EvolDir

July 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

Bainbridge Washington ChromosomeEvolution Aug17-20

REGISTRATION CLOSING JUNE 30TH

The AGA PresidentÂÂs Symposium, Chromosome Evolution: Molecular Mechanisms and Evolutionary Consequences, will be held at the beautiful IslandWood retreat on Bainbridge Island, outside Seattle, Washington. This will be a small meeting, 100-125 people, in an idyllic setting, providing an opportunity to interact with top researchers and dedicated students at talks, meals, and after-hour get-togethers.

Registration with shared lodging is only $400, and includes all meals from a reception the evening of Monday, Aug 17 through breakfast on Thu, Aug 20. The food is fabulous, and weÂÂve even thrown in a couple of drinks every evening.

For more information, poster abstract submission, and registration, go to: http://www.theaga.org/-program.htm We still have a few spaces, but theyÂÂre filling up fast, so register soon!

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 ÂV 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 MendelÂÂs 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 OÂÂNeill (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 Baker

Managing Editor, Journal of Heredity http://jhered.oxfordjournals.org/ Manager, American Genetic Association http://www.theaga.org/ 2030 SE Marine Science Dr Newport, OR 97366 https://www.facebook.com/AmericanGeneticAssociation AGAJOH@oregonstate.edu

---

Bainbridge Washington ChromosomeEvolution Aug17-20 2

**** REGISTRATION CLOSING JUNE 30TH! *****

There are a few spots left at IslandWood X if you wish to attend the symposium, but stay elsewhere, please email Anjanette at agajoh@oregonstate.edu<mailto:agajoh@oregonstate.edu>.

The AGA Presidents Symposium, Chromosome Evolution: Molecular Mechanisms and Evolutionary Consequences, will be held at the beautiful IslandWood retreat on Bainbridge Island, outside Seattle, Washington. This will be a small meeting, 100-125 people, in an idyllic setting, providing an opportunity to interact with top researchers and dedicated students at talks, meals, and after-hour get-togethers.

Registration with shared lodging is only $400, and includes all meals from a reception the evening of Monday, Aug 17 through breakfast on Thu, Aug 20. The food is fabulous, and weve even thrown in a couple of drinks every evening.

For more information, poster abstract submission, and registration, go to: http://www.theaga.org/program.htm 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 V 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 Mendels 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 ONeill (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 Baker

Managing Editor, Journal of Heredity http://-jhered.oxfordjournals.org/ Manager, American Genetic Association http://www.theaga.org/ 2030 SE Marine Science Dr Newport, OR 97366 https://-www.facebook.com/AmericanGeneticAssociation AGAJOH <AGAJOH@oregonstate.edu>

Biddeford Maine EvolGenomics YoungInvest Jul12-17 Deadline

Application Deadline Approaching - Ecological & Evolutionary Genomics Gordon Conference Reply-To: “Werren, Jack” <werr@mail.rochester.edu>

Applicants for the Ecological & Evolutionary Genomics Gordon Conference (12-17 July) will be accepted through 14 June 2015. The conference descriptor is at this link - http://www.grc.org/programs.aspx?id=-3D13135 The general theme is “From Genomes to Biomes: Using Biodiversity to Explore Biocomplexity” If you are interested in attending the conference, please check out our outstanding assemblage of speakers and topics, and apply by June 14.

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>

Bologna ItalianSocEvolution Aug31-Sep3

Less than 20 days to the abstract submission deadline for the 6th Congress of the Italian Society for Evolutionary Biology.

- submit your abstract. - share & follow us on Twitter @Evoluzione_2015 - see you in Bologna!!

http://www.evoluzione2015.net https://twitter.com/-Evoluzione_2015 The University of Bologna, the Department of Biological Geological and Environmental Sciences and the Molecular Zoology Lab (MoZoo Lab) invite you at the 6th Congress of the Italian Society of Evolutionary Biology that will be held in Bologna (Italy) from August 31 to September 3, 2015.

The 6th SIBE congress wants to specifically promote exchanges and discussion among Italian and non-Italian evolutionary Biologists, with particular attention to young researchers. Symposia will cover different topics, including the most up-to-date thematic areas of Evolutionary Biology. A paricular attention will also be given to the dissemination of the nature and social role of evolutionary biologists to general public.

The Conference is organized into 7 thematic symposia covering most of the fields of Evolutionary Biology. The Conference warmly welcomes all professional and non-professional Evolutionary Biologists, as well as teachers and science writers. It is also particularly addressed to young students and scientists and, through an informal and easy going atmosphere, wants to promote exchanges and synergies among scientists and/or amateurs.

The Congress venue is conveniently located in the University Area, which is close to the historic part of the beautiful city of Bologna, the house of the oldest Univeristy in the world.

We hope to see you in all in Bologna

The Organizing Committee of the 6th Congress of the Italian Society of Evolutionary Biology

Marco Passamonti <marco.passamonti@unibo.it>

Edinburgh UKPopGenet Dec15-18

Please make a note in your diary:

The 49th UK Population Genetics Group meeting (aka 'PopGroup') will be held in Edinburgh from the 15th to the 18th of December 2015.

Further details will follow when registration opens later in the year.

On behalf of the organisers,

Darren Obbard

EdinburghPopGroup@ed.ac.uk

– Institute of Evolutionary Biology and Centre for Immunity, Infection, and Evolution University of Edinburgh http://obbard.bio.ed.ac.uk/ The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

"darren.obbard@ed.ac.uk" <darren.obbard@ed.ac.uk>

IllinoisStateU ManagingUndergradRes Oct9

Do you want to keep track of your research group activities, involve professors and students from other departments or universities in common research, or make the pathway to publication in journals like SPORA or LiB easier? Join us at BEER 2015 to kick off an online network that will be focused on using QUBES Hub to manage research groups in quantitative and mathematical biology education and research.

Dates & Location: Friday, October 9, 2015 from 1:30 PM - 4:30 PM preceding the International Symposium on Biomathematics and Ecology Education and Research < https://about.illinoisstate.edu/biomath/beer/Pages/default.aspx > meeting at Illinois State University in Normal, IL.

Description: The Quantitative Undergraduate Biology Education Synthesis (QUBES) team sponsors online mentoring networks and an online hub (https://qubeshub.org) focused on quantitative biology education. QUBES Hub can be used to run a variety of computational tools in the cloud, for everything from agent-based modeling simulations in NetLogo to big data analysis in R. Be one of the first user groups to see how QUBES Hub could be used to manage your current undergraduate research, classroom-based research, or undergraduate education research agendas. This Faculty Mentoring Network will begin in-person, then continue online all semester to facilitate the sharing of resources and expertise.

Prior to the BEER kick-off meeting, participants will have the opportunity to review tutorials for QUBES Hub and begin participating in the online environment. The network will run from 1 October 2015 to 26 February 2016 and will be hosted online at https://qubeshub.org/groups/beer2015 . During the October 9th kick-off, participants will develop a plan for integrating QUBES Hub into their research team. After the in-person meeting, network participants will continue to interact online to refine the workflow for their research groups (classroom-based or undergraduate research), discuss various implementation challenges, define strategies to overcome these challenges, and engage in user experience feedback for the QUBES Hub team. Participants will implement during the late fall and/or spring and share their experiences with each other.

This mentoring network is most relevant for faculty who have already defined research agendas in mathematical or quantitative biology which incorporate undergraduate students or the scholarship of teaching and learning. No more than 14 participants will be selected from the applications. To qualify, participants must identify at least one current research topic in mathematical or quantitative biology, identify at least one quantitative tool that they use with their students, and must have an ongoing research collaboration either with an undergraduate student(s) or with another faculty member in the scholarship of teaching and learning.

We particularly encourage applications from research groups that involve faculty and students from more than one college/university.

Participants must also be able to commit ~1 hour per week to online discussions throughout the span of the mentoring network dates. Additional time outside of these discussions will also be required for independent work on adapting the framework for managing research online.

Although we are unable to provide travel support, BEER has its own travel funding opportunities for early-career faculty. There is no additional cost to participate in the QUBES Faculty Mentoring Network.

To apply, please go to: https://goo.gl/REgTok. Application deadline is June 25th. Accepted applicants will be notified by July 2th.

QUESTIONS?

You can find more information here: https://qubeshub.org/groups/beer2015/ Questions can also be directed via email to Carrie Diaz Eaton at ceaton@unity.edu.

“Hale, Alison Nicole” <anm116@pitt.edu>

Marseilles 19thEvolBiol Sep15-18 Deadline 2

Dear all

The dead line for the registration at the “19th evolutionary biology meeting at Marseilles” is June 30 we will then shift to the late registration stage.

more info http://sites.univ-provence.fr/evol-cgr/ or contact marie-helene.rome@univ-amu.fr

best regards Pierre

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

Oxford Systematics Aug26-28 Deadline

The Biennial Meeting of the Systematics Association is taking place on 26th-28th August in Oxford (UK). This is the flagship meeting of the Systematics Association and promises an exciting program of international speakers and cutting edge research talks on systematic approaches to biodiversity and its evolution. Hope to see you there.

Symposia include: - The value of long term monitoring plots for plant systematics and ecology in the tropics - Comparative approaches to the origin of biodiversity - Accelerating the pace of taxonomy - Rooted in deep time: Palaeontological contributions to systematics

Plenary lectures will be given by Michael Sanderson and Peter Holland There is still time to register and the opportunity to present a talk or poster in the open sessions. The deadline for Abstract submission is July 1st and the deadline for registration is June 26th. Full details of the conference, abstract submission and links to registration can be found at: http://www.systass.org/biennial2015/ *Registration Rates* £220 Full 3 day rate SA member £250 Full 3 day rate non-member £130 Student 3 day rate SA member £160 Student 3 day rate non-member £85 Full 1 day rate £60 Student 1 day rate The 3 day rate includes sandwich lunch (meat, fish and vegetarian) and 2 drinks receptions. The day rate includes sandwich lunch.

Accommodation All accommodation, if desired must be booked for three nights. The accommodation is at Christchurch for 25th, 26th and 27th August with breakfast included. Prices shown are for all 3 nights. £186 Single standard room £261 Single ensuite room £384 Twin ensuite room £306 Twin set room (would suit two students sharing) £40 Conference dinner (menu choice available at conference)

For further contact / queries, email: sabiennial2015@systass.org

mark wilkinson <apodauk@gmail.com>

Oxford Systematics Aug26-28 Deadline 2

Please note CORRECTION to the named PLENARY SPEAKERS (with apologies to Mike Sanderson!)

The Biennial Meeting of the Systematics Association is taking place on 26th-28th August in Oxford (UK).

This is the flagship meeting of the Systematics Association and promises an exciting program of international speakers and cutting edge research talks on systematic approaches to biodiversity and its evolution. Hope to see you there.

Symposia include:

- The value of long term monitoring plots for plant systematics and ecology in the tropics

- Comparative approaches to the origin of biodiversity

- Accelerating the pace of taxonomy

- Rooted in deep time: Palaeontological contributions to systematics

Plenary lectures will be given by Michael Donoghue and Peter Holland

There is still time to register and the opportunity to present a talk or poster in the open sessions.

The deadline for Abstract submission is July 1st and the deadline for registration is June 26th.

Full details of the conference, abstract submission and links to registration can be found at:

http://www.systass.org/biennial2015/ *Registration Rates*

Â£220 Full 3 day rate SA member

Â£250 Full 3 day rate non-member

Â£130 Student 3 day rate SA member

Â£160 Student 3 day rate non-member

Â£85 Full 1 day rate

Â£60 Student 1 day rate

The 3 day rate includes sandwich lunch (meat, fish and vegetarian) and 2 drinks receptions. The day rate includes sandwich lunch.

Accommodation

All accommodation, if desired must be booked for three nights. The accommodation is at Christchurch for 25th, 26th and 27th August with

breakfast included. Prices shown are for all 3 nights.

Â£186 Single standard room

Â£261 Single ensuite room

Â£384 Twin ensuite room

Â£306 Twin set room (would suit two students sharing) Â£40 Conference dinner (menu choice available at conference)

For further contact / queries, email: sabiennial2015@systass.org

–

Dr Mark Wilkinson Natural History Museum London SW7 5BD

Mark Wilkinson <apodauk@gmail.com>

Stockholm MammalBiol Aug17-21 Programme Registration

Dear everyone,

A conference programme is now available for the 7th European Congress of Mammalogy, and can be directly downloaded using this link: http://www.zoologi.su.se/ecm7/Programme%20Talks%20ECM.pdf There are only 10 days left to register for the conference (the deadline is on June 15th)!

Registration can be done here: 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>

Stockholm MammalBiol Aug17-21 RegistrationExtended

Dear all,

There is still room for more participants at the 7th European Congress of Mammalogy (ECM7), so we have extended the registration deadline until July 15.

The conference, which will be held in Stockholm on 17-21 August, will feature a wide range of presentations by some of the world's leading mammal biologists.

The full conference programme can be downloaded here: http://www.zoologi.su.se/ecm7/Programme%20ECM_2015-06-18.pdf To register, please follow this link: 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: 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 Love Dalén <Love.Dalen@nrm.se>

UGraz CichlidEvolution Sep6-9

- registration and abstract submission deadline extended to July 3! - includes workshop addressing oil drilling project in Lake Tanganyika

CICHLID SCIENCE 2015

We are pleased to announce that the 4th Cichlid Science meeting will take place from Sept 6 to Sept 9, 2015, at the University of Graz, Austria.

We invite all cichlid scientists to come and present their work. We also welcome everybody interested in cichlids and cichlid research to attend the meeting.

The Cichlid Science meeting series was launched in 2010 at the University of Basel. After subsequent meetings in Leuven and Bangor, it is now our pleasure to host this yearïs meeting in Graz. Cichlid Science meetings provide a relaxed and informal ambience promotive of stimulating discussions, exchange of ideas and networking among scientists from the many different fields of cichlid research.

The deadline for registration and abstract submission is July 3; the registration fee is euro 70.

Please consult the meeting website for information on the venue, keynote speakers, program, registration etc. http://www.uni-graz.at/~sefck/CichlidScience/home.htm The organizers look forward to welcoming you in Graz!

Kristina Sefc (kristina.sefc@uni-graz.at), Stephan Koblmueller(stephan.koblmueller@uni-graz.at)

"kristina.sefc@uni-graz.at" <kristina.sefc@uni-graz.at>

UMichigan AnnArbor PopGenet Jul25-26

Dear Colleagues,

The field of population genetics has a remarkable tradition of being a tight-knit and nurturing community. In order to better foster that sense of community for the popgen groups in the Midwest, we thought it would be fun to organize a short scientific conference to which we could bring our labs and have meaningful introductions and interactions. After a successful first trial last year (Evidence on https://midwestpopgen.wordpress.com/), we are excited to run this meeting again.

Thus, we'd like to invite you to come and bring your group to the meeting of the MidWest Population Genetics group, which will be held on July 25-26th at the University of Michigan. The meeting will begin Saturday and continue to Sunday with a BBQ on Saturday evening.

The keynote speaker will be Goncalo Abecasis, chair of Biostatistics at the University of Michigan. Thirteen 25 minute talks will be selected from submitted abstracts. Students are especially encouraged to attend and present their work. There will be a small prize for best poster and best talk by a student or postdoctoral fellow.

Space is limited, so if you do plan to attend, please RSVP to szoellne@umich.edu or sign up on http://tinyurl.com/kv3vtx4 by June 1, and submit your abstracts by June 1 to dconrad@genetics.wustl.edu so we can finalize our program. There is no registration fee.

The tentative schedule follows below. We do hope that you can make it and help establish this as an important meeting for the population geneticists in our region!

All the best,

Don Conrad, WashU

John Novembre, Chicago

Bret Payseur, Wisconsin

Sebastian Zollner, Michigan

Draft Agenda:

Saturday

12:00-1:30pm Registration and light lunch

1:30-3:30 Four 25 minute talks

3:30-4:30 Posters

4:30-5:30 Keynote

7:30-11 BBQ

Sunday

8-9 Breakfast

9-10:30 Three 25 minute talks

10:30-10:45 Break

10:45-12:15 Three 25 minute talks

12:15-1:30pm Lunch

1:30-2:25pm Three 25 minute talks

UMichigan AnnArbor PopGenet Jul25-26 2

Dear Colleagues,

The field of population genetics has a remarkable tradition of being a tight-knit and nurturing community. In order to better foster that sense of community for the popgen groups in the midwest, we thought it would be fun to organize a short scientific conference to which we could bring our labs and have meaningful introductions and interactions. After a successful first trial last year (Evidence on https://midwestpopgen.wordpress.com/), we are excited to run this meeting again.

Thus, we'd like to invite you to bring your group to the meeting of the MidWest Population Genetics group, which will be held on July 25-26th at the University of Michigan. The meeting will begin Saturday and continue to Sunday with a BBQ on Saturday evening.

The keynote speaker will be Goncalo Abecasis, chair of Biostatistics at the University of Michigan. Thirteen 25 minute talks will be selected from submitted abstracts. Students are especially encouraged to attend and present their work. There will be a small prize for best poster and best talk by a student or postdoctoral fellow.

If you do plan to attend, please RSVP to szoellne@umich.edu or sign up on http://tinyurl.com/-kv3vtx4 by July 1, If you are interested in presenting a talk, submit your abstracts by July 1 to dconrad@genetics.wustl.edu so we can finalize our program.

The tentative schedule follows below. We do hope that you can make it and help establish this as a fun meeting for the population geneticists in our region!

All the best,

Don Conrad, WashU

John Novembre, Chicago

Bret Payseur, Wisconsin

Sebastian Zollner, Michigan

Draft Agenda:

Saturday

12:00-1:30pm Registration and light lunch

1:30-3:30 Four 25 minute talks

3:30-4:30 Posters

4:30-5:30 Keynote

7:30-11 BBQ

Sunday

8-9 Breakfast

9-10:30 Three 25 minute talks

10:30-10:45 Break

10:45-12:15 Three 25 minute talks

12:15-1:30pm Lunch

1:30-2:25pm Three 25 minute talks

Sebastian Zoellner <szoellne@umich.edu>

UStAndrews EnvironmentalOmics Jul6-8

LAST CALL - LIMITED SPACES AVAILABLE

THIRD INTERNATIONAL ENVIRONMENTAL 'OMICS SYNTHESIS CONFERENCE - IEOS2015 University of St Andrews 6-8 July 2015 http://-environmentalomics.org/ieos2015 DEADLINE for registration and abstract submission (posters only): EXTENDED to 19 June 2015

DEADLINE for application for postgraduate student bursaries: EXTENDED to 19 June 2015

STUDENT BURSARIES:

Postgraduate students who submit abstracts are eligible for a bursary, covering 100% of the registration fee. When submitting an abstract, students should indicate they wish to be considered for a bursary. Successful applicants will receive a code for FREE registration.

KEYNOTE SPEAKERS:

Professor ELIZABETH THOMPSON, University of Washington http://www.stat.washington.edu/-thompson Professor MARK BLAXTER, University of Edinburgh http://bit.ly/1AG0jpq Professor BARBARA METHE, J Craig Venter Institute http:/-/www.jcvi.org/cms/about/bios/bmethe INVITED SPEAKERS:

Dr LOGAN KISTLER, University of Warwick http://www2.warwick.ac.uk/fac/sci/lifesci/people/-lkistler Dr UMER ZEESHAN IJAZ, University of Glasgow http://userweb.eng.gla.ac.uk/umer.ijaz Professor JIANQUAN LIU, Lanzhou University https://www.researchgate.net/profile/Jianquan_Liu2 Dr NATHAN BAILEY, University of St Andrews http://biology.st-andrews.ac.uk/staff/nwb3 Professor C-H CHRISTINA CHENG, University of Illinois at Urbana-Champaign http://www.life.illinois.edu/ccheng Dr DAVID MARSHALL, James Hutton Institute http://www.hutton.ac.uk/staff/david-marshall Professor DAVID WALLOM, Oxford University http:/-/www.oerc.ox.ac.uk/people/david-wallom Professor DANNIE DURAND, Carnegie Mellon University http:/-/www.cmu.edu/bio/faculty/primary/durand.html IEOS2015:

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 are 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.

PRE- and POST- MEETING WORKSHOPS

http://environmentalomics.org/ieos2015-workshops/ 6 July - training workshops provided by the NERC Biomolecular Analysis Facility Gene expression analysis Metabolomics workshop Restriction-site Associated DNA (RAD) Data Analysis eDNA & metabarcoding

9 July Analyzing environmental DNA: Bio-Linux on the EOS Cloud (T. Booth, CEH Wallingford) >From reads to genes, a NGS analysis (Dr M. Pinheiro, University of St Andrews)

SUMMER OF V'S

IEOS2015 attendees are also welcome at a separate meeting on Data Science, The Summer of V's, immediately preceding the main registration event for IEOS. Separate registration is required for the Summer of V's: http://www.idir.st-andrews.ac.uk/vs IEOS2015: http://environmentalomics.org/ieos2015 With best wishes,

Professor Thomas Meagher, Chair The IEOS Conference Organising Committee http://environmentalomics.org/ieos2015-committee The University of St Andrews is a charity registered in Scotland : No SC013532

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

— / —

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

Vienna SMBE2015 Jul12-16 RegistrationDeadline

Hello evoldir community,

this is a reminder of the upcoming final registration deadline for SMBE 2015 (July 12-16) in Vienna, Austria. We're currently not planning for the possibility of on site registration. Therefore, please 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.

Registration deadline is this upcoming Sunday, June 21.

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

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

- Five poster sessions

- 28 symposia on cutting edge topics with 42 invited speakers http://smbe2015.univie.ac.at/program/symposia/ - A special symposium on NGS library construction

- Plenary speakers: Doris Bachtrog (UC Berkeley), Joe Felsenstein (Univ. of Washington), Dmitri Petrov (Stanford Univ.) 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, local poster service 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

WashingtonDC OriginOfLife Nov9-13

Upcoming Conference on

Re-conceptualizing the Origin of Life

Nov. 9-13^th, 2015 at Carnegie Institution of Washington, Washington D.C.

Physics and chemistry have arrived at a deep understanding of the non-living world. Can we expect to reach similar insights, integrating concepts and quantitative explanation, in biology? Life at its origin should be particularly amenable to discovery of scientific laws governing biology, since it marks the point of departure from a predictable physical/chemical world to the novel and history-dependent living world. This conference aims to explore ways to build a deeper understanding of the nature of biology, by focusing on modeling the origins of life on a sufficiently abstract level. The conference will cover a diverse range of topics bearing on the problem of solving life's origins, starting from prebiotic conditions on Earth and possibly on other planets and moving up through the hierarchy of structure in biology all the way to social complexity. The focus is therefore on studying the origin of life as part of a larger concern with the origins of organization, including major transitions in the living state and structure formation in complex systems science.

