics

Postdoc:FredHutch.ImmuneRepertoireDynamics

A new postdoctoral position is available in the groups of Trevor Bedford and Erick Matsen at the Fred Hutchinson Cancer Research Center located in Seattle, WA. This position will focus on analyzing immune repertoire sequence data from an evolutionary perspective.

Deep sequencing of B cell repertoires has opened up the possibility of understanding the immune response at a molecular level. This project will analyze repertoire data to compare processes of clonal expansion and affinity maturation in primary and secondary immune responses. These studies will allow, for the first time, a detailed mechanistic understanding of original antigenic sin in viral infection; results from these studies may allow construction of vaccines that better deal with a diversity of pathogen exposures. This work represents a collaboration with experimental colleagues at the Fred Hutch, Emory University and Adaptive Biotechnologies. There will be no want of fresh data.

The ideal candidate will have experience with working with sequence data and a strong interest in model-based statistical analysis of real data sets. Data sets will comprise millions of B cell repertoire sequences and so strong coding abilities are essential. Candidates should have experience in at least one programming language and a proven track-record of peer reviewed publications. Candidates with PhDs from diverse backgrounds are encouraged to apply, including biology, mathematics, statistics, physics and computer science. However, experience in phylogenetics or immunological bioinformatics is especially opportune. The Fred Hutch is an equal opportunity employer, committed to workforce diversity. Women and minorities are particularly encouraged to apply.

The position is available immediately with flexible starting dates for a 2-year appointment with possibility of extension. Informal inquires are welcome. Applications will be accepted until the position is filled. The Fred Hutchinson Cancer Research Center offers competitive salaries commensurate with experience and skills, complete with benefits.

To apply please send (1) cover letter that includes the names and contacts for three references and a short statement of research interests, (2) a current CV and (3) code samples or links to published/distributed code to trevor<at>bedford.io.

For more information, please see: http://bedford.io/ http://matsen.fredhutch.org/

INRA France ConservationModeling

Call for applications for a Postdoctoral Fellowship Provisioning and stability of multiple ecosystem services in agroecosystems A postdoctoral fellowship is proposed at CNRS Moulis and INRA Agroecology in collaboration with CNRS CEBC to develop theory on the magnitude and stability of multiple ecosystem services, such as crop production, pollination and conservation, and their synergies and trade-offs depending on the spatial arrangement of agricultural landscapes.

Application deadline: 9 May 2015 Eligibility deadline by Agreenskills (see below): 26 April 2015 Date of recruitment: from 1st August 2015 Open to: Young researchers holding a PhD with less than 7 years of postdoctoral research experience Fellowship: â¬3500/â¬5000*permonth*

Eligibility Applicants must: - Hold a PhD (or PhD will have been awarded by the date of recruitment); - Have less than 7 years of research experience after their PhD; - Have spent no more than 12 months in France during the 3 years prior to the date of recruitment; - Be able to write and speak English or French fluently; - Have at least 1 publication in a peer-reviewed journal;

Application Candidates interested in the postdoctoral research position should contact Sabrina Gaba (sabrina.gaba@dijon.inra.fr). The postdoctoral project is part of Agreenskills (http://www.agreenskills.eu/), hence candidates are evaluated and selected through two selection rounds per year for both programs: - Before April 26th 2015: Candidates interested in the research project will have to fulfil the eligibility criteria (described below) and to complete an online application through the secure area of the AgreenSkills web portal. Applicants will have to provide a detailed CV. - Before May 9th 2015: Once declared eligible, candidates will be able to apply by proposing a research project that is relevant to the fields of interest of the research teams.

INRA < http://www.inra.fr > *SabrinaGaba* *Chargée de recherches * sabrina.gaba@dijon.inra.fr *Centre INRA de Dijon* Tèl. : +33 (0)3 80 69 31 87 Fax : +33 (0)3 80 69 32 62

17, rue de Sully, BP 86510 21065 Dijon Cedex France http://www6.dijon.inra.fr/umragroecologie Sur twitter: @sabrina_gaba Sur twitter: @ZA_PVS

Sabrina Gaba <sabrina.gaba@dijon.inra.fr>

IPasteur PopCompGenomics

POSTDOC IN POPULATION/COMPUTATIONAL GENOMICS, Institut Pasteur

A postdoctoral position in population/computational genomics is available in the Human Evolutionary Genetics Unit (Quintana-Murcis Lab), in the Department of Genomes and Genetics at Institut Pasteur in Paris. The lab combines large empirical datasets and computation approaches to study human population genetics, for more information see http://www.pasteur.fr/research/-heg. Current work in the lab focuses on a wide range of topics, including (i) the study of the relative effects of demography and natural selection in the shaping of human genome variability using next-generation sequencing data, (ii) the genetic control of gene expression related to immunity-related processes, (iii) the influence of genetic variation and changes in lifestyle and ecologies of human populations on patterns of epigenetic variation. Our lab benefits from the large and outstanding community of researchers in population genetics, epigenetics, microbiology, immunology and computational biology at the Institut Pasteur, providing a working interdisciplinary research environment.

Applicants must have a strong background in statistics and computer science and a desire to do research in genetics and evolutionary biology, or a strong background in theoretical population genetics with experience analyzing genomewide datasets. Programming skills and proficiency in unix-based computational environments are essential.The applicants will have the freedom to choose their own projects as long and they fit within the general interests of our lab.

US citizens are encouraged to apply to the prestigious Pasteur Foundation Postdoctoral Fellowships (Deadline September 10, 2015). Detailed information can be found at http://www.pasteurfoundation.org/scientific-careers/fellowship-program Informal inquiries as well as applications (including a CV, research statement, copies of relevant publications and contact information for at least two references) should be emailed to Lluis Quintana-Murci at <quintana@pasteur.fr>.

Lluis QUINTANA-MURCI Unit of Human Evolutionary Genetics, CNRS URA3012 Institut Pasteur 25, rue du Dr. Roux 75724 Paris Cedex 15 France

Tel: +33 1 40 61 34 43 Fax: +33 1 45 68 87 27 e-mail: quintana@pasteur.fr

Lab Website: www.pasteur.fr/research/heg Lluis Quintana-Murci <lluis.quintana-murci@pasteur.fr>

LoyolaU Chicago MadagascarBird PhylogeneticsMacroevolution

Postdoc:LoyolaUChicago.MadagascarBirdsPhylogeneticsMacroevolution

An NSF-funded postdoc is available for a project on the comparative biogeography and diversification of birds in Madagascar. The postdoc will work jointly with Sushma Reddy at Loyola University Chicago and Dan Rabosky at University of Michigan.

The project aims to investigate the origins and history of the avifauna of Madagascar and study the general drivers of species diversification in this iconic macroevolutionary laboratory. Birds inhabiting this island are the result of several independent colonizations from surrounding regions. Despite arriving in Madagascar millions of years ago, only half the endemic lineages have subsequently speciated within this large island. The project aims at a comprehensive investigation of the poorly-studied bird diversity on Madagascar to determine what causes some groups to diversify while others fail to speciate. Specifically we will examine (1) broad-scale phylogenetic and biogeographic patterns to determine the timing and origins of endemic lineages (2) phylogeographic structure within the island to investigate cryptic diversity (3) phenotypic diversity of Malagasy species and their relatives to assess rates of evolutionary change, and (4) the predictability of speciation by com paring factors that may influence diversification across these clades.

The postdoc will be involved in several different aspects of the project, including collecting and analyzing data (genetic, biogeographic, and phenotypic), writing manuscripts, giving presentations, mentoring students, and participating in fieldwork. The postdoc will have a unique opportunity to be part of an international collaboration and to gain well-rounded skills in evolutionary biology.

The ideal candidate will have a good publication record and some experience with NGS data analysis, programming in R, and avian systematics. The position is funded for 3 years and will be based in Chicago for the first of the half term and Ann Arbor for the second. Applicants must have a Ph.D. in biology or a related field. Start date is flexible and salary is competitive with NSF/NIH rates.

Please email Sushma at sreddy6{at}luc.edu < http://luc.edu/ > with your interests, availability, CV, and questions. The position will be open until filled.

Loyola University Chicago is an Equal Opportunity/Affirmative Action employer with a strong commitment to diversifying its faculty. Applications from women and minority candidates are especially encouraged.

sreddy6luc@gmail.com

McGill PopulationGenetics

Graduate and postgraduate positions in mathematical and population genetics

Graduate student and postdoc positions in mathematical and population genetics are available in Simon Gravel's group at McGill University in Montreal, Canada. The project aims at creating mathematical models of historical human migrations, family histories, and high-throughput genomic data. Students will be involved in conceptual methods development, implementation, and applications to exciting datasets. This is a unique opportunity to be involved in work that is relevant and interesting from a mathematical, medical, and historical perspectives.

We welcome applications from qualified candidates from diverse backgrounds, including biology, anthropology, mathematics, physics, and computer science. Programming experience and a demonstrated interest in mathematics, statistics, or related fields is required.

The position offers an exceptional opportunity to develop theoretical and computational ideas and apply them to cutting-edge data in a supportive and thriving research environment.

Applications and queries should be sent to gravellab@gmail.com. Please include a statement of interest (1 page) and a CV with a list of publications, contact information for three references, and a low-resolution scan of official transcripts.

simon.gravel@gmail.com

MichiganStateU ElectricFishGenomics

A National Science Foundation postdoctoral position is now available in the Electric Fish Laboratory in the

Department of Integrative Biology at Michigan State University (http://efish.zoology.msu.edu) concerning the genomic basis of electric signal diversity in mormyrid electric fish. Electric signals are crucial in the evolution of reproductive isolation among the rapidly diverged Paramormyrops genus. This interdisciplinary project will involve the combination of gene expression analysis (RNA-seq), population genomics, and the application of new and exciting transgenic techniques in non-model systems. For an overview of approaches see Gallant et al. (2014, Science) and Gallant et al. (2014, Nature Communications).

This position is available as of May 2015, but start dates are negotiable. Appointment for this position will be initially for 12 months, with the possibility of renewal for up to three years, contingent on the continued availability of funds as well as satisfactory output of successful applicant.

Duties: The successful applicant will be responsible for constructing genomic and transcriptomic libraries, as well as their assembly and analysis using bioinformatics tools in a high-performance computing environment. Work will require the development of new research methodologies and tools, and publishing results in high-impact journals. In addition, successful applicants will be responsible for co-training undergraduate, graduate students and technicians, as well as contributing to the overall research environment of the University. Successful applicant will be encouraged to participate in a one-of-a-kind NSF-sponsored BEACON center for the study of evolution in action (http://bit.ly/GN0Rhx), for which MSU is the host institution. Professional development opportunities will be provided in conjunction with the MSU Office of Postdoctoral Training and the Center For Academic Excellence.

Required qualifications: Ph.D. or equivalent degree in biology, evolution, bioinformatics, genetics or related field. Publication of work based on Ph.D. thesis is required, as well as teaching and supervisory experience. A strong working knowledge of next-generation sequencing technologies, as well as proficiency in the use of UNIX/Linux command line operating systems. Competence in at least one computer scripting language (R, Python, Perl, MATLAB). Must be willing and able to perform fieldwork in Gabon, West-Central Africa.

Preferred qualifications: Experience with genomic assembly and analysis, population genetics, experience and background in communication systems and aquatic vertebrates, fluency or competency in French. To apply, email the following: a cover letter, current CV, and the contact information (phone number and email address) of three referees to jgallant [at] msu.edu.

Dr. Jason R. GallantAssistant Professor Room 38 Natural Sciences Department of Integrative Biology Michigan State University East Lansing, MI 48824 jgallant@msu.edu

office: 517-884-7756

Jason Gallant <jgallant@msu.edu>

Montpellier 2 PathogenEvolution

Postdoctoral position at Montpellier on Analysis of pathogen interactions and pathogen communities

A 24 months Postdoctoral Scientist position is available in September 2015 at the Institute of Research for Development (IRD), in Montpellier, France. The work will be performed in the research group headed by Dr. Benjamin Roche. The project is funded by a grant from the Agence Nationale de la Recherche (ANR).

Scientific context: The proposed project will study how pathogen interactions, through immunological, ecological or social mechanisms, can take place in space and time to shape pathogen communities in human populations. In addition of the intriguing knowledge produced in fundamental ecology by this project, major public health perspectives are also expected. To answer these questions, two unique datasets are available in this project. The first one, focusing at a population scale, includes weekly notifications of more than 30 pathogens within an homogeneous area. The second dataset, targeting an individual scale, relies on a human cohort involving more than 4,000 individuals who have been screened for about 15 pathogens.

Position description: The candidate will combine theoretical modeling of multi-pathogen systems with cutting-edge statistical analysis of the available dataset in order to: (i) characterizing robustly the different kind of pathogen interactions, (ii) understanding the ecological pressures shaping pathogen communities and (iii) predicting the outcomes of the different public health strategies on the structure of pathogen communities.

The candidate will have a PhD in Biological Sciences and a demonstrated experience in ecological/epidemiological modeling of infectious diseases (through statistical and/or mathematical approach). Interested candidates should apply by June 10th by sending (1) a letter of motivation, (2) a CV with publication list, and (3) the names, institutions and email addresses of three references to Dr. Benjamin Roche at benjamin.roche@ird.fr.

– Benjamin Roche, PhD

Labs: International Center for Mathematical and Computational Modeling of Complex Systems (UMMISCO) Infectious Diseases: Vector, Control, Genetic, Ecology and Evolution (MIVEGEC) Centre for Ecological and Evolutionary Research on Cancer (CREEC)

Postal address: Research Institute for Development (IRD) 911, avenue Agropolis BP 64504 34394 Montpellier Cedex 5 France

Phone:+33629585460 e-mail:roche.ben@gmail.com web:http://roche.ben.googlepages.com ——

Post-doc position at Montpellier on disease ecology of malaria in Bobo-Dioulasso

During the last century, WHO have led public health interventions that resulted in spectacular achievements such as the worldwide eradication of smallpox and the elimination of malaria from the Western world. However, besides major successes achieved in control of infectious diseases, most elimination/control programs remain frustrating in many tropical countries where specific biological and socio-economical features have prevented implementation of disease control over broad spatial and temporal scales. Emblematic examples include malaria, dengue, yellow fever, measles and HIV. There is consequently an urgent need to develop affordable and sustainable disease control strategies that can target the core of infectious disease transmission in highly endemic areas.

Focusing on Dengue transmission in Phnom Penh (Cambodia) and on malaria spreading in Bobo-Dioulasso (Burkina Faso), the PANIC project (PathogenÂs NIChe: a new approach for infectious diseases control) aims to develop conceptual, empirical and theoretical frameworks to envision optimized public health strategies for vector-borne diseases by considering the most recent advances in ecology and evolution of infectious diseases. Funded by the Agence Nationale de la Recherche (ANR, www.agence-nationale-recherche.fr) for five years, this project involves French, Burkinabese and Cambodian researchers from various fields (entomology, virology, epidemiology, disease ecology, modeling) to tackle this issue.

Within this context, we are seeking for a post-doctoral fellow who will focus on data analyses to quantify the contribution of (i) mosquito population dynamics, (ii) change in human behavior and (iii) resident immunity on the spatio-temporal transmission of malaria in Bobo-Dioulasso. Most of the data relevant to this project (household socio-economic data, epidemiological time series and mosquito population dynamics from different neighborhoods) are already available, and additional data will be collected in the field at the beginning of the project. Therefore, several stays have to be expected in Bobo-Dioulasso, with flexible durations.

The ideal candidate will have a PhD in epidemiology or in ecology and

— / —

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 PathogenEvolution

Postdoctoral Scientist in Analysis of pathogen interactions and pathogen communities

A 24 months Postdoctoral Scientist position is available in September 2015 at the Institute of Research for Development (IRD), in Montpellier, France. The work will be performed in the research group headed by Dr. Benjamin Roche. The project is funded by a grant from the Agence Nationale de la Recherche (ANR).

Scientific context: The proposed project will study how pathogen interactions, through immunological, ecological or social mechanisms, can take place in space and time to shape pathogen communities in human populations. In addition of the intriguing knowledge produced in fundamental ecology by this project, major public health perspectives are also expected. To answer these questions, two unique datasets are available in this project. The first one, focusing at a population scale, includes weekly notifications of more than 30 pathogens within an homogeneous area. The second dataset, targeting an individual scale, relies on a human cohort involving more than 4,000 individuals who have been screened for about 15 pathogens.

Position description: The candidate will combine theoretical modeling of multi-pathogen systems with cutting-edge statistical analysis of the available dataset in order to: (i) characterizing robustly the different kind of pathogen interactions, (ii) understanding the ecological pressures shaping pathogen communities and (iii) predicting the outcomes of the different public health strategies on the structure of pathogen communities.

The candidate will have a PhD in Biological Sciences and a demonstrated experience in ecological/epidemiological modeling of infectious diseases. Interested candidates should apply by June 1st by sending (1) a letter of motivation, (2) a CV with publication list, and (3) the names, institutions and email addresses of three references to Dr. Benjamin Roche at benjamin.roche@ird.fr.

Living at Montpellier:http://www.agropolis.org/english/guide/index.html

– Benjamin Roche, PhD

Labs: International Center for Mathematical and Computational Modeling of Complex Systems (UMMISCO) Infectious Diseases: Vector, Control, Genetic, Ecology and Evolution (MIVEGEC) Centre for Ecological and Evolutionary Research on Cancer (CREEC)

Postal address: Research Institute for Development (IRD) 911, avenue Agropolis BP 64504 34394 Montpellier Cedex 5 France

Phone:+33629585460 e-mail:roche.ben@gmail.com web:http://roche.ben.googlepages.com Benjamin Roche <roche.ben@gmail.com>

Montpellier PopulationGenomics

Post-Doctoral position in population genomics " Montpellier, France

Purpose and responsibilities: The research program GENESIS focuses on the role of GENetic diversity and phenotypic plasticity in adaptations to changing Environments: a genomic analySIS of a biological invasion. It involves four academic research teams from UK and France for the three next years and is opening a post-doctoral position to work on the conservation genomics of fish topmouth gudgeon Pseudorasbora parva, a small cyprinid species native to East Asia. The post-doc will be in charge of the analysis of genomic data (GBS) for conservation genomics and estimating heritability of fitness related traits using a molecular based pedigree.

Research program The main question for the program is to assess the role of genetic diversity and phenotypic plasticity in adapting to changing environmental conditions. GENESIS uses the framework of biological invasion to answer this question as the challenge for an invasive species is to respond quickly and efficiently to changes in the selective regime imposed by the colonized ecosystem. In addition, a series of stochastic sampling events associated with the colonization process is predicted to result in strong genetic drift in invasive populations, providing the opportunity for rapid evolutionary change through both selection and drift, and the majority of studies report marked phenotypic change in invasive populations. The information on heritability of ecologically significant life history traits or behaviors is crucial in accurately predicting responses to selection and is therefore a key element of GENESIS that aims at increasing our understanding of factors that promote establishment success of invasive species and the response of small fragmented populations to climate change. A phylogeography will be constructed based on the genomics data. Further, in order to identify genomic regions under selection between populations, an ≪ outlier analysis ≫ will be conducted. The problem of identifying statistically significant departure from neutrality is complicated and results related to assumptions made, by example to the demographic history of the samples. A variety of tests have been developed either making strict assumptions about demographic history of the populations or estimating for evolutionary non independence among samples. The candidate will have a significant experience of such tests including methods based on summary statistics (eg Fst) as well as bayesian hierarchical modelling. The candidate will be able to choose a justified approach taking into account the characteristic of the data (SNP and NGS sequencing), the robustness of the methods to departures from assumptions, and the consideration of false positive rate.

Practical information for applications The post-doc position will be hold at the Center for Biology and Management of Populations at the international capus of Baillarguet, near Montpellier, France (http://www1.montpellier.inra.fr/CBGP/). Applicants are expected to speak and write English although French is always welcome given the location of this position. Applicants will find some information about living at Montpellier here: http://www.agropolis.org/english/guide/index.html The position is available for 2 years and starts at the latest in November 2015. We will start reviewing the applications from now but will continue to consider incoming applications until the position is filled. The gross salary of the post-doc candidate would be around 24 271 euro per year.

Qualifications Ph.D. in population genomics and biostatistics Specific skills and technical/administrative training required: One or more programming languages Scientific writing Interpersonal communication

Preferred Experience: Experience in genome scan, GBS data analysis

Informal enquiries and applications should be sent to jean-francois.martin@supagro.fr. Applications should include a cover letter with a statement of research interests and qualifications for the position, complete CV with publication list, and contact details of three referees, embedded in a single pdf file.

You may link to this post at : http://www1.montpellier.inra.fr/CBGP/?q=fr/content/post-doctoral-position-population-genomics jean-francois.martin@supagro.fr

---

NorthCarolinaStateU EvolGenomicsCichlids

A postdoctoral position is currently available in the lab of Reade Roberts in the North Carolina State University Department of Biological Sciences (Raleigh, NC), to study the evolution of sex determination and sex chromosomes in cichlid fish using genomic approaches.

An ideal candidate will have demonstrated bioinformatics expertise working with high-throughput sequencing data for genome assembly and annotation, comparative genomics, and/or gene expression analysis. Molecular or organismal biology skills are a plus, but not required. Candidates must have a PhD in an appropriate field, and the motivation, creativity, and analytical skills to drive and develop a multi-faceted research project.

The overarching research aim of the Roberts Lab is to understand the genetic basis of adaptive evolution and developmental differences, using East African cichlid fishes as a comparative model system. Research in the lab draws on a number of skill sets, including genetic mapping, gene expression analysis, comparative genomics, bioinformatics, fieldwork, and evolutionary, developmental, and molecular biology. Active projects focus on polygenic sex determination systems and dietary adaptation at the level of the gastrointestinal tract, and the successful candidate would be expected to contribute to these on-going research themes. An extensive bioinformatics research community at NC State University provides access to computing resources and technical expertise, and opportunities for collaboration with allied faculty.

The position is full-time for one year, with further extension subject to satisfactory performance in the first year.

Interested applicants should send a brief note (˜1 page) describing previous research experience and their interests and goals in our lab, as well as a current CV including contact information for at least two references. Please send application materials or any questions regarding the position to robertslabncsu@gmail.com. Applications will be considered on an on-going basis until the position is filled.

nbhodges@ncsu.edu

Philadelphia HerpetologyBiodiversity

BIODIVERSITY (HERPETOLOGY) POSTDOCTORAL SCHOLAR IN PHILADELPHIA

The Center for Biodiversity at Temple University (Philadelphia) is interested in hiring a Biodiversity Postdoctoral Scholar to conduct research in the laboratory of Professor Blair Hedges (www.hedgeslab.org/). The specific area of focus is herpetology, involving systematic studies of large numbers of species, and, most likely, field work. The successful applicant will generate DNA sequences and work with both molecular phylogenies and preserved specimens, and will pursue academic questions in evolutionary biology, systematics, taxonomy, biogeography, and conservation.

The Center for Biodiversity is located in the new Science, Education, and Research Center (SERC building) on Temple's main campus (www.biodiversitycenter.org). Members and affiliates of the Center for Biodiversity include Erik Cordes, Amy Freestone, Blair Hedges, Matthew Helmus, Tonia Hsieh, Sudhir Kumar, Julie Marin, Robert Sanders, Brent Sewall, and Rachel Spigler. The Philadelphia region is already a growing center for herpetology in the U.S., with faculty research laboratories at multiple institutions.

Interested persons should send an e-mail to temple.biodiversity@gmail.com stating their interest in this position and briefly discussing past research experience and skills. Please attach a curriculum vitae that contains contact information for three references. Review of applications will begin on June 10th and continue until the position is filled. The start date is negotiable.

Temple University is located in the heart of historic Philadelphia and is the sixth largest provider of graduate school education in the USA. Situated in close proximity to New York City and Washington DC, Philadelphia is the birthplace of America and home to many academic and research institutions as well as numerous cultural attractions.

Temple University is an equal opportunity, equal access, affirmative action employer committed to achieving a diverse community (AA, EOE, m/f/d/v).

"sbh@temple.edu" <sbh@temple.edu>

RiceU EvolutionaryBiology

Postdoctoral Research Position in Evolutionary Biology

A postdoctoral position is available in the laboratory of Dr. Scott Egan, in the Department of BioSciences at Rice University. Our lab is broadly interested in understanding the origin and maintenance of biodiversity, including integrative studies of ecology, evolution, and population genetics. Primary work in the lab focuses on speciation, the evolution of specialization, and plant-insect interactions. This work is naturally interdisciplinary and we use a combination of ecological field experiments, common garden and greenhouse studies, behavioral observations, and molecular genetic techniques to thoroughly address these topics. Postdoctoral scholars will develop their own independent projects, but will have the opportunity to collaborate on grant-funded projects dealing with speciation in insects and their parasitoids, the genetic basis of adaptation and speciation, and applied projects dealing with conservation and invasive species genetics. Additional information about our lab may be found at https://sites.google.com/-site/scottpegan/ The selected postdoc will have great latitude in selecting their specific research focus, as the goal of this position is to recruit a strong, innovative researcher to investigate any research topic closely aligned to the focus of the Egan Lab. Research could be field-based or lab-based, or both. Scientists that integrate genome level data with studies of ecology and evolution are especially encouraged to apply, especially those with experience handling both large genotype datasets and full-genome sequence analyses (e.g. programming in C, or scripting language Python and/or Perl).

Requirements: The postdoctoral researcher should have a Ph.D. in evolution, ecology, behavior, or a closely related field, demonstrate a record of successful publications, possess excellent analytical and communication skills, and excel at both independent and collaborative research.

Research Topics: The successful candidate can investigate a wide range of topics under the umbrella of evolutionary ecology, including ecological speciation, evolutionary consequences of anthropogenic impacts, tritrophic interactions, predator-prey or host-parasite coevolution, phylogeography, phenotypic plasticity, and eco-evolutionary dynamics.

Start Date / Position Details: The position will begin approximately September 1st, 2015 (very negotiable), and continue for 24 months. Salary will be highly competitive and commensurate with experience and qualifications. The position will also include research funds ($2500 per year), health insurance, and benefits.

Application: To apply, please send a cover letter stating your proposed interests and overlap with our lab, a detailed CV, two letters of recommendation, and up to three relevant papers as a SINGLE PDF to Dr. Egan (scott.p.egan@rice.edu). In the cover letter, please include a general description of the proposed research topic(s), and how the work would fit into the overall focus of our lab. Review of applications will begin immediately, and continue until filled.

Location: Our lab is part of the Department of BioSciences at Rice University, which is home to a vibrant community of faculty, postdoctoral, graduate, and undergraduate scholars in Ecology and Evolution, Biochemistry, Cell Biology, Genetics and Neuroscience. Our EEB program has particular strengths in species interactions, animal behavior, population and community ecology, conservation biology, evolutionary ecology, and evolutionary genetics and genomics. We are located in Houston, Texas, an exciting, diverse, and affordable city with world-class opportunities for dining, arts, and entertainment and access to diverse terrestrial and aquatic environments. Rice is located beside one of the country's largest medical research centers, providing additional opportunities in bioinformatics and genomics. Additional information about our department may be found at http://biosciences.rice.edu . "scott.p.egan@rice.edu" <scott.p.egan@rice.edu>

RoyalBotanicGardensKew TreePhylogenomics

Two Phylogenomics Research Fellows posts

We are seeing to recruit two interlinked active phylogenomic research fellows who will join a team of plant phylogenetic and evolutionary experts in the Department of Comparative Plant and Fungal Biology at Royal Botanic Gardens, Kew, UK. The posts will provide the appointed research fellows with the opportunity to engage with the latest advances in next generation sequencing technologies to address both pure and applied research questions, with a focus on tree genomics, conservation and seed science. The focus of the two posts are 1) Establishing a genomic library for South-East Asian trees for biodiversity analysis, conservation and authentication, and 2) Evolution and diversification of a "recalcitrant" tree family in the Asia-Pacific.

For further information, including an overview of the research proposed for each post, and to apply, please see https://careers.kew.org/vacancy/-phylogenomics-research-fellows-217344.html Dr Ilia Leitch (i.leitch@kew.org) Dr William Baker (w.baker@kew.org) Dr Felix Forest (f.frest@kew.org)

F.Forest@kew.org

Sydney MolecularEvolutionPhylogenetics

Postdoc: Molecular evolution and/or phylogenetic methods

Description Fellowships are available to come and work with my group in Sydney, Australia, for up to 6 months (indeed, you could apply to work with any group in Australia).

If you are a recent PhD graduate, and have interests that overlap with our lab, please get in touch with an email that outlines your interests, along with a copy of your CV, to:

robert.lanfear@mq.edu.au

Specific projects include (but are not limited to):

1. Investigating the accumulation of somatic mutations in individual plants

2. Various projects examining the causes and consequences of variation in rates of molecular evolution among taxa (plants and animals)

3. Developing and applying methods for model selection and data filtering in phylogenetics

For more information on the research our lab, please visit:

www.robertlanfear.com/research The fellowships provide a good salary, as well as covering all travel and other costs. They are competitive, but success rates are quite high. Recent PhD graduates with at least one publication are competitive. More information on the fellowships themselves can be found here:

https://internationaleducation.gov.au/endeavour%20program/scholarships-and-fellowships/international-applicants/pages/international-applicants.aspx and the list of eligible countries can be found here:

https://internationaleducation.gov.au/Endeavour%20program/Scholarships-and-Fellowships/Participating_countries/Pages/Participating%20Countries%20and%20Regions.aspx Yours,

Rob Lanfear

– Rob Lanfear ARC Future Fellow and Senior Lecturer, School of Biological Sciences, Macquarie University, Sydney

phone: +61 (0)2 9850 8204 www.robertlanfear.com robert.lanfear@mq.edu.au

---

TempleU PlantReproductiveEvolution

A Postdoctoral Fellow position is available in the Spigler lab in the Department of Biology at Temple University. The Postdoctoral Fellow will be involved in an ongoing project on variation in plant-pollinator interactions and phenotypic selection on floral traits across a fragmented landscape and in the design and implementation of new field, greenhouse, or population genetic studies related in areas. There are numerous opportunities to mentor undergraduates in research and to participate in outreach efforts. Additional information about the Spigler lab can be found at http://rachelspigler.weebly.com . Candidates must have a PhD in Ecology, Evolutionary Biology, Botany, or related field; experience designing, conducting, and managing field and greenhouse studies; and strong quantitative skills. A demonstrated track record of publications, excellent interpersonal, communication, and time-management skills, a strong work ethic, and attention to detail are also essential. Additional preferred qualifications include standard molecular skills (e.g., DNA extraction, PCR, microsatellite genotyping) and related statistical experience.

The position is available immediately and to last for one year, with the possibility of extension based on satisfactory progress and funding. Salary, commensurate with experience, and benefits are provided. Interested applicants should send the following as a SINGLE PDF file by email to Rachel Spigler (rachel.spigler@temple.edu): 1) a short statement (1-2 pages) on research interests, previous experience, and motivation for applying, 2) your curriculum vitae, and 3) contact information for three references. Informal inquiries about the position are welcome. Review of applications will begin immediately and continue until the position is filled.

About the Biology Department at Temple University

Temple University is a large, comprehensive public research university in Philadelphia, PA, with more than 37,000 undergraduate, graduate, and professional students enrolled in over 400 academic degrees. The Biology Department at Temple (https://bio.cst.temple.edu/) represents an active research community with strengths in ecology, genomics, conservation, and evolutionary biology and is home to the newly formed Center for Biodiversity (http://cst.temple.edu/research/centers-and-institutes/center-biodiversity), Center for Computational Genetics and Genomics (https://bio.cst.temple.edu/ ˜ hey/CCGG/), and Institute for Genomics and Evolutionary Medicine (http://igem.temple.edu/).

Philadelphia is the fifth largest city in the US, rich in history, known for its arts and culture, and is brimming with a vibrant science community. There are approximately 90 colleges and universities in the Greater Philadelphia region, with plenty of opportunities for collaboration. Philadelphia is also home to Fairmount Park, one of the worlds largest city park systems.

Rachel Spigler <rachel.spigler@temple.edu>

TreeOfLife ComputableSemantics

Postdoctoral fellow in Computable Semantics for the Tree of Life

The Phyloreferencing project seeks a postdoctoral fellow for researching and developing computational semantics approaches to large-scale biodiversity data integration problems. The project aims to enable addressing elements in the Tree of Life by unambiguous, transparent, and fully computable semantics of their patterns of evolutionary descent. The work involves researching and developing OWL models and ontologies, tools for converting existing data into OWL format, and online proof-of-concept applications for using machine reasoning to navigate biodiversity data by Tree of Life-semantics.

The project is a collaboration between Dr. Nico Cellinese < http://www.flmnh.ufl.edu/museum-voices/nico-cellinese/ > (Florida Museum of Natural History < http://www.flmnh.ufl.edu/ >, University of Florida < http://www.ufl.edu/ >) and Hilmar Lapp (Center for Genomic and Computational Biology < http://www.genome.duke.edu/ >, Duke University) newly funded by NSF for 3 years. The incumbent will be based in the lab of Dr. Cellinese, but will work closely with both PIs and will periodically travel to Lapp's lab at Duke University. Starting date is negotiable but the sooner the better. Salary starts at $45,000.

Why phyloreferencing? Integrating and querying biological data across organisms, whether on small or large scales, to this day relies on traditional names for organisms and groups of organisms based on Linnaean nomenclature. However, when it comes to integrating and communicating data, these suffer from two major limitations. Firstly, because they are simple text-strings, machines cannot access the meaning intended by those who coin a name and those who apply it, resulting in rampant ambiguity and inconsistency in what organism names are interpreted to mean. Secondly, there are many groups of organisms for which a Linnaean name does not and may never exist, but for which valuable biological knowledge needs to be communicated. The Phyloreferencing project aims to address these challenges by defining ontology-based references ('phyloreferences') to elements on the Tree of Life that are unambiguous have fully computable semantics. To accomplish this, we are using OWL, OWL ontologies, and machine reasoning. Phyloreferences build on a large body of theoretical and applied work on phylogenetic taxonomy.

The overall deliverables of the project include a formal specification for phyloreference encoding and reasoning in OWL; ascertaining correctness of the specification using small-scale tests verifiable by domain experts; and a large-scale proof-of-concept application for using phyloreferences to navigate biodiversity data resources.