Each day of the conference is organized around a different integrative theme, kicked off by an invited keynote presentation. Themes include: information in the living world, the origin of organization, the self in the world, re-conceptualizing the nature of the living state, and an integrated view of the origin and organization of the biosphere. Keynotes include: Chris Adami (Michigan State U.), Lee Cronin (U. Glasgow), Sara Imari Walker (Arizona State U.), Eric Smith (ELSI/Sante Fe Institute) and Douglas Erwin (Smithsonian Institution).

The goal of the conference is to concentrate on integrative conceptual and foundational themes, and not to review the field. We hope to facilitate new collaborations and identify specific experimental and theoretical projects that significantly advance our understanding of the origin of life. To maintain a productive workshop-style atmosphere, the conference is limited to 100 participants. Participants must therefore apply to ensure a space at the meeting. There is no registration fee.

Applications for participation are now open and may be submitted at: https://easychair.org/conferences/-?conf=3Dmol20150 We encourage submission of abstracts for the poster session, which will be held throughout the entire week and will central to fostering lively discussion. Abstract submissions for poster presentations are being accepted through Aug. 1st 2015 and should be submitted at the link above.

For more information on the meeting, including a full list of confirmed speakers, please visit our conference website:

https://carnegiescience.edu/events/lectures/-re-conceptualizing-origin-life Sara Walker <sara.i.walker@asu.edu>

WoodsHoleMA MobileDNA Sep3-5

We apologize for a non-functional web link. Please use the working link below.

Registration and abstract submission is underway for the 2015 meeting "Mobile Genetic Elements: in silico, in vitro, in vivo":

https://ws3.mbl.edu/iebms/wri/-wri_p1_display.aspx?oc=10&cc=MOBILEDNA
Abstract submission deadlines: August 1 for talk and fellowship consideration; August 15 for poster presentations.

Dear Evoldir community:

The 2015 meeting "Mobile Genetic Elements: in silico, in vitro, in vivo" will take place from Thursday, September 3 to Saturday, September 5 at the Marine Biological Laboratory (MBL) in Woods Hole, MA, USA. The meeting will bring together experimental and computational scientists seeking to narrow the existing gap between the fast-paced discovery of transposable elements (TEs) in silico, stimulated by exponential growth of comparative evolutionary genomic and metagenomics studies, and a limited number of experimental models amenable to in vitro and in vivo studies of structural, mechanistic, and regulatory properties of TEs and their impact on their prokaryotic and eukaryotic hosts. It will also feature a bioinformatics workshop. Special attention will be paid to the evolutionary aspects of TE-host interactions.

The meeting continues the series of bi-annual regional meetings held since 2007 in Woods Hole and in Cold Spring Harbor and will now cover a broader swath of the continent, following the recent affiliation between the MBL and the University of Chicago. Participants from any interested US and international labs are welcome. Half of the talks will be selected from submitted abstracts. We especially encourage abstract submissions from young scientists at the graduate, postdoctoral, and early-stage investigator levels, and have allocated funds for fellowship awards to cover registration costs for selected presenters, as well as members of under-represented minority groups.

We look forward to seeing you on Cape Cod in September!

Meeting organizers: Phoebe Rice, University of Chicago
Irina Arkhipova, Marine Biological Laboratory

"iarkhipova@mbl.edu" <iarkhipova@mbl.edu>

WoodsHoleMA MobileDNA Sept3-5

Registration and abstract submission is underway for the 2015 meeting "Mobile Genetic Elements: in silico, in vitro, in vivo":

https://ws3.mbl.edu/iebms/wri/-wri_p1_display.aspx?oc=3D10&cc=3DMOBILEDNA

Abstract submission deadlines: August 1 for talk and fellowship consideration; August 15 for poster presentations.

Dear Evoldir community:

The 2015 meeting "Mobile Genetic Elements: in silico, in vitro, in vivo" will take place from Thursday, September 3 to Saturday, September 5 at the Marine Biological Laboratory (MBL) in Woods Hole, MA, USA. The meeting will bring together experimental and computational scientists seeking to narrow the existing gap between the fast-paced discovery of transposable elements (TEs) in silico, stimulated by exponential growth of comparative evolutionary genomic and metagenomics studies, and a limited number of experimental models amenable to in vitro and in vivo studies of structural, mechanistic, and regulatory properties of TEs and their impact on their prokaryotic and eukaryotic hosts. It will also feature a bioinformatics workshop. Special attention will be paid to the evolutionary aspects of TE-host interactions.

The meeting continues the series of bi-annual regional meetings held since 2007 in Woods Hole and in Cold Spring Harbor and will now cover a broader swath of the continent, following the recent affiliation between the MBL and the University of Chicago. Participants from any interested US and international labs are welcome. Half of the talks will be selected from submitted abstracts. We especially encourage abstract submissions from young scientists at the graduate, postdoctoral, and early-stage investigator levels, and have allocated funds for fellowship awards to cover registration costs for selected presenters, as well as members of underrepresented minority groups.

We look forward to seeing you on Cape Cod in September!

Meeting organizers:

Phoebe Rice, University of Chicago

Irina Arkhipova, Marine Biological Laboratory

"iarkhipova@mbl.edu" <iarkhipova@mbl.edu>

GradStudentPositions

AMU Marseille DrosophilaEvolution

PhD position available in the Prud'homme lab Aix Marseille University (France)

Evolution of egg laying site choice in Drosophila

We are looking for a PhD student to study the evolution of egg laying site selection in Drosophila. While most fruitflies species use decaying plant or fruit substrates to lay their eggs, some species have evolved a preference for ripe fruit substrates. One of these species is Drosophila suzukii, an invasive species that causes severe damage to the fruit industry in many countries.

The goal of the project is to peer into the genetic and neuronal mechanisms involved in the selection of egg laying site in Drosophila, and the changes responsible for the evolution of this innate behavior in Drosophila suzukii. The approaches we are using to tackle this question include behavioral tests and functional (genetic) manipulations in an inter-species comparative context.

The project is funded by the A*MIDEX foundation, supported by the Initiative of Excellence at the Aix-Marseille University (AMU). The PhD position is funded for 3 years and should start in September or October 2015. The position is exclusively for students outside the AMU.

Please send applications, including a motivation letter, a CV, a description of research experience and interests, and contact information for 2-3 references to: benjamin.prudhomme@univ-amu.fr

Applicants with a background in Drosophila behavior /genetics/ chemosensory biology will be considered favorably.

Our lab is part of the Institute of Developmental Biology of Marseille (IBDM), an interdisciplinary research center studying developmental biology and neurobiology. More information about the lab and the institute can be found here : (http://www.prudhommelab.com/ www.ibdm.univ-mrs.fr /)

Benjamin Prud'homme <benjamin.prudhomme@univ-amu.fr>

CarletonU EvolutionOfSex

Graduate Position: CarletonU. (Ottawa, Canada): Evolution of Sex

If interested in pursing an MSc or PhD in evolution of sex with Root Gorelick at Carleton University in Ottawa, please send the following information, preferably in a single e-mail attachment:

(1) a thoughtful and passionate 1-2 page essay on why you would like to pursue this degree and your vision of what the research might entail (2) your CV (3) a scanned copy of your university transcript (4) contact information for at least two faculty members who could recommend you

Tentative, less formal inquires are also welcomed. Funding is currently only available for citizens and permanent residents of Canada.

My current interests in evolution of sex are in origins of meiosis and in differences between females and males. However, I am open to research projects in other areas of evolution of sex. I am especially interested in sex of organisms other than plants and animals, such as chromalveolates.

Root Gorelick Carleton University Ottawa, Ontario, Canada Root.Gorelick@carleton.ca http://www.carleton.ca/~rgorelic Root.Gorelick@carleton.ca

CarletonU IndigenousPerspEvolution

Graduate Position: CarletonU. (Ottawa, Canada): Indigenous/Aboriginal perspectives in evolution and ecology

If interested in pursing an MSc or PhD in Indigenous/Aboriginal perspectives in evolution and ecology with Root Gorelick at Carleton University in Ottawa, please send the following information, preferably in a single e-mail attachment:

(1) a thoughtful and passionate 1-2 page essay on why you would like to pursue this degree and your vision of what the research might entail (2) your CV (3) a scanned copy of your university transcript (4) contact information for at least two faculty members who could recommend you.

Tentative, less formal inquires are also welcomed. Funding is currently only available for citizens and permanent residents of Canada.

Root Gorelick Carleton University Ottawa, Ontario, Canada Root.Gorelick@carleton.ca http://www.carleton.ca/~rgorelic

Root.Gorelick@carleton.ca

ColoradoStateU EvolutionManagementSystems

A position for a Ph.D. student is available at Colorado State University. Human societies vary widely in the approaches used to manage natural resources. The funded project seeks to address long-standing debates in multiple academic disciplines (e.g., anthropology, geography, economics, and human behavioral ecology) regarding what factors shape the subsistence and land tenure systems used by societies across the globe, and to examine the evolutionary pathways of these natural resource management systems. The senior project personnel have, in recent years, adapted methods originally developed in biogeography and evolutionary biology to explore the factors that drive the evolution and geographic patterns of cultural diversity. In addition, the research group has developed a database that maps cultural features onto language family trees for over 1400 societies, and links these to ecological and environmental variables, empowering new lines of investigation into drivers of cultural change. The team is now uniquely positioned to conduct the first, integrated empirical tests of theories regarding the geography and evolution of natural resource management. The successful candidates will be based at Colorado State University and collaborate with an interdisciplinary team of researchers from the U.S., Australia, Canada, Germany and the United Kingdom.

Field of Work: The successful candidate is expected to:

- play a key role in designing, implementing, completing and writing up analyses, and also complete project-related research and coordination tasks.

- apply for and be accepted to the PhD program in Human Dimensions of Natural Resources at Colorado State University to begin starting in August 2015 or January 2016

Offer:

- full graduate tuition waiver and a monthly stipend

- valuable research experience as part of the education received in the doctoral program at CSU

- office space and computer facilities

- costs for research expenses and related travel will also be covered by the project

The position will be reviewed annually and, contingent upon performance and available funds, be appointed to additional years. Three years of potential funding is expected to be available.

Your qualifications: Selection will be made on a competitive basis using the following criteria:

- A strong academic background in cultural evolution, geography, anthropology, ecology, evolutionary biology or allied disciplines

- Some knowledge of research methods and statistical analyses used to examine spatial patterns of diversity and/or evolution (e.g., spatial models, GLM, and/or phylogenetic methods)

- Interest in studying in a program that emphasizes the application of social science theory to environmental issues and conservation.

Your application: By July 31, 2015, please submit a letter of interest detailing how you meet each of the qualifications, curriculum vitae (indicating previous academic performance indicators, publication history, and prior research experience), and contact information for three references to Michael Gavin (Michael.gavin@colostate.edu)

"Gavin,Michael" <Michael.Gavin@colostate.edu>

Germany Biodiversity

The DFG-funded Research Training Group RTG 2118 âIntegrating Biodiversity Research with Movement Ecology in Dynamic Agricultural Landscapes [BioMove]' (Speaker: Prof. Dr. Florian Jeltsch) at the University of Potsdam (UP), the Freie Universität Berlin (FU), the Leibniz Institute for Zoo and Wildlife Research (IZW, Berlin), and the Leibniz Centre for Agricultural Landscape Research (ZALF, Müncheberg) offers several positions:

At the University of Potsdam 7 doctoral candidates (PhD); Registration Number: 147/2015; 26 hours per week (65%) for three years. 1 postdoctoral researcher (PostDoc); Registration Number: 148/2015; 40 hours per week (100%) for two years.

The salary scale is in accordance with the German public service 13 TV-L (area east). Contracts are time-limited according to the Academic Fixed-Term Contract Law (WissZeitVG).

At the Leibniz Institute for Zoo and Wildlife Research (IZW), Berlin 2 doctoral candidates; the doctoral positions are initially limited to two years, with the possibility of extension to a maximum of three years. Salary is according to TVöD (65% for doctoral students).

At the Freie Universität Berlin 1 doctoral candidate; Salary is according to TV-L FU E13 (65%), 3-year contract.

At the Leibniz Centre for Agricultural Landscape Research (ZALF) Müncheberg 1 doctoral candidate, 26 hours per week (65%) for three years. The salary is in accordance with the German public service 13 TV-L (area east). Contracts are time-limited according to the Academic Fixed-Term Contract Law (WissZeitVG).

beginning on October 1st, 2015. The scientific disciplines involved in the RTG are movement ecology, biodiversity research, behavioural and evolutionary ecology, conservation biology,ecological modelling, and related topics.

The research projects of the RTG strategically combine empirical, experimental and modelling approaches based in one common study area (AgroScapeLab-Quillow, north-eastern Brandenburg, Germany) to test a unifying set of hypotheses on the linkage of movement ecology and biodiversity research. The postdoctoral researcher is expected to play a leading role in model-based synthesis and theory advancement. Acknowledging the importance of variability, BioMove shifts the focus from âaverage' movement towards incorporating potential effects of individual variation in movement properties and decisions for biodiversity dynamics. This will not only advance our mechanistic understanding of how biodiversity patterns emerge but also improve our ability to predict biodiversity responses to ongoing changes in land use or climate. Projects will cover different spatial and temporal scales and groups of organisms ranging from bacteria, fungi, plankton, plants, and insects to mammals (for more details see http://www.biomove.org). Ideal doctoral candidates have a background in one of the scientific disciplines (or related fields) represented in this RTG. The postdoctoral researcher additionally should have a strong background in ecological modelling, synthesis or theory refinement. A strong interest in interdisciplinary research and the willingness to engage in scientific exchange with other disciplines is essential for applicants. Knowledge of German or willingness to learn German will be an advantage in some projects.

Doctoral candidates should fulfill the following requirements: a very good M.Sc. degree (or equivalent) in Ecology, Zoology, Botany, Behavioura l or Evolutionary Biology, Microbiology or other natural sciences if mechanistic modelling was involved. very good English skills (written and spoken) very good statistical and analytical skills (preferentially sound knowledge in R) experience in one or more of the following areas is expected: experimental field and laboratory studies, ecological modelling, individual-based modelling, telemetry, spatial data analysis (GIS), molecular ecology.

The PostDoc candidate should fulfill the following requirements: a strong expertise in ecological modelling and theory documented by high ranking peerreviewed publications. experience in synthesis work is beneficial.

The University of Potsdam, the Freie Universität Berlin, the Leibniz Institute for Zoo and Wildlife Research and the Leibniz Centre for Agricultural Landscape Research are equal opportunities employers and place particular emphasis on fostering career opportunities for women. Qualified women are therefore strongly encouraged to apply as they are underrepresented in this field. Disabled persons with equivalent aptitude will be favored.Detailed information on the application process, the research topics with their specific tasks and the training program are available at http://www.biomove.org. Candidates are required to indicate up to three preferred projects and explain their motivation for choosing them. Interviews will take place in July.

— / —

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

HasseltU EuropeanNightjar PopGenetics

The Faculty of Sciences, research institute Research Institute: Centre for Environmental Sciences of Hasselt University seeks a (m/f): PhD student Zoology

Background

http://www.uhasselt.be/CMK-en Task description

Your research will aim at elucidating the population-genetic structure of European Nightjar (Caprimulgus europaeus) on a regional (Flemish) as well as a European scale. You will make use of several molecular-genetic techniques. The project fits in with a larger research regarding the ecology, behaviour and protection of this bird species.

Profile

Good relational, communicative and reporting skills

Good knowledge of English

Can work well in team

The candidate has research interest

Diploma

Ms Biology, Applied Biosciences (or equivalent).

Final-year students are (likewise) encouraged to apply.

Employment

Scholarship for a period of 2 x 2 years (with evaluation after 2 years).

Further information

Content job responsibilities:

Prof. dr. Tom ARTOIS, +32-11-268309, tom.artois@uhasselt.be

Content terms of employment and selection procedure:

http://www.uhasselt.be/jobs Application

You can only apply online up to and including 26 June 2015.

Selection procedure

Preselection on the basis of CV. Interview with the selected candidates.

Luc Lens <Luc.Lens@ugent.be>

Leiden MovingHybridZones

PhD-position at Naturalis Biodiversity Center Naturalis has a position for a PhD Candidate, 36 hours a week PhD project: The genomics of moving hybrid zones

About the project Hybrid zones between species are recognized as Âwindows on the evolutionary processÂ because they provide insights into the nature of species, species boundaries, introgression and speciation. Comparatively little attention has been given to the spatial dynamics of hybrid zones, how they shift across the landscape and how movement impacts introgression. In this PhD project, the candidate will investigate hybrid zone movement in European large bodied newts of the genus *Triturus*. Questions to be addressed include: Is introgression large-scale and unidirectional as models predict ? Is hybrid zone movement depending on the landscape ? Can the history of introgression be reconstructed from the size of the introgressed blocks of genes ? The project is funded by the Dutch research organization NWO. The project will be carried out in international collaboration and the possibility exists to work at the Shaffer Lab at UCLA, Los Angeles, USA, in one or two sessions for up to eight months.

General requirements and skills The successful candidate has a MasterÂs degree in biology with proven experience in genomics and in evolutionary biology and, preferably, biogeography and GIS. Laboratory skills, a good command of the English language and proven writing abilities are essential. The ideal candidate will be highly motivated, adaptable to different laboratory settings and have a demonstrated capacity for multidisciplinary research.

On offer We offer a dynamic research environment with involved research staff for supervision; a national and international academic network and a well-equipped and modern laboratory environment with highly qualified technical staff. The candidate will also be affiliated with either Leiden University, the University of Amsterdam, or Wageningen University. A full-time contract (36 hours per week) for a period of one year, to be extended with three years after successful first year evaluation. A salary of circa Â 2.567,- per month. The successful candidate will be employed by Naturalis in Leiden. All our employees are incorporated into a pension fund. The candidate will be supervised by Dr. J. W. Arntzen. Feel free to contact him at pim.arntzen@naturalis.nl with questions about this position. Also see http://science.naturalis.nl/arntzen . *Procedure* Applicants are invited to submit their application, including a cover letter and CV, and the names and e-mail addresses of at least two referees, no later than July 16 by e-mail to: sollicitaties@naturalis.nl.

About Naturalis Biodiversity Center The focus of Naturalis is biodiversity. Naturalis curates a collection of 37 million specimens; this is one of the world's largest natural history collections. We present the history of our planet and the diversity of life on Earth with permanent and temporary exhibitions, educational programmes and websites. Our research and education are maintained at a high academic level. Naturalis is appealing to a wide audience, attracting over 300.000 visitors and 5 million hits to its website annually. Co-operation with international institutions, including three renowned Dutch universities, and the outstanding collections, are all factors that attract hundreds of visiting scientists every year. Expectations and ambitions for the next few years are high. Naturalis will invest significantly in infrastructure for collections and research, including new buildings. In short, we are a developing, world-class institution, and present this exciting opportunity for you to help us achieve our ambitions and meet our challenges.

Pim Arntzen pim.arntzen@naturalis.nl

–

T 071-5271921 Sylviusweg 72 - 2333 BE Leiden E Pim.Arntzen@naturalis.nl I http://science.naturalis.nl/arntzen Pim Arntzen <pim.arntzen@naturalis.nl>

LinnaeusU Sweden 2 ImmunityEvolution

The Centre for Ecology and Evolution in Microbial Model Systems (EEMiS), Linnaeus University, Sweden, is currently recruiting five new PhD students in subjects ranging from marine microbiology to ecoimmunology. Full details of all five studentships, with information on how to apply, can be found at: http://lnu.se/about-lnu/jobs-and-vacancies?l=en . Applications (in English) should arrive no later than July 31, 2015.

Two of these studentships will be hosted by the Zoonotic Ecology and Epidemiology Group headed by Prof Jonas Waldenström. Further details of these two PhD positions are provided below:

—–

POSITION 1

TITLE: Innate immunity of waterfowl - from genes to function. Reference number: PA 2015/292-2.2.1

PROJECT DESCRIPTION: The extent to which naturally occurring polymorphisms in immune genes result in individual differences in pathogen susceptibility remains an open question. While inbreeding has been linked to increased disease susceptibility in many species, it is not currently known whether low heterozygosity in general, or at specific immune loci, is responsible. Beta-defensins are key effector molecules of the innate immune repertoire of higher vertebrates, including birds. Their primary mode of action is the disruption of microbial membranes. However, they are increasingly recognised to have multifaceted roles in immune defence. Beta-defensins represent an ideal system for the study of host ecoimmunology. Firstly, they have a direct role in killing invading pathogens, and secondly, the functional peptide is encoded by a single exon of 36-38 amino acid residues. These genes thus represent a tractable and biologically relevant tool for elucidating the genetic basis for host immunity. The current project aims to build on knowledge of Beta-defensin allelic variation within and between wild populations and species in order to develop an in vitro model for assessing host-pathogen interactions. Based on allelic profiles the student will compare the bactericidal properties of defensin alleles in their native conformations. This work may involve folding and oxidation of native peptides, liquid chromatography, structure determination based on NMR data, and development of bioassays for testing. The successful applicant will interact with other students and researchers within EEMiS, a multidisciplinary centre of excellence within Linnaeus University that comprises expertise in ecology, evolution, and microbiology.

—–

POSITION 2

TITLE: Re-addressing Campylobacter jejuni epidemiology and evolution. Reference number: PA 2015/291-2.2.1

PROJECT DESCRIPTION: Campylobacter jejuni is the most common zoonotic infection in Europe. Despite a well described epidemiology and targeted interventions to reduce carriage in food animals (especially poultry), human campylobacteriosis remains high in Sweden and the EU. In this doctoral student project, we want to turn the question of campylobacteriosis around. Instead of asking how humans become infected, we will investigate what properties that make specific campylobacters so adapted to their food animal niche. Identifying the genes responsible to a 'life on the farm' will: (1) enable a more comprehensive understanding of C. jejuni evolution, (2) pinpoint which traits that underlie emergence of new genotypes in food animals and human disease, and (3) provide new entry points for measures to reduce C. jejuni carriage in food animals.

A vital part in this line of research is to combine epidemiology with phylogenomics where genotypes and phenotypes of C. jejuni from food producing animals are contrasted with strains isolated from non-food animal sources. At our disposal, we have the largest collection in the world of C. jejuni strains from wild birds which, together with new strains, will form the basis for gene-by-gene comparisons with C. jejuni genomes from a reference strain repository. Based on the genetic studies the student will set up phenotypic assays, perform experimental binding studies, and carry out experimental infections in bird models to test the predictions arising from the genomic approach. The successful applicant will interact with other students and researchers within EEMiS, a multidisciplinary centre of excellence within Linnaeus University that comprises expertise in ecology, evolution, and microbiology.