The full grant proposal is available at http://dx.doi.org/10.6084/m9.figshare.1401984 . Postdoctoral project responsibilities The postdoc will work closely with the project PIs and graduate students to generate the major project deliverables, which include the following:

1. As part of creating a specification for encoding phyloreferences and phylogenies in OWL, the postdoc will participate in OWL model and ontology development for phylogenies and phyloreferences; develop templates for constructing phyloreferences in OWL; and develop tools to convert published phylogenies and phyloreferences to OWL ontologies. 2. The postdoc will create an online proof-of-concept application that uses OWL reasoning to allow users to query biodiversity data resources using phyloreferences and Tree of Life-scale phylogenies.

All software source code, ontologies, and related products will be developed collaboratively on Github and be made available under open-source licenses.

Qualifications:

* PhD in Computer Science, Computational Biology, Bioinformatics or a related field * Domain knowledge in biology, biodiversity, or evolution is helpful, but not required. * Strong knowledge of Description Logic semantics, ontologies and modeling (ideally OWL ontologies). * Experience with logic machine reasoning (ideally OWL DL reasoners and entailments). * Strong programming experience in languages frequently used in scientific computing, and especially for computing with ontologies (Java, Scala, functional languages) and for managing or converting scientific data (e.g., Python). * Experience programming with OWL API or other APIs to working with machine reasoners. * Experience with web-application development (in particular using JavaScript, or microframeworks).

How to apply: To apply please submit a letter of interest and CV, together

— / —

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

UBern ConservationBiol

Our research group offers:

A postdoc position in conservation biology/restoration ecology 80-100% during 1 year

The candidate will work in an applied research program co-funded by the Swiss National Science Foundation, entitled: Grassland management: designing tomorrow's farmland for biodiversity

The successful candidate will work in the lowland module of the research program that experimentally tests, at field scale, novel management regimes that can restore and/or improve biodiversity in extensively managed meadows declared under the Swiss agri-environment scheme (AES). The research program was launched in 2010 with the objective to deliver evidence-based grassland management policy guidelines (see e.g. Buri et al. 2013 Agr. Ecosyst. Env.). The main task of the postdoc will be to analyse data collected in 2014 and 2015 (plants and field invertebrates) and prepare manuscripts. The ideal candidate must have a PhD degree, is familiar with agro-ecological issues and can justify of previous research experience in the field (assessed by publications). He/she must master modern analytical techniques and software. Strong writing skills in English is prerequisite. Starting date flexible, optimally between October 2015 and January 2016. Salary according to SNSF conditions (ca 6'300 - 6'800 CHF per month). Send a letter of motivation, your CV including a list of publications, summary of PhD thesis, as well as the names, institutional addresses, emails and phone numbers of two references to jean-yves.humbert@iee.unibe.ch.

Application deadline is 1 August 2015. Interviews of selected candidates will take place in Bern Tuesday 22 September 2015.

Prof. Raphaël Arlettaz and Dr Jean-Yves Humbert 12 May 2015

Jean-Yves Humbert, PhD University of Bern Institute of Ecology and Evolution Office: Erlachstrasse 9a Trakt 2 Mail: Baltzerstrasse 6, CH-3012 Bern Tel. +41 31 631 31 73 jean-yves.humbert@iee.unibe.ch http://www.iee.unibe.ch/cb/content/about_us/staff/jhumbert jean-yves.humbert@iee.unibe.ch

---

UBritishColumbia ConiferPopGenomics

We are looking for a postdoctoral fellow to join the AdapTree research team (http://adaptree.forestry.ubc.ca) at the University of British Columbia (UBC), Vancouver, BC, Canada. This large research team includes scientists at several universities, including Loren Rieseberg, Mike Whitlock, Sam Yeaman, and Tongli Wang (UBC), Andreas Hamann (University of Alberta), Jason Holliday (Virginia Tech), Katie Lotterhos (Wake Forest University), and Kay Hodgins (Monash University). We are assessing the genomics of local adaptation and climate-related traits with large sequence capture and SNP datasets for hundreds of populations of two widespread conifers. The boring bioinformatics is largely finished and we are looking for help with the exciting task of sifting through millions of SNPs to find interesting patterns. The ideal candidate will have experience with population genomics, analysis of next generation sequence data and SNP genotypes, GWAS methods, strong R skills, and fluency in perl or python, awk, and shell scripting. Alternatively, candidates with extensive knowledge of the molecular biology of abiotic stress response in plants but less familiarity with population genomics are also encouraged to apply.The position is initially for one year, starting July 1, 2015, but may be extended pending funding. Please send a CV and names of three references to Project Leader Sally Aitken, Department of Forest and Conservation Sciences, UBC (Sally.Aitken@ubc.ca).

"sally.aitken@ubc.ca" <sally.aitken@ubc.ca>

UBritishColumbia ProtistBiodiversity

RA in freshwater and marine protist biodiversity

The Department of Botany seeks a well-trained highly motivated and enthusiastic individual interested in exploring the diversity of protists in marine and costal environments using a combination of molecular environmental microbiological survey methods and microscopic identification.

The applicant must have a PhD or equivalent and at least three additional years of research experience. Essential skills include a well developed expertise in eukaryotic biodiversity, evolutionary history, and protist identification (in particular the testate amoebae), the use of single cell isolation and cultivation methods, developing next generation sequencing libraries for environmental tag sequencing, and basic skills in molecular biology and interpretation of large environmental sequence data sets. The applicant must have excellent written and oral communication skills and be highly organised.

The position is available starting Sept 1 2015 for an initial period of one year with a possibility for extension subject to a satisfactory performance and funding. To apply, please send a cover letter outlining research experience and interest, a curriculum vitae and the names and contact information for 3 referees to Patrick Keeling, Department of Botany, University of British Columbia, 3259-6270 University Boulevard, Vancouver, B. C. V6T 1Z4, Canada.Emailpkeeling@mail.ubc.ca. Fax (604) 822-6089. Closing date is June 26.

UBC hires on the basis of merit and is committed to employment equity. We encourage all qualified persons to apply, however, Canadians and permanent residents of Canada will be given priority.

"pkeeling@mail.ubc.ca" <pkeeling@mail.ubc.ca>

UCalifornia Riverside PlantBacteriaSymbiosis

The Sachs Lab at UC Riverside is recruiting a postdoctoral scholar to join our team.

The primary goals for this postdoc are flexible, but research will focus on the evolution, ecology, and genetics of plant-bacterial symbioses. To learn more about our lab see our website (http://www.sachslab.com/).

We work on wild, model, and crop legume species that interact with the bacterial symbiont lineages Bradyrhizobium and Mesorhizobium. The postdoc can propose research or can choose their primary research foci once they join the lab. Major projects in our lab include i) investigating the evolution and mechanisms of 'host control' traits in legumes that constrain exploitation in rhizobial symbiont populations, ii) uncovering competitive interactions among rhizobia in soil communities to explain the genomic and phenotypic drivers of rhizobial strain dominance, and iii) using greenhouse, in vitro experiments, and genotyping to generate novel applications to improve crop growth. Our group is broad and has included students focusing on plant biology, microbiology, genetics and genomics, and evolutionary ecology.

Candidates should have a Ph.D. in evolutionary biology, genetics, genomics, population biology, or related disciplines. Most importantly, the ideal candidate is a highly motivated scientists who can work independently and take projects from initiation to publication. Solid bacteriology skills and computational competence are both a plus for this position. A strong background in evolutionary and or molecular genetics would also be very useful. Finally, the ideal candidate would also have experience with next-generation sequencing techniques, which might include RADseq and highly-multiplexed-whole genome sequencing. Irrespective of experience, the postdoc must be able to learn new techniques and quickly and easily troubleshoot protocols. He or she will likely work closely with graduate students and the PI to manage multiple research projects and thus we seek a team player with excellent leadership skills.

The start date is flexible. The position will be available as early as July 2015, but can begin later if necessary. The position is initially for a one-year period, with possible extension of another year, dependent upon satisfactory performance. Salary is commensurate with experience and qualifications.

Interested individuals should send a CV, contact details of three referees, and a detailed cover letter describing their interest in the position to joel.sachs@ucr.edu. The cover letter should outline what types of research you would like to do in our lab and how your past experience prepares you for this research. Feel free to e-mail Joel Sachs to ask any questions about the position or our lab.

The University of California, Riverside has an active career partner program, and is an Affirmative Action equal opportunity employer committed to excellence through diversity.

joel.sachs@ucr.edu

UChile HumanGenomics

We are seeking candidates for a Postdoctoral position in Genetics to study the demographic history of settlers of Patagonia. The postdoc will work in a genomics and bioinformatics laboratory and will have available microarray genotyping data and whole genome sequence data from modern and ancient DNA from Patagonia (Chile and Argentina). He/she will also be responsible for generating and analyzing new data. Travel opportunities to our collaborators laboratory, Carlos Bustamante < http://med.stanford.edu/bustamantelab/ > in Stanford University.

Requisites:

* PhD in Genetics, Evolution or related field obtained between January 1st 2012 and November 1st 2015. * A motivation letter * A recommendation letter from a direct supervisor * Writing fluency in English

Desired skills:

* Strong background in quantitative or population genetics * Bioinformatic skills at user level * Spanish or willingness to learn

Funding:

* Through a FONDECYT Postdoctoral fellowship < http://www.conicyt.cl/fondecyt/2015/04/08/-concurso-postdoctorado-2016/ > (Spanish). * Successful applicants will apply for funding with the sponsorship and assistance of the laboratory PI (application will be in English).

Deadline:

* *May 8 2015*

Postdoc start date:

* November 2015

Interested should inquiries and application material to Dr. Ricardo Verdugo (raverdugo@u.uchile.cl).

Ricardo A. Verdugo S., M.V., Ph.D. Assistant Professor Human Genetics Program, ICBM Faculty of Medicine, University of Chile Independencia 1027, Santiago, Chile Phone: +56 (2) 2978 9527 raverdugo@u.uchile.cl http://genomed.med.uchile.cl “Ricardo A. Verdugo” <raverdugo@u.uchile.cl>

UCincinnati DrosophilaSensoryDivergence

A postdoctoral position is available in the Department of Biological Sciences at the University of Cincinnati to work on an NSF-funded study examining the genetic and neural factors underlying phenotypic divergence. The work will be conducted in the laboratories of Drs. Stephanie Rollmann and John Layne. The goal of the work is to elucidate the genetic and neurophysiological mechanisms underlying changes in the olfactory system that accompany adaptation to different ecological environments in Drosophila mojavensis. The successful candidate will have demonstrated expertise in evolutionary genomics and/or sensory biology. Technical expertise in single sensillum/electrophysiological recordings, and/or next generation sequencing technology, as well as bioinformatics analysis is strongly desired. The successful candidate will also have excellent verbal, written, and organizational skills. The appointment is for one year with the possibility of renewal contingent upon sufficient progress.

To apply, visit https://jobs.uc.edu and search for Requisition ID 2742. Applications should include: (a) cover letter outlining your research interests, scientific accomplishments, and your motivation to work on this project; (b) curriculum vitae (c) names of three references with their contact information. Questions should be addressed to stephanie.rollmann@uc.edu. Application review will continue until the position is filled.

The University of Cincinnati is an affirmative action/equal opportunity employer/ M/F/Vet/Disabled.

rollmasm@ucmail.uc.edu

UCollegeCork 5 EvolutionaryBehaviouralBiol

Up to 5 Research positions in Evolutionary Behavioural Ecology

[3]The evolutionary ecology of cognition across a heterogeneous landscape[2] (EVOECOCOG: ERC funded project)

Why do individuals vary in their cognitive abilities? EVOECOCOG takes the disciplines of cognition and evolutionary biology into a natural setting to answer this question. It aims to do this by investigating a variety of proximate causes and population-level consequences of individual cognitive variation using a great tit Parus major population. The project represents one of the first large-scale integrative studies of cognitive performance on any wild population.

Three objectives capture the project^{1}s broad scope: 1) To characterise proximate causes of variation in cognitive and other associated traits, including personality, all of which can influence similar ecologically important behaviour. Quantitative genetic, social, parasite-mediated, and physiological causes will be explored. 2) To examine links between these traits, key functional behaviours and trade-offs, e.g., space use, niche specialization, predation, parental care and promiscuity; and 3) To examine the consequences of this variation for life histories, fitness, natural and sexual selection.

Dates: Application deadline is 1 June 2015. Interviews will be held initially by Skype within 2 weeks. Start dates are mid-July or as soon thereafter as possible.

For further information, please contact Prof. John L. Quinn at j.quinn@ucc.ie

University College Cork is one of Ireland^{1}s largest and most successful universities. The research would be conducted in the School of BEES which consists of 20 faculty (including 3 holders of current ERC grants), ca. 20 postdocs and 50 PhD students across Zoology, Ecology, Plant Sciences and Geology. Cork is situated on the south coast of Ireland, 2.5 hours from Dublin,is served by an international airport, has a population of about 200,000, and is on the doorstep of some of the most beautiful coastline in Europe.

"Quinn. John" <J.Quinn@ucc.ie>

UEdinburgh QuantitativeGenetics

Postdoctoral Researcher in Quantitative Genetics

Salary Range: Â£31,342 - Â£37,394 per annum

The Roslin Institute is a world-class centre for quantitative genetics, particularly of managed animal populations such as livestock and companion animals. We have a vacancy for a post-doctoral researcher in quantitative genetics to work alongside Dr. Pam Wiener (Roslin), Dr. John Hickey (Roslin) and Dr. Marie Haskell (Scotland's Rural College) on the genomic dissection of behavioural characteristics in dogs. The post will involve the development of a low-density platform for genotyping two major dog breeds, characterisation of behavioural traits based on questionnaire data and genomic association and prediction analyses of the behavioural data.

The successful applicant will have (or be close to having) a PhD in Quantitative Genetics, Population Genetics, Statistics, Biology, or a related area. The candidate will be expected to have experience of working with large-scale SNP marker data, for example, genome-wide association mapping and genomic prediction, and experience with multivariate statistical analysis. Demonstrable skills in project and sample management, ability to communicate effectively with the public and the oral and written communication of scientific results are also essential.

The post-holder will join the Genetics and Genomics department at the Institute, which comprises 24 research groups. He/she will also join a large and active group of scientists across Edinburgh researching the genetics of complex traits. The successful candidate will have the chance to collaborate with leading researchers in the field and to present results at meetings and conferences.

The post is funded for two years with the possibility of extension.

For further information, please see http://www.roslin.ed.ac.uk/vacancies/033268/research-fellow/ or contact pam.wiener@roslin.ed.ac.uk

Closing Date: 12 June 2015

Applications can be made via this weblink: http://www.roslin.ed.ac.uk/vacancies/033268/research-fellow/ Pam Wiener The Roslin Institute and Royal (Dick) School of Veterinary Studies University of Edinburgh Easter Bush, Midlothian EH25 9RG, UK

phone: 44 (0) 131 651 9209 email: pam.wiener@roslin.ed.ac.uk Â "The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336

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

"pam.wiener@roslin.ed.ac.uk"
<pam.wiener@roslin.ed.ac.uk>

UHelsinki EcolGenetics

Postdocoral reseacher position in Ecological Genetics

The University of Helsinki, founded in 1640, is one of the world's leading universities for multidisciplinary research. The university has an international academic community of 40,000 students and staff members. The University of Helsinki offers comprehensive services to its employees, including occupational health care and health insurance, sports facilities, and opportunities for professional development. The International Staff Services office assists employees from abroad with their transition to work and life in Finland.

The Department of Biosciences situated at the Viikki science park belongs to the Faculty of Biological and Environmental Sciences of University of Helsinki and is the largest research and teaching unit in biosciences in Finland. The Department of Biosciences is one of the largest departments of Helsinki University with its c. 25 million euro budget and over 400 staff members.

The Department of Biosciences invites applications for a

TWO-YEAR POST DOCTORAL RESEARCHER POSITION

in the Ecological Genetics Research Unit, headed by Prof. Juha Merilä.

The Ecological Genetics Research Unit is part of the Department of Biosciences which hosts research community of experimental, computational, and theoretical labs with common interest in Evolutionary Biology. Cutting edge infrastructure is available at all levels, including high-performance computer clusters, access to next-generation sequencing facilities, molecular biology labs and animal breeding facilities.

The main goal of this Academy of Finland funded postdoctoral project is to address questions about the genetic underpinnings of quantitative trait variation within and among different populations of stickleback fishes. Large datasets (SNPs and full genome sequences) will be analysed with QTL- and association mapping, along with other population genomic approaches. Questions relating to phylogeographical relationships among different populations and species of sticklebacks, as well as the relative roles of selective and neutral processes underlying the inferred relationships, are also to be addressed within this project. Opportunities for collaborative projects with other unit members and research associates are possible. The candidate would be given freedom to pursue their own ideas and research interests within the general framework of the main project.

We are looking for an ambitious postdoctoral researcher with strong enthusiasm towards science. The successful candidate should have PhD / post doctoral experience within the fields of evolutionary genetics/genomics, bioinformatics and/or animal breeding, with genuine interest towards addressing problems at the population level (rather than comparative genomics). Excellent bioinformatics skills and experience in handling both large marker datasets and full-genome sequence analyses (e.g. programming in C, or scripting language Python and/or Perl), as well as good written and verbal communication skills in English are required. The preferred starting date is 1st January 2016, but an earlier start date is negotiable (earliest possible start date: 1st October 2015). The employment contract includes a trial period of 4 months.

The salary will be based on level 5 of the demands level chart for teaching and research personnel in the salary system of Finnish universities. In addition, the appointee will be paid a salary component based on personal work performance. The total minimum salary at the beginning of the employment is 3127,54 euro/month.