—

For more information about either of these positions, please contact: Professor Jonas Waldenström (jonas.waldenstrom@lnu.se) +46(0)-480-446195; Dr Joanne Chapman (joanne.chapman@lnu.se) +46(0)-480-447394 (position 1 only); Head of Department Per-Eric Betzholtz (per-eric.betzholtz@lnu.se), +46-(0)480-446249; or Personnel Officer Ulrika Petersson (ulrika.petersson@lnu.se), +46-(0)480-446996.

More information and details of how to apply can be found at

— / —

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

---

LouisianaStateU RatAdaptation

PhD position in molecular ecology: Inquiries are invited for a PhD assistantship to examine the effects of the Deepwater Horizon oil spill on marsh rice rats in Louisiana. Research would include examining the relationship between genetic variation at immune genes and bayou virus infection on oiled and unoiled plots. Additional work could include gene methylation or other measures of response to PAH exposure depending on the candidate's experience and interest. Work will include a lab and a field component. Qualifications: experience with genetic analyses (lab and statistical), experience coordinating and collecting field data (particularly handling rodents and operating boats), excellent writing and organizational skills, and ability to work in a large collaborative group. Salary for the position is $22K/year. Interested candidates are welcome to contact Dr. Sabrina Taylor, School of Renewable Natural Resources, Louisiana State University, staylor at lsu.edu, 225-578-4137. To apply, send a cover letter, CV, and a list of 3 references (with phone #s and/or email addresses). Equal Employment Opportunity applies to this position.

With best wishes,

Sabrina

Sabrina Taylor Assistant Professor School of Renewable Natural Resources 227 RNR Bldg. (Office 331) Louisiana State University and AgCenter Baton Rouge, LA 70803 USA

225-578-4137, fax 4227

http://www.rnr.lsu.edu/people/taylor/default.htm
"Taylor, Sabrina S" <staylor@agcenter.lsu.edu>

Lund InsectSystematics

TWO PHD STUDENT POSITIONS IN LEPIDOPTERA PHYLOGENETICS AND EVOLUTION

The positions form part of a group of 15 PhD students now being recruited to the EU-funded Marie Sklodowska-Curie Innovative Training Network BIG4 (http://big4-project.eu/). 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 two PhD student positions advertised here will be formally associated with the Department of Biology at Lund University, Sweden (http://biology.lu.se/). The positions will be supervised by Niklas Wahlberg, who has recently been hired by Lund University as a Professor in Biological Systematics. The Wahlberg lab has a strong research tradition in Lepidoptera systematics and evolutionary biology (http://www.nymphalidae.net/).

Position 1: Lepidoptera phylogenomics

The successful candidate for this position will be using Next Gen sequencing approaches to elucidate the phylogenetic relationships of several species rich groups of Lepidoptera. The project will be particularly focussed on retrieving large amounts of genetic information from museum specimens using similar approaches to those used in sequencing fossils. The student will work in the lab developing protocols, do bioinformatics on resulting sequences and analyze data using phylogenomic methods. Apply here: https://lu.mynetworkglobal.com/en/what:job/jobID:67668/where:4/ Position 2: Lepidoptera diversification dynamics

The successful candidate for this position will be estimating times of divergence for selected groups of Lepidoptera, in particular Noctuoidea and Geometroidea, and elucidating factors behind diversification of those clades. The candidate will be using the latest algorithms for finding correlations between diversification rates and factors such as host plant use and historical biogeography. Apply here: https://lu.mynetworkglobal.com/en/what:job/jobID:67677/where:4/ More information from Niklas Wahlberg (niklas.wahlberg@biol.lu.se)

"niklas.wahlberg@utu.fi" <niklas.wahlberg@utu.fi>

MaxPlanckInst Jena MicrobialEvolution

PhD Evolution of metabolic cross-feeding interactions

Dr. Christian Kost, Experimental Ecology and Evolution Research Group,

Max Planck Institute for Chemical Ecology

A 3-year PhD position is available in my lab at the Max Planck Institute for Chemical Ecology in Jena, Germany. This DFG-funded project will study the evolution of metabolic cross-feeding interactions within bacterial model communities. Using an approach of experimental coevolution between members of the same or different bacterial species, this project aims at (i) identifying the impact of genetic relatedness, and (ii) determining the role of phenotypic heterogeneity during the evolution of cooperative cross-feeding interactions. By combining individual-based modelling with detailed analyses of derived genotypes (whole-genome re-sequencing) and phenotypes (i.e. microscopic analyses on a single-cell level, chemical analyses), unprecedented mechanistic insights into the dynamics that shape the evolution of cooperative cross-feeding interactions can be gained.

The project is part of the DFG-funded Priority Programme Phenotypic Heterogeneity and Sociobiology of Bacterial Populations (http://spp1617.de) and will be conducted in close collaboration with other experimental and theoretical working groups.

The position requires a master's degree in biology (or a related field). The successful candidate should be highly motivated, be able to work independently, and have a strong background in microbiology, evolutionary biology and/ or ecology. Previous research experiences in bioinformatics, theoretical biology, analytical chemistry, or molecular biology are advantageous.

My group offers an international, dynamic, and interactive scientific environment as well as state-of the art, newly equipped laboratories. Information on our scientific work including recent publications can be found here: http://www.ice.mpg.de/ext/633.html?&L=1index.phpd%3D571202 Please do not hesitate to contact me (christiankost@gmail.com; 0049-(0)3641-571212) for informal enquiries.

Your application should consist of:

i) Letter of motivation (max. 2 pages: Why you think the project is relevant, why are you interested in it, and what makes you a suitable candidate?)

ii) Statement of research experience and interests (max. 1 page)

iii) CV (incl. grades of B.Sc and M.Sc)

iv) Publication list (if applicable)

v) Names and e-mail addresses of three academic referees

Please send your application as a single PDF file to Dr. Christian Kost (christiankost@gmail.com). Screening of applications will begin immediately and continue until the position is filled.

Dr. Christian Kost Experimental Ecology and Evolution Group Max Planck Institute for Chemical Ecology Beutenberg Campus Hans-Knöll-Straße 8 D-07745 Jena Germany Tel.: ++49 (0)3641 57 1212 Fax.: ++49 (0)3641 57 1202 Email: christiankost@gmail.com http://www.ice.mpg.de/ext/633.html www.jsmc.uni-jena.de/fileadmin/website/media/pdf/people/faculty/facu lty_kost.pdf

Christian Kost <christiankost@gmail.com>

MaxPlanck Tuebingen GeneNetworkEvolution

* Genetic mapping of evolutionary developmental variation using hybrid mouse in vitro crosses *

One postdoctoral position, one PhD position and a staff scientist position are available in the Chan Lab at the Max Planck Institute in T^{1}bingen as part of a prestigious 1.5M EUR European Research Council grant investigating the role of gene regulatory network evolution in mice by studying *in vitro*± genetic crosses.

The goal of our research is to adopt cutting-edge tissue culture techniques for studying evolutionary divergence in gene networks. We will generate recombinant inbred panels from mouse hybrids spanning increasing evolutionary divergence. We will assay expression and tissue phenotypes at the tissue, fitness and even organismal levels. This ground-breaking research will elucidate the gene network evolution underlying tissue function and speciation in mammals.

PhD position in computation and statistical genomics of gene network evolution in mammals

Your role: Your goal will be to understand the patterns and processes driving mammalian gene network evolution using in vitro crosses of tissue from interspecific mouse hybrids. You will work closely with a postdoc responsible for the derivation and generation of mouse recombinant inbred panels. You will be responsible for the generation, processing and analysis of DNA and RNAseq data to build detailed genotype-phenotype maps from in our in vitro± crosses between interspecific mouse hybrids spanning increasing evolutionary divergence. You will link evolutionary changes in gene expression and phenotypes to specific genetic changes and identify general rules of mammalian gene network evolution. You will integrate into our broader research team and will have the opportunity to collaborate in many other exciting mapping and genomic studies (both intra- and interspecies) in mice and other vertebrates.

Requirements: You will have a Masters or equivalent degree, in Biostatistics, Bioinformatics or Statistical Genetics and in-depth research experience in these fields. You should demonstrate expertise and proficiency in handling large-scale computational data analyses, and advanced skills in statistical analysis (e.g. QTL or GWAS approaches, genotype imputation, Hidden Markov Models, and haplotype phasing of whole genome data). Experience with UNIX and fluency in statistical or programming languages (R and C++, Python or Perl) is essential. We are interested in candidates who are keen to apply new and innovative statistical approaches. Passion for research, team spirit and enthusiasm are essential.

Our Team: You will work in a multidisciplinary team that focuses on mammalian EvoDevo, combining population and comparative genomics with molecular biology and tissue engineering techniques to study the evolution of gene regulatory network in mouse and its close relatives. Our research group is funded by the European Research Council (ERC) and the Max Planck Society and is located on the Max Planck Campus in T^{1}bingen, Germany. T^{1}bingen is one of the best locations in the world in evolutionary genomics research. Our campus hosts world-class research groups, including a Nobel laureate and 11 other ERC-funded teams. We operate state-of-the-art sequencing and other core facilities. English is the working language. All seminars and communications are in English.

Our Offer: Funding is available for the duration of a PhD project (expected length: 3.5 years). Positions will supported by a scholarship contract with salary and benefits based on the German public service pay scale (TVoeD) and are commensurate with training and experience. The Max Planck Society seeks to increase the number of women in areas where they are underrepresented, and therefore explicitly encourages women to apply. The Max Planck Society is committed to employing more handicapped individuals and especially encourages them to apply.

For more information please see: http://fml.tuebingen.mpg.de/chan-group/open-positions
To Apply: Consideration of applications will begin on June 15th 2015, and will remain open until filled. Please send your application with 1. a statement of research interests and why you have applied for this position, 2. your CV, and 3. three reference letters to Dr Frank Chan at frank.chan@tue.mpg.de or the postal address below. Incomplete applications will not be considered.

Dr. Frank Chan

Friedrich Miescher Laboratory of the Max Planck Society

Spemannstrasse 39

72076 T^{1}bingen

Germany

Please see related posts for other positions

–

Frank Chan Max Planck Research Group Leader Friedrich Miescher Laboratory of the Max Planck Society Spemannstrasse 39 72076 T^{1}bingen Germany

T: +49 (0)7071 601 888 F: +49 (0)7071 601 801 @: frank.chan@tue.mpg.de http://www.fml.tuebingen.mpg.de/chan-group.html

— / —

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

MichiganTechU WatermilfoilPopulationGenetics

We are looking for one graduate MS/PhD student to work on the population genetics and ecology of invasive watermilfoil in Michigan waterways. Student will focus on describing patterns of hybridization using microsatellites and how genetic variation influences resistance to control measures (herbicide) and community dynamics of native species in various waterways. Student will collaborate with each other and other members of a multifaceted team that includes scientists, community and state agencies, and private and corporate interest groups.

Minimal qualifications include a background in ecology, evolution, invasive species, and/or population genetics (through coursework OR research positions) and a growing interest in these fields. A strong academic record, evidence of excellent written and analytical skills, and enthusiasm for field and laboratory research will be highly favored.

Interested persons should contact Dr. Erika Hersch-Green (eherschg@mtu.edu) by email and include a CV and a statement about their research interests in general and in particular their interest and compfortability with genetic approaches. Suitable candidates will then be contacted for an interview to discuss projects and reference letters will be requested. Invited students will need to submit a formal application to the graduate school at Michigan Technological University. Start date can be Fall or Spring semester, with a preference for the Fall 2015. Current funding is for two years.

Review of applications will begin immediately and continue until positions are filled.

Erika Hersch-Green, Assistant Professor Department of Biological Sciences Michigan Technological University 1400 Townsend Drive Houghton, MI 49931 Office: 906-487-3351 Fax: 906-487-3167

Erika Hersch-Green <eherschg@mtu.edu>

Montpellier StatisticalPopGenomics

A PhD position is available at the Centre of Biology for the Management of Populations (CBGP) in Montpellier (France), co-funded by the French National Institute for Agricultural Research (INRA) and the European network BiodivERsA

Analysing genetic differentiation to identify genomic signatures of selection

The rapid development of high throughput sequencing and genotyping technologies (Next Generation Sequencing, NGS) permits the comparison of patterns of polymorphisms at a very large number of molecular markers, which allows a detailed characterization of the genomic regions involved in the adaptation of organisms to their environment. However, most of the statistical methods developed so far to identify signatures of selection in the genomes rely on over-simplified demo-genetic models, and generally ignore the information brought by linkage disequilibrium (LD) between genetic markers.

The aim of this PhD project is to propose and evaluate new model-based methods to identify signatures of selection using allele frequency data in a Bayesian framework, along two main axes:

(i) improving the underlying demo-genetic models, by extending existing approaches based on a migration-drift equilibrium model (Vitalis et al. 2014), or the explicit modelling of the divergence history of populations (Gautier et Vitalis, 2013). An alternative approach will consist in estimating the correlation structure of allele frequencies between populations (Guillot et al., 2014).

(ii) using the information brought by the spatial organization of markers (LD). This might be achieved, e.g., by integrating the correlation of gene frequencies at neighbouring SNPs in the models, using hidden Markov models or autoregressive models; or by analysing phased data (obtained by haplotype reconstruction using unsupervised classification techniques) and considering haplotype blocks as multi-allelic loci. These new methods will be directly applied on NGS (pool-seq) data obtained within the European (BiodivERsA) programme EXOTIC, which aims at characterizing the genetic bases of adaptation during the invasion of an iconic species: the Harlequin ladybird Harmonia axyridis (Lombaert et al. 2014). These data, which are already available, will be used to contrast the genomic characteristics of native and invasive populations, at a worldwide scale.

We seek a highly motivated candidate with a Master degree, trained in mathematical modelling and/or biostatistics, with a strong interest for evolutionary biology and the analysis of data (NGS in particular). A good knowledge of population genetics principles and likelihood-based inference techniques will be appreciated. Advanced programming skills in one programming language (e.g., C, C++, Fortran), and the statistical software R, are required.

This PhD will be co-supervised by Renaud Vitalis and Mathieu Gautier, at the Centre of Biology for the Management of Populations (CBGP), in Montpellier, France. The application of the new methods developed on the Harlequin ladybird will benefit from a close collaboration with Arnaud Estoup and Benoit Facon.

We invite the interested candidates to send us a detailed CV, a motivation letter and the e-mail address of one referee, at: renaud.vitalis@supagro.inra.fr and mathieu.gautier@supagro.inra.fr, before July 1st 2015. A first selection round will be done based on this information, and the successful candidates will be interviewed through Skype before July 10th 2015.

Funding: ca. 1 757 euros (gross) per month (for 3 years), starting October 1st 2015.

Montpellier is located in Southern France, and benefits from a vibrant scientific community, in particular in the fields of Ecology and Evolution.

Selected publications in relation to the subject:

Gautier M and Vitalis R (2012) rehh : An R package to detect footprints of selection in genome-wide SNP data from haplotype structure. Bioinformatics, 28: 1176-1177

Gautier M and Vitalis R (2013) Inferring population histories using genome-wide allele frequency data. Molecular Biology and Evolution, 30: 654-668

Guillot G, Vitalis R, le Rouzic A and Gautier M (2014) Detecting correlation between allele frequencies and environmental variables as a signature of selection. A fast computational approach for genome-wide studies. Spatial Statistics, 8: 145-155

Lombaert E, Guillemaud T, Lundgren J, Koch R, Facon B, Grez A, Loomans A, Malausa T, Nedved O, Rhule E, Staverlokk A, Steenberg T and Estoup A (2014) Complementarity of statistical treatments to reconstruct worldwide routes of invasion: the case of the Asian ladybird Harmonia axyridis. Molecular Ecology, 23: 5931ÂV6205.

Vitalis R, Gautier M, Dawson KJ, and Beaumont MA (2014) Detecting and measuring selection from gene frequency data. Genetics, 196: 799-817

– Renaud Vitalis

Centre de Biologie pour la Gestion des Populations
755 avenue du campus Agropolis CS 30016 34988
Montferrier-sur-Lez cedex

— / —

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

Munich EvolutionaryGenomics

PhD Student Position: Evolutionary and Functional Genomics

A PhD student position in Evolutionary and Functional Genomics is available at the University of Munich

(LMU). The student will participate in research related to the Germany-wide priority program 'Rapid Evolutionary Adaptation'.

The specific project focuses on the rapid evolution of gene regulation. It involves the analysis of gene expression variation in natural populations of Drosophila melanogaster using next-generation sequencing technology (RNA-seq) and transgenic reporter gene studies. Although there is a bioinformatic component, most of the work will be experimental.

The University of Munich has a strong, interactive group in evolutionary biology, including theoreticians and experimentalists working on both plant and animal systems. We have an international group and the everyday working language is English. The Department of Biology is housed in the state-of-the-art BioCenter on the University of Munich High-Tech campus.

The PhD student will receive a salary according to the German pay scale (65% E13 TV-L). Applicants should have a master's degree or equivalent in biology or a related field. In addition, laboratory experience in molecular biology and/or genetics is desired. Interested candidates should send a CV, statement of interest, and contact information of at least two potential referees as a single PDF file to Prof. John Parsch (parsch@bio.lmu.de).

Website: http://evol.bio.lmu.de/research/john_parsch/index.html Review of applications will begin on July 20, 2015 and will continue until the position is filled.

The University of Munich is an Equal Opportunity/Affirmative Action Employer and has an affirmative action policy for the disabled.

John Parsch <parsch@zi.biologie.uni-muenchen.de>

NHM UOslo EvolutionaryGenomics

Natural History Museum Doctoral Research Fellowship in Evolutionary Genomics and Zoology

A 4-year PhD position (SKO 1017) is available at the Natural History Museum (NHM), University of Oslo.

The Natural History Museum, University of Oslo, is the largest of its kind in Norway with approximately 150 employees engaged in research, teaching, curating collections and popularizing the sciences of botany, mycology, zoology, paleontology and geology.

Job description

The subject of the PhD project will address the genomic foundations of cryptic speciation in marine interstitial invertebrates. The detection of cryptic species is exponentially increasing in the past two decades. This includes many interstitial species living in the space between the sand grains, for which the "Meiofauna paradox" is long known. That is, morphological identical species with very limited dispersal capacities exhibit a global distribution. The paradox is related to cryptic speciation, but several aspects are unknown. 1) What is driving speciation? 2) How strongly is gene flow limited between populations? 3) Does sympatry of cryptic species occur? 4) Why are the species morphologically static? These questions shall be addressed using European populations from the interstitial polychaete Stygocapitella subterranea as a model system. Population and evolutionary genomic approaches will be explored to assess gene flow, signatures of different selection regimes and phylogeography.

The project will be based on morphological and molecular methods. NHM have access to modern DNA-laboratory facilities. The PhD will be associated with the professor of evolutionary genomics at NHM, Torsten Struck.

Requirements * We seek a person with strong motivation for evolutionary genomics. * The candidate must be skilled in laboratory practices relating to DNA extraction, next-generation sequencing of genomes including RAD sequencing and preferably working with small amounts of tissue material (i.e., whole genome amplification). * Very good computing skills and background in bioinformatics are required for handling and analyzing large data sets emerging from next-generation sequencing approaches. * General knowledge about annelid morphology and identification of interstitial species will be advantageous. * Collaboration and communication skills (including written and spoken English) * Applicants must hold a Master's degree or equivalent in biology or related disciplines like bioinformatics.

We offer * Salary based on salary level 50-55 (NOK 430 500 - 467 700 per year) * A challenging and friendly working environment * Membership in the Norwegian Public Service Pension Fund * Attractive welfare benefits

The purpose of the fellowship is research training leading to the successful completion of a PhD degree. The fellowship requires admission to the PhD program at the Faculty of Mathematics and Natural Sciences. Appointment to a research fellowship is conditional upon admission to the Faculty's research training program. A plan for the research training must be submitted no later than two months after taking up the position, and the admission approved within three months.

Compulsory service, duty work, shall represent 25% of the total hours of work.

Evaluation of the application

In assessing applications, particular emphasis will be placed upon the academic and personal ability of the candidate to complete the project within the given timeframe and write a PhD thesis under supervision. Interviews with selected candidates will be arranged. Please also refer to the English translation of regulations pertaining to the conditions of employment for research fellowship positions:

http://www.uio.no/english/research/doctoral-degree-and-career/phd/appli cation/

http://www.mn.uio.no/english/research/doctoral-degree-and-career/phd-pr ogramme/index.html

A good command of English is required.

http://www.mn.uio.no/english/research/doctoral-degree-and-career/regula tions/proficiency-requirements.html

The application must include: * Application letter * CV (summarizing education, positions and academic work, scientific publications and other relevant activities) * Copies of educational certificates and letters of recommendation * List of publications and academic work that the applicant wishes to be considered by the evaluating committee * A one page explanation of how a PhD in evolutionary genomics will fit into the applicant's career plan * Names and contact details of 2-3 referees (name, relation to candidate, e-mail and telephone number)

— / —

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

Seville Spain GenomicDivergenceSpeciation

PhD position (FPI fellowship) at the Doñana Biological Station in Seville

(ver debajo versión en castellano)

We are seeking a highly motivated PhD candidate to apply for a FPI fellowship associated with the recently granted project "Patterns and processes of genomic divergence along the speciation continuum in two recent evolutionary radiations: a multidisciplinary and integrative approach" (DIVERGEN). The project will integrate genomic and phenotypic data for taxonomic delimitation in two species complexes of montane orthoptera and analyze the evolutionary and demographic trajectories of the delimited species in relation to landscape heterogeneity and past environmental changes. These questions will be addressed combining genomic data obtained using high-throughput DNA sequencing techniques, morphometric geometrics and species distribution modelling, among other analytical approaches.

The PhD will be developed under the supervision of Joaquín Ortego and Anna Papadopoulou at Estación Biológica de Doñana (EBD-CSIC, Seville, Spain), a reference center for ecological and evolutionary research. For more information about this center and our research group visit: http://www.ebd.csic.es/, http://www.consevol.org/, and https://sites.google.com/site/joaquinortegolozano/ Although the official call will open in the next days, the deadline for submitting applications is expected to be around the end of June. The candidates should fulfil the requirements of the call (i.e., to hold a master degree and have been admitted in a PhD program from a Spanish university). A background in molecular techniques, bioinformatics, population genetics, phylogenetics and/or biogeography will be positively evaluated.

Candidates should send their CV and a letter of motivation stating their interest in DIVERGEN to Joaquín Ortego (joaquin.ortego@csic.es)

Best, Joaquín Ortego

Se busca candidat@ para solicitar un contrato predoctoral FPI asociado al proyecto “Patrones y procesos de divergencia genómica a lo largo del continuo de especiación en dos radiaciones evolutivas recientes: una aproximación multidisciplinar e integrativa” (DIVERGEN) concedido por el Programa Estatal de Fomento de la Investigación Científica y Técnica de Excelencia. El proyecto tiene como objetivo combinar datos genómicos y fenotípicos para realizar análisis de delimitación de especies en dos complejos de ortópteros montanos y estudiar las trayectorias demográficas y evolutivas de los distintos taxones en relación a la heterogeneidad del paisaje y cambios ambientales acontecidos durante el Pleistoceno. El proyecto combinará el procesado bioinformático de datos genómicos obtenidos mediante técnicas de secuenciación masiva, análisis de morfometría geométrica y modelado de la distribución de las distintas especies, entre otras aproximaciones analíticas.

La tesis se realizaría en la Estación Biológica de Doñana (EBD-CSIC) bajo la supervisión de Joaquín Ortego y Anna Papadopoulou. Para más información sobre el centro y grupo de investigación: http://www.ebd.csic.es/, http://www.consevol.org/ y https://sites.google.com/-site/joaquinortegolozano/ Aunque la convocatoria oficial será publicada en los próximos días, el plazo para presentar las solicitudes se estima que finalice alrededor del 30 de junio. Los candidat@s deberán cumplir los requisitos de la convocatoria (entre ellos, estar admitidos o matriculados en un programa de doctorado para el curso 2015/2016 en la fecha en la que se formalice el contrato). Se valorará positivamente (aunque no es imprescindible) la experiencia previa en técnicas moleculares, bioinformática, genética de poblaciones, análisis filogenéticos y/o biogeografía.

Los interesad@s pueden enviar su CV y motivaciones para realizar la tesis en el contexto de este proyecto a Joaquín Ortego (joaquin.ortego@csic.es)

Saludos, Joaquín Ortego

– Joaquín Ortego Department of Integrative Ecology Estación Biológica de Doñana Avda. Américo Vespucio s/n 41092 Sevilla, Spain e-mail: joaquin.ortego@csic.es Website: https://sites.google.com/site/-joaquinortegolozano/ Anna Papadopoulou <a.papadopoulou05@alumni.imperial.ac.uk>

StockholmU Sweden PopulationGeneticsConservation

PhD position in Population Genetics closing date for application: July 30, 2015

We announce a four-year full time graduate student position with a focus on conservation genetics issues in the aquatic environments of the Baltic Sea and freshwater mountain lakes of central Sweden. We look for a student who is highly motivated and interested in theoretical and empirical population genetics but also in conservation issues and how genetics information can be used in conservation management. The PhD will be carried out within the Baltic Sea Marine Biodiversity project (BAMBI; www.bambi.gu.se) and the Lakes Bävervattnen long term genetic monitoring study of brown trout populations (www.zoologi.su.se), and be affiliated with the Department of Zoology at Stockholm University.

Stockholm University is situated in the beautiful surroundings of a National City Park were you can stroll in ancient forests and swim off rocks or beaches just within short walks from campus. It is a modern university with a long history that is characterized by an open atmosphere and a multicultural environment. Stockholm University is one of the world’s top 100 higher education institutes.

The Department of Zoology has a long history of basic and applied research of animal species, from arthropods to large mammals, from the perspectives of its five divisions: Ecology, Ethology, Population Genetics, Functional Morphology, and Systematics and Evolution. The Department has c. 100 staff including c. 40 PhD students. The advertised position will be affiliated to the Division of Population Genetics, which has a strong tradition of theoretical and empirical focus on conservation genetics issues and with recent research also focusing on developing and using genomic tools.

Read more and apply here: https:/-/web103.reachmee.com/ext/I007/927/-job?site=8&lang=UK&validator=-d3e6a58db9058c5eab7ea3e324f063f6&job_id=330 Read more about the department: www.zoologi.su.se/en/-index.php, Stockholm University: http://www.su.se/-english/ We look forward to your application! Exact date to start the PhD work will be as agreed with the successful applicant. However, our ambition is to start work as soon as possible. Do not hesitate to contact us if you have any questions: Prof. Linda Laikre linda.laikre@popgen.su.se and Eeva Jansson eeva.jansson@zoologi.su.se (we will both supervise this project).

Linda Laikre <linda.laikre@popgen.su.se>

Sweden Macroevolution

Dear colleagues,

Please help us advertise this fully funded PhD position in Biology to any potential candidates.

The applicant will work on macroevolutionary analyses of living and extinct taxa. The project, funded through a Wallenberg Academy Fellowship, aims at identifying major drivers of speciation and extinction through time and space. We aim at answering questions such as why some lineages have produced many more species and genera than others; how climate change has affected biodiversity in the past; which regions, biomes and traits are most closely associated with the evolutionary success of clades; how clades compete with each other over evolutionary time; what is the biogeographical history of particular lineages; and what is the influence of phenotypic traits on biogeographical processes.

The project will involve compiling (or generating) and analysing phylogenetic and fossil data, and potentially the development of methods aimed at macro evolutionary inferences. The details of the project can be adjusted based on the candidates skills and interests.

A full description and information on how to apply can be found at: http://www.gu.se/-omuniversitetet/aktuellt/ledigaanstallningar/-?id144&Dnrp6081&Type=E (and in Swedish): http://www.gu.se/omuniversitetet/aktuellt/-ledigaanstallningar/?id144&Dnrp6081&Type=S Many thanks and best wishes,

Alex

Alexandre Antonelli, PhD Wallenberg Academy Fellow

Associate professor, Department of Biological and Environmental Sciences, University of Gothenburg Delivery address: Box 461, SE 405 30 Göteborg, Sweden Visiting address: Carl Skottsbergs gata 22B, 413 19 Göteborg, Sweden

Scientific curator, Gothenburg botanical garden

Lab homepage: http://antonelli-lab.net Phone: + 46 (0) 703 989570 E-mail: alexandre.antonelli@bioenv.gu.se

Alexandre Antonelli <alexandre.antonelli@bioenv.gu.se>

Switzerland WSL SpatialEcology

The Swiss Federal Institute for Forest, Snow and Landscape Research WSL is a part of the ETH domain. Approximately 500 people work on the sustainable use and protection of the environment and on the handling of natural hazards.

The Research Unit Biodiversity and Conservation Biology, which deals with all aspects of biodiversity from genes to ecosystems and which has strong links into practical management, is looking, per August 1, 2015, for a PhD student in spatial ecology and habitat network modelling.

The interdisciplinary project CHECNET focusses on coupling ecological habitat networks with land-use/transport networks. You will develop a new method for constructing habitat networks that predicts occurrences of animal species resulting from changes in land-use and/or traffic flows on the Swiss Plateau. You work with existing occurrence data from a range of animal groups. You publish your work in international scientific journals and present them at conferences.

You have a Master in Biology, Environmental Sciences or Geography, are interested in spatial ecology and have experience with the modelling of habitat connectivity, habitat suitability and/or networks. You also have experience with programming (R, Python, Matlab) and GIS (ArcGIS, QGIS). You enjoy communication and collaboration in an interdisciplinary project and are fluent in English.

For more information: https://apply.refline.ch/-273855/0509/pub/1/index.html “vanstrien@ethz.ch” <vanstrien@ethz.ch>

UAlberta LynxEvolution

MSc opportunity

Density estimation of lynx during a snowshoe hare peak and decline

We are seeking a motivated student interested in using camera trapping to estimate the abundance of lynx in our study area in the southwestern Yukon. We have been studying snowshoe hares and lynx at Kluane Lake for almost 40 years. During much of that time we have obtained a relative abundance estimate of lynx via winter snow track transects. We are now poised to deploy camera arrays to estimate actual lynx density changes during a hare peak and decline. We have good estimates of snowshoe hares and numbers suggest they will peak in 2015-16. The successful candidate will be part of an energetic team (5 professors and 7 graduate students) studying the lynx-hare cycle. The project will involve extensive fieldwork during autumn and winter meaning that scholarship (NSERC or equivalent) support will be necessary. The successful applicant would enroll at the University of Alberta, Department of Biological Sciences.

If you enjoy fieldwork and want to experience one of the most beautiful places in Canada during an exciting time in the hare-lynx cycle, this thesis opportunity is for you. Work could begin as early as September 2015.

Applicants should provide a CV plus a copy of their transcripts via email to Stan Boutin (sboutin@ualberta.ca). The competition will remain open until a suitable candidate is found.

"asykes@ualberta.ca" <asykes@ualberta.ca>

UEasternFinland FishEvolution

PHD STUDENT POSITION IN EVOLUTIONARY FISH ECOLOGY, 15.6.2015

We announce a four-year graduate student position (01.09.2015 - 31.08.2019) at the Department of Biology, University of Eastern Finland (UEF), Joensuu campus in the Project "Evolutionary restoration of trout populations impacted by human-induced selection", funded by the Academy of Finland. PhD work will take place in our new project that is based on a large breeding experiment, and in which we study the genetic basis of vulnerability to angling, life-history variation and trait co-variation (pace-of-life syndromes) especially with respect to migration behaviour in brown trout. The PhD student is expected to have a background in genetics and to have basic knowledge on next generation sequencing techniques and associated bioinformatics methods. The work will require occasional visits to and a 2-12 month stay at the Department of Biology, University of Turku, but basic work such as DNA extraction can be conducted at the local department in Joensuu. The recruited PhD-student would join an appropriate graduate school of University of Eastern Finland and be supervised by Dr. Anssi Vainikka (Joensuu), Dr. Silva Uusi-Heikkilä (Turku) and Prof. Robert Arlinghaus (Berlin, Germany).

We encourage applications from highly motivated candidates interested in evolutionary genetics, animal personality research and fishing/hatchery-induced evolution. We offer a competitive salary according to the UEF standards (also based on the candidate's progress, ca. 2000 - 3500 eur / month) the benefits of a young, very productive research group and an international network of collaborations. Some teaching obligations are included in the position (to be negotiated). Four month trial period is used in the recruitment. Joensuu is a small (about 75 000 inhabitants) rather international university town in Eastern Finland, but well connected through railways and an airport. Joensuu offers a nice environment especially for a person interested in nature-related hobbies. Fishing skills are appreciated but by no means compulsory. Field work is conducted in Kainuu Fisheries Research station in Paltamo, located 270 km north from Joensuu.

We expect the successful candidate to be fluent in English, since modern academic research is based on international collaboration, and all scientific reports (Finnish PhD thesis consists of 4-5 research articles/manuscripts and a summary) will be written in English. We require some demonstrations of good writing skills, and therefore ask the applicants to attach a motivation letter (two pages) describing in English, why would you be a suitable person for the work, how do you see research on fish genetics could help to solve sustainability issues and what are your personal ambitions in science. Please also analyse your strengths and weaknesses. We do not expect you to be a PhD during admission phase, but ready to work hard enough to become a highly qualified PhD in four years.

Please send your application together with your CV to anssi.vainikka@uef.fi by 30.7.2015. You can also send a voluntary recommendation letter separately to the e-mail address above from one referee. The best three candidates will be interviewed through Skype.

Please ask for more information: Dr. Anssi Vainikka, tel. +358 500 443290 or anssi.vainikka@uef.fi or Dr. Silva Uusi-Heikkilä, silva.uusi-heikkila@utu.fi

More information about our research: https://www2.uef.fi/en/aquatic-ecology/home & http://www.kfrs.fi & http://pnp.utu.fi/silva.html anssi.vainikka@uef.fi

UKoblenzLandau GroundWaterGenetics

German(speaker)s!

Since part of this job will be to interact with locals during sampling campaigns, German proficiency is mandatory and therefore, the job advertisement is held in German.

Im Rahmen des BMBF-geförderten Vorhabens GROUNDCARE (Ausschreibung ReWaM - Regionales Wassermanagement) sucht dasInstitut für Grundwasserökologie IGÃ GmbH in Landau in der Pfalz für das Teilprojekt TP3: ÂGrundwasserfauna - Diversität und Bewertung“

eine/n Doktoranden/in

Thema: Molekulare Ãkologie von Grundwasser-Metazoen

Ziel: Im Mittelpunkt steht die Frage, inwieweit genetische Verfahren für die Bewertung des GrundÂ’wassers sowie für die Bestimmung der Biodiversität (Fauna) geeignet sind. Im Vordergrund stehen genetische und genomische Analysen von Grundwasser-Metazoen in Abhängigkeit von ökologischen Gradienten sowie die Beschreibung phylogeographischer Muster ausgewählter Arten.

Zeitraum der Arbeit: 01.09.2015 - 31.08.2018.

Das Projekt: Biologische Indikatoren dienen als Standardparameter für die Ãberwachung des ökoÂ’logischen Zustands von Oberflächengewässern. Für Grundwasserökosysteme gibt es derartige Ãberwachungskonzepte allerdings bislang noch nicht. Zudem ist kaum bekannt, wie GrundÂ’wasserÂ’ökosysteme auf verschiedene anthropogene Störungen reagieren, und wie schnell sie sich davon wieder erholen. Das Projekt ”Grundwasserfauna - Diversität und Bewertung “ ist Teil eines vom BMBF geförderten Projekteverbundes zur ”Parametrisierung und Quantifizierung von Grundwasser-ÃkosystemÂ’dienstleistungen als Grundlage für eine nachhaltige Bewirtschaftung“ (GroundCare). Dabei sollen u.a. molekulare Kengrößen, die Aussagen über die Grundwasserqualität und den ökoloÂ’gischen Status eines Grundwasserleiters erlauben, ermittelt und getestet werden.

Die Betreuung der Promotion erfolgt gemeinsam mit der AG Molekulare Ãkologie der Universität Koblenz-Landau.

Ihre Qualifikation: Voraussetzungen sind ein mit Diplom, MSc oder vergleichbarem Abschluss beÂ’endetes Studium der Biologie oder vergleichbarer Fächer, sowie Erfahrungen in Molekulargenetik. Führerschein Klasse B und die Bereitschaft zu Dienstreisen. Wünschenswert sind Erfahrungen mit Codezeilen-basierten Datenanalysen (z.B. R, S-Plus, Python, Perl, Matlab, Java) bzw. Erfahrungen mit Bioinformatik und multivariater Statistik.

Bewerbungsschluss ist der 17.07.2015.

Die Vorstellungsgespräche finden statt am 30.07.2015.

Ihre aussagekräftige Bewerbung senden Sie bitte elektronisch an Frau Dr. Susanne Schmidt, E-Mail: schmidt@groundwaterecology.de

Bei Fragen wenden Sie sich bitte ebenfalls an Frau Dr. Susanne Schmidt (Tel: 06341/280-31339). Institut für Grundwasserökologie IGÃ GmbH An der Universität, Fortstr. 7 76829 Landau

www.groundwaterecology.de

UmeaU UngulateEvolution

I am advertising a PhD position in animal community ecology, partly using molecular methods. I think this position could be of interest for the readers of evoldir.

Joris

The department of Wildlife, Fish & Environmental studies (SLU, Umea, Sweden) offers a fully funded PhD project in Animal Community Ecology.

Beyond Moose: community ecology of Sweden’s novel diverse ungulate communities

Project description

Sweden's ungulate communities have changed dramatically, resulting from introductions of non-native (e.g., fallow deer) and native ungulates (e.g., wild boar) and expansion of ranges northwards beyond historic distributions due to milder winters. We lack a comprehensive understanding of the functioning of these novel diverse ungulate communities in landscapes modified by humans. The Swedish EPA has funded our program Beyond Moose to increase this understanding and to move from single- to multispecies wildlife management. This also feeds into the international discussion on how to manage increasing ungulate communities throughout Europe and North America. The PhD will study trophic interactions among species, and effects on individual and population performance, for varying ungulate community compositions and along gradients of land use practices. The project combines field methods with state of the art DNA tools. Results will be crucial for finding trade-offs among competing ecosystem services such as game meat and recreation from hunting vs. fiber from forests and food from crops. The PhD student will closely collaborate with an advertised PhD position in the Governance project that focuses on social dimensions of multi-species wildlife management.

Qualifications

The applicant should have an MSc degree in Ecology or similar discipline. We are looking for a candidate that is prepared to combine extended field work periods with work in the lab (DNA analyses) as well as complex data analyses, such as bioinformatics. Documented skills in one or more of these three aspects are highly valued. The candidate should be fluent in spoken and written English. The candidate should be able to work independently as well as in a team. Experience in writing and publishing scientific papers is a plus.

How to apply:

Deadline for applications is 26^th July 2015. Preferred start date is 1^st of September 2015. Please use below link for more information on how to apply:

http://www.slu.se/en/education/postgraduate-studies/-new-phd-student/Rea d-more/?sprak=e&Uid02

Further information:

Joris Cromsigt, joris.cromsigt@slu.se; Navinder Singh, navinder.singh@slu.se.

Read about being a PhD at the department at http://phdatvfm.weebly.com/ and about the PhD education at SLU at www.slu.se/en/education/postgraduate-studies/ . Joris Cromsigt <joris.cromsigt@slu.se>

USunshineCoast CrustaceanEvolution

Genomics of Masculinity in Crustaceans:

Crustaceans are considered ancestral to insects. They represent a diverse phylum, with unique features such as the androgenic gland which defines masculinity in Malacostraca. Applications for PhD positions in evolutionary genetics are invited in the lab of Tomer Ventura at the University of the Sunshine Coast (Queensland, Australia). Our group uses an array of bioinformatics approaches combined with in vitro and in vivo techniques (including gene silencing), in order to understand the molecular basis and evolution of sexual differentiation. We developed de novo transcriptome assemblies and assays that enable us to explore the function of specific genes in masculinity followed by elucidating the evolutionary pathway of these genes, through comparative phylogenetics.

Prior training in the following areas is highly desirable but not essential: quantitative or population genetics, bioinformatics, genomics or evolutionary biology.

Qualifications: Applicants require either a Bachelor's degree with Honours, 'Master of Science, MPhil or equivalent degrees. International applicants usually will have published some work in peer-reviewed journals. Australian and New Zealand applicants must have received first class Honours degrees. Scholarship schemes at the University of the Sunshine Coast are highly competitive. The USC Graduate School website provides further information on the entry requirements for admission to the PhD program and scholarship details. Individuals successful in gaining a tuition-fee waiver scholarship usually also obtain a living stipend.

Application process Interested candidates should send a cover letter describing their motivation and research interests along with a CV to tventura@usc.edu.au no later than Tuesday July 7th 2015. Short-listed candidates will be asked to provide further information and documentation and will be interviewed over Skype. Following, the final applicants will be invited to apply for a PhD at USC.

Tomer Ventura FoSHEE University of the Sunshine Coast Sippy Downs, QLD 4556 Australia tventura@usc.edu.au

Tomer Ventura <tventura@usc.edu.au>

UValencia BacterialGenomics

We are seeking a highly motivated PhD candidate to apply for a FPI fellowship associated with the recently granted project “Fast bacterial evolution: processes and opportunities for the development of genomic epidemiology” (FASTBACGENOMEPI) recently funded by MINECO (Spanish Office for Economy and Competitiveness). The main goal of this project is to expand the advances in new sequencing technologies to derive the complete genome sequence of difficult-to-culture bacteria from uncultured samples of clinical or environmental origin. We will work with the three sexually transmitted bacteria (Chlamydia trachomatis, Neisseria gonorrhoeae and Treponema pallidum), and we will also pursue the analysis of natural populations of Legionella pneumophila. The project will encompass wet-lab approaches with the use and eventual development of bioinformatic tools to allow the fast and precise analyses of complete genome sequence information for its integration in evolutionary and epidemiology frameworks.

The PhD will be developed under the supervision of Fernando González-Candelas at the Evolution and Health Unit (Cavanilles Institute for Biodiversity and Evolutionary Biology, University of Valencia, Spain) and Genomics and Health Unit (FISABIO, Valencia, Spain), reference centers for evolutionary and epidemiological research. For more information about this research centers and our group visit: http://www.uv.es/gonzalef/ ; http://www.uv.es/evosalud/ ; http://fisabio.san.gva.es/ ; http://www.uv.es/uvweb/institut-universitari-cavanilles-biodiversitat-biologia/en/institut-cavanilles-biodiversitat-biologia-evolutiva-1285893448913.html

The PhD fellowship will extend for 4 years with a starting salary of 16,422 euro with additional funds for enrollment in a PhD program and to support short stays at other research centers. The research is funded through project BFU2014-58656R. The deadline for submitting applications is June 29, 2015 at 15.00 (Spanish time). The candidates should fulfil the requirements of the call (i.e., to be acceptable in a PhD program from a Spanish university). A background in molecular techniques, bioinformatics and molecular evolutionary biology will be positively evaluated.

Candidates should send their CV and a letter of motivation stating their interest in this project to Fernando González-Candelas (fernando.gonzalez@uv.es). Formal applications must be submitted through the Facilit@ application at the MINECO web site (https://sede.micinn.gob.es/)

Best regards,

Fernando González-Candelas

Prof. Fernando Gonzalez Candelas Catedrático de Genética / Professor of Genetics Unidad Mixta Infección y Salud PÃºblica FISABIO/Univ. Valencia Universitat de Valencia Phone: (+34) 963543653 - 961925961 C/ Catedrático Jose Beltran, 2 FAX: (+34) 963543670 E-46980 Paterna (Valencia) SPAIN e-mail: fernando.gonzalez@uv.es http://www.uv.es/gonzalef ResearcherID: G-5681-2010 ORCID http://orcid.org/0000-0002-0879-5798 Fernando <fernando.gonzalez@uv.es>

UWestEngland Biodiversity

We are offering a fully-funded PhD bursary studying the evolutionary relationships of tropical arthropods and their ecological interactions with the environment. Essentially, the student will investigate the link between biodiversity and ecosystem function in a tropical rainforest.

Supervisor: Dr Farnon Ellwood, University of the West of England Applicants are encouraged to email in advance of application: farnon.ellwood@uwe.ac.uk http://people.uwe.ac.uk/Pages/person.aspx?accountname=3Dcampus/mdf-ellwood Background: The world is changing. Climate change and food security are of increasing concern, while the loss of biodiversity and ecosystem services are forcing us to question how ecological communities interact with the physical environment. Answering this question is becoming increasingly urgent; we are in a mass extinction crisis and few theories can predict how communities of species will respond to environmental disturbance and shifting weather patterns. Tropical rainforests are particularly vulnerable to anthropogenic disturbance. The student will spend their first year studying a model rainforest at the Eden Project in Cornwall; fieldwork in the second and third years will be based in Malaysia alongside members of our research group currently taking part in the Royal Society South East Asia Rainforest Research Programme. This programme is designed to facilitate the study of rainforest under different levels of disturbance; the study area is made up of forest fragments logged in a chronological sequence. The size and shape of each fragment is known, as are the identities of every tree species.