To apply, please send your CV with publication list and contact details of two references, and a letter (max 2 pages) with a description of your research interests and career goals. In particular, please provide clear motivation for your suitability as a candidate for this position. Send these documents as a single pdf-file to hy-kirjaamo@helsinki.fi.

Apply at latest 31 July 2015 by 15.45 local Helsinki time.

For more information, please contact Prof. Juha Merilä (juha.merila@helsinki.fi), Tel: +358-40-8374165.

More information about host groups research profile, please consult e.g. http://www.helsinki.fi/biosci/-egru/publications/publications.html Apply at latest 31.07.2015

Apply for job

Baocheng Guo <baochengguo@gmail.com>

UHelsinki EvolGenomics

Postdoctoral position in evolutionary genomics at University of Helsinki

The project

The main goal of this Academy of Finland funded postdoctoral project is to address questions about the genetic underpinnings of quantitative trait variation within and among different populations of stickleback fishes. Large datasets (SNPs and full genome sequences) will be analysed with QTL- and association mapping, along with other population genomic approaches. Questions relating to phylogeographical relationships among different populations and species of sticklebacks, as well as the relative roles of selective and neutral processes underlying the inferred relationships, are also to be addressed within this project. Opportunities for collaborative projects with other unit members and research associates are possible. The candidate would be given freedom to pursue her/his own ideas and research interests within the general framework of the main project.

Requirements

We are looking for an ambitious postdoctoral researcher with strong enthusiasm towards science. The successful candidate should have PhD / post doctoral experience within the fields of evolutionary genetics/genomics, bioinformatics and/or animal breeding, with genuine interest towards addressing problems at the population level (rather than comparative genomics). Excellent bioinformatics skills and experience in handling both large marker datasets and full-genome sequence analyses (e.g. programming in C, or scripting language Python and/or Perl), as well as good written and verbal communication skills in English are required.

Starting date

The preferred starting date is 1st January 2016, but an earlier start date is negotiable (earliest possible start date: 1st October 2015). The employment contract includes a trial period of 4 months.

Salary

The salary will be based on level 5 of the demands level chart for teaching and research personnel in the salary system of Finnish universities. In addition, the appointee will be paid a salary component based on personal work performance. The total minimum salary at the beginning of the employment is 3127,54 euro/month.

How to apply

To apply, please send your CV with publication list and contact details of two references, and a letter (max 2 pages) with a description of your research interests and career goals. In particular, please provide clear motivation for your suitability as a candidate for this position. Send these documents as a single pdf-file to hy-kirjaamo@helsinki.fi Apply at latest 31 July 2015.

Information

For more information, please contact Prof. Juha Merilä (juha.merila@helsinki.fi), Tel: +358-40-8374165.

More information about host groups research profile, please consult e.g. http://www.helsinki.fi/biosci/egru/-publications/publications.html About the host institute

The University of Helsinki, founded in 1640, is one of the world's leading universities for multidisciplinary research. The university has an international academic community of 40,000 students and staff members. The University of Helsinki offers comprehensive services to its employees, including occupational health care and health insurance, sports facilities, and opportunities for professional development. The International Staff Services < http://www.helsinki.fi/intstaff/ > office assists employees from abroad with their transition to work and life in Finland.

The Department of Biosciences situated at the Viikki science park belongs to the Faculty of Biological and Environmental Sciences of University of Helsinki and is the largest research and teaching unit in biosciences in Finland. The department of is one of the largest departments of Helsinki University with its c. 25 million euro budget and over 400 staff members. It hosts research community of experimental, computational, and theoretical labs with common interest in Evolutionary Biology. Cutting edge infrastructure is available at all levels, including high-performance computer clusters, access to next-generation sequencing facilities, molecular biology labs and animal breeding facilities.

Juha Merilä <juha.merila@helsinki.fi>

UKansas EvolutionaryAdaptation

Where: Reuman lab, Department of Ecology and Evolutionary Biology, University of Kansas

What: Postdoctoral researcher position available in population/community ecology

Dr Daniel Reuman is recruiting into his lab in the University of Kansas Department of Ecology and Evolutionary Biology. The broad research goal of the lab is to mechanistically understand and predict the consequences of human impacts such as global warming on populations, communities, and ecosystems. We use quantitative tools and collaborate widely with field and laboratory workers to explain observations, confront theory with data, and make predictions. Example projects can be found at http://www.reumanlab.res.ku.edu/. Two to three years of funding are currently available. Several diverse opportunities exist to contribute to and take leadership roles in ongoing research directions in collaboration with current lab members and a network of collaborators in the USA and Europe, and to develop new directions.

We seek individuals who are demonstrably passionate about quantitative approaches to questions in population, community and landscape ecology that fit into the broad goals of the lab. A PhD or ABD in a related field is required. Researchers with backgrounds in life or physical sciences or computing or mathematics will be considered if they can demonstrate a driving motivation for both the quantitative approach and the biological questions of the lab.

The University of Kansas (KU) is a major research university with special strength in ecology and evolutionary biology. The EEB department has >40 tenured and tenure-track faculty working in a wide variety of areas, with National Research Council and Chronicle of Higher Education rankings in the top 10 in the USA. KU is located in the town of Lawrence, Kansas, about 40 miles from Kansas City. Lawrence is a progressive and cosmopolitan university town of about 100,000 people, with vibrant art, music, and sports scenes. Lawrence was ranked among the top ten college towns in the country in 2012 by livability.com, beating, for instance, Ann Arbor, MI, and Austin, TX.

For questions contact Dan Reuman at reuman@ku.edu. To apply see http://employment.ku.edu/staff/1768BR. To apply, please submit a CV, cover letter of up to two pages, and your best publication. Initial review of applications begins 20 June, 2015. Position open until filled.

“d294r143@ku.edu” <d294r143@ku.edu>

UKonstanz 2and5year ComparativeGenomics

Postdoc positions (2-years or 5-years) available in molecular evolution, comparative genomics and evo-devo at the University of Konstanz in Germany

The Zukunftskolleg at the University of Konstanz provides generous funding for two types of Postdoctoral fellowships. The funding for 2-year or 5-year fellowships is meant to support postdocs on their way towards academic independence. These fellowships also offer the opportunity to apply for significant internal funding for research expenses.

Zukunftskolleg Fellows need an academic sponsor and host laboratory. Zukunftskolleg Fellows should therefore propose research projects that fit with a particular host laboratory at the University of Konstanz and should be of collaborative and interdisciplinary nature.

Please visit https://www.zukunftskolleg.uni-konstanz.de/funding-programmes/fellowship/ for more information.

DEADLINE: May 18th 2015

Axel Meyers lab at the Department of Biology at the University of Konstanz welcomes applications from motivated Ph.D. biologists or postdocs who are interested in the fields of either molecular evolution, comparative genomics, and / or the evolution of developmental mechanisms. More specific information on our ongoing research projects can be found on the Meyer-Lab’s www pages.

http://www.evolutionsbiologie.uni-konstanz.de The University of Konstanz is among the most highly ranked institutions in Germany and provide a lively and academically outstanding research environment. Konstanz is a lovely historic town located on Lake Constance on the southern German border to Switzerland.

Additional information can be obtained from: axel.meyer@uni- konstanz.de , phone: +49 (0) 7531 / 88 - 4163, fax + 49 (0) 7531 / 88 - 3018 or from our website: http://www.evolutionsbiologie.uni-konstanz.de . Applications should be received by the Zukunftskolleg before May18th, 2015.

Prof. Axel Meyer, Ph.D. Lehrstuhl f^{1}r Zoologie und Evolutionsbiologie Department of Biology Building M, Room M806 University of Konstanz 78457 Konstanz Germany

fon + 49 (0)7531 88 4163 fax + 49 (0)7531 88 3018

secretary: Ingrid.Bader@uni-konstanz.de tel. + 49 (0)7531 88 3069

www.evolutionsbiologie.uni-konstanz.de Axel Meyer <a.meyer@uni-konstanz.de>

ULausanne Bioinformatics

Postdoc in bioinformatics

A postdoc position is available on a project to study the evolutionary dynamics of genomes and transcriptomes. The postdoc will work in collaboration on two projects:

(1) Evo-devo genomics, in the Robinson-Rechavi lab: evolutionary study of the duplication history of chordate genomes, including de novo assembly of a Mediterranean amphioxus genome from PacBio long reads, and comparative transcriptomics analysis from RNA-seq: (2) Evolution of sex chromosomes, in the Pannell and Perrin labs: assembly and polymorphism analysis of sex chromosomes from plants and amphibians.

The postdoc would be expected to take a leading position on the bioinformatics of the genomics of non-model organisms, and to participate actively in evolutionary analyses and interpretation. The postdoc will work closely with other bioinformaticians and evolutionary genomicists on both projects. In the medium term, the postdoc will be expected to develop his or her own subproject and publications.

The position will be in co-supervision between Profs Marc Robinson-Rechavi, John Pannell and Nicolas Perrin, all three in the Department of Ecology and Evolution. Prof Robinson-Rechavi is also a group leader at the Swiss Institute of Bioinformatics, and the postdoc will also be a full member of the SIB. The starting contract will be for 1 year, starting as soon as possible, renewable for up to five years; the postdoc will participate in some undergraduate and/or masters teaching, in English or in French.

The ideal candidate would have a doctorate degree in bioinformatics, genomics, or a related field; a good command of Unix and another programming language; hands-on experience with genomic data; and an interest in pursuing research on non model organisms. Experience with the R language and cluster computing would be beneficial. Funds for the position are available immediately, and our preference would be to appoint someone to the position this summer, if possible.

Full applications, which should include a cover letter, a CV, and the contact information of 3 referees, should be sent to marc.robinson-rechavi@unil.ch as a single PDF document. Informal enquiries should be directed to marc.robinson-rechavi@unil.ch; john.pannell@unil.ch; and/or nicolas.perrin@unil.ch.

Deadline for applications: all applications received by May 22, 2015, will be given full consideration, but the position will remain open until the right candidate has been appointed.

For background on the labs in which you would be working, please see: Robinson-Rechavi lab: http://bioinfo.unil.ch/ Pannell lab: http://www.unil.ch/dee/home/menuinst/research/group-pannell.html Perrin lab: http://www.unil.ch/dee/home/menuinst/research/group-perrin.html John Richard Pannell <John.Pannell@unil.ch>

UmeaU PopulationGenetics

Please find below an ad for a post doc position in my lab. The full ad and form for online application can be found at:

https://umu.mynetworkglobal.com/en/what:job/jobID:64261/where:4/ We are looking for a postdoc in population genetics within the project “An integrated approach to understanding the annual growth cycle in trees” funded by the Knut & Alice Wallenbergs foundation. The position is full time for two years and is placed in UmeÃ. The deadline for applications is 2015-06-01 and the position is expected to start in September 2015 or upon agreement.

Project description We are looking for a postdoc for a project aimed at investigating genetic variation in European aspen (Populus tremula) and association with naturally occurring variation in phenology. The project will be based on data from whole-genome re-sequencing of a reference population consisting of approximately a hundred individuals and data on epigenetic variation from the same population. The goal is to identify the genes that regulate natural variation and local adaptation in important phenology traits to local growing conditions, such as temperature and daylength.

Formal requirements Successful candidates will have a PhD degree, or equivalent, in ecology or genetics. To be eligible for this position, you should have completed your doctoral degree maximum three (3) years before the end of the application period, unless certain circumstances exist.

Qualifications The work will primarily involve bioinformatic and statistical analyses of Next Generation Sequencing (NGS) data, although there are also possibilities for doing field work, greenhouse and lab experiments. The project is run in collaboration with a number of research groups at UmeÃ Plant Science Centre. Excellent proficiency in English is required, as English is the working language in the research group. Prior experience of working with NGS data in a population genetics context is required. Knowledge in bioinformatics/statistics and prior experience of working with epigenetic questions is a merit.

Terms of employment The candidate should preferably be available from September 2015 but a later start can be arranged. The position is for full time, funded for two years and placed in UmeÃ.

How to apply You apply through our recruitment system MyNetwork Pro. Log into the system and apply via the button on the web page. The application should contain the following, written in English or in Swedish:

* A personal cover letter including why you are interested in this position and how you can contribute to the research group (max two pages) * CV including list of publications * Certified copies of certificates as well as other relevant documentation. * Names and contact details of three references.

The Department of Ecology and Environmental Science carries out research and postgraduate education in ecology, environmental science and physical geography. The department has about 160 employees, about 20 of whom are post-docs. For more information, visit www.emg.umu.se . Pär K. Ingvarsson Professor, Evolutionary Genetics UmeÃ Plant Science Centre Department of Ecology and Environmental Science Linneaus väg 6 UmeÃ University, SE-901 87 UmeÃ, Sweden tel. +46-(0)90-786-7414, fax. +46-(0)90-786-6705

Pär Ingvarsson <par.ingvarsson@umu.se>

UMelbourne LightAdaptation

A fixed term full-time Postdoctoral position (Level A) is available at the School of BioSciences (Faculty of Science), University of Melbourne.

The Research Fellow will be responsible for designing, executing, and analysing field and laboratory experiments, as part of the research project “The dark side of night: species and community impacts of night lighting”, which is funded by an ARC Discovery grant.

The research is part of an international collaboration between the University of Melbourne (Dr Theresa Jones and Prof Mark Elgar), the University of Exeter (Prof Kevin Gaston) and the Netherlands Institute of Ecology (Prof Marcel Visser).

The position is located at The University of Melbourne and reports to the Chief Investigator.

Salary: $64,863* - $88,016 p.a. (*PhD entry Level $81,998 p.a.) plus 9.5% superannuation

For further information please see the attached PDF.

Dr Theresa Jones Senior Lecturer - The Behaviour and Evolution Group The School of BioSciences, The University of Melbourne Victoria 3010, Australia

Tel: +61 (0)3 90359576

Theresa Melanie Jones <theresa@unimelb.edu.au>

UMelbourne LightAdaptation 2

A fixed term full-time Postdoctoral position (Level A) is available at the School of BioSciences (Faculty of Science), University of Melbourne.

The Research Fellow will be responsible for designing, executing, and analysing field and laboratory experiments, as part of the research project “The dark side of night: species and community impacts of night lighting”, which is funded by an ARC Discovery grant.

The research is part of an international collaboration between the University of Melbourne (Dr Theresa Jones and Prof Mark Elgar), the University of Exeter (Prof

Kevin Gaston) and the Netherlands Institute of Ecology (Prof Marcel Visser).

The position is located at The University of Melbourne and reports to the Chief Investigator. Salary: $64,863* - $88,016 p.a. (*PhD entry Level $81,998 p.a.) plus 9.5% superannuation

For further information please visit the website: http://jobs.unimelb.edu.au/caw/en/job/885888/-research-fellow .

Dr Theresa Jones Senior Lecturer - The Behaviour and Evolution Group The School of BioSciences, The University of Melbourne Victoria 3010, Australia Tel: +61 (0)3 90359576

Theresa Melanie Jones <theresa@unimelb.edu.au>

UMichigan AntibioticResistanceEvolution

Evolutionary Medicine

We are looking for a brave, ambitious, fun and skilled post-doc with a very strong background in evolutionary biology who is interested in real time evolution in a US hospital setting. We want to do evolutionary risk analyses with a view to understanding the clinical decisions which drive resistance evolution. It is our contention that much of the conventional wisdom in this area has a very poor evidence base, and that understanding what is going on quantitatively will make possible evidence-based resistance management. This project is a collaboration between an Infectious Disease physician with a very strong background in evolutionary biology (Woods MD/PhD) and an evolutionary biologist with a strong interest in hospital infections (Read PhD), and will be primarily focused on data generated by clinicians during patient care. The position is based in the University of Michigan Hospital, Ann Arbor, with the expectation of considerable time at the Center for Infectious Disease Dynamics, Penn State.

Here's the formal stuff:

RESEARCH FELLOW

Job Summary The Department of Internal Medicine, Division of Infectious Diseases is seeking a post-doctoral applicant to take the lead on development, implementation and analysis of ecological and evolutionary models of antibiotic resistance, which could include agent-based models and compartmental dynamical model, including model fitting and parameter estimation. Additionally, the application will be expected to gather and critical synthesize literature for metanalyses, as well as take the lead on writing of manuscripts for publication.

This is a collaborative project between the labs of Robert Woods at the University of Michigan and Andrew Read at Pennsylvania State University. The position will be based at the University of Michigan, with some time spent at the Center of Infectious Disease Dynamics at Penn State.

Required Qualifications Ph.D. required. Experience coding in R or python is a requirement. Significant publication track record in this area, ideally with postdoctoral experience.

Desired Qualifications Experience fitting microbiological data to ecological and evolutionary models, and a track record of collaboration with mathematicians, statisticians, biologists, and public health officials is an advantage.

Full details and application process at http://-umjobs.org/job_detail/110426/research_fellow Informal inquiries to Bob Woods (robertwo@med.umich.edu) or me (a.read@psu.edu).