Aims: The overall aim of the project is to explore whether functional redundancy (i.e. overlap in ecosystem services) can buffer against disturbance-induced species extinctions. Studies of the link between biodiversity and ecosystem function have yet to show how the removal of certain species affects nutrient cycling and the transfer of energy within ecosystems. By studying the evolutionary relationships of invertebrates against a background of microbial activity and nutrient stoichiometry (i.e. relationships between the relative quantities of nutrients cycling through the epiphytes), the student will show how the nutritional requirements of organisms shape ecological communities. Moreover, this work will reveal how disturbing the chemical balance of organisms changes the fluxes of elements and energy through ecosystems. In summary, we will reveal what happens when environmental disturbance upsets the balance of nature.

Methods: The student will manipulate physical and biological conditions within epiphytic bird's nest ferns (Asplenium nidus), an ecosystem model developed by us specifically for this purpose. Experimental manipulations within the epiphytes will be replicated in habitats where the ferns occur naturally, and which represent increasing severities of disturbance: in pristine rainforest; in selectively logged forest of different times since logging; and in oil palm plantations. Bird's nest ferns are increasingly important as reservoirs of biodiversity in these progressively degraded habitats. This project will advance our knowledge in two ways: first, using ferns as ecosystem models, the student will manipulate invertebrate diversity and microclimate within the ferns and thus quantify the specific impacts of disturbance on biodiversity and ecosystem function; second, using ferns as naturally-occurring sampling units, the student will compare the results from their manipulative experiments with the genuine effects of large-scale habitat degradation. The ferns are ideal natural microcosms for this purpose: they are abundant, widely distributed, easy to manipulate, and can be sampled thoroughly. Moreover, the ferns contain suspended soil which not only provides the fern with nutrients but creates a unique habitat for a wide range of organisms.

Further details: The studentships consist of an annual stipend of £14,057. In addition, full-time tuition fees will be covered for 3 years. Please submit your completed application to graduateschool@uwe.ac.uk by Monday 29 June 2015. The studentship will start on 1 October 2015 or 1 January 2016.

How to apply: http://www1.uwe.ac.uk/research/-postgraduateresearchstudy/studentshipopportunities/-studentships2015/has.aspx Farnon Ellwood <Farnon.Ellwood@uwe.ac.uk>

UZurich EvolutionaryBiol

PhD thesis in experimental or computational evolutionary biology

A three-year Ph.D. studentship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. We are looking for a researcher to study innovation in biological systems that range from molecules to genome-scale genetic networks. The lab's projects range from the directed evolution of macromolecules to laboratory evolution in E.coli and computational analyses of genetic networks (e.g., Hayden et al., Nature 2011; Payne and Wagner, Science 2014;). A sample of the laboratory's research can be found at http://www.ieu.uzh.ch/wagner/. Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and life's fundamental organizational principles.

The successful candidate for an experimental project will have a strong background in molecular biology and microbiological techniques. The successful candidate for a computational project will have a strong background in bioinformatics and computational biology, fluency in a major scripting language such as perl, and experience in software development. Applicants without a demonstrated interest and research history in evolutionary biology, and without a Masters Degree or equivalent cannot be considered further. We are looking for an individual who is highly self-motivated and can work independently.

The working language in the laboratory is English. German skills, although helpful, are not essential. Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file merged from the following parts to annette.schmid@ieu.uzh.ch: CV including publication list, a statement of research interests not exceeding three pages, and three academic references. A brief sketch of a potential experimental evolution project is also desirable. Please include the word “EXPPHD15” in the subject line. The application deadline is August 15, 2015. The position is available from January 1, 2016.

Annette Schmid Administrative Assistant of Prof. A. Wagner University of Zurich Institute of Evolutionary Biology and Environmental Studies Wagner lab, Y27-J52 Winterthurerstrasse 190 CH-8057 Zürich Switzerland Mail to: annette.schmid@ieu.uzh.ch Phone +41 (0)44 635 61 42 Fax +41 (0)44 635 61 44 at the office on Monday and Thursday

annette.schmid@ieu.uzh.ch

WageningenU GenomicSelectionNaturalEnemies

A PhD student position within the EU-funded Marie Skodowska-Curie Innovative Training Network BINGO (Breeding Invertebrates for Next Generation Biocontrol) is available at the Laboratory of Genetics and the Animal Breeding and Genomics Centre of Wageningen University in the Netherlands.

About the position: The candidate will work on the development of genome-based selection for the improvement of natural enemies in biocontrol. Intraspecific genetic variation in arthropods is often studied in the context of evolution and ecology. Such knowledge can also be very usefully applied for selection of genotypes with optimal trait values to develop more effective biocontrol agents. For complex life-history or behavioural traits that lack easily recordable morphological phenotypes (i.e. longevity, development time, fecundity), the selection process can be laborious. Knowledge of the genomic regions underlying the traits can facilitate the screening and selection process. Genome-based selection (GS) methods use information from genome-wide DNA-markers to efficiently select for such complex traits. While they have been shown to hold great potential for plant and animal breeding, GS methods have not yet been applied for the improvement of natural enemies. This project seeks proof-of-principle for the use of genome-based selection for key life history and natural enemy traits in the model parasitoid wasp Nasonia vitripennis. The aim is to develop selection protocols for insect natural enemies and apply these for the genome-based selection of Nasonia lines for complex life-history traits. The project will involve: (1) A quantitative genetics approach, known as (genomic selection,) to accommodate the haplodiploid nature of parasitoids and other natural enemies; (2) Genomic data generation and analysis using next-generation sequencing technologies; (3) Large-scale phenotyping of complex traits in Nasonia. For more details on this position, see http://-bit.ly/1D3tcLT Qualifications: We seek a bright, highly motivated, and enthusiastic researcher with a skill set suitable to the project and who is able to work both as part of a team and independently. Our ideal candidate has a strong quantitative or statistical genetic background, experience with bioinformatic analysis, and life-history or behavioural work in insects. You have a master degree in quantitative genetics, statistical genetics, animal or plant breeding, or evolutionary biology, with a good background in population genetics, bioinformatics, genomics or computational biology. Candidates from other programs, with a strong interest in the application of quantitative methods in genetics are also invited to apply. Experience with NGS technologies and genomic data analysis is a plus, but training will be provided. Insect experimental work will be part of the project. The language in the lab is English. Therefore, a high standard of spoken and written English is required.

Eligiblity: Candidates must be, at the time of recruitment by the host organisation, in the first four years (full-time equivalent) of their research careers and have not yet been awarded a doctoral degree. This is measured from the date when they obtained the degree, which would formally entitle them to embark on a doctorate (e.g. Master degree). Eligible candidates may be of any nationality but must not, at the time of recruitment have resided or carried out their main activity (work, studies, et cetera) in The Netherlands for more than 12 months in the 3 last years immediately prior to the recruitment date.

BINGO-ITN: The BINGO-ITN is funded by the EU Horizon2020 programme and involves 12 partners from academia, non-profit organizations, and biocontrol industry located in the Netherlands, Germany, France, Spain, Czech Republic, Austria, Switzerland, Greece and Portugal. BINGO's approach is multidisciplinary, encompassing a broad range of scientific disciplines, including the application of state-of-the-art population genomics. The BINGO programme combines integrated training workshops and internship opportunities across the network, with career opportunities in academia, public or the private sectors. You will work in close cooperation with PhD students and researchers involved in related BINGO research projects. Secondments are planned to other BINGO participants. For more information about the BINGO project and other PhD projects see www.bingo-itn.eu How to apply: To apply, please provide a letter of motivation and a detailed CV by e-mail to: 1. Dr. Bart Pannebakker, bart.pannebakker@wur.nl & Dr. Piter Bijma, piter.bijma@wur.nl 2. CC to: info@bingo-itn.eu 3. Add subject: BINGO-Application RP13

We will be considering applications until 1st of August

2015, the ideal starting date is 1 September 2015

"bart.pannebakker@wur.nl"

<bart.pannebakker@wur.nl>

Jobs

23andMe Computational Biologist

Computational Biologist - Population Genetics

23andMe Mountain View, CA, United States

We are looking for a colleague with training and experience in computational biology to join our highly productive Research Team. This person will be involved in the analysis of human genetic data and the development of computational methods, which requires a mix of computational skills, statistical knowledge, creativity and biological insight.

Who we are

Since 2006, 23andMes mission has been to help people access, understand, and benefit from the human genome. We are a group of passionate individuals pushing the boundaries of whats possible to help turn genetic insight into better health and personal understanding.

Our Research Team

23andMes Research Team prides itself on driving cutting edge, industrial-scale science that makes an impact which belies the teams size, in an environment and culture that fosters creativity, innovation, collaboration and fun. Our science has garnered the respect of many members of the broader scientific community. As 23andMe continues to grow, we are looking for people who are excited by the potential discoveries we can make with our innovative research framework.

Who you are

You have a medley of mathematical, statistical and computation skills and a passion for understanding evolution. You get motivated when working on something that feels valuable. You appreciate the power of statistics and believe in the value of accessing ones genetic information. You enjoy working as part of a team, are goal-driven and are excited to contribute to something that truly impacts peoples lives.

What youll contribute to

- Developing methods and performing genetic analyses that will advance the understanding of human genetics and shape 23andMes consumer product. - Long term R&D projects that bring research advances into 23andMes consumer product. - Providing scientific support to a variety of teams across the company, including communications and public relations, making scientific knowledge accessible to the average person.

We hope you have

- PhD in Computational Biology or related field such as Genetics, Computer Science, Engineering, Physics, Math, or Bioinformatics. - Strong bioinformatics and biostatistics background, with experience in algorithm development and machine learning approaches. - Evolutionary or population genetics research experience. - Track record of applying innovative methods to drive project success. - Strong programming skills, especially in scripting languages such as Python and R. - At ease in a Linux environment. - Familiarity with the fundamentals of human genetics. - Enthusiasm for working in a highly collaborative environment. - The ability to be proactive, thorough and independent, but also to work effectively within a dynamic, fast-paced and interdisciplinary team.

Other skills we are looking for

- Demonstrated record of developing and distributing tools for the analysis and visualization of genomics data. - Experience with C/C++, Django, HTML, Git.

Apply online: 23andme.com/careers/oFga1fwQ/

ABOUT US

23andMe, Inc. is the leading personal genetics company. Founded in 2006, the mission of the company is to help people access, understand and benefit from the human genome. 23andMe has over 900,000 customers worldwide with over 80 percent consented to participate in research. 23andMe, Inc. is located in Mountain View, CA. More information is available at www.23andMe.com . Kasia Bryc <kbryc@23andme.com>

AncestryHealth 2 ComputationalGenomics

POSITION TITLE: Clinical Genomics Scientist, AncestryHealth LOCATION: San Francisco, CA

AncestryHealth (www.AncestryHealth.com) is seeking a motivated, collaborative and talented computational biologist with experience in the analysis of clinical and genomic data. Working with a nimble team of geneticists, statisticians, computer scientists and epidemiologists, the Clinical Genomics Scientist will invent algorithms and methods to interpret our singular data set of genotypes, pedigrees and phenotypes. We are seeking applicants who are eager to develop novel ways to extract actionable and accurate clinical genomics discoveries for consumers.

Requirements/Qualifications: * The successful candidate for the position will have an M.D. or Ph.D. in Computational Biology, Genetics, Statistics, Computer Science (or a related field). * The candidate must have a passion for using genomic data to advance healthcare, population health, and wellness. * Demonstrated excellence in algorithm development using "- omics" data in clinical applications is important. * The successful applicant will have a strong working knowledge of statistics and proficiency in one or more of Python, Java, C/C++ or R. * Excellent verbal and written communication skills are required. * Strong organizational and interpersonal skills will be needed in our fast-paced team.

Interested? Here's how to apply:

Begin your online application http://smrtr.io/yKH7rw or if you have any problems please submit your CV/resume to careers@ancestryhealth.com Please reference CLINICAL GENOMICS SCIENTIST in the subject field of your e-mail.

Ancestry (www.ancestry.com) is a private equity owned company with large US offices in Provo, Utah, and San Francisco, as well as several international offices including London, Dublin, Munich, Toronto, and Sydney. Ancestry is the world's largest online resource for family history with an extensive collection of over 13 billion historical records that have been digitized, indexed, and made available online over the past 15 years. These digital records and documents enabled Ancestry's 2.7 million plus paying subscribers and over 12 million registrants to create nearly 60 million family trees. While most of Ancestry's subscribers are in the US, the company has a strong presence in the UK, Canada, and Australia, and is in the process of a large international expansion into Eastern Europe and Mexico. In 2014, Ancestry had non-GAAP revenue of $619.5 million (up 10.3% YOY) and adjusted EBITDA of $214.8 million.

AncestryDNA (www.ancestryDNA.com) has become the fastest growing direct-to-consumer genomic company by providing consumers insights into their ancestral origins. A team of scientists leverages pedigrees, documents, demographics, and genomes to conduct innovative research in population

—

POSITION TITLE: Epidemiologist, AncestryHealth LOCATION: San Francisco, CA

AncestryHealth (www.AncestryHealth.com) is seeking a self-starting scientist to define and build a corpus of clinical data that will maximize the value of our genomics, pedigree and self-reported phenotype data. Working with a nimble team of geneticists, statisticians, computer scientists and clinical genomics specialists, the Epidemiologist will create consumer-facing health reports and help design data collection protocols that will maximize the research value of our data now and in the future. We are looking for a collaborative, visionary and dedicated individual eager to create novel resources for clinical and public health research.

Requirements/Qualifications: * The successful candidate for the position will have an M.D. or Ph.D. in Epidemiology or Public Health. * Experience designing and/or managing large cohort studies is extremely important. * The successful applicant will have a strong working knowledge of statistics. * Demonstrated ability to critically evaluate genetics studies will be valuable. * Excellent verbal and written communication skills are required. * Strong leadership and interpersonal skills will be needed in our fast-paced team.

Interested? Here's how to apply: Begin your online application http://smrtr.io/ViJLKg or if you have any problems please submit your CV/resume to careers@ancestryhealth.com Please reference EPIDEMIOLOGIST in the subject field of your e-mail.

— / —

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

BangorU AlgalBioinformatics

Two-year PDRA to look at blue energy sources/algae - analysing GBS data and GWAS

Based at Bangor University (School of Environment, Natural Resources and Geography and the Centre for Applied Marine Sciences)

Part of the Sustainable Biotechnology and Biofuels SuBBSea Seaweed project (BBSRC and DBT India) led by Durham University with a consortium of partners in the UK and India. Required PhD standard in bioinformatics/statistical genetics/molecular biology and experience of working with large datasets. Knowledge of Stacks and other bioinformatics software desirable.

Advert on jobs.ac.uk:

http://www.jobs.ac.uk/job/ALJ741/postdoctoral-research-officer/ Full details and application at Bangor University:

https://jobs.bangor.ac.uk/details.php.en?id=-3DQLYFK026203F3VBQB7V68LOTX&n PostingID 32&nPostingTargetID“58&mask=stdext&lg=UK

Thanks,

Katherine

http://www.bangor.ac.uk/emailtpl/logo-a2.png Katherine Steele Darlithydd mewn Cynhyrchu Cnydau Cynaliadwy Ysgol Amgylchedd, Adnoddau Naturiol a Daearyddiaeth E-bost: k.a.steele@bangor.ac.uk Ffôn: 00 44 (0) 1248 388655 Prifysgol Bangor, Bangor, Gwynedd, LL57 2DG http://www.bangor.ac.uk/emailtpl/twitter-16.png @prifysgolbangor http://www.bangor.ac.uk/emailtpl/facebook-16.png /PrifysgolBangor

Katherine Steele Lecturer in Sustainable Crop Production School of Environment, Natural Resources and Geography Email: k.a.steele@bangor.ac.uk Phone: 00 44 (0) 1248 388655 Bangor University, Bangor, Gwynedd, LL57 2DG http://www.bangor.ac.uk/emailtpl/twitter-16.png @BangorUni http://www.bangor.ac.uk/emailtpl/facebook-16.png /BangorUniversity

Rhif Elusen Gofrestredig 1141565 - Registered Charity No. 1141565

Katherine Steele <k.a.steele@bangor.ac.uk>

BayerCropSci WestSacramento Bioinformatics

The primary responsibilities of this role, as a Grad Scholar, are to:

- Participating in a multi-disciplinary team of scientists at the Biologics Bayer CropScience West Sacramento, CA R&D Facility to offer bioinformatics, genomics, transcriptomics and metagenomics for controlling pests and diseases in plant and promoting plant health using microbes;

- Proactively identifying and incorporating new algorithms and technology to automate the analysis of microbial genomes and to extend the features of existing analysis pipelines;

- Understanding the dynamics of plant, microbe and pest/pathogen interaction using various omics technologies;

- Managing next-generation sequencing (NGS) data and analyses;

- Training scientific staff on the use of relevant bioinformatics software and tools;

- Working with other non-bioinformatics team member in the CLS group to understand their roles and to serve as backups as needed;

- Communicating effectively through listening, documentations and presentations, especially using compelling visualization tools to share analysis and interpretation of data.

More specifically related to this position, Bayer seeks an incumbent who possesses the following:

- PhD in Computational Biology, Ecology and Evolution, Plant Biology,Bioinformatics, Genomics or related field with 0-1 year of post-graduate experience or a Master's with 4+ years, or BSc. with 6+ years of post-graduate experience and currently enrolled in a graduate program.

- Proven ability to handle large data sets efficiently using scripts, databases, and other tools;

- Familiar with state-of-the-art open source and commercial bioinformatics tools;

- In depth familiarity with various public genomic databases, statistical software tools and packages such as R and bioinformatics algorithms, particularly for the analysis of NGS data (Illumina and PacBio);

- Should be comfortable enough with some basic statistical concepts and able to converse with other scientists about how to interpret basic statistical analyses such as ANOVA, linear regression, and power analyses.

- Experiences in three or more of the following areas: Comparative genomics; Transcriptome sequencing analysis; Phylogenetic analysis; Pathway modeling and analysis; and/or Metagenomics analysis;

Preferred Skills/Qualifications:

- Familiarity with SQL and relational database, particularly PostgreSQL;

- Fluent in Python, Perl, or other scripting languages;

- Previous laboratory experience;

- Knowledge of fungal, bacterial, insect, or plant genetics;

- Working with high performance computing clusters and/or cloud services.

Interested applicants should please send a resume and a cover letter to

Dilara Ally (Sr Bioinformatics Scientist) : email: dilara.ally@bayer.com

ColdSpringHarborLabs CompSciDeveloper

Position Description The Simons Center for QB at Cold Spring Harbor Laboratory (CSHL) is seeking a highly motivated Computational Science Developer to work with the Siepel Lab on evolutionary genomics. This is a full-time position. This person will develop software tools, databases, and web resources. Requirements include experience with C/C++, proficiency in shell scripting and a language such as Perl or Python, experience with relational databases and computer clusters and ability to work in a Linux environment. This individual will work under the direct supervision of Dr. Siepel.

Specific Responsibilities include, but are not limited to the following: X Maintenance, refinement, and support for a software package called PHAST (PHylogenetic Analysis with Space/Time models) for phylogenetic analysis and comparative genomics. Includes implementing new statistical models, algorithms, and analysis features;

improving integration with the UCSC Genome Browser; developing web interfaces to popular programs; optimizing code for improved scalability; and responding to occasional user questions and bug reports.

X Maintenance of a local mirror of the mysql-based UCSC Genome Browser, and development of new annotation tracks for visualization of analysis results.

X Assisting in genome-wide analyses. Includes developing scripts to parse, convert, and otherwise process large data sets; running analysis programs in parallel on large compute clusters; and integrating, organizing, and analyzing program output.

X Development and maintenance of general software and database infrastructure of the lab. Includes organizing large data sets, software tools, and web resources, and supporting lab members and close collaborators in tool development and data analysis.

Qualifications: X Applicants should have a minimum of a Bachelors degree in computer science, engineering, or a related field and 2-3 years of experience in software development.

X Experience with C/C++.

X Basic knowledge of algorithms and data structures.

X Experience in a Unix/Linux environment, including proficiency in shell scripting, and scripting in a language such as Perl or Python.

X Experience with relational databases (mysql or similar). Basic knowledge of web programming (HTML).

X Strong interpersonal skills and ability to work as part of a diverse team.

X Good oral and written communication skills, with the ability to communicate effectively to colleagues and staff across multidisciplinary areas.

X Ability to manage multiple projects in a dynamic environment with changing priorities.

X Ability to help establish realistic goals and deliver work on schedule.

X Ability to work independently and solve problems as they arise.

X Interest in molecular biology, genetics, and evolution, and willingness to learn concepts and terminology from these fields as needed.

Preferred Qualifications: X Masters degree and/or 4-5 years of related experience.

X Some experience or training in bioinformatics.

X Experience working with very large data sets and compute clusters.

X Basic knowledge of statistics.

X Experience with R and/or Matlab.

X Coursework or job experience in genetics, molecular biology, or evolutionary biology.

Job location: CSHL, One Bungtown Road, Cold Spring Harbor, NY 11724

TO APPLY: visit the CSHL Careers website at www.cshl.edu/careers. Position Number:01134-R.

"Gill, Irene" <gill@cshl.edu>

Cornell HumanGeneticsProgrammer

The Research Programmer will develop and extend high performance software, manage data, and perform analyses to further computational genetics research. The lab does interdisciplinary research at the interface of computer science, genetics (primarily human genetics), and statistics, with a key emphasis on developing novel computational methods that can analyze massively sized datasets (tens to hundreds of thousands of samples). Responsibilities of the position include but are not limited to:

* Development, maintenance, and support of high performance software packages for analysis of genetic data in order to infer relationships of samples to one another, the population of origin of regions of a sample's genome, and other related genetic properties of samples. Includes implementing novel algorithms using data structures designed for efficient processing of huge datasets; providing documentation for users; and responding to occasional user questions and bug reports.

* Assisting in genome-wide analyses. Includes developing scripts to parse, convert, and otherwise process large data sets; running analysis programs in parallel on large compute clusters; and integrating, organizing, and analyzing program output.

* Development and maintenance of general software and data storage infrastructure of the lab. Includes organizing large data sets, software tools, and web resources, and supporting lab members and close collaborators in tool development and data analysis.

Research in the Williams Lab aims to elucidate human genetic history, evolution, and the genetic basis of human disease, with a focus on uncovering population and individual relationships from the past several thousand years. The algorithms under development utilize machine learning techniques, including hidden Markov models (HMMs) and expectation-maximization (EM) approaches, and utilize specialized data structures to achieve high efficiency that scale to very large datasets. This work depends critically on the development and maintenance of efficient, reliable software tools, and the organization and management of large data sets. For more information on the lab's research, see http://-williamslab.bscb.cornell.edu/ . Qualifications:

Required: * Bachelor's degree in computer science, engineering or related field, and 3-5 years of experience in software development. * Experience with C/C++, high performance programming, and machine learning. Knowledge of algorithms, data structures, and object-oriented programming, and a familiarity with probability and statistics. * Experience in a Unix/Linux environment, including proficiency in shell scripting, and scripting in a language such as Perl or Python. * Strong interpersonal skills and ability to work as part of a diverse team, while contributing to a high-quality and respectful work environment. * Excellent oral and written communication skills, with the ability to communicate effectively to colleagues and staff across multidisciplinary areas. * Ability to manage multiple projects in a dynamic environment with changing priorities. * Ability to help establish realistic goals and deliver work on schedule. * Ability to work independently and solve problems as they arise. * Interest in genetics, bioinformatics, and evolution, and willingness to learn concepts and terminology from these fields as needed.

Preferred:

* Master's degree. * Some experience or training in bioinformatics. * Experience working with very large data sets and compute clusters. * Basic knowledge of statistics. * Experience with R and/or Matlab. * Coursework or job experience in genetics, molecular biology, or evolutionary biology. * Strong judgment, organization, and leadership skills, and a high capacity for critical, creative thinking.

Amy Williams <alw289@cornell.edu>

FordhamU LabTech PopGenomics

Laboratory technician in population genomics

Louis Calder Center, Fordham University

Armonk, NY 10504

DUTIES & RESPONSIBILITIES

The Munshi-South Lab at the Louis Calder Center, Fordham Universitys biological field station, is looking for a lab technician to join a dynamic research group and contribute to a number of projects that use population genomic tools to address fundamental questions about the evolution of urban wildlife. The research technician will be involved in collecting and analyzing molecular datasets, with a particular emphasis on RAD-Seq and whole genome resequencing. Particular molecular techniques will include DNA extraction, DNA quantification, restriction digests, ligations, and gel electrophoresis. Running and maintenance of a liquid handling robotic platform will also be part of the technicians duties. The technician will share responsibility for day-to-day lab operations including laboratory administration, sample and data organization, and mentoring undergraduate researchers. The position may also include occasional assistance with field work, including trapping and sample collection from mammals, amphibians, and insects. More information about research activities in the Munshi-South Lab is available at http://nycevolution.org *QUALIFICATIONS:*

Required: Bachelor's degree in Biology (or related field) with at least six months of experience with molecular wet-lab research, and excellent organizational skills. Ability to communicate clearly, work independently, and interact collaboratively is essential.

*Preferred: *Experience with RADSeq or SNP genotyping; familiarity with Geneious, R, or programming languages (e.g. Python / PERL).

SALARY & APPOINTMENT INFORMATION

The initial term of appointment is for one year, with renewal for a second year contingent on satisfactory progress. The pay rate is $17.50 / hour for up to 35 hours / week (i.e. $32,000 annually). The Calder Center is located 25 miles north of New York City, and has the advantages of an idyllic, forested setting and potential for subsidized housing.

APPLICATION PROCEDURES

To apply for this position, please send application materials as a single PDF to Jason Munshi-South at jmunshisouth@fordham.edu. A complete application will include a cover letter explaining your research interests and qualifications for the position, a CV, and contact information for up to three professional references. Full consideration will be given to complete applications received by *13 July 2015*.

Jason Munshi-South, Ph.D. Associate Professor Louis Calder Center & Dept of Biological Sciences Fordham University Armonk, NY 10504 jmunshisouth@fordham.edu (914) 273-3078 ext 20 http://NYCevolution.org/ jason.munshisouth@gmail.com

GMI Vienna EvolutionaryGenomics

Evolutionary Genomics Group Leader

The Gregor Mendel Institute (GMI) is recruiting a Group Leader. The GMI is devoted to basic research in plant biology, a field we consider ripe with opportunity. Presently, we are targeting evolutionary genomics, however, we welcome all applications with relevance to plant biology. Our main criterion is scientific excellence and we favor projects with a potential for high impact. Candidates are expected to develop an independent research program at the highest level. The GMI offers outstanding research support, including a very substantial yearly research budget and access to state-of-the-art facilities. The initial contract will be for five years (a three-year extension is subject to review).

The GMI is part of the Vienna Biocenter, a research cluster with over 1,700 researchers from over 40 countries, located close to the center of Vienna, and 20 minutes from the airport. English is the working language. The working environment is family-friendly, with subsidized on-campus child care facilities. The GMI is core-funded by the Austrian Academy of Sciences and also receives funding from numerous national and international agencies.

Please send your application, including a curriculum vitae, a brief description of your proposed research (no more than four pages), and contact details for at least three referees to Carmen Ilic.

Informal inquiries can be directed to Dr. Magnus Nordborg.

Review of applications will begin September 1, 2015 and will continue until the position is filled.

“Nordborg, Magnus” <magnus.nordborg@gmi.oeaw.ac.at>

MaxPlanck Tuebingen EvolDevelVariation

* Genetic mapping of evolutionary developmental variation using hybrid mouse in vitro crosses *

One postdoctoral position, one PhD position and a staff scientist position are available in the Chan Lab at the Max Planck Institute in Tübingen as part of a prestigious 1.5M EUR European Research Council grant investigating the role of gene regulatory network evolution in mice by studying *in vitro* genetic crosses.

The goal of our research is to adopt cutting-edge tissue culture techniques for studying evolutionary divergence in gene networks. We will generate recombinant inbred panels from mouse hybrids spanning increasing evolutionary divergence. We will assay expression and tissue phenotypes at the tissue, fitness and even organismal levels. This ground-breaking research will elucidate the gene network evolution underlying tissue function and speciation in mammals.

Staff scientist in molecular biology and tissue engineering

Your role: You will be a central team member working closely with postdocs and PhD students on molecular genetic and tissue engineering projects. You will be responsible for the derivation and maintenance of specialized iPS and embryonic stem cell lines, tissue differentiation and high-throughput sequencing library preparation for DNA and RNAseq. In addition to your own research role, you will share lab management duties that include ordering and equipment maintenance and training of newcomers together with other existing lab members.

Requirements: You should hold a Masters, equivalent degree or higher in the areas of genetics, molecular biology or regenerative medicine. We are looking for a strong track-record and demonstrated research experience and training particularly in tissue culture and aseptic techniques. Passion for research, team spirit and enthusiasm are essential. English is required.

Our Team: You will work in a multidisciplinary team that focuses on mammalian EvoDevo, combining population and comparative genomics with molecular biology and tissue engineering techniques to study the evolution of gene regulatory network in mouse and its close relatives. Our research group is funded by the European

Research Council (ERC) and the Max Planck Society and is located on the Max Planck campus in Tübingen, Germany.

Our campus hosts world-class research groups, including 11 other ERC-funded teams, and operates state-of-the-art sequencing and other core facilities. English is the working language. All seminars and communications are in English.

Our Offer: The position is available for an initial 2 years with the possibility of extension based on performance. Salary and benefits are according to the German public service pay scale (TVöD Bund up to and including E13) and are commensurate with training and experience.

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

For more information please see: http://fml.tuebingen.mpg.de/chan-group/open-positions To Apply: Consideration of applications will begin on June 15th 2015, and will remain open until filled. Please send your application with 1. a statement of research interests and why you have applied for this position, 2. your CV, and 3. three reference letters to Dr Frank Chan at frank.chan@tue.mpg.de or the postal address below. Incomplete applications will not be considered.

Dr. Frank Chan

Friedrich Miescher Laboratory of the Max Planck Society

Spemannstrasse 39

72076 Tübingen

Germany

Please see related posts for other positions –

Frank Chan Max Planck Research Group Leader Friedrich Miescher Laboratory of the Max Planck Society Spemannstrasse 39 72076 Tübingen Germany

T: +49 (0)7071 601 888 F: +49 (0)7071 601 801 @: frank.chan@tue.mpg.de http://www.fml.tuebingen.mpg.de/chan-group.html Frank Chan <frank.chan@tue.mpg.de>

MaxPlanck Tuebingen FishTechnician

Animal Husbandry Technician - Fish

Our lab investigates the molecular mechanisms of adaptation and speciation in threespine stickleback fish. Using functional genetics and genomics we aim to understand the molecular changes that contribute to phenotypic differences, affect individual fitness and play a role in adaptive divergence.

Your responsibilities: You will be responsible for the feeding, care, husbandry and maintenance of threespine stickleback fish in a state-of-the-art aquarium facility. You will be actively involved in the day-to-day running of the facility including the administering of food, monitoring of animal health, water chemistry changes, aquarium cleaning, and record keeping in a husbandry database, and technical maintenance of the aquarium facility. Basic knowledge and experience working with fish husbandry would be advantageous. As we study natural populations of sticklebacks, your help and participation with field collections and logistics may occasionally be required.

Our requirements: We are looking for a reliable, enthusiastic and motivated individual with training in animal husbandry, biological sciences or similar qualification. Prior experience with fish husbandry and technical running of aquatic facilities (handling, crossing, breeding, care, and water chemistry) would be advantageous but not required. The ability to carry out clean and physically demanding work is an absolute requirement. Willingness to learn and troubleshoot new techniques is important. Experience or understanding of basic genetics would be helpful, but is not necessarily a requirement. We expect from you interest and enjoyment in basic research, goal-oriented and self-motivated work ethic, flexibility and the readiness to learn new skills. English communication skills would be useful, as English is the working language in our lab.

We offer: interesting work in an interdisciplinary team with scientists, and international atmosphere and excellent lab working conditions. We will provide comprehensive on-the-job training. We offer remuneration in accordance to the TVöD standard based on qualification and previous experience. The position is initially limited to 2 years, with the possibility of extension. The Max Planck Society seeks to increase the number of women in those areas where they are underrepresented and therefore explicitly encourages women to apply. The Max-Planck society is committed to increasing the number of individuals with disabilities in its workforce and therefore encourages applications from such qualified individuals.

Application deadline: 10th July 2015. Please send your applications with CV and contact details of at least two referees by post or e-mail to:

Dr. Felicity Jones Friedrich Miescher Laboratory of the Max Planck Society Spemannstrasse 39 72076 Tübingen Germany

fcjones@tuebingen.mpg.de

Felicity Jones <fcjones@tuebingen.mpg.de>

MaxPlanck Tuebingen GeneticBasisVariation

Staff Scientist in genetics and molecular biology

A staff scientist position in genetics and molecular biology is available in the Jones Lab at the Max Planck Institute in Tuebingen, Germany as part of a Max Planck and ERC-funded research team investigating the molecular genetic basis of variation and adaptation in natural populations. Your role: You will be a central team member working closely with postdocs and PhD students on molecular genetic, transgenic, and genomic projects. You will be responsible for running functional genetic assays (cloning, microinjection and fish embryonic phenotyping) and preparation of genomic DNA, RNA and ChIPSeq libraries. In addition to your own research role, you will share lab management duties that include ordering and equipment maintenance with other existing lab members.

Requirements: You should hold a Masters, equivalent degree or higher in the areas of genetics, molecular biology. We are looking for someone with a strong track-record and demonstrated research experience and training particularly in genetics and molecular biology. Passion for research, team spirit and enthusiasm are essential. English is required.

Our Team: You will work in a multidisciplinary team that uses genetics, molecular, developmental, and evolutionary biology to study the molecular mechanisms of adaptation and speciation in threespine stickleback fish. Our research group is funded by the European Research Council (ERC) and the Max Planck Society and is located on the Max Planck campus in Tübingen, Germany. Our campus hosts world-class research groups, including 11 other ERC-funded teams, and operates state-of-the-art sequencing and other core facilities. English is the working language. All seminars and communications are in English.

Our Offer: The position is available for an initial 2 years with the possibility of extension based on performance. Salary and benefits are according to the German public service pay scale (TVöD Bund up to and including E13) and are commensurate with training and experience. The Max Planck Society seeks to increase the number of women in those areas where they are underrepresented and therefore explicitly encourages women to apply. The Max-Planck society is committed to increasing the number of individuals with disabilities in its workforce and therefore encourages applications from such qualified individuals. For more information please see: fml.tuebingen.mpg.de/jones-group/open-positions

To Apply: Consideration of applications will begin on July 20th 2015, and will remain open until filled. Please send your application with 1. a statement of research interests and why you have applied for this position, 2. your CV, and 3. three reference letters to Dr Felicity Jones at fcjones@tuebingen.mpg.de or the postal address below. Incomplete applications will not be considered.

Dr Felicity Jones, Friedrich Miescher Laboratory of the Max Planck Society, Spemannstrasse 39, 72076 Tuebingen, Germany.

Felicity Jones <fcjones@tuebingen.mpg.de>

MuseumNS NorthCarolina 3yr Curation

North Carolina Museum of Natural Sciences Full-Time Project Technician Position

Description The North Carolina Museum of Natural Sciences (NCSM) is looking to hire a 3 year, full-time project technician in the Fishes Unit of the Research and Collections Section. This position will be funded via an NSF CSBR grant. The person in this position will work closely with the Collections Manager of Fishes and Project Manager in the processing of recently-acquired collections. Processing will include all aspects of curation, such as stabilizing, labeling, databasing, etc.

Essential Functions - Stabilizing specimens in ethanol

- Cataloging specimens using an MS Access database - Georeferencing locality information - Updating taxonomic information - Labeling and shelving specimens - Assisting with Citizen Science Curator project - Supervising volunteers and student interns

Qualifications Preferred - Bachelor's Degree in biology or related field - Curatorial experience in natural history collections - Databasing experience, preferably with Microsoft Access - Efficient attention to detail - Ability to work both independently and as part of a team - Must be able to lift up to 50 lbs and work with various chemicals

Location NCSM Research Lab, located at 1671 Gold Star Drive, Raleigh, North Carolina, 27606

Approximate starting date Mid-July 2015

Please submit a cover letter and resume to Gabriela Hogue (gabriela.hogue@naturalsciences.org) by June 15, 2015.

Thanks, -Gabriela

Gabriela M. Hogue Collections Manager of Fishes North Carolina Museum of Natural Sciences 11 West Jones Street, Raleigh, NC 27601-1029 USA 919.707.8868 fax 919.715.2294 www.naturalsciences.org "Hogue, Gabriela" <gabriela.hogue@naturalsciences.org>

Queens Belfast MarineEvolution

Queen's University Belfast, Lecturer in Marine Biology

Job title - Lecturer in Marine Biology (fixed term, three years, not tenure-track)

Job reference - 15/103923 Salary - Â£34,233 - Â£40,847

Closing date for applications is 29 June.

Full details https://hrwebapp.qub.ac.uk/-tlive_webrecruitment/wrd/run/-ETREC107GF.open?VACANCY_ID=-8050225aEw&WVID=6273090Lgx&LANG=USA
The post will be based in the University's off campus marine station in Portaferry, Northern Ireland (Queen's University Marine Laboratory: www.qub.ac.uk/qml).

This is a fixed term lectureship (=assistant professor) position that will serve as sabbatical cover for the director of the Queen's University Marine Laboratory; however there is no expectation of the new post taking on any major administrative responsibility. Teaching responsibilities are expected to include short field courses based in the marine station and one on-campus course (preferably direct cover for the established course 'Adaptations in the Marine Environment').

Enquiries should be directed to the Head of School, Biological Sciences, Aaron Maule <hos.biolsci@qub.ac.uk>

j.sigwart@qub.ac.uk

SanDiegoZoo ConservationBioinformatics

A postdoc position is immediately available in the Genetics Division of the San Diego Zoo Institute for Conservation Research.

The Bioinformatics Postdoctoral Associate will work within the Genetics Division at the San Diego Zoo Institute for Conservation Research, analyzing genomic data from several projects involving species of conservation concern such as the white rhinoceros and California condor. Genomic analyses will focus on applications to the management of captive populations and address questions on the genetic basis of adaptations underlying populations and species differences.

Applicants must have completed a Ph.D. in bioinformatics or related fields (evolutionary biology/genomics) with strong experience in data analysis. Understanding of comparative genomics and population genomics is REQUIRED, including knowledge of principal components analysis, admixture, phylogenomics, coalescent methods, genome scan of positive selection, and relatedness.

For more information or to apply: bit.ly/1IappMW

Oliver Ryder San Diego Zoo Institute for Conservation Research www.sandiegozoo.org "oryder@ucsd.edu" <oryder@ucsd.edu>

TexasAM EvolutionaryGenomics

The Biology Department at Texas A&M (the main campus in College Station) has openings for TWO tenure-track positions in evolutionary genomics, very broadly defined. The following advertisement will appear in this week's issue of Science:

The Department of Biology at Texas A&M University invites applications for two tenure-track Assistant Professor positions in evolutionary genomics, starting in the fall of 2016. We will consider candidates pursuing innovative research in any area of evolutionary genomics, including empirical, theoretical or computational approaches applied to any taxonomic group. The criteria for selection will be uniqueness, creativity and excellence in research and scholarship. We require all candidates to have a Ph.D. and strongly encourage applications from candidates who will increase the exposure of our students to a diverse culture. Successful candidates will be expected to develop externally funded research programs and to teach undergraduate and graduate courses. The Department of Biology (www.biology.tamu.edu) is part of an interactive and collegial research environment, offering a modern infrastructure and competitive startup packages. The broader Texas A&M research community includes a number of exciting interdepartmental programs, such as the new Ecology and Evolutionary Biology Doctoral Program (eeb.tamu.edu), the Texas A&M Institute for Genome Sciences and Society (genomics.tamu.edu), and the Genetics Interdisciplinary Graduate Program (genetics.tamu.edu). Applicants should email a letter of intent, curriculum vitae, statements of research and teaching interests, and should arrange to have three letters of recommendation sent to evosearch@bio.tamu.edu. Review of applications will begin September 1, 2015.

Questions regarding this search should be directed to Dr. Adam G. Jones, chair of the search committee, at evosearch@bio.tamu.edu.

Texas A & M University is an Equal Opportunity/Affirmative Action employer that is dedicated to the goal of building a culturally diverse and pluralistic faculty and staff who are committed to teaching and working in a multicultural environment. We strongly encourage applications from women, minorities, veterans, individuals with disabilities, and the LGBTQ community. In addition, the University is responsive to the needs of dual career couples.

“ajones@bio.tamu.edu” <ajones@bio.tamu.edu>

UInnsbruck AquaticEvolutionaryEvol

The University of Innsbruck invites applications for the position of University Professor of AQUATIC EVOLUTIONARY ECOLOGY at the Research Institute of Limnology on Mondsee of the Faculty of Biology. The position according to Â§99 University law 2002 will be based on a five-years civil-law employment contract with the University.

Responsibilities include

- Representing the subject of Aquatic Evolutionary Ecology both in research and teaching. - Teaching of undergraduate and graduate students and supervision of theses. - Participating in the University’s research focus entitled “Alpine region - man and biosphere”. - Acquisition of third party funded research projects.

Eligibility requirements include

a pertinent degree in higher education, a pertinent habilitation or equivalent qualification, publications in leading international peer-reviewed journals, involvement in international research, experience abroad / practical experience with acquisition of research grants and qualification in leadership.

The University of Innsbruck is committed to increasing the percentage of female employees, especially in leading positions and therefore explicitly invites women to apply. In the case of equivalent qualifications, women will be given preference.

Applications must reach us at the latest by September 17th, 2015 and should include the usual documentation (motivation letter, curriculum vitae, publications and grants list, description of current and intended research - max. 5 pages, samples of the 5 most important works). All documents have to be submitted in digital form (e-mail, one file in .pdf format) to: Leopold-Franzens-Universität Innsbruck, Fakultäten Servicestelle, Standort Technikerstraße 17, A-6020 Innsbruck (fss-technik@uibk.ac.at).

The basic salary is set down in the collective bargaining agreement for university employees. Professors are in the remuneration group A 1. For the position the monthly salary is 4.782,40 Euro (14 x). Depending on qualification and experience a higher salary can be a topic in the negotiations with the rector. Beyond that the university offers attractive additional benefits (http://www.uibk.ac.at/universitaet/zusatzleistungen/).

The full, authoritative text in German (published in the official bulletin of the University of June 17th, 2015) as well as additional information on the current status of the application process may be found at: http://www.uibk.ac.at/fakultaeten-servicestelle/standorte/technikerstrasse/berufung/index.html Further information can be gained from the head of the search committee the Dean Univ.-Prof. Dr. Ulrike Tappeiner: Büro der Dekanin, Technikerstraße 15, 6020

Innsbruck, Ãsterreich; Tel.: + 43 512 507-30 191; email Dekanat-Biologie@uibk.ac.at

Univ.-Prof. Dr. Dr. h.c. mult. Tilmann Märk Rector

"Wanzenböck, Sabine" <Sabine.Wanzenboeck@uibk.ac.at>

ULausanne Genomics

The Faculty of Biology and Medicine of the University of Lausanne, Switzerland invites applications for a position as :

Tenure-track Assistant Professor or Associate Professor at the Center for Integrative Genomics

Entrée en fonction: To be agreed Durée du contrat: 6 ans, renouvable selon art. 62 Loi sur l'Université de Lausanne Taux d'activité: 100% Lieu de travail: Lausanne Référence: Offre nÂ3610 Annonce du: 26.05.2015 Offre parue en: Français, English

Description des tÃches

We seek candidates with post-doctoral experience who have demonstrated excellence in conducting research and have an interest in teaching. The successful candidate will be expected to : - establish a world-class independent and innovative research program that will attract extramural funding, - participate in teaching at the undergraduate and graduate levels. The rank of the position - which comes with competitive starting packages and running budget - will be determined according to the level of the selected candidate. The Center for Integrative Genomics (CIG) (http://www.unil.ch/cig/-home.html) is a highly interactive research center of the Faculty of Biology and Medicine at the University of Lausanne, comprising both research groups and state-of-the-art core facilities. It is located on the Dorigny campus overlooking Lake Geneva. Areas of particular interest for this position include but are not limited to the structure and function of genomes and their evolution, signal transduction, the regulation of gene expression and cell proliferation, and the genomics of complex process such as development, physiology, and behavior. Note that a second position with focus on molecular evolution, population genetics, human genetics and computational biology is currently open at the CIG. (http://www.unil.ch/fbm/home/menuinst/la-releve-academique/mises-au- concours.html).