– Andrew Read PhD, Director, Center for Infectious Disease Dynamics, Evan Pugh Professor of Biology and Entomology, Eberly Professor in Biotechnology, The Pennsylvania State University, University Park PA 16802, USA

www.thereadgroup.net www.cidd.psu.edu www.bio.psu.edu www.ento.psu.edu +814 867-2396 (office, biology) +814 863-4444 (office, entomology) +814 867-2397 (lab) +814 865-1250 (fax) +814 321-5004 (cell) Staff Assistant Monica Arismendi mha15@psu.edu; +814 863-6471

"a.read@psu.edu" <a.read@psu.edu>

UMinnesota PopulationGenomics

Mexican cave tetras offer a unique opportunity to study how recombination, selection, drift, and introgression shape genomic divergence. Cave tetras experience vastly different selection pressures than do conspecifics living in surface waters. Distinct phenotypes and behavioral differences have evolved and are maintained in the cavefish populations, while in some caves, substantial gene flow between surface and cavefish is ongoing. There are multiple, independent origins of cavefish in separate caves, providing a naturally replicated experiment.

In collaboration with most of the US-based cavefish labs, we have generated whole genome resequencing data. The postdoctoral position would include analysis of these data and writing manuscripts. In addition, the successful candidate would gather data for some work on recombination, stress, and aging and help with maintenance of the lab.

The postdoc will be a 'go-to' person in our group for troubleshooting everyday computational and molecular methods, and therefore seek applicants with extreme persistence and patience, as well as excellent communication skills. In addition to the duties above, the postdoc will be encouraged to develop an independent research project that complements ongoing research in the McGaugh lab and submit this as an NIH-NRSA within the first year of employment. If the candidate desires an opportunity to hone teaching skills, opportunities to guest-lecture in large enrollment classes may also be arranged.

A background in genomics is preferred.

There is flexibility in the start date, but ideally the candidate would start by Summer or Fall 2015. The position is initially available for one year with additional renewals contingent on performance. A longer appointment may be based on both performance and funding.

Interested applicants should send a preliminary inquiry with CV, references, and statement of why you are interested in joining the lab to [smcgaugh AT umn d0t edu] prior to submitting an application.

Completed applications should be submitted via the UMN website and should include: a CV, a cover letter describing your interest and suitability, undergraduate and graduate transcripts (if applicable), contact information for three references.

myu.umn.edu/employment

Job opening ID- 300477

For more information on the McGaugh lab see https://sites.google.com/site/mcgaughlab/ Minimum Qualifications

1) A PhD in genomics, evolution, genetics, or related fields (by the start of employment)

2) Experience with next-gen sequence data and a unix/command line interface.

3) Demonstrated ability to produce high-quality publications.

4) A desire to help lead an integrative and motivated group of young scientists.

5) Patience, dedication, flexibility, and enthusiasm.

6) Excellent communication skills.

Preferred Qualifications

1) Working knowledge of population genetics

2) Working knowledge/interest of the genetics underlying aging, stress, and recombination.

3) Experience with scripting/programming languages including R, python, and/or C++

Suzanne McGaugh <smcgaugh@umn.edu>

UMontreal PrimateFunctionalGenomics

Post-doctoral Position in nonhuman primate functional genomics

A postdoctoral position in nonhuman primate functional genomics is available under the co-mentorship of Dr. Luis Barreiro (University of Montreal and at the Sainte-Justine Hospital Research Center) and Dr. Jenny Tung (Duke University). Collaborative projects between our labs focus on the biological consequences of social relationships and social stressors in primates, using genomic and computational tools. More details on some of our ongoing projects can be found at http://luis-barreirolab.org/ or http://www.tung-lab.org . Postdoctoral applicants should have a strong background in evolutionary, behavioral, or computational genomics. Strong data analysis skills, including programming and statistical modeling experience, are essential. Familiarity or experience with primate behavior or population genetics is a plus. The applicants will have the freedom to choose their own projects as long as they fit within the general interests of our collaborative research.

Our labs offer congenial research environments that foster strong interdisciplinary training and collaborative exchange. This position is posted through the University of Montreal, with flexibility to be physically based either in Montreal or in North Carolina.

To apply for the position please send an email to Luis Barreiro (luis.barreiro@umontreal.ca) and Jenny Tung (jt5@duke.edu) including a cover letter, current CV, and contact information for at least two references.

Luis Barreiro, PhD. *Assistant Professor * *CHU

Sainte-Justine/University of Montreal* *Canadian Research Chair in Functional and Evolutionary * *Genomics of the Immune System. * 3175, Côte Sainte-Catherine, *Phone# : 514-345-4931 ext. 2544* *e-mail: luis.barreiro@umontreal.ca

lbbarreiro@gmail.com

UMuenster 2 GenomicEvolution

The Bornberglab has the following openings:

POSTDOCtoral research associate (TVL13 100%FTE): to work on COMPARATIVE GENOMICS OF SOCIAL INSECTS and/or MOLECULAR EVOLUTION UNDERLYING AGEING and caste development. Application deadline is June 30th 2015 and commencing date is either late 2015 or early/mid 2016. Candidates should have experience in molecular evolutionary biology, insect genome analysis and life history traits, good skills scripting languages for bioinformatics and excellent communication skills for interaction with collaborations partners across Germany and abroad.

See http://bornberglab.org/positions for further details.

POSTDOCtoral research associate (TVL13 100%FTE): to work on the DE NOVO EMERGENCE AND EVOLUTION OF new PROTEINS using candidate genes from genomic data and their reconstructed presumed ancestors, but with an emphasis on EXPERIMENTAL VERIFICATION of biophysical properties and biochemical functions of expressed proteins. Application deadline is July 31st 2015 and commencing date is either late 2015 or early/mid 2016. Candidates should have experience in some of the following fields: molecular and/or structural biology concerning proteins, NMR spectroscopy or related techniques, protein cloning, purification and crystallisation, enzymatic kinetic assays.

See http://bornberglab.org/positions for further details.

Erich Bornberg-Bauer PhD, Prof. of Molecular Evolution + Genomeinformatics Institute for Evolution and Biodiversity, Huefferstrasse 1 D-48149 Germany Westfalian Wilhelms University Muenster, bornberglab.org ebb.admin@wwu.de Phone / Fax / Direct Line: +49 (0) 251 83 21630 / 24668 / 21011

"E. Bornberg" <ebb@uni-muenster.de>

UNamur Belgium Bioinformatics

Postdoctoral bioinformatician in Evolutionary genomics, UNamur, BELGIUM

A 3-year postdoctoral bioinformatician position is available to work on the genome evolution of bdelloid rotifers within the group of Prof.Karine Van Doninck (Laboratory of Evolutionary Genetics and Ecology) atthe University of Namur (Belgium). The postdoctoral researcher will work on two projects, funded by ARC and FNRS-MIS, with as main objective to investigate the origin and causes of the genomic peculiarities found in the bdelloid rotifer /Adineta vaga./

Using next-generation sequencing (NGS) we previously characterized the degenerate tetraploid genome structure of the bdelloid rotifer /Adineta vaga/ with massive genomic rearrangements involving most of the longest scaffolds. As a consequence, no homologous pair of chromosomes could be identified within this genome providing the first genomic hallmark of ameiotic evolution within this bdelloid rotifer clade. Another peculiarity observed in the genome of /A. vaga/ is the high percentage of genes (8%) of non-metazoan origin and probably acquired through horizontal gene transfer (HGT) (see Flot et al_Nature_2013). These features could be conferred by their long-term ameiotic evolution. Nonetheless, the unusual lifestyle of many bdelloid rotifers, involving repeated cycles of desiccation and the associated DNA DSBs (see Hespeels et al_JEB_2014), may also contribute to genome structure evolution. In order to determine the origin and causes of these genomic peculiarities we are starting a comparative analysis of genomes of different bdelloid species that diverged a long time ago, including lineages that have lost the ability to withstand desiccation, and of an /A. vaga/ clone submitted to several rounds of desiccation. The postdoc will conduct bioinformatic analyses of genomic (and transcriptomic) data being generated.

The current team of researchers working on bdelloid rotifers within the 2 projects include 3 Principal Investigators (Prof. K. Van Doninck and Dr. F. Chainiaux from UNamur and Prof. B. Hallet from UCL), 2 postdoctoral researchers, 3 PhD students, 2 Master students and 2 technicians.

Contacts: Prof. Karine Van Doninck, karine.vandoninck@unamur.be University of Namur, Laboratory of Evolutionary Genetics and Ecology http://www.lege-unamur.be Application: Applicants should have a PhD in a relevant area. Priority will be given to candidates with a proven track record (with several publications as a first author) who will express their motivation to the project. The position is for 3 years starting preferably on the 1st of July 2015.

The closing date for applications is 15th of May 2015.

Interested applicants should send a cover letter (briefly describing research experience, interests, and career goal), curriculum vitae (with list ofpublications), and the names of three references (including address,phone number and Email) to Karine VAN DONINCK (karine.vandoninck@unamur.be)

Karine VAN DONINCK Full Professor Department of Biology

T. +32 (0)81 724 407 F. +32 (0)81 724 362 karine.vandoninck@unamur.be http://perso.fundp.ac.be/~kvandoni/

Université de Namur ASBL Rue de Bruxelles 61 - 5000 Namur Belgique

Let's respect the environment together. Only print this message if necessary!

Karine Van Doninck <karine.vandoninck@fundp.ac.be>

UppsalaU ComputationalMolEvol

Investigating insertion and deletion in genomic inference —

A post-doctoral fellowship in molecular evolution is available working with Simon Whelan at Uppsala University, Sweden. The postdoc will join a project working on the development and application of phylogenetic methods for studying insertion and deletion both within protein families and on the genome scale.

The project has two broad aims. The first is to apply probabilistic methods we have been developing to study insertion and deletion rates from aligned or unaligned sets of sequences. We will use these estimated rates to study how patterns of insertion and deletion vary through the genome, both in genes and intergenic DNA, and how evolutionary forces affect these fundamental processes. The second aim of the project is to use this acquired knowledge of insertion and deletion to filter or rearrange multiple sequence alignments to better reflect the true homologous relationships between bases or residues. These approaches will be assessed through their ability to correctly estimate sequence divergence, natural selection and phylogeny using both empirical and simulation data sets. There is also the possibility for the fellow to develop their own research interests, providing they fit within the broad scope of the project outlined above.

The fellowship will be located at the Evolutionary Biology department at the Evolutionary Biology Centre (EBC), Uppsala, Sweden. Uppsala is a leading centre for evolution and ecology research, with a large number of research groups in the subject area. The Evolutionary Biology department (http://www.ebc.uu.se/Research/IEG/evbiol/?languageId=1) is a diverse and multi-cultural department, with both computational and laboratory based research groups working on evolutionary genomics, speciation, population genetics and phylogenetics. The fellowship will be supported by the Carl Tryggers Stiftelse (CTS) and will be initially for one year, with the possibility of extending for an additional year. Details of this fellowship are available (in Swedish; Google Translate works reasonable well) at http://www.carltryggersstiftelse.se/ and CTS make the final appointment of the fellow based on the conditions outlined there. The fellowship would be expected to start as soon as possible. If you have any questions regarding the research project or anything else about the fellowship please contact me.

Please send your application to simon.whelan@ebc.uu.se in a single pdf file containing the following information:

* Cover letter; * CV, including publication record; * A brief statement (max. 2 page) outlining your research interests, experience, and ambitions; and * Contact information (name/address/phone/e-mail) for 2-3 referees.

The recruitment will be ongoing until a suitable candidate is found.

Regards,

Simon Whelan

Simon Whelan | Evolutionary Biology Centre, Uppsala University | T: +46-(0)18-4716483

simon.whelan@ebc.uu.se

UVirginia Bioinformatics Genomics

Bioinformatics/Genomics Postdoc in Gut Microbiome Studies

Gut microbes play important roles in human health and disease. Central to gut microbial community dynamics is how nutrients flow between community members as well as between the community and its host. The laboratory of Dr. Martin Wu at the Department of Biology University of Virginia is seeking a postdoctoral research associate to work on a project to map and predict metabolic fluxes between gut microbiome and host. Activities will include RNA-Seq, whole genome shotgun metagenomics and 16S RNA sequencing library preparations and next-generation sequencing data analyses. This is a collaborative project funded by NIH. More information about the project can be found at https://grantome.com/grant/NIH/R01-GM108501-02 Applicants will have a Ph.D. in the field of biology, computational biology, or related field by the start date. Molecular biology skills are highly desirable. Applicants should have substantial experience with scripting (e.g. Perl or Python), Linux and bioinformatics tools. Experience with next-generation sequencing data analysis is also required. This is a one-year appointment; however, appointment may be renewed for an additional two one-year increments, contingent upon available funding and satisfactory performance.

To apply, please submit a candidate profile through Jobs@UVA (https://jobs.virginia.edu) and electronically attach: curriculum vitae with list of publications, a cover letter that summarizes your background and career interests, and contact information for three (3) references. Search on posting number 0616383. Review of applications will begin May 31, 2015. However, the position will remain open until filled.

Questions regarding this position should be directed to: Dr. Martin Wu (mw4yv@virginia.edu).

Questions regarding the Candidate Profile process or Jobs@UVA should be directed to: Rich Haverstrom (rkh6j@virginia.edu).

The University will perform background checks on all new hires prior to making a final offer of employment.

The University of Virginia is an Equal Opportunity/Affirmative Action Employer. Women, minorities, veterans and persons with disabilities are encouraged to apply.

"mw4yv@virginia.edu" <mw4yv@virginia.edu>

UVirginia EvolutionaryGeneticsGenomicConflict

The Department of Biology at the University of Virginia invites applications for a postdoctoral Research Associate position in the lab of Dr. Robert Cox. The aims of the position will be tailored to the expertise of the successful applicant and will be closely associated with our NSF-funded research on the evolutionary and ecological genetics of sexual dimorphism and genomic conflict in Anolis lizards.

Our research blends perspectives from ecology, genetics, and physiology to study the evolutionary dynamics associated with the highly divergent reproductive roles of males and females. Using sexually dimorphic Anolis lizards as a model system, we study a variety of questions related to the quantitative genetics of sexually dimorphic phenotypes and fitness optima, the physiological and endocrine mechanisms that underlie sex differences in development, and the roles of natural and sexual selection in shaping the evolutionary trajectories of males and females in the wild. Our typical approaches include large-scale breeding studies in the lab, phylogenetic comparative analyses, phenotypic manipulations, and long-term studies of natural selection, sexual selection, and quantitative genetics of wild lizard populations in Florida and The Bahamas.

The Research Associate will work closely with the PI, collaborators, and lab personnel to design and lead research in the lab and field. The position also involves preparation of grant proposals, conference presentations, and manuscripts, management and analysis of data, and mentoring of graduate and undergraduate students. The ideal candidate will demonstrate the ability to integrate across biological disciplines and use the appointment to develop and pursue novel, exciting questions. Demonstrated expertise in ecological or evolutionary genetics is required. Preferred skills include expertise in some combination of the following: selection analysis, RAD-seq, RNA-seq, programming and bioinformatics related to the above, and quantitative genetics of wild populations using an animal-model framework.

The completion of a PhD degree in Biology or related field by the start date of the appointment is required. Preferred appointment start date is September 1, 2015, but alternative start dates are possible. This is a one-year appointment; however, appointment may be renewed for an additional two one-year increments, contingent upon available funding and satisfactory performance.

To apply, please submit a candidate profile through Jobs@UVA (https://jobs.virginia.edu) and electronically attach: curriculum vitae with list of publications, a cover letter that summarizes research interests and professional goals, and contact information for three (3) references. Search on posting number 0616288.

Review of applications will begin May 17, 2015. However, the position will remain open until filled.

Questions regarding this position should be directed to: Dr. Robert Cox (rmc3u@virginia.edu).

Questions regarding the Candidate Profile process or Jobs@UVA should be directed to: Rich Haverstrom (rkh6j@virginia.edu).

The University will perform background checks on all new hires prior to making a final offer of employment.

The University of Virginia is an Equal Opportunity/Affirmative Action Employer. Women, minorities, veterans and persons with disabilities are encouraged to apply.

Robert Cox <rmc3u@virginia.edu>

UWisconsinMadison PopGenomics

*Post-doctoral Position on the Population Genomics of a rapidly evolving agricultural pest ***

“Do Hyper-Diverse Genomes Run The Pesticide Treadmill: Resequencing Colorado Potato Beetle Genomes To

Understand Rapid Pest Evolution”, University of Wisconsin, Madison, Department of Entomology

A postdoctoral position will be available in Dr. Sean Schoville's lab at the University of Wisconsin-Madison, in collaboration with Dr. Yolanda Chen (University of Vermont) and Dr. David Hawthorne (University of Maryland).

Summary:

Understanding the mechanisms underlying rapid evolutionary change, particularly at the scale of the whole genome, is an important challenge for both theoretical and applied evolutionary biology. This genome resequencing project focuses on the Colorado potato beetle, and its relatives, to understand the structural and functional genomic changes associated with the beetle's host range expansion onto potato, the colonization of novel climatic regimes, and the rapid development of insecticide resistance (to over 50 classes of insecticides!).

Position Responsibilities:

The post-doctoral associate will be expected to analyze whole-genome resequence data to assess the population genomics and structural genomic changes across a diverse sample of Colorado potato beetle genomes. This project will provide training opportunities in bioinformatics analysis, population genetic modeling and phylogenomic analysis. Desirable skills for this project include familiarity with Linux operating systems and computer programming (Perl, Python, and R), as well as previous experience analyzing population genetic data.