Profil souhaité

A more detailed job description is available on the Internet site http://www.unil.ch/fbm/home/menuinst/la-releve-academique/mises-au-c oncours.html.

Dossier de candidature

Applications should include a motivation letter, the curriculum vitae, a list of publications highlighting the five most significant ones, a brief statement of the past and future research, and a summary of previous teaching experience (if any). Please include also names and contact information of at least three references. The full application should be submitted to www.unil.ch/iafbm/-application as a single PDF.

Remarques

Further information may be obtained from Prof. L. Keller (Laurent.Keller@unil.ch), Chairman of the search committee. Seeking to promote an equitable representation of men and women among its staff, the University encourages applications from women.

Délai de candidature

Candidatures jusqu'au: 05.08.2015

–

The Faculty of Biology and Medicine of the University of Lausanne, Switzerland invites applications for a position as :

Tenure-track Assistant Professor or Associate Professor at the Center for Integrative Genomics

Entrée en fonction: To be agreed Durée du contrat: 6 years, to be renewable, according to art. 62 of Lausanne University Statute Taux d'activité: 100% Lieu de travail: Lausanne Référence: Offre nÂ3609 Annonce du: 26.05.2015 Offre parue en: Français, English

Description des tÃches

We seek candidates with post-doctoral experience who have demonstrated excellence in conducting research and have an interest in teaching. The successful candidate will be expected to : - establish a world-class independent and innovative research program that will attract extramural funding, - participate in teaching at the undergraduate and graduate levels. The rank of the position - which comes with competitive starting packages and running budget - will be determined according to the level of the selected candidate. The Center for Integrative Genomics (CIG) (http://www.unil.ch/cig/-home.html) is a highly interactive research center of the Faculty of Biology and Medicine at the University of Lausanne, comprising both research groups and state-of-the-art core facilities. It is located on the Dorigny campus overlooking Lake Geneva. Areas of particular interest for this position include but are not

— / —

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

UNAM Mexico AquaticOrganismGenomics

INSTITUTO DE CIENCIASDEL MAR YLIMNOLOGÃA

The Marine Science and Limnology Institute of the National Autonomous University of Mexico (UNAM) is opening a position as Full Time Associate Researcher level Cto be filled as fixed-term contract as described in Article 51 but with possibility of yearly renewals.

SPECIALTY AREA:

Genomics of Aquatic Organisms

REQUIREMENTS:

position will be made available as part of the University's Program for Renovating the Academic Staff, Subprogram for the Incorporation of Young Career Academics. The Program's requirements specify that the candidates must be younger than 39 years of age for women and younger than 37 for men at the date of approval by the corresponding Technical Committee.

to settle in Mazatlán, Sinaloa (México).

Academic Level: Ph. D., with two years of postdoctoral experience.

research project addressing national problems related to aquatic organisms using a Genomics approach must be proposed

's curriculum vitae without original documents, which should include 10 or more scientific papers published with SCI and IF, teaching experience and graduate and undergraduate theses directed

BASE SALARY: $MXN 16,651.16

DEADLINE TO RECEIVE SUBMISSIONS: 27 July2015.

Contact person: Dr. María Adela Monreal Gómez

Academic Secretary ICML Phone number: (+52) (55) 5622-5772

E-mail:icmlsa@cmarl.unam.mx

Samuel Gomez <samuelgomez@ola.icmyl.unam.mx>

UPennsylvania Adaptation

Tenure-track faculty position in Ecology at The University of Pennsylvania.

The Department of Biology at the University of Pennsylvania invites applications for a tenure-track faculty position in Ecology. The appointment will be at the level of Assistant Professor. We are searching broadly for a community or ecosystem ecologist working at any spatial scale, from local to global, and using theoretical and/or empirical approaches. Areas of interest include, but are not limited to, mechanisms of community assembly, coexistence, diversity, adaptation and the interplay between biotic and abiotic processes in the face of climate and land-use change. We welcome applicants working on any domain of life, from micro- to macroscopic.

We are especially interested in candidates who utilize novel approaches that span levels of biological organization or transcend traditional boundaries.

Penn's Department of Biology has a long-standing tradition of maintaining an integrated research and educational program across all basic biological sciences, from Ecology and Evolution, Plant Sciences, Molecular and Cellular Biology, Genomics, to Neuroscience. The Department values interdisciplinary research, collaboration, and collegiality, and has a vision emphasizing Life in its Natural Context. Candidates are expected to have demonstrated excellence and productivity in research and will be expected to excel in undergraduate and graduate teaching.

Interested candidates should submit materials online at http://facultysearches.provost.upenn.edu/postings/606 and include a curriculum vitae, concise statements of research and teaching interests, a short annotated description of up to five publications, and the name and contact information of at least three referees. Recommenders will be contacted by the University with instructions on how to submit a letter to the website. Review of applicants will begin September 11, 2015 and continue until the position is filled.

The Department of Biology is strongly committed to Penn's Action Plan for Faculty Diversity and Excellence and to creating a more diverse faculty (for more information see: http://www.upenn.edu/almanac/volumes/v58/n02/diversityplan.html). The University of Pennsylvania is an equal opportunity employer. Minorities, women, individuals with disabilities, and protected veterans are encouraged to apply.

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

USalford 4 Biodiversity

The School of Environment & Life Sciences at the University of Salford, UK, is seeking to appoint up to four new academics in the broad areas of ecology, biodiversity and conservation. Candidates with a research focus on evolutionary processes relevant to human/wildlife/pathogens interactions, environmental management and ecosystem services are all encouraged to apply.

Please see details here: http://www.jobs.ac.uk/job/ALH727/lectureships-in-global-ecology-and-conservation-x4/ Closing date for application: July 5th, 2015. Interviews: in July. Informal enquiries: Prof.Judith E. Smith, Head of School, j.e.smith@salford.ac.uk

S.Mariani@salford.ac.uk

Other

Call SSB Symposia

Reminder: Call for 2016 SSB Symposia

The Society for Systematic Biologists invites proposals for symposia 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. 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

DGE special issue

Dear colleagues,

with this mail we invite contributions for a Special Issue on “Size and Shape” to be submitted to Development, Genes and Evolution (DGE) (http://www.springer.com/life+sciences/-evolutionary+%26+developmental+biology/journal/-427). This Special Issue is based on the Symposium “Size and Shape - Integration of morphometrics, mathematical modelling, developmental and evolutionary biology” that took place in April 2014. Please find more information about the symposium here: http://www.evolution.uni-goettingen.de/ If you or your colleagues have are interested in contributing to this special issue with a review or perspectives/opinion article or with an original data paper that is related to one of the topics covered by the Size and Shape meeting, you are welcome to submit your article until September 15th, 2015.

If you are not sure whether your contribution fits the scope of the Special Issue, please send the following information to nposnie@gwdg.de until July, 15th 2015: a) Name(s) of potential authors b) type of article (review, perspective, original article) c) max. 0.5 A4 page summary.

Otherwise, just submit your article until September 15th, 2015 to Development Genes and Evolution. In order to identify your article as contribution for the Special Issue make sure that you choose the Article Type Name: “SI: Size and Shape” from the dropdown menu during the submission. For more information about any formal requirements, please refer to the following journal website: http://www.springer.com/life+sciences/-evolutionary+%26+developmental+biology/journal/-427 If you have any question, feel free to contact us at any time.

Best wishes,

Niko Prpic Nico Posnien

– Nico Posnien Georg-August-University Göttingen Johann-Friedrich-Blumenbach Institute for Zoology and Anthropology Department of Developmental Biology Ernst-Caspari-Haus (GZMB) Justus-von-Liebig-Weg 11 37077 Göttingen Germany

Phone: +49 (0) 55139 20817 E-mail: nposnie@gwdg.de web: http://www.evolution.uni-goettingen.de/-posnienlab/index.html web: http://www.uni-goettingen.de/en/44993.html web: http://www.uni-goettingen.de/en/44993.html

Exploitative Biology positions

If you would like to highlight particularly exploitative volunteer opportunities, internships, and “work experiences” posted to job boards, there is a new site for that!

http://crapwildlifevolunteerjobs.tumblr.com/ >From the about page:

Volunteer 'jobs' that offer no pay are rampant in wildlife ecology and conservation biology, and it's time for them to stop. They're unprofessional, exploitative, limit diversity, immoral, and in some jurisdictions illegal.

Gas stations don't volunteer their products to run field trucks; airlines don't offer up free flights 'for the experience'. Staff should be paid. No money for salaries = no staff.

This site isn't about slogging any individual or organization, but the practice of using volunteers in place of paid staff. This practice has got to stop. And from time to time, we come across 'job' adverts that are simply ridiculous. To highlight the problem and widespread nature of the practice, submit unpaid jobs in ecology, wildlife, and conservation and help spread the word.

Sean McCann <smccann27@gmail.com>

Intl J Genomics

Dear Sir I would like to ask you if it is possible to announce in Evoldir the text below which is a call for submission of manuscript to a special issue in Conservation Genomics

Sincerely Cino Pertoldi

dear collegues interested in conservation biology, this advertisement is to draw your attention to a forthcoming special issue entitled: "How Can Genomic Tools Contribute to the Conservation of Endangered Organisms" in the journal International Journal of Genomics which is in ISI WEB OF SCIENCE, the call is at the following web page:

http://www.hindawi.com/journals/ijg/si/134520/cfp/ if some of you have a manuscript which you think fit in the aim of this issue please submit it.

I think it is an interesting opportunity to make a nice special issue on this important topic, in addition the journal is an open access journal which means that it will have a broader audience.

Cino Pertoldi

Long Term DNA storage

Dear Evoldir Community,

Recently in our lab we have been experiencing intermittent problems with long term DNA storage.

The samples causing problems would have been extracted using a variety of different methods, stored at 4 degrees during use and then moved to -20 or -80 degrees for long term storage. These samples all have good nanodrop values and have been successfully PCR'ed.

Once the samples are taken out of long term storage and are nanodropped again the DNA seems to have disappeared!!! The samples have been stored in a variety of plastic ware (different types of tubes and plates) all made from polypropylen. While it is possible that the DNA is somehow becoming stuck to the plastic, the fact that the problem is happening so infrequently makes us think it may be something else.

Thankfully we have managed to recover the samples by heating and shaking at 60 degrees continuously for ~48 hours, but are puzzled as to why this is happening in the first place.

Has anyone else experienced this before or have any insights into the causes?

Thanks in advance for your help and I will of course re-post responses,

Nicole Foley

Nicole Foley European Research Council PhD Fellow University College Dublin School of Biological and Environmental Sciences Science Center West Belfield Dublin 4 Ireland

nicole.ma.foley@gmail.com

Long Term DNA storage answers

Dear Evoldir Community,

We've had some very interesting responses to our problem regarding our disappearing DNA. Below, please find all responses on the matter and more.

Thanks to everyone for all their help,

Nicole Foley

Original Query

Dear Evoldir Community,

Recently in our lab we have been experiencing intermittent problems with long term DNA storage.

The samples causing problems would have been extracted using a variety of different methods, stored at 4 degrees during use and then moved to -20 or -80 degrees for long term storage. These samples all have good nanodrop values and have been successfully PCR'ed.

Once the samples are taken out of long term storage and are nanodropped again the DNA seems to have disappeared!!! The samples have been stored in a variety of plastic ware (different types of tubes and plates) all made from polypropylen. While it is possible that the

DNA is somehow becoming stuck to the plastic, the fact that the problem is happening so infrequently makes us think it may be something else.

Thankfully we have managed to recover the samples by heating and shaking at 60 degrees continuously for ~48 hours, but are puzzled as to why this is happening in the first place.

Has anyone else experienced this before or have any insights into the causes?

Thanks in advance for your help and I will of course re-post responses,

Nicole Foley

Responses

It could simply be that the samples stored below -20C become insoluble and the DNA tends to crystallize to the walls of the tube. Thus you cannot pick up any signal on the nanodrop and when you re-suspend the DNA you find it again.

Another cause could be the quality of the buffer you are using and the tubes you store the DNA in.

You could either precipitate the samples and store them dry or just keep them at 4C - DNA is generally quite stable.

Peter

shum.p@hotmail.com

Hi Nicole

I have seen good DNA go bad but not since I started using low bind plastic. I use eppendorf lo-bind tubes and twin.tec plates. The plates are designed for PCR, but also work fine for DNA template storage. But I know from others that it is not always the solution. Sometimes DNA just mysteriously disappears.

http://www.eppendorf.com/int/index.php?sitemap=-3D2.1&action=3Dproducts&contentid=-1&catalognode=14136 There is an interesting paper by Gaillard and Strauss about this issue: international biotechnology laboratory / august 2000 Eliminating DNA loss & denaturation during storage in plastic microtubes

good luck

Arjen

A.E.Van-T-Hof@liverpool.ac.uk

My lab has experienced this from time to time with a small number of samples. In all cases, the DNA had been stored in water rather than a buffer like TE. DNA eventually denatures in water, especially if dilute. It can often be (partially) renatured by treatments similar to the one you used, and this can be facilitated by adding a small amount of concentrated TE (or that old standby, SSC) to the denatured DNA sample before heating. It is less successful if the storage water was acidic (below pH of about 6.0) to begin with or has become so with time or upon initial thawing from the freezer.

Our Sanger sequencing facility on campus (like many others) requires samples to be submitted in water. There is a temptation therefore to elute our fish DNA samples from purification columns with water and then store them that way. If such samples are stored at - 20 or even -80 C for some time, we encounter the denaturation problem. So with precious samples we elute withTE (or with the elution soln. provided by the supplier of the columns, generally Qiagen or Zymo) and then repurify an aliquot and elute with water for sequencing.

Bruce Turner

fishgen@vt.edu

Dear Nicole Foley,

I would like to share with you my experience: nanodrop measurements are not very reliable. Sometimes at all. I dont know how old are your DNAs, however, my DNAs were PCRable after 4 years of -20 storage (very good amplification at variable loci).

Another option might be to lyophilisate DNA for long-term storage and keep it at -20 or - 80 C. Then dilute when you will need this DNA again. Just an idea.

Nothing really new from my site, perhaps others will have bigger expertise in DNA storage.

All the best,

Josef Janou^{1}ek

Mendel University in Brno, Czech Republic

janousek.jose@gmail.com

Hi Nicole,

How was the DNA extracted and what is it stored in (e.g. TE, water, etc)? Some extraction methods such as boiling are good for short term yield, but can damage the DNA. Similarly some may leave other compounds in the solution that degrade the DNA. The final solution it is stored in is also important as it needs some buffering capacity.

Theresa

theresa.burg@uleth.ca

Dear Nicole

That's not a big problem at all, we know DNA is a macro molecule and has a

— / —

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

MaxPlanckInst Gabon VolResAssist ApeSampleCollection

Volunteer Research Assistant Chimpanzee and Gorilla genetic sample collection

Hiring Organization: Max Planck Institute for Evolutionary Anthropology

Date Posted: 2015-04-06

Position Description: We have one research assistant position available in Loango National Park, Gabon. We initiated a project to habituate chimpanzees and western gorillas in Loango in January 2005. In addition, in 2014, we started a project to assess group composition and group dynamics of chimpanzees and gorillas in the study area. For this, genetic samples have to be collected in a systematic manner.

We are looking for a person to support the sample collection starting in July 2015, for a one year period. The assistant's tasks will include: walking recces within grid cells as part of a team and searching for genetic samples (feaces) and signs of apes. This will require long hours in the forest, a lot of walking, a high degree of self-motivation and reliability. Other tasks include handling of samples, data entry, chimpanzee habituation and possible assistance with other projects like phenology, vegetation surveys and camera traps. Loango National Park is located on the coast of Gabon and consists of several ecosystems including coastal forest and swamps. The living conditions at this project are basic. We have two main camps, with only basic amenities (no running water, only minimal solar power for electricity). The typical day consists of approximately 10 hours walking in the forest, often through swamps, an average of 12 km per day, rain or shine. The work is physically demanding.

Qualifications/Experience: The applicant must have at least a BSc in biology, zoology, anthropology or a related discipline. Previous field experience with primates or other animals will be viewed as a great asset. Basic laboratory skills (like handling a pipette) are advantageous but not mandatory. The applicant should demonstrate an ability to handle the living conditions at the site. A minimum knowledge of French is required. Interested applicants should send a letter of interest, CV, and names and email addresses of 3 references via email by June 12^th. However, we will be reviewing applications as they arrive; please don't send repeated letters of inquiry or telephone calls.

Salary/funding: 150 euros per month to be paid within Gabon.

Support provided for internship/volunteer positions (travel, meals, lodging): One round trip airfare to Gabon and transportation to study site will be provided. Accommodation (a tent) and basic equipment is provided. Basic food is also provided, but if you want anything special you need to purchase it yourself. You will be required to have basic health insurance that also covers emergency repatriation and liability. You also must have vaccinations for measles, yellow fever, TB, hepatitis A and B, polio, and meningitis.

Term of Appointment: 1 year

Application Deadline: June 12^th, 2015

Comments: Interested applicants should send a letter of interest, CV, and names of 3 references (since the deadline is tight the can be handed in later in exceptional cases) to laura_hagemann@eva.mpg.de. If you do not hear from me by June 20th, please assume that you are not being considered for the position.

Laura Hagemann, PhD student Max Planck Institute for Evolutionary Anthropology Department of Primatology Deutscher Platz 6 04103 Leipzig, Germany +49 (0)341 9952 269

Laura Hagemann <laura_hagemann@eva.mpg.de>

Medfly samples

Dear all,

I am looking to get some medfly (Ceratitis capitata) collections from around Europe- ideally I would like 50+ individuals from multiple locations- I was wondering if anyone would be able to send me some samples (either on dry ice or in RNAlater/trizol as I want to extract RNA) or would be able offer help me in collecting some individuals. We have some money to cover expenses. Please get in touch if you think you may be able to help in any way.

Many thanks,

Ben

– Ben Longdon Department of Genetics University of Cambridge +44 (0) 1223 333945 b.longdon@gen.cam.ac.uk http://benlongdon.wordpress.com http://www.gen.cam.ac.uk/research/Jiggins/Ben.html

Software 4273pi

Dear Evoldir,

4273pi is for those wishing to teach, learn or use research-grade bioinformatics on the low-cost Raspberry Pi computer. 4273pi includes Open Access teaching material and a customised Linux operating system for the Raspberry Pi.

Coverage of particular interest to Evoldir includes: delimiting gene/protein families; multiple alignment and phylogeny; gene family evolution; looking at species differences; and function and evolution of enzymes.

We are happy to announce 4273pi version 1.31. This has the best software and teaching material yet, and may be downloaded at:

http://eggg.st-andrews.ac.uk/4273pi For further details on 4273pi, see also:

http://dx.doi.org/10.1186/1471-2105-14-243 and http://bit.ly/1Nn9QU3 - Daniel

–

http://biology.st-andrews.ac.uk/staff/db60 The University of St Andrews is a charity registered in Scotland : No SC013532

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

Software DISSECT genomeAnalysis

Dear All,

Computational tools are quickly becoming the main bottleneck to analyse large-scale genomic and genetic data.

To address this, we have developed DISSECT, a new, free and user-friendly software that can run on computer systems that range from simple desktop computers to large supercomputers. This allows analysing small genomic datasets as well as datasets containing hundreds of thousands of records.

Among the things the software can currently do are: standard GWAS Analysis, Principal Components Analysis, Fit Univariate and Bivariate Mixed Linear Models or Genomic Prediction.

Further details on the software and what it can do can be found at: http://biorxiv.org/content/early/2015/06/05/020453 The software can be downloaded from our dedicated web site at: http://www.dissect.ed.ac.uk If you have questions, please contact us at: dissect@roslin.ed.ac.uk

Or follow us on twitter for updates and new functionalities: @DissectRoslin

Best wishes,

Albert

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

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

Software RpackageLEA

Dear All

We have recently released the R package LEA that enables users to run genome-wide ecological association studies from the R command line.

Genome-wide ecological association studies aim at detecting allele frequencies that exhibit significant statistical association with ecological gradients. Ecological association studies can provide lists of genetic polymorphisms that are potentially involved in local adaptation to environmental conditions through natural selection.

The package LEA runs (very fast) STRUCTURE-like analyses of population structure, and performs genome scans for selection from large genomic data sets. It derives advantages from R programming functionalities to adjust significance values for multiple testing issues and to visualize results.

The package is available from the Bioconductor resource repository http://www.bioconductor.org. Online documentations and tutorials are available from the authors' webpages http://www.membres-timc.imag.fr/-Olivier.Francois . See also the application note here: http://onlinelibrary.wiley.com/doi/10.1111/2041-210X.12382/full If you have any questions or want to send feedback, do not hesitate to contact us at: olivier.francois@imag.fr

Best regards,

Olivier

"olivier.francois@imag.fr" <olivier.francois@imag.fr>

SouthAfrica VolFieldAssist MoleRatEvolution

SouthAfrica.VolResearchAssistant.SocialMoleRats

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

Position 1: Voluntary field research assistant: 9th of July to Mid-October (3 months)

Position 2: Voluntary laboratory research assistant: From July onwards for 6 months

Position 1 (Field based):

We are looking for one voluntary field research assistants to conduct research on the completely subterranean, highly social Damaraland mole-rat (Fukomys damarensis). Specifically, this project investigates the group augmentation hypothesis and how benefits of living in large groups can generate selection for altruism in animals. We are currently conducting a large scale capture-mark and recapture experiment running over one year in which the voluntary research assistant would play an important role. Field work takes place in the southern Kalahari, Northern Cape province of South Africa. Entire groups of mole-rats will be captured and individually marked. Morphological measurements and tissue samples will be obtained before the release of the animals. The work is physically extremely demanding (long hours, heavy digging to capture mole-rats) and weather conditions are very challenging (heat during the day, very cold during the night). Field work will make trapping during the night necessary. The assistant will mostly be working along one more experienced scientist but will need to work independently at times.

Applicants should be enthusiastic, willing to work hard and keen to get involved in an ecological research project in the African bush. The research assistants are expected to be willing to work at night when trapping schedules require it and need to be fit as capturing mole-rats requires the capacity to do hard physical work (digging) in a challenging environment. Applicants must be holders of a driving license. A zoology related degree and/or previous field experience will be considered an asset. The successful applicant will work in a small team of 2 persons and hence need to be a team player and generally a person that enjoys collaboration under sometimes challenging and isolated circumstances.