How to Apply:

Funding for this position is available for 1 year with the possibility of extension. To apply, please send a single pdf with a cover letter, a CV, 1-2 representative publications, and names and contact information for 3 references to Dr. Sean Schoville, email: sean.schoville@wisc.edu, by June 30, 2015. Start date is flexible but preference will be given to candidates that can begin in late-August or early-September 2015. The University of Wisconsin is an equal opportunity/affirmative action employer.

For more information about the research in our groups, please go to:

http://labs.russell.wisc.edu/molecularecology/ http://blog.uvm.edu/yfanslow/ http://entomology.umd.edu/hawthorne-david.html – Sean Schoville University of Wisconsin-Madison Department of Entomology 1630 Linden Drive 637 Russell Labs Madison, WI 53706 Office phone: 608-262-2956 http://labs.russell.wisc.edu/molecularecology sean.schoville@wisc.edu

WorkshopsCourses

Armenia Colombia ELAEVO Jul27-Aug4

*IV **Latin American School of** Evolution*

The Latin American School of Evolution (ELAEVO) is an international theoretical and practical course that primarily aimed to provide to participants advanced concepts in selected topics of evolutionary biology, and encourage interaction and integration among Latin American students, professors and researchers in evolutionary biology.

About 120 graduate students from Argentina, Bolivia, Brazil, Chile, Colombia, Mexico, Peru and Uruguay have been part of the three previous versions of ELAEVO: Montevideo 2009, Buenos Aires Valdivia 2011 and 2013.

The IV Latin American School of Evolution will be held between July 27 and August 4, 2015 in Armenia, Colombia. It is organized by the Colombian Network of Evolutionary Biology and at the University of Quindío. The central topic of this ELAEVO will be evolutionary genetics with a component of paleontology. We will also have workshops on scientific writing in English.

TEACHING FACULTY

Evolutionary genetics

Michael L. Arnold - University of Geogia Daniel Ortiz-Barrientos - University of Queensland Daniel R. Matute - University of North Carolina at Chapel Hill Ferran Palero - Institut Sophia Agrobiotech Andrew J. Crawford - Universidad de los Andes Camilo Salazar - Universidad del Rosario

*Paleontology *

Carlos Jaramillo - Smithsonian Tropical Research Institute Javier Luque - University of Alberta

COSTS

COP 200.000 (Colombian pesos) USD 100

ACCOMMODATION GRANTS

Not available yet

ACADEMIC COMMITTEE

Víctor Hugo García-Merchan - Universidad del Quindío, Colombia Fernando Vargas-Salinas - Universidad del Quindío, Colombia Hugo Mantilla-Meluk - Universidad del Quindío, Colombia Enrique Lessa - Universidad de la República, Uruguay Daniel Naya - Universidad de la República, Uruguay Juan Opazo - Universidad Austral, Chile Francisco Bozinovic - Pontificia Universidad Católica, Chile Esteban Hasson - Universidad de Buenos Aires, Argentina Juan Jose Fanara - Universidad de Buenos Aires, Argentina

ELIGIBILITY

Graduate students from Latin American universities working on evolutionary biology. Applicants must submit their CV (max. 3 pages), a motivation letter (max. 1 page) and recommendation letter from advisor (max. 2 pages).

APPLICATION

March 30 until May 8. Applicants must complete the form and attach the three documents required.

Contact: elaevo2015@ gmail.com

——

La Escuela Latinoamericana de Evolución (ELAEVO) es un curso internacional teórico-práctico que tiene como objetivos principales brindar a sus participantes conceptos avanzados en tópicos selectos de biología evolutiva y fomentar la interacción e integración entre estudiantes, docentes e investigadores latinoamericanos que trabajan en biología evolutiva.

Cerca de 120 estudiantes de posgrado de Argentina, Bolivia, Brasil, Chile, Colombia, México, Perú y Uruguay han sido parte de las tres versiones anteriores de la ELAEVO: Montevideo 2009, Valdivia 2011 y Buenos Aires 2013.

La IV Escuela Latinoamericana de Evolución se realizará entre el 27 de julio y el 4 de agosto de 2015 en Armenia, Colombia. Es organizada por la Red Colombiana de Biología Evolutiva con el apoyo de la Universidad del Quindío. El tema central de esta versión de la ELAEVO será genética evolutiva con un componente de paleontología. También habrá espacio para tres talleres de escritura científica en inglés.

INSTRUCTORES

Genética Evolutiva Michael L. Arnold - University of Geogia (Visitar su pagina web) Daniel Ortiz-Barrientos - University of Queensland (Visitar su pagina web) Daniel R. Matute - Univ of North Carolina at Chapel Hill (Visitar su pagina web) Ferran Palero - Institut Sophia Agrobiotech (Visitar su pagina web) Andrew J. Crawford - Universidad de los Andes (Visitar su pagina web) Camilo Salazar - Universidad del Rosario (Visitar su pagina web)

Paleontología Carlos Jaramillo - Smithsonian Tropical Research Inst (Visitar su pagina web) Javier Luque - University of Alberta (Visitar su pagina web)

COSTO DE INSCRIPCIÓN Pesos Colombianos: COP 200.000 Dólares: USD 100

BECAS DE HOSPEDAJE Información no disponible aún.

COMITÉ ACADÉMICO Víctor Hugo García-Merchan - Universidad del Quindío, Colombia Fernando Vargas-Salinas - Universidad del Quindío, Colombia Hugo Mantilla-Meluk - Universidad del Quindío, Colombia Enrique Lessa - Universidad de la República, Uruguay Daniel Naya - Universidad de la República, Uruguay Juan Opazo - Universidad Austral, Chile Francisco Bozinovic - Pontificia Universidad Católica, Chile Esteban Hasson - Universidad de Buenos Aires, Argentina Juan Jose Fanara - Universidad de Buenos Aires, Argentina

ELEGIBILIDAD Estudiantes de posgrado de universidades latinoamericanas trabajando en biología evolutiva. Los aspirantes deberán presentar su CV (max. 3

— / —

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

Barcelona DataAnalysisR Jan18-22

Dear Colleagues, Registration is open for the course MULTIVARIATE DATA ANALYSIS FOR ECOLOGY AND EVOLUTION IN R. Date: January 18-22, 2016. Instructors: Dr. Dean Adams((Iowa State University, USA) and Dr. Antigoni Kaliontzopoulou (Centro de Investigação em Biodiversidade e Recursos Genéticos (CIBIO), Portugal). Course Webpage: http://www.transmittingscience.org/courses/stats/multi-ecol-evol-in-r/ This course is directed towards PhD students and researchers interested in exploring the potential of R language for multivariate analyses in ecology and evolution. The course will provide a general presentation of major statistical tools for multivariate analyses, including exploratory methods, multivariate GLM, methods for controlling for evolutionary and ecological non-independence, model selection and analysis of dispersion. The course will include a morning and an afternoon session. During the morning session, the instructors will discuss major themes in ecology and evolution and associate them to the statistical tools available for exploring specific scientific questions. The afternoon session will begin with a short (1h) demonstration of R code based on a worked, biological example and followed by practical training by the participants. At the end of the course, participants will each give a presentation on their research system, potentially including some analyses carried out during the course, or ideas of how they might incorporate the knowledge acquired during the course to their research. This course will be held in the Sabadell facilities of the Institut Català de Paleontologia (Barcelona, Spain) and is co-organized by Transmitting Science and the Institut Catalá de Paleontologia M. Crusafont. Place are limited and will be covered by strict registration order. please feel free to distribute this information between your colleagues if you consider it appropriate.

With best regards Soledad De Esteban-Trivigno, PhD.courses@transmittingscience.org Transmitting Science www.transmittingscience.org soledad.esteban@transmittingscience.org

Copenhagen SpeciesDistModelling 24-28Aug

LAST WEEK TO REGISTER!

The Center for Macroecology, Evolution and Climate is now accepting applications for our annual PHD course entitled “Modelling species distributions under climate change”, to be held at the University of Copenhagen August 24-28.

Read more about it here, including information on how to apply:

http://macroecology.ku.dk/teaching/int_phd_course/ Please note that this course is available to PhD students ONLY, and applications received outside of the application period will not be considered; this year’s deadline is June 1.

Applications and other inquiries should be directed to David Nogués-Bravo: dnogues@snm.ku.dk.

kamarske@snm.ku.dk

Glasgow ViralBioinformatics Aug10-14

Training course on Viral Bioinformatics and Genomics

Monday 10th - Friday 14th August Application deadline 25th May Cost Ì250

http://bioinformatics.cvr.ac.uk/Downloads/-OIE_announcements.pdf The need for effective and automated analyses of viral sequences has increased exponentially with the new high-©-throughput sequencing technologies. An understanding of the different bioinformatic approaches available for processing these data is an essential step in most virological studies.

We will be giving a 5-©day course, which will consist of a series of lectures and practical exercises that directly address bioinformatic challenges posed by the current deluge of sequence data. We will enable participants to understand and deal with high-©- throughput sequence datasets and encourage the exchange of ideas among diagnosticians, virologists, bioinformaticians and evolutionary biologists.

The 2015 course will introduce the participants to the power of the UNIX command-©- line and bash scripts, as well as a suite of bioinformatics tools covering the following topics:

- HTS sequencing technologies: overview of the different HTS platforms and sample preparations. - Unix primer: introduction to Bio-©-Linux and essential bash scripting. - Reference assembly: aligning sequence reads to a known reference and visualizing the alignment; (e.g., bowtie2, BWA, Tanoti, Tablet, UGENE). - Variant calling: consensus sequence generation, low frequency variant calling and error correction; (e.g., LoFreq, VPhaser). - De-©-novo assembly: overlap layout and De Bruijn graphs approaches for sequence assembly; (e.g., Velvet, IDBA-©-UD). - Metagenomic analyses: sanitizing sequence datasets, assembling, annotating, visualizing; (e.g., MetAMOS, Krona, MEGAN). - Genomics: scaffolding, improving the assembly, finishing the assembly, gene annotation; (e.g., ICORN, Artemis). - Phylogenetic analysis: introduction to multiple sequence alignment and phylogenetic reconstruction; (e.g., clustal, PhyML).

The course will be held at the CVR, Garscube Campus, University of Glasgow, Glasgow, UK. The CVR has been designated an World Organisation for Animal Health (OIE) Collaborating Centre for Viral Genomics and Bioinformatics at the 82nd OIE General Session.

Richard Orton <Richard.Orton@glasgow.ac.uk>

Guaruja Brazil SystematicReviews Jun25-26

Short Workshop: Introduction to Meta-Analysis and Systematic Reviews, June 25-26 (before Evolution 2015) Deadline extended

A 1.5 day workshop will be held before the Evolution meeting in Guarujá, Brazil, starting on the afternoon of June 25. The cost is $60 U.S. per participant. SPECIAL TRAVEL FELLOWSHIPS ARE AVAILABLE TO QUALIFIED PARTICIPANTS.

Instructors: Jessica Gurevitch (Stony Brook University, State University of New York) Marc Lajeunesse (University of South Florida)

Participation is limited to 24 people. Sponsored by the American Society of Naturalists. Applications and registration details are available at: http://-lajeunesse.myweb.usf.edu/ASN_workshop_2015.html < https://t.e2ma.net/click/xdgtk/9exss/xl6uhd >

Thanks! Jessica

Jessica Gurevitch <jessica.gurevitch@stonybrook.edu>

Kish Iran PhylogeographyPhylogeny Aug8-12

"Workshop on Phylogeography and Phylogeny based on Molecular data"

Kish Island, Persian Gulf, Iran.

This course is for students who want to learn the analysis of molecular sequences and genotype frequencies data at several levels: clades, species or populations. We will address different questions regarding the evolutionary relationships among data presented, as well as the demographic history of the populations at different scales.

The objectives of the course are: a) to learn how to prepare molecular data for (b) to be able to perform some basic phylogenetic analysis, c) to learn some historical demographic analyses and d) to learn how to interpret the results obtained and how to present the data for a publication.

Hours: 40h Dates: 08-12/August/2015 Schedule: 9h00-13h00, 15h00-19h00 Place: Kish Island, Persian Gulf, Iran. Minimum Participant Number: 20 Maximum Participant Number: 30 Deadline: 15/06/2015 Requisites: Basic knowledge of Systematics, Molecular Biology and user level Computer. Bring your own laptop. It is preferable to bring your own data (optional). Price: 650 Euro, breakfast, lunch and 5 nights hotel is included. Payment Method: 20% reservation, 80% first July. Account information: Hamid Ghanavi± IBAN: ES17 0239 2011 6830 4003 9107 SWIFT/BIC: EVOBESMMXXX Please include your name and family name on your payment title as follows: Name + Family name + PhyloIran±. Example: Charles Darwin PhyloIran±. Send us your proof of payment. Contact: phylo.iran@gmail.com More info: " https://drive.google.com/file/d/-0B575Uo8XkdyfZEJnbXUtYmtWTDA/view?usp=-3Dsharing "

Important Note Citizens of the most countries in the world need a visa to visit the country. You have to arrange your visa on your own, but we offer to obtain your visa if it is needed. International flights to Kish Island are quite expensive; the option we suggest is to fly to Tehran and take another flight to Kish Island from there. If you are interested, contact us as soon as possible at phylo.iran@gmail.com.

Speakers: -Mario Garcia Paris. PhD. National Museum of Natural Sciences, Madrid, Spain. mparis@mncn.csic.es PhD obtained at the University Complutense of Madrid (UCM, Spain), on the evolutionary history of midwife toads (Amphibia). Postdoctoral researcher at the University of California at Berkeley (USA) working on Systematics and Phylogeny of tropical salamanders (Amphibia). Current work, as a permanent researcher at Museo Nacional de Ciencias Naturales± (MNCN-CSIC), centred on phylogeography and phylogeny of insects, and especially on the evolution of complex morphological structures. Author of more than 150 papers (70 indexed in JCR journals), including Evolution, Molecular Ecology, Molecular Phylogenetics and Evolution, Proceedings of the Royal Society... (see profile at http://scholar.google.com/citations?user=-3DkhsdwwEAAAAJ&hl=3Den) his main interest is the field observation of the consequences of evolutionary processes.

-Elena Guacimara Gonzlez. PhD. National Museum of Natural Sciences, Madrid, Spain. elenag@mncn.csic.es My research program focuses on the study of evolutionary biology, adaptive traits, and origin of species diversity by combining the use of molecular systematic and proteomic-base data as analytical tools. Over the past few years, I have made progress in unravelling the evolutionary history, biogeography, and population genetics of a variety of vertebrate groups (specially marine fishes). Results of my research have been published in more than 30 peer-review journals, one book chapter, and one patent.

-Diushi Keri Corona Santiago. MSc. National Museum of Natural Sciences, Madrid, Spain. diushi.keri@mncn.csic.es Biologist degree obtained of the Universidad Michoacana de San Nicols (UMSNH, Mexico) in 2010. In 2013, Diushi gets two M. Sc. degrees of the UMSNH and of the Universidad Complutense de Madrid (UCM, Spain) in Biological Sciences and

Evolutionary Biology, respectively. His studies are focused in evolutionary biology and molecular evolution, population genetics, conservation biology, systematics and bioinformatics. Currently in his PhD work try to explain the evolution of allopolyploid species of Iberian Peninsula to infer in general process for biodiversity origin in special of vertebrates.

— / —

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

Lausanne TeachingEvolution Aug9

Do you teach evolution as part of your courses? Are you involved in evolution outreach? If you answered yes to either of these questions, do not miss our workshop, Sunday 9th August: "Actively Teaching Evolution± max. 30 participants, at L'prouvette in Lausanne. As part of the 15th European Society for Evolutionary Biology congress in Lausanne, this workshop is organised to provide methods and resources available for active learning of evolution that engage students of all ages. Congress and workshop registration are separate: you can attend the workshop and not the congress. The day will include talks on education and outreach, research talks by evolutionary biologists and hands-on activities to bring back to the classroom. Poster presentations are encouraged, but not mandatory. Graduate students and postdocs are particularly encouraged to apply. Apply here : http://bit.ly/1OZcZZy More information here : http://bit.ly/1b6umtX For any questions, comments, please email eseb2015outreach@gmail.com This workshop is supported by: *ESEB, CERCLE FSER*

xanasapinto@gmail.com

Lisbon Portugal 3 PhylogeographyBiodiversity Jul6-31

Three advanced courses from cE3c Portugal.

---

cE3c - Centre for Ecology, Evolution and Environmental Changes Advanced Course Practical Course on Phylogeography

organized by Octavio Paulo| July 6-10 2015 @ Lisbon, Portugal

Objectives: Phylogeography is one of the recent scientific areas emergent from the dissemination of highthroupt technologies of sequencing starting in the 90's of the XXth century, with the consequent development of intraspecific genetic variance analysis and its geographic distribution. The analysis of phylogeographic data allows to study the processes of population differentiation and the underlying evolutionary and demographic history. Applications of this body of knowledge go from conservation genetics to the study of the evolution of species and populations. This course is aimed at students and professionals that intend to get started on phylogeographic analysis as well as researchers already with some experience that want to deepen or update their knowledge in the field. The course involves theoretical classes as well as hands-on practical sessions using software. Participants are encouraged to bring their own sequence data for analysis.

Course instructor

Octavio Paulo (octavio.paulo@fc.ul.pt)

Professor at the Faculty of Sciences of the University of Lisbon, researcher at the Centre for Ecology, Evolution and Environmental Changes (cE3c - http://ce3c.fc.ul.pt/), Coordinator of the Computational Biology & Population Genomics Group (http://cobig2.com)

Intended audience

This course will be open to a maximum number of 20 participants.

Minimum formation: Bachelor in Biology or related area.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of fees for other participants see the programme details (access link below)

Deadline for applications: June 12, 2015

Candidates should send a short CV and motivation letter to Octavio Paulo (octavio.paulo@fc.ul.pt)

For additional details about the programme of the course, fees and to know how to register, click here, and access the specific course

http://cba.fc.ul.pt/education/-

advanced_courses_2015.php For more information about the course, please contact: octavio.paulo@fc.ul.pt

----

cE3c - Centre for Ecology, Evolution and Environmental Changes Advanced Course Island Biogeography organized by Ana Margarida Santos| July 27-31 2015 @ Lisbon, Portugal

Island Biogeography

Objectives: This course introduces the field of island biogeography, a discipline that has long influenced other research areas such as macroecology, community ecology, evolution and conservation biology. This course covers the main aspects of island biogeography, and on completion of the course the students shall have acquired knowledge and understanding on: Ecological/evolutionary theories developed from studies on islands, and its applications in other research areas; Processes that occur during and after island colonization, that shape island community characteristics; Island evolutionary processes; Applications of island biogeography to conservation biology

Course coordinator

Ana Margarida Santos (http://guidasanto1.wix.com/-anamcsantos2)

Marie Curie Research Fellow, Departamento de Biogeografía y Cambio Global, Museo Nacional de Ciencias Naturales (MNCN-CSIC), Madrid (Spain)

Intended audience

This course will be open to a maximum number of 20 participants.

Minimum formation: Bachelor in Biology or related area.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of fees for other participants see the programme details (access link below)

Deadline for applications: May 24, 2015

Candidates should send a short CV and motivation letter to Ana Margarida Santos (ana.margarida.c.santos@googlemail.com)

For additional details about the programme of the course, fees and to know how to register, click here, and access the specific course

http://cba.fc.ul.pt/education/-advanced_courses_2015.php For more information about the course, please contact: ana.margarida.c.santos@googlemail.com?

----

cE3c - Centre for Ecology, Evolution and Environmental Changes Advanced Course Measuring Biodiversity: How to get data, assess its quality and measure different aspects of diversity organized by Joaquin Hortal| July 20-24 2015 @ Lisbon, Portugal

Objectives: This course offers an overview of the different ways to

— / —

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

Lisbon Portugal ClimateChangeAdaptation Jul13-17

cE3c - Centre for Ecology, Evolution and Environmental Changes Advanced Course Climate Change: scenarios, impacts and responses

organized by Maria Joao Cruz and Elisabeth Robert | July 13-17 2015 @ Lisbon, Portugal

Climate Change: scenarios, impacts and responses

Objectives: The goal of this short course is to introduce the students to the main climate change research concepts and prepare them to use available information on scenarios, impacts and adaptation. Specific goals include: Study climate change and socio-economic scenarios and have an overview of what are the predictions for Portugal, Europe and the World; Explore the main expected impacts of climate change in a range of sectors; Explore direct and indirect impacts on biodiversity; introduction vulnerability assessment methodologies; Study specific responses to climate change, namely Mitigation and Adaptation (including Ecosystem based Adaptation), looking at specific examples in a range of scales.

Course Coordinators:

Maria Joao Cruz (cruz.mjoao@gmail.com)

Elisabeth Robert (liesrobert1@gmail.com)

Researchers at the Centre for Ecology, Evolution and Environmental Changes (cE3c - http://ce3c.fc.ul.pt/), Research Group CCIAM

Intended audience

This course will be open to a maximum number of 20 participants.

Minimum formation: Bachelor in Biology or related area.

The course is free for 1st year PhD students in the Doctoral programme in Biology (FCUL), Biodiversity, Genetics and Evolution (UL; UP) and Biology and Ecology of Global Changes (UL, UA). For information of fees for other participants see the programme details (access link below)

Deadline for applications: June 19, 2015

Candidates should send a short CV and motivation letter to Ângela 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://cba.fc.ul.pt/education/-advanced_courses_2015.php For more information about the course, please contact: amantunes@fc.ul.pt

Margarida Matos, PhD

Centro de Ecologia, EvoluçÃ£o e AlteraçÃµes Ambientais (cE3c - Centre for Ecology, Evolution and Environmental Changes)

Faculdade de Ciências da Universidade de Lisboa Campo Grande, Edificio C2 - 5Âº Piso Phone: +351 217500000 ext. 22141 1749-016 Lisboa Portugal

Margarida Matos <mmmatos@fc.ul.pt>

Montana PopGenomicDataAnalysis Aug31-Sep5

We are pleased to announce and invite you to the forthcoming edition of ConGen!

7th ConGen- Population Genomic Data Analysis Course: Recent Application of Next Gen Sequence Data to Understand Genetic Population Structure and Detect Natural Selection

31-Aug/ 5-Sept 2015, Flathead Lake Biological Station, Montana, USA

Applications for 2015 edition are now open!

Objective: To provide training in conceptual and practical aspects of data analysis for the population and evolutionary genomics of natural and managed populations. Emphasis will be on next generation sequence data analysis (RADs, exon capture, and whole genome sequence analyses) and interpretation of output from recent novel statistical approaches and software programs. The course also will allow daily discussions among young researchers (student participants) and >10 leaders in population genomics (instructors) to help develop the next generation of conservation and evolutionary geneticists. We will identify and discuss developments needed to improve data analysis approaches. This course will cover analysis methods including the coalescent, Bayesian, approximate Bayesian, and likelihood-based approaches.

Who should apply: Ph.D. students, post-docs, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. Applicants must have a basic background in population genetic data analysis, including testing for Hardy-Weinberg proportions and gametic disequilibrium. Participation will be limited to 25-30 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own data to analyze (for example graduate students well into their degree program).

Deadline for early bird application is 1 July, 2015

Course/Workshop Format: For each subject, we typically provide 30-45 minutes of background, theory, discussion and introduction to concepts. Immediately following, we will conduct data analyses together for 30-60 minutes using relevant software programs and real data sets. Evening hands-on computer sessions and lodging together of the instructors and students in the same location (the beautiful Flathead Lake field station) will allow for extensive exchange and facilitate learning.

For detailed information (on instructors etc.) see http://www.umt.edu/sell/cps/congen/ [dinner at McD (Large)] Field trip dinner with instructors in Glacier National Park

"Luikart, Gordon" <gordon.luikart@mso.umt.edu>

NIMBioS UTennessee EvolQuantGenetics Aug10-15

The National Institute for Mathematical and Biological Synthesis (NIMBioS) is now accepting applications for its Tutorial, “Evolutionary Quantitative Genetics,” to be held August 10-15, 2015, at NIMBioS.

*Objectives: *Quantitative genetic theory has been applied to a wide range of phenomena including the evolution of differences between the sexes, sexual preferences, life history traits, plasticity of traits, as well as the evolution of body size and other morphological measurements. This tutorial is for evolutionary biologists interested in how quantitative genetics theory can be tested with data, both from single species and with multiple-species phylogenies. Participants V graduate students, postdocs, and junior faculty V will learn how to use R to build and test evolutionary models. There is a need for evolutionary biologists to understand the field of evolutionary quantitative genetics because of the ability to collect large amounts of data by computer, the development of statistical methods for changes of traits on evolutionary trees and for changes in a single species through time, and the realization that quantitative characters will not soon be fully explained by genomics.

The content of this tutorial will be similar to the workshop held at NIMBioS in 2014. For information about the Evolutionary Quantitative Genetics 2014 tutorial held at NIMBioS, visit http://www.nimbios.org/tutorials/TT_eqg . *Location: *NIMBioS at the University of Tennessee, Knoxville

*Co-Organizers: *Stevan J. Arnold, Integrative Biology, Oregon State Univ. and Joe Felsenstein, Genome Sciences, Univ. of Washington, Seattle

*Instructors: *Patrick Carter, Evolutionary Physiology, Washington State Univ., Pullman; Tyler Hether, Biological Sciences, Univ. of Idaho, Moscow; Adam Jones, Biology, Texas A&M Univ.; Emilia Martins, Biology, Indiana Univ., Bloomington; Brian O’Meara, Ecology & Evolutionary Biology, Univ. of Tennessee; Liam Revell, Biology, Univ. of Massachusetts, Boston; and Michael Whitlock, Zoology, Univ. of British Columbia

Co-Sponsor: The American Society of Naturalists

For more information about the tutorial and a link to the online application form, go to http://www.nimbios.org/tutorials/TT_eqg2015 There are no fees associated with this tutorial. Tutorial participation in the tutorial is by application only. Individuals with a strong interest in the topic, including post-docs and graduate students, are encouraged to apply, and successful applicants will be notified within two weeks of the application deadline.

*Food and Lodging: *Breakfast and lunch will be provided at NIMBioS each day of the tutorial, as well as coffee and mid-morning and mid-afternoon snacks. NIMBioS is not covering other expenses for participants, but a block of rooms will be reserved at a nearby hotel. More information will be available on our website soon about lodging, room rates, and how participants can make reservations.

Application deadline: May 10, 2015

The National Institute for Mathematical and Biological Synthesis (NIMBioS) (http://www.nimbios.org) brings together researchers from around the world to collaborate across disciplinary boundaries to investigate solutions to basic and applied problems in the life sciences. NIMBioS is sponsored by the National Science Foundation, with additional support from The University of Tennessee, Knoxville.

Catherine Crawley, Ph.D. Communications Manager National Institute for Mathematical and Biological Synthesis (NIMBioS) University of Tennessee 1122 Volunteer Blvd, Ste. 106 Knoxville, TN 37996 e ccrawley@nimbios.org t +1 865 974 9350 <tel:%2B1%20865%20974%209350> f +1 865 974 9461 <tel:%2B1%20865%20974%209461> http://www.nimbios.org http://www.facebook.com/nimbios http://twitter.com/nimbios To receive email notifications of blog updates, click here < http://www.nimbios.org/wordpress/subscribe2updates/ > To subscribe to our bi-monthly newsletter, click here < http://visitor.r20.constantcontact.com/manage/optin/ea?v=001RgvbKVLa7a4Psoj8H7c43A%3D%3D >

Catherine Crawley <ccrawley@nimbios.org>

Oeiras Portugal ViralEvolution May25-May28

Dear All,

We are happy to announce the course

MEVR15 Molecular Epidemiology of Viruses using R

IMPORTANT DATES for this Course Deadline for applications: May 15th 2015 Latest notification of acceptance: May 16th 2015 Course date: May 25th - May 28th 2

with Simon Frost from the University of Cambridge, Cambridge, UK

Details at: http://gtpb.igc.gulbenkian.pt/bicourses/MEVR15 Duration: 4 days Course fee: Euro 360.00

Note: Travelling to Portugal is relatively cheap. Oeiras is 15 km away from Lisboa International Airport (LIS). Subsistence in Oeiras can cost as low as Euro 30 (Lodging and dinner) the rest is covered by the course fee.

Thanks for your interest, Pedro

– Pedro Fernandes GTPB Coordinator Instituto Gulbenkian de Ciência Apartado 14 2781-901 OEIRAS PORTUGAL Tel +351 21 4407912 http://gtpb.igc.gulbenkian.pt

---

Portugal NGS DataAnalysis Jun23-25

Introduction to next-Generation Sequencing (NGS) Data and Analysis June 23-26, 2015 | CIBIO-InBIO, Vairao, Portugal

The course Introduction to next-Generation Sequencing (NGS) Data and Analysis, which will take place at CIBIO-InBIO, Vairao, Portugal on June 23-26, 2015, provides an introduction to the basics of next generation sequencing data and analysis, and includes hands-on exercises throughout.

Topics covered include:

1. basics of the Linux command line;
2. DNA/RNA preparation and sequencing technologies, including reduced- representation sequencing;
3. what to do with newly-delivered sequencing data;
4. assembling sequences of varying sizes and complexities;
5. variant discovery;
6. annotation of small to large datasets;
7. ancient and variable-coverage DNA;
8. transcriptomes and gene expression analysis; and
9. walkthroughs of example analyses.

Emphasis throughout is on understanding fundamentals, and on developing skills for design of practical sequencing projects and analysis of sequencing data in light of research questions and biological and practical limitations.

Click here (http://cibio.up.pt/workshops–courses/details/introduction-to-next-generation-sequencing-data-and-analysis) to see the PROGRAMME for this course.

COURSE INSTRUCTORS Douglas Scofield John Archer Antonio Muñoz

INTENDED AUDIENCE The course is aimed for postgraduate researchers with particular interest in the analysis of NGS, genomics and transcriptomics data (preferably already working on such kind of projects). Pending upon the number of applications received, PhD students directly involved in NGS & genomic studies can also be accepted.

REGISTRATION DEADLINE Deadline for registration is May 25, 2015.

To know more about this course, please visit CIBIO-InBIO's website (http://cibio.up.pt/workshops–courses/details/introduction-to-next-generation-sequencing-data-and-analysis) or contact us at newgen.course@cibio.up.pt.

CIBIO Divulgação

Portugal SpeciesNicheModelling Jul6-10

INTRODUCTION TO NICHE MODELLING 6-10 July 2015 Observatório Astronómico Prof. Manuel de Barros Alameda do Monte da Virgem, Vila Nova de Gaia

Do you want to know what is an Ecological Niche Model and how to calculate it? Do you want to use ecological niche models to support a species' description? Or to evaluate niche conservatism inside a taxonomical group? This course will teach you the base theory of ecological niche modelling and its main methodologies. By the end of this 5-day practical course, you will have the capacity to perform ecological niche models and understand their results. You will be able to choose and apply the correct methodology depending in the aim of your study and type of datasets.

This course is orientated to PhD and MSc students, as well as other students and researchers working on biogeography, evolutionary biology, systematists, or related disciplines. Participants will receive a diploma of course attendance, copies of presentations and materials used, one selection of the most relevant articles on Ecological Niche Modelling, and a copy of programs and other tools used in the course.

The course will be mainly practical, with some theoretical lectures. Students will use two modelling programs: ModEco (http://gis.ucmerced.edu/ ModEco/) and R, the free software environment for statistical computing and graphics (http://www.r-project.org/). Students will learn to use modelling algorithms like Maxent and ENFA, and R packages for computing ENMs like dismo and biomod2. Also, students will learn to compare different ecological niche models by ENMTools (http:/-/enmtools.blogspot.pt/) .

Recommended Background Basic knowledge in Geographical Information Systems and R statistical package is necessary.

Course Format The first course day will be mainly theoretical. The following days will be mainly practical with some short theoretical presentations. The course will be lectured in English.

Lecturer NeftalíSillero Centro de Investigação em Ciências Geo-Espaciais (CICGE), Faculdade de Ciências, Universidade do Porto

Course Information and Registration Only 24 inscriptions! *The registration fee is 120 EURO*. Students must bring their own laptops!

Dates: 6-10 July 2015. Venue: Observatório Astronómico Prof. Manuel de Barros, Alameda do Monte da Virgem, Vila Nova de Gaia (Portugal). https://-goo.gl/maps/Xaxfe *More information in*:

https://www.facebook.com/ pages/Introduction-to-Ecological-Niche-Modelling/ 359229247606906 < https://sites.google.com/site/neftalisillero/Home/enm-course >

NeftalíSillero <neftali.sillero@gmail.com>

Portugal WildlifeConservaton May25-27

CIBIO-InBIO Advanced Course Applied Wildlife Population Ecology with L. Scott Mills | May 25-27, 2015 @ Vairao, Portugal

During this 3 days course, the participants will be exposed to the scientific basis and practical applications of the study of wildlife population biology. The modern study of wildlife population ecology orchestrates a dance at the interface of reliable fieldwork and the use of mathematical tools and population genetic techniques. Participants will learn how to collect the data necessary to study wildlife populations, and how to assess the factors that affect population growth and interactions with other species. This will include descriptors of population dynamics (eg. Trends in abundance, cycles), projections of deterministic and stochastic population models with stage structure, mechanisms and modeling of density dependence (positive and negative), targeting specific conservation actions through sensitivity analysis, metapopulation and source-sink dynamics, viability analysis, and the interface between genetic variation and population performance. The focus will be on how to rigorously analyze population dynamics and apply the inferences to better conservation decision-making.

Click here to see the PROGRAMME (http://-cibio.up.pt/workshops–courses/details/applied-wildlife-population-ecology) for the course.

COURSE INSTRUCTOR L. Scott Mills (http:/-/cnr.ncsu.edu/fer/people/l-scott-mills/), Chancellor's Faculty Excellence Program in Global Environmental Change Department of Forestry and Environmental Resources, North Carolina State University

INTENDED AUDIENCE This course will be open to a maximum number of 20 participants. Priority will be given to:

- 1st year PhD students attending the BIODIV Doctoral Programme;
- Other BIODIV PhD students;
- PhD students attending other courses.

REGISTRATION Registration deadline: May 19, 2015 Participation is free of charge for BIODIV students | Registration fee for other participants: euro 100,00.

For additional details about the course and to know how to register, click here (http://cibio.up.pt/workshops–courses/details/applied-wildlife-population-ecology).

For more information about the course, please contact: post.graduation@cibio.up.pt

CIBIO DivulgaçÃ£o

SCENE Glasgow GeneticDataAnalysis Aug3-7

PR˜Statistics

Genetic data analysis using R (statistics course) 3ˆrd-7ˆth August 2015 - There are 4 last places left on this course

The course is being delivered by Dr. Thibaut Jombart who has contributed towards a number of R packages (adegenet, adephylo, geography, outbreaker, Outbreakertools, bmmix, episerve (author) and ade4 and phylobase (contributor) and Caitlin Collins (Imperial College London) who also contributes to the R packages adegenet, Outbreakertools and episerve)

This 5 day course will be held at SCENE (Scottish Centre for Ecology and the Natural Environment), Glasgow, United Kingdom from August 3rd - 7th 2015

This course will provide an extensive overview of exploratory methods for the analysis of genetic data using the R software. We will address a number of key problems in population genetics, such as: How to examine genetic diversity using phylogenetic trees as well as multivariate methods, identify genetic clusters, and unravel spatial genetic patterns. Participants will be provided with the theoretical background and statistical methodology necessary to approach each problem from a number of different angles (considering, for example, univariate and multivariate approaches). Hands-on practical sessions will then provide an opportunity to highlight the pros and cons of methods introduced by the lectures, while conferring to participants advanced knowledge of the R packages adegenet, ape, and phangorn. Altogether, the aim of this course is to equip participants with powerful resources for tackling increasingly common challenges in genetic data analysis.

Course timetable:

Day 1: Intro to phylogenetic reconstruction

Lecture 1a: Reconstructing phylogenies from genetic sequence data. Three main approaches covered: distance-based phylogenies; maximum parsimony; and likelihood-based approaches.

Lecture 1b: Short R refresher.

Practical 1: Phylogenetic reconstruction using R. Three main approaches plus rooting a tree; assessing/testing for a molecular clock; and bootstrapping.

Main packages: ape, phangorn.

Day 2: Intro to multivariate analysis of genetic data

Lecture 2: Key concepts in multivariate analysis. Focus on using factorial methods for genetic data analysis.

Practical 2: Basics of multivariate analysis of genetic data in R. Topics include: data handling, population genetic tests of population structure (PCA, PCoA).

Main packages: adegenet, ade4, ape.

Day 3: Exploring group diversity

Lecture 3: Approaches to identifying and describing genetic clusters. Topics include: hierarchical clustering, K-means, population-level multivariate analysis (between-group-PCA, DA, DAPC).

Practical 3: Applying the approaches covered in morning lecture and emphasising their strengths and weaknesses.

Main packages: adegenet, ade4.

Day 4: Genome-Wide Association Studies (GWAS)

Lecture 4: Intro to GWAS study design and statistical approaches: univariate, regression-based and multivariate analysis.

Practical 4: Applying each class of methods covered in morning lecture, with emphasis on their strengths and weaknesses.

Main packages: adegenet, glmnet.

Day 5: Spatial genetic structures

Class 1: Discussing the origin and significance of spatial genetic patterns, and how to test for them.

Practical: 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.

Cost is Â£490 for the 5 days including lunches and refreshments or Â£665 for an all-inclusive option which includes the addition of accommodation, breakfast, lunch, dinner and refreshments.

For further details or questions or to register please email oliverhooker@prstatistics.co.uk or visit www.prstatistics.co.uk Please feel free to distribute this material among colleagues if you think it is suitable

Additional upcoming courses; BIOINFORMATICS FOR BIOLOGISTS AND GENETICISTS; APPLIED BAYESIAN MODELLING FOR ECOLOGISTS AND EPIDEMIOLOGISTS; SPATIAL ANALYSIS OF ECOLOGICAL DATA USING R; ADVANCING IN R; STABLE ISOTOPE MIXING MODELS USING SIAR, SIBER AND MIXSIAR;

"oliverhooker@prstatistics.co.uk"
<oliverhooker@prstatistics.co.uk>

SwissAlps Social Interactions Jul6-9

THE COSTS AND BENEFITS OF INFORMATION ACQUISITION AND USE IN SOCIAL INTERACTIONS

When? 6-9 July 2015 Where? Arolla (Swiss Alps), Switzerland

This workshop is organized by Prof. Michaël Taborsky and Dr. Leif Engqvist from the University of Bern (CH).

Invited speakers: Dr. Sarah Brosnan, Georgia State University (US) Prof. Thomas Bugnyar, University of Vienna (AT) Dr. Sasha Dall, University of Exeter (UK) Dr. Keith Jensen, University of Manchester (UK) Prof. Alex Kacelnik, University of Oxford (UK) Prof. Jens Krause, Leibniz Inst. Berlin (DE) Prof. David Stephens, University of Minnesota (US)

The program of the workshop will consist of a combination of plenary talks by invited speakers and work performed in small groups, in which the participants will discuss a particular theme together with one of the invited speakers. The results of these small-group sessions willl be presented to the plenum by student participants, followed by a general discussion.

Adaptive decision making depends on the quality of available information. The significance of direct or indirect information involved in social decisions is little understood. Evidence for constraints and substantial costs in the acquisition and processing of information is accumulating. Accordingly, behavioural decisions often seem to be made with imperfect knowledge, following “rules of thumb” rather than applying prudent assessment to make optimal choices. Furthermore, individuals may or may not benefit from sharing information; hence they may transmit only partial or false information. The aim of this workshop is to discuss these issues in an evolutionary framework, both from an empirical and theoretical perspective. Questions discussed in this workshop will include, for instance, how different costs of information acquisition and use will change predictions on adaptive decision making; or, whether seemingly irrational or “wrong” decisions may actually make sense when tak ing costs and constraints on information use into account. These are topics of great interest to students and scientists from different disciplines, such as behavioural ecology, neurobiology, cognitive sciences, and psychology. Interaction between different fields will identify open questions and directions for future interdisciplinary research.

For more info and registration: http://www.cuso.ch/-activity/?p=3D1128&id=3D2242 Queries: ecologie-evolution@cuso.ch

Caroline Betto-Colliard <Caroline.Betto-Colliard@unil.ch>

Switzerland GenomeEvolutionMicrobsPathogens Aug24-Sep4

ZHAW-SIB Summer School GEMP 2015: “Genomics and Evolution of Microbial Pathogens”

Date: 24 August - 4 September 2015 Place: Wädenswil (Zürich lake), Switzerland Organizers: Maria Anisimova and Theo Smits

Target audience are researchers who: - wish to study microbial pathogens, their genomes & evolutionary dynamics as a result of host-pathogen interaction interaction or environmental changes - willing to learn how to use bioinformatics tools for genome analyses

Summary: With > 28’000 microbial genomes sequenced today, a broader range of researchers can step into NGS genomics without the prior knowledge of the complexity involved. GEMP2015 offers a steady and hands-on introduction to the analysis of raw NGS data, from the assembly of raw reads into a high-quality genome, to annotation and the evolutionary analyses of sequences. GEMP 2015 aims to show how computational analyses of genomic data may bring insights into the molecular evolution of pathogenicity and host-pathogen interactions. Special attention is dedicated to statistical hypothesis testing to detect non-neutral evolution, which may point to functionally relevant molecular changes due to adaptive processes.

GEMP 2015 offers a combination of lectures, exercises and discussions around problems arising with real NGS data. Participants will acquire practical experience of handing large NGS data with a variety of free and commercial software packages. As a highlight of the course, internationally renowned experts will present their work on pathogen genomics in a mini-symposium.

Program and registration: http://-gemp2015.lifeinnumbers.ch/ “Anisimova Maria (anis)” <anis@zhaw.ch>

Tjrn Sweden Bioinformatics Nov2-6

Dear all,

Please find below the preliminary schedule and general aims of the course, “An introduction to bioinformatic tools for population genomic and metagenetic data analysis”, offered November 2-6 2015 at the Sven Lovén Centre for Marine Sciences on the island of Tjärnö outside of Strömstad on the Swedish West Coast (http://loven.gu.se/english/stations/tjarno/?languageId=100001&disableRedirect=true&returnUrl=http%3A%2F%2Floven.gu.se%2Fstationer%2Ftjarno%2F)

There is no course fee. Accommodation and meals for students are provided by the Royal Academy of Sciences of Sweden. Students will need to provide their own means of transportation to and from the course, however.

The course will be open to a maximum of 18 students, as large parts of the course will consist of hands-on exercises. The aim is a broad mix of students both from the University of Gothenburg and from the outside, mainly PhD students but postdocs are also welcome to apply.

Knowledge of general molecular biology and genetics is necessary, as is some previous experience with commandline interfaces. Previous experience working on a remote server will also be beneficial. No previous bioinformatics skills are needed, however.

For registration, please fill out the form at http://goo.gl/forms/umXf64qlcs Deadline for registration is September 15th 2015.

Please note that ALL students must bring their own computers.

Best wishes,

Pierre De Wit Sarah Bourlat

—

An introduction to bioinformatic tools for population genomic and metagenetic data analysis, 2.5 higher education credits Third Cycle

Faculty of Science; Department of Marine Sciences

The Swedish Royal Academy of Sciences

-----

1 Confirmation

The syllabus was confirmed by the Steering Committee of the Department of Marine Sciences 200X-XX-XX, 200X-XX-XX.

Discipline: Natural Science Responsible department: Department of Marine Sciences Main fields of study: Bioinformatics

2. Position in the educational system

Elective course; third-cycle education.

3. Entry requirements

Admitted to third cycle education.

4. Course content

This course aims at detailed understanding and hands-on experience of using state of the art bioinformatics pipelines for one’s own biological research questions. An important aspect of the course is to show how genomic data can be applied to address and answer research questions in the fields of genetics, ecology, population biology, biodiversity monitoring and conservation. The students will be trained in the latest bioinformatic methods to analyze high throughput sequencing data, which is present in many research projects. The course will cover basic computing tools required to run command line applications, processing high throughput sequencing data of the CO1 gene from environmental samples to reveal biodiversity and analysis of sequencing data from whole genome scans for population genomic studies.

The first part of the course introduces general computing tools for beginners such as the UNIX command line environment, bash commands, data formatting using regular expressions and basic scripting in the unix shell with a series of examples and exercises. The course introduces bioinformatics software for analysis of sequence data from metagenetics (The high-throughput sequencing of a molecular marker from an ecosystem or a community of organisms, used for large-scale analyses of biodiversity), through a series of live demonstrations (AmpliconNoise, TaxAssign, QIIME). The course also introduces basic and advanced concepts of population genomics data analysis such as genome/transcriptome assembly, annotation (BLAST), alignment/mapping, differential Gene expression, functional enrichment tests, SNP genotyping, PCA, outlier tests. The course corresponds to 1 week of full time studies and and is composed of lectures, demonstrations and computer labs.

5. Outcomes

1. Knowledge and understanding 1a. Demonstrate advanced knowledge of experimental strategies, applications and tools of DNA barcoding/metabarcoding and population genomics. 1b. Demonstrate advanced knowledge of the potential of genomics approaches to answer

ecosystem-wide questions, in particular for biodiversity monitoring.

2. Skills and abilities 2a. Ability to use basic commands in the Unix command line environment (reformatting data with regular expressions, basic scripting, running python scripts from the unix shell)

2b. Ability to use metagenetics software tools to analyse sequence data from environmental samples (data cleaning steps, clustering of reads into operational taxonomic units (OTUs) and taxonomic assignment through hidden markov models and database matching (BLAST, barcode of life database).

— / —

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

---

UMaryland CollegePark Bioinformatics Jun8

Hello all,

The UMD Bioinformatics Core will be offering hands-on Bioinformatics training again this summer. This week long course is perfect for those with little to no bioinformatics experience but whom have a need to learn next-generation data handling methods. The workshop, Bioinformatics Crash Course, was offered last summer and was a huge success. The space is limited to 25 people and filled in two days last year. If youre interested I recommend registering quickly. For details on the workshop or other bioinformatic needs see the following link. As always feel free to share this with colleagues who may be interested.

http://biology.umd.edu/workshops.html The workshop will cover the following and is geared towards beginners:

NGS Sequencing Platforms Raw data quality control and processing De novo genome assembly RNA-seq differential expression analysis Transcriptome assembly Experimental Design Linux and Python training HPC utilization and job submission

This hands-on workshop will provide training on the most common aspects of NGS analysis and methodology. Participants should have an understating of general biological concepts but no bioinformatics knowledge is required. The course will begin with an introduction to the command line and using High Performance Computer Clusters (HPCC, DeepThought2). By combining lectures with hands-on examples participants will gain an understanding of the most common bioinformatic workflows and tools. The workshop is held in a computer lab so there is no need for participants to bring a laptop.

Bioinformatics Crash Course Where: U of Maryland - College Park When: June 8th - June 12th When: 9:00am - 4:30pm each day What: This hands-on workshop will provide training on the most common aspects of NGS analysis and methodology. Participants should have an understanding of general biological concepts but no bioinformatics knowledge is required. The course will begin with an introduction to the command line and using High Performance Computer Clusters (HPCC, DeepThought2). By combining lectures with hands-on examples participants will gain an understanding of the most common bioinformatic workflows and tools.

Who should attend: Undergrads, Grad Students, Postdocs, and Faculty that want to learn the basic tools and techniques involved in NGS analysis and bioinformatics.

Registration and fees: Please register using the link below. The registration fee is $750 and includes lunch. Payment is required to hold your place in the class. UMD-CP should provide an FRS number for payment. Payment via Credit Card is also accepted.

Registration Link: http://goo.gl/forms/k1Rtgi99xR imisner@umd.edu

---

UMaryland CollegePark Bioinformatics Jun8-12

Only 8 spots left! If you can register then there is still space registration will automatically close once capacity is reached.

Hello all,

The UMD Bioinformatics Core will be offering hands-on Bioinformatics training again this summer. This week long course is perfect for those with little to no bioinformatics experience but whom have a need to learn next-generation data handling methods. The workshop, Bioinformatics Crash Course, was offered last summer and was a huge success. The space is limited to 25 people and filled in two days last year. If youre interested I recommend registering quickly. For details on the workshop or other bioinformatic needs see the following link. As always feel free to share this with colleagues who may be interested.

http://biology.umd.edu/workshops.html The workshop will cover the following and is geared towards beginners:

NGS Sequencing Platforms

Raw data quality control and processing

De novo genome assembly

RNA-seq differential expression analysis

Transcriptome assembly

Experimental Design

Linux and Python training

HPC utilization and job submission

This hands-on workshop will provide training on the most common aspects of NGS analysis and methodology. Participants should have an understating of general biological concepts but no bioinformatics knowledge is required. The course will begin with an introduction to the command line and using High Performance Computer Clusters (HPCC, DeepThought2). By combining lectures with hands-on examples participants will gain an understanding of the most common bioinformatic workflows and tools. The workshop is held in a computer lab so there is no need for participants to bring a laptop.

—

Bioinformatics Crash Course

Where: U of Maryland - College Park

When: June 8th - June 12th

When: 9:00am - 4:30pm each day

What: This hands-on workshop will provide training on the most common aspects of NGS analysis and methodology. Participants should have an understanding of general biological concepts but no bioinformatics knowledge is required. The course will begin with an introduction to the command line and using High Performance Computer Clusters (HPCC, DeepThought2). By combining lectures with hands-on examples participants will gain an understanding of the most common bioinformatic workflows and tools.

Who should attend: Undergrads, Grad Students, Postdocs, and Faculty that want to learn the basic tools and techniques involved in NGS analysis and bioinformatics.

Registration and fees: Please register using the link below. The registration fee is $750 and includes lunch. Payment is required to hold your place in the class. UMD-CP should provide an FRS number for payment. Payment via Credit Card is also accepted.

Registration Link: http://goo.gl/forms/k1Rtgi99xR Ian Misner, Ph.D. Bioinformatics Coordinator Bioinformatics Core Department of Biology 1247 Biology Psychology Building #144 University of Maryland College Park, MD 20742

Ph. 301-405-8134 Office: BPS 1247

http://www.biology.umd.edu/bioinformatics-core.html imisner@umd.edu

---

UPadova EvoDevo Sep28-Oct1

Summer School on Evolutionary Developmental Biology Conceptual and Methodological Foundations

4th Edition: The Evolution of Developmental Processes

Venice, 28 September 1 October 2015

Organizers: Alessandro Minelli, Gerd B. Müller and Giuseppe Fusco School director: Johannes Jaeger

School sponsors: Istituto Veneto di Scienze, Lettere ed Arti, Venice and Konrad Lorenz Institute for Evolution and Cognition Research, Vienna. Location: Istituto Veneto di Scienze, Lettere ed Arti, Palazzo Franchetti, Venice

Taching panel: J. Jaeger (School Director, CRG Barcelona), P. Beldade (Gulbenkian Institute, Lisbon), G.E. Budd (University of Uppsala), G. Fusco (University of Padova), R. Jenner (Natural History Museum, London), A. Khila (Institut de Génomique Fonctionnelle de Lyon), A. McGregor (Oxford Brookes University), A. Minelli (University of Padova), C. Mirth (Instituto Gulbenkian de Ciencia, Oeiras, Portugal), G.B. Müller (Konrad Lorenz Institute, Vienna, and University of Vienna), A. Peel (University of Leeds)

Deadline for applications: May 30th 2015

For details, visit < http://www.istitutoveneto.org/-EDB2015/ >

Giuseppe Fusco Department of Biology University of Padova Via U. Bassi 58/B I-35131 Padova Italy tel. +39.049.827.6238 fax +39.049.827.6230 e-mail giuseppe.fusco@unipd.it webpage http://-dept.bio.unipd.it/fusco

Giuseppe Fusco <giuseppe.fusco@unipd.it>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. ...plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.