Position 2 (Laboratory based):

This position entails assisting in a study on hormonal manipulations of subordinate and dominant mole-rats. We are interested in the effects of prolactin and testosterone on allo-parental care in non-reproducing mole-rats. The research assistant holding this position will be involved in all steps of the experiments and will mainly work in the laboratory with our captive mole-rats which are housed in large semi-natural tunnel systems. The responsibilities include behavioural observations, hormonal measures (blood sampling, urine sampling) and hormonal manipulations.

The successful applicant will work in a small team of 5-6 persons. The research station is also the home of several other projects studying meerkats (www.kalahari-meerkats.com), pied babblers, forktailed drongos, bat-eared foxes and hornbills resulting in a stimulating scientific environment. Around 20-30 research assistants are based at the station year round. Research assistants will learn a range of skills such as remote sensing of behaviour, endocrine sampling techniques, capture-mark-recapture techniques, behavioural observations, data handling and management.

Accommodation is provided, and research assistants are paid a monthly allowance to cover their personal costs and food. Costs for travelling from Johannesburg to the field site will be covered.

Applications received until the 8thth of June 2015 are ensured full consideration. Later applications can be considered especially for position 2.

To apply (CV + cover letter) or enquire further information see pdf version of this ad http://bit.ly/1M3J5mN or contact:

Dr Markus Zöttl

Research associate

University of Cambridge

+441223336673

Mz338@cam.ac.uk

Markus Zoettl <mz338@cam.ac.uk>

SouthAfrica VolFieldAssist StripedMouseEvol

Volunteers needed from now onwards as field assistants for the project: Reducing Daily Energy Expenditure as an Adaptive Response to Droughts - Physiology and Behavior

Opportunity: This is a great opportunity for anybody who wants to get more experience in field work relating to eco-physiology, animal behavior, evolution, and ecology before starting an MSc or PhD project.

Project: We study the evolutionary and ecological reasons as well as physiological mechanisms of group living, paternal care, communal nesting and social flexibility in the striped mouse. One focus is on the adaptation to droughts, combining physiological, behavioral, ecological and evolutionary research. As this species is diurnal and the habitat is open, direct behavioral observations in the field are possible.

What kind of people are needed? Biology/zoology/veterinary students are preferred as candidates. Applicants must have an interest in working in the field and with animals. Hard working conditions will await applicants, as the study species gets up with sunrise (between 5 and 6 o‘ clock), and stops its activity with dusk (19 o‘ clock). Work in the field will be done for 5 days a week. Applicants must be able to manage extreme temperatures (below 0 at night in winter, sometimes over 40C during summer days). Applicants must both be prepared to live for long periods in the loneliness of the field and to be part of a small social group.

Work of volunteer field assistants: Trapping, marking and radio-tracking of striped mice; all-day observations in the field. Volunteers will also see how blood samples are collected for physiological measurements. Volunteers are expected to help with maintenance of the research station (water pump, solar power, etc.).

Confirmation letter: Students get a letter of confirmation about their work and can prepare a report of their own small project to get credit points from their university for their bachelor or masters studies.

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 1350 (around 180 US$, 110 Euro) must be paid for accommodation at the research station. Students must buy their own food etc in Springbok (costs of about R 3000, approx. 360 US$ or 250 Euro/month). Including extras (going out for dinner; shopping), you should expect costs of about 600 US$ / 450 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country.

Place: The field site is in the Goegap Nature Reserve near Springbok in the North-West of South Africa. The vegetation consists of Succulent Karoo, which has been recognized as one of 25 hotspots of biodiversity. It is a desert to semi-desert with rain mainly in winter (June to September).

When and how long: At the moment we are looking for several volunteers. Volunteers are expected to stay at least three months, but longer periods of up to 6months are preferred.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to rrimbach@gmail.com

More information under http://stripedmouse.com/-site1_3_5.htm Contact via e-mail: rrimbach@gmail.com

Succulent Karoo Research Station A registered South African non-profit organization Dr. Rebecca Rimbach

(Postdoctoral Fellow) South Africa

Dr. Rebecca Rimbach

School of Animal, Plant and Environmental Sciences University of the Witwatersrand South Africa

Rebecca Rimbach <Rebecca.Rimbach@wits.ac.za>

Teaching evolutionary mechanisms

Hi,

I m teaching Evolution for Biology students and now we are working about variation, genetic drift, gene flow and natural selection.

When searching for videos in the internet about evolutionary mechanisms I saw many examples with incomplete explanations and also presenting the mechanisms in a way my students dont understand how they act together.

I would like to know if some in the list have a good suggestion about an animation or video to be used in classroom.

Thanks for any help!

Prof. Dr. J. C. VOLTOLINIÃ

Grupo de Pesquisa e Ensino em Biologia da ConservaÃÂ§ÃÂ£o - ECOTROP

Universidade de TaubatÃÂ©, Departamento de Biologia TaubatÃÂ©, SP. 12030-010.Ã

E-Mail: jcvoltol@uol.com.br

* Grupo de pesquisa ECOTROP CNPq: http://dgp.cnpq.br/buscaoperacional/detalhepesq.jsp?pesq=81371558097356 35Ã

* CurrÃculo Lattes: http://lattes.cnpq.br/8137155809735635Ã * Assessoria EstatÃstica: http://assessoria-estatistica.blogspot.com.br/ * Fotos de Cursos e Projetos: http://www.facebook.com/ecotrop VOLTOLINI <jcvoltol@uol.com.br>

Women Evolutionary Biol

Dear Colleagues

I need help gathering any protocols that are currently available to improve the number of women invited to conferences or as editor of the journals. If you are a member or is familiar with such policies from any societies (such as CSE, SMBE, american naturalists, but not limited to these) I would really appreciate it if you could forward the information to me. email: abouchakra@evolbio.mpg.de

Your help is greatly appreciated

Best regards

Maria

Maria Abou Chakra Max Planck Institute Evolutionary Biology: theory group Plön Germany http://web.evolbio.mpg.de/~abouchakra Maria Abou Chakra <abouchakra@evolbio.mpg.de>

PostDocs

AarhusU PDF ResAssist QuantComputationalBiol

Postdoc and Research Assistant in Quantitative Computational Biology

Post doc position

A post doc position is available at the Center for Quantitative Genetics and Genomics (QGG) at Aarhus University to work on development and implementation of methods large scale computational biology with a focus on genetic investigations using genomic information in combination with large scale phenotyping programs. The position is part of the strategic research center “GenSAP” (http://gensap.au.dk) that aims to develop models and applications for use of computational biology in animals, plants, and model species. The position is available for two years from 1 August 2015 or as soon as possible thereafter, with the possibility of extension depending on performance.

QGG has extensive experience in development and implementation of computing methods for genetic studies. Results are implemented in software which is routinely used at QGG and by several Danish and international research groups and commercial breeding companies. Such studies commonly include analysis of very large stochastic mixed models that require efficient numerical implementation. In recent years the use of genomic information, with thousands or millions of genetic markers per individual, has been increasing and this development demands new efforts to update the methodology used for genetic studies. The candidate is expected to work on several computational issues in computational algorithms to analyze large linear models, parallelization, and maximization problems in likelihood or Bayesian statistical methods, and will be expected to be involved in writing publications in the area. The candidate will also be involved in a continuing process of restructuring the existing large volume of code to ensure code of high quality, robustness, and easy future maintenance.

Qualifications for the post doc: * Ph.D.- degree in computer science, engineering, quantitative genetics or similar fields with a strong emphasis on computational methods. * Strong background in computational methods and experience with development of algorithms for analyzing mixed models. * Experience in computer languages used for high performance computing such as C or FORTRAN or similar languages. * Preferably experience working with UNIX systems for high performance computing. * Preferably experience with computational methods analyzing large mixed models. * Good oral and written communication skills in English. * Able to work in a large and diverse research group and with many external scientific and commercial partners.

Research assistant position

A research assistant position is available at the Center for Quantitative Genetics and Genomics (QGG) at Aarhus University to work on development and implementation of methods and models for large scale genetic investigations using genomic information in combination with large scale phenotyping programs. The position may be filled by research assistant and is available for two years from 1 August 2015, with the possibility of extension.

QGG has extensive experience in development and implementation of methods and models for genetic studies. This has led to a number of software packages which are routinely used at QGG and by several Danish and international research groups and commercial breeding companies. Genetic studies commonly involve analyzing very large mixed models. The use of genomic information, with thousands or millions of genetic markers per individual, has been increasing and this new development demands new efforts to update the methodology used for genetic studies. The candidate will work on several computational issues in computational algorithms to iteratively analyze large stochastic models, parallelization, and maximization problems in likelihood or Bayesian statistical methods. The candidate will also be involved in a continuing process of restructuring the existing large volume of code to ensure code of high quality, robustness and easy future maintenance. Furthermore the candidate will be involved in interaction with users and in updating information to users.

Qualifications for the research assistant position: * MSc degree in computer science, engineering, genetics or similar field with a strong emphasis on computational methods. * Experience in computer languages used for high performance computing. * Preferably experience working with UNIX systems for high performance computing. * Good communication and project organization skills, and good oral command of English.

Place of work: The Center for Quantitative Genetics and Genomics (QGG) at Aarhus University (AU) is a major center for research and education in quantitative genetics, quantitative genomics, and breeding. It comprises 20 senior staff and a group of 45 PhDs and postdocs. The center is part

— / —

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 EvolutionMedicine 2

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, with flexibility as needed. 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 Genomics

POST-DOCTORAL RESEARCH ASSOCIATE POSITION IN REGENERATIVE GENOMICS

The School of Life Sciences at Arizona State University invites applications for a postdoctoral position working in regenerative genomics and bioinformatics. ASU is a dynamic and progressive university dedicated to interdisciplinary collaborations and integrating excellence in research and teaching. The School of Life Sciences at ASU contains over 100 faculty members who foster a culture of basic research and teaching with an eye toward applicability.

Duties will include generation and analysis of differential gene expression in regeneration (RNA-Seq and proteomic data analysis using tools such as TopHat, Bowtie, Cuffdiff, and DESeq), transcriptome assembly (using tools such as Trinity), whole genome assembly and annotation (using tools such as ABySS, DISCOVAR, and MAKER). Position will entail studies of regeneration using genomic and bioinformatic approaches.

Qualifications: Candidates must have earned a doctoral degree in genomics, bioinformatics, genetics, regenerative medicine, or developmental biology, or in a related field prior to appointment; candidate must not currently hold a permanent faculty position. Those with a demonstrated productive and innovative research experience will be given preference. Background in bioinformatics, mathematical biology, or computer science is desired but not essential.

To apply: Send cover letter summarizing your qualifications and interests, curriculum vitae, and names and email addresses of three professional references to Dr. Kenro Kusumi, School of Life Sciences, Arizona State University, PO Box 874501, Tempe, AZ 85287-4501, Email: kenro@asu.edu. The initial closing date for receipt of applications is June 15, 2015; applications will be reviewed weekly thereafter until the search is closed. The search will be closed on August 1, 2015. A

background check is required for employment. Arizona State University is an equal opportunity/affirmative action employer committed to excellence through diversity. Women and minorities are encouraged to apply. For additional information on this position and the School of Life Sciences, please visit http://sols.asu.edu/jobs .
"Kenro.Kusumi@asu.edu" <Kenro.Kusumi@asu.edu>

Bethesda Maryland HIVEvolution

The Henry M. Jackson Foundation for the Advancement of Military Medicine Inc. (HJF) is seeking a post-doctoral fellow for the HIV Research Program (MHRP) located in Bethesda, Maryland. HJF provides scientific, technical and programmatic support services to MHRP. The U.S. Military HIV Research Program (MHRP) (www.hivresearch.org) is at the forefront of the battle against HIV to protect U.S. troops from infection and to reduce the global impact of the disease. MHRP is one of the leading clinical research programs developing a vaccine to prevent HIV, improving treatments for HIV and co-infections and also working towards a cure.

Job Summary The post-doctoral fellow will be part of a team of biologists, clinicians and statisticians working on a range of questions related to HIV vaccine research. The candidate will investigate HIV evolutionary processes both within and between hosts, focusing on a unique, comprehensive cohort of acutely infected individuals followed over time.

Major Duties The post-doctoral fellow will contribute to MHRP's research agenda through independent and collaborative research resulting in presentations and publications.

The incumbent may perform some or all of the following responsibilities: 1. Independently perform comprehensive molecular epidemiological analysis 2. Use state-of-the-art Bayesian phylogenetic and phylogeographic approaches 3. Contributing to the science through independent and collaborative research including authoring papers 4. Maintaining current knowledge of and contributing to advancements in the field through participation in professional organizations, scientific conferences, reading industry journals, and publication of manuscripts 5. Performing other tasks as required

Qualifications The successful candidate will have a Ph.D. in computational biology, molecular biology, or microbiology/virology. The candidate should be a dedicated, social, detail-oriented person, who is able to work independently within a team of researchers. Excellent written and verbal communication skills are required.

To apply Please contact Morgane Rolland mrolland@hivresearch.org

"mrolland@hivresearch.org"
<mrolland@hivresearch.org>

CarnegieMuseum Pittsburgh Systematics

POSTDOCTORAL FELLOW at Carnegie Museum of Natural History, Pittsburgh

A one-year NSF-funded postdoctoral fellowship is available immediately and provides taxonomic, systematic, and curatorial training in entomology at the Carnegie Museum of Natural History in Pittsburgh, Pennsylvania, USA. We are seeking a highly motivated, well organized, and creative individual to conduct original systematic research on a targeted insect lineage, so as to enable imaging and data capture as specified by our NSF-funded project. The individual will work directly with one or more curators in the Section of Invertebrate Zoology < http://www.carnegiemnh.org/science/-default.aspx?id=3D16656 >, who will serve as supervisors and mentors throughout the term of the fellowship.

* Fellowship Term.- The fellowship period is for one (1) year, starting on July 1, 2015 thru June 30, 2016. * Eligibility.- Candidate must possess a doctoral degree (or international equivalent) in entomology or a related field and must be able to conduct original research that will lead to the advancement of scientific knowledge at the Carnegie Museum of Natural History. Research interests should focus on collection- based, field-oriented studies in systematics that will have broad applications and impacts in theory, conservation, evolution, and/or biogeography. The candidate must have a publication record in international journals demonstrating her/his adequacy for the position offered. * Knowledge, Skills, Abilities.- The candidate must have prior graduate training in entomology with an emphasis on lineages that are well-represented but under-worked in the CMNH collection, including Siphonaptera, Mecoptera, Odonata, Hymenoptera, Heteroptera, and others (less emphasis on Coleoptera, Lepidoptera, Diptera, and Homoptera). The capacity to talk with and engage public audiences about her/his research while participating in public events at the museum is highly encouraged, as is par-

ticipation as a lecturer in museum-sponsored scientific seminars. The appropriate skills, experience, and education of the Fellow will be determined by the curators, with emphasis placed on a postdoctoral program to train early career Ph.D. scientists, helping them to acquire scientific training under the tutelage of Carnegie curators to further their academic and/or research careers. * Funding.- The fellow will receive an annual salary of $38,000, plus fringe benefits. Funding is provided by the InvertNet Project (https://invertnet.org/), which is a project funded through the NSF Advancing Digitization of Biological Collections (ADBC) program and nationally coordinated by the iDigBio Team (www.idigbio.org).

A review of applications will begin on June 25th but applications will be accepted until the position is filled. The start date planned for this position is July 1, 2015. Applications should be completed online at http://www.carnegiemuseums.org/interior.php?pageID (search for "Postdoctoral" and select Requisition ID #1020). Then create a profile and follow the on-screen instructions. The following items should be submitted as part of the application: 1) a CV, 2) a short statement of research interests, and 3) names and contact information for three references familiar with the candidate and his/her research. Questions about the position should be directed to either James Fetzner (FetznerJ@CarnegieMNH.Org) or John Rawlins (RawlinsJ@CarnegieMNH.Org), or Bob Davidson (DavidsonR@CarnegieMNH.Org).

"Fetzner, Jim" <FetznerJ@CarnegieMNH.Org>

ColdSpringHarborLab EvolutionaryGenomics

Position Description: Postdoctoral Positions in Computational Genomics are available in Dr. Adam Siepels research group in its new location at the Simons Center for Quantitative Biology (SCQB) at Cold Spring Harbor Laboratory (CSHL). The Siepel Group specializes in the development of probabilistic models, algorithms for inference, prediction methods, and application of these methods in large-scale genomic data analysis. Of particular interest is research relevant to existing, NIH supported projects in (1) human population genomics, including demography inference using Bayesian coalescent-based methods, inference of natural selection on regulatory and other noncoding sequences, and prediction of fitness consequences for noncoding mutations; and (2) transcriptional regulation in mammals and Drosophila, including the estimation of rates and patterns of transcriptional elongation from GRO-seq data, prediction of transcription factor binding sites from DNase-seq data, and regulatory network inference based on joint patterns of transcription and binding in inducible systems. The research on transcriptional regulation will continue to be carried out in close collaboration with Dr. John Lis at Cornell University.

Relevant recent papers include the following: Rasmussen MD, Hubisz MJ, Gronau I, Siepel A. Genome-wide inference of ancestral recombination graphs. PLoS Genet. 10(5):e1004342, 2014.

Freedman AH, Gronau I, Schweizer RM, Ortega-Del Vecchyo D, Han E, et al. [30 coauthors]. Genome sequencing highlights the dynamic early history of dogs. PLoS Genet. 10(1):e1004016, 2014.

Capra JA, Hubisz MJ, Kostka D, Pollard KS, Siepel A. A model-based analysis of GC-biased gene conversion in the human and chimpanzee genomes. PLoS Genet. 9(8):e1003684, 2013

The ideal candidate will be enthusiastic, highly motivated and independent; will have a strong background in comparative genomics, population genomics, or transcriptional regulation, a serious interest in molecular biology and genetics combined with good skills in mathematics and computer science, and a strong record of accomplishment in research. Postdoctoral associates in the group are expected to participate in both methods development and data analysis, to be comfortable in a fast-moving, interactive, and collaborative research environment, and to actively publish and present results.

Required Qualifications: Ph.D. in bioinformatics, computer science, statistics, genetics, molecular biology, applied mathematics, or a related field. Research experience (with first-author publications) in computational genomics or a closely related field. Fluency in probabilistic modeling and computational statistics. Proficiency in programming, ideally in C or C++, as well as in scripting languages such as python, Perl, mat lab, or R. Should be comfortable in a Linux environment, with large data sets, computer clusters, and databases.

Job location: CSHL, One Bungtown Road, Cold Spring Harbor, NY 11724

TO APPLY: visit the CSHL Careers website at www.cshl.edu/careers. Position Number:01229-R.

"Gill, Irene" <gill@cshl.edu>

ColoradoStateU EvolutionManagementSystems

A position for a Postdoctoral researcher is available at Colorado State University on a funded project focused on the geography and evolution of natural resource management systems. Human societies vary widely in the approaches used to manage natural resources. The funded project seeks to address long-standing debates in multiple academic disciplines (e.g., anthropology, geography, economics, and human behavioral ecology) regarding what factors shape the subsistence and land tenure systems used by societies across the globe, and to examine the evolutionary pathways of these natural resource management systems. The senior project personnel have, in recent years, adapted methods originally developed in biogeography and evolutionary biology to explore the factors that drive the evolution and geographic patterns of cultural diversity. In addition, the research group has developed a database that maps cultural features onto language family trees for over 1400 societies, and links these to ecological and environmental variables, empowering new lines of investigation into drivers of cultural change. The team is now uniquely positioned to conduct the first, integrated empirical tests of theories regarding the geography and evolution of natural resource management. The successful candidate will be based at Colorado State University and collaborate with researchers at MPI SHH and an interdisciplinary team of researchers from the U.S., Australia, Canada, Germany and the United Kingdom.

Field of Work: The successful candidate is expected to:

- begin work in August/September of 2015 (exact date negotiable)
- assist in directing the project
- help guide work of the PhD student and undergraduate assistants
- lead 1-2 subprojects on the use of phylogenetic analyses to examine the evolution of land tenure and/or subsistence
- have the opportunity to help shape future research directions

Offer:

- salary commensurate with research experience
- mentoring by senior research personnel from multiple fields and institutions
- office space and computer facilities
- costs for research expenses and related travel will be covered by the project.

The position will be reviewed annually and, contingent upon performance and available funds, be appointed to additional years. Three years of potential funding is expected to be available.

Your qualifications: Selection will be made on a competitive basis using the following criteria:

- A strong academic background with demonstrated experience using computationally intensive phylogenetic methods (e.g. to examine co-evolution, evolutionary trajectories, ancestral states, etc).
- Preference will be given to candidates with experience working on evolution of cultural diversity, however candidates with strong analytical skills whose prior focus has been with other taxa are also encouraged to apply.
- Preference will also be given to candidates with the proven communication and collaboration skills needed to work as part of interdisciplinary research teams.

Your application: By July 31, 2015, please submit a letter of interest detailing how you meet each of the qualifications, curriculum vitae (indicating previous academic performance indicators, publication history, and prior research experience), and contact information for three references to Michael Gavin (Michael.gavin@colostate.edu

"Gavin,Michael" <Michael.Gavin@colostate.edu>

FieldMuseum Chicago InsectPlantEvolution

POSTDOCTORAL RESEARCH ASSOCIATE IN THE MOREAU AND REE LABS AT THE FIELD MUSEUM ON INSECT-PLANT COEVOLUTION

DEADLINE FOR APPLICATIONS SUBMISSION: 7 July 2015

When, where, and how did insect-plant associations arise, and how did this affect their evolutionary and ecological trajectories?

We seek an outstanding postdoctoral researcher to address this general question, including but not limited to studies emphasizing data-mining and phylogenetic reconstructions of co-evolutionary history. Potential general topics include plant-pollinator, plant-herbivore, or other symbiotic interactions, or questions involving historical biogeography and ecological assembly (e.g., did insect groups specialized on desert plants evolve from non-plant-associated desert insects, or from plant-associated relatives outside the deserts?).

The successful candidate will work in collaboration between Dr. Corrie Moreau (www.moreaulab.org) and Dr. Richard Ree (www.reelab.net) in the museum's Integrative Research Center. In addition to conducting primary research, the candidate will work with educators in the museum's Learning Center to create a K-12 level classroom exercise and lesson plan focused on the tree of life.

The Field Museum offers a dynamic research community in evolutionary biology that includes resident curators, senior scientists, postdocs, and graduate students, as well as numerous associates at the University of Chicago, the University of Illinois at Chicago, the Chicago Botanic Garden, the Morton Arboretum, and Argonne National Labs. Chicago combines world-class urban amenities and culture with affordable costs of living.

Applications should include: 1) CV including contact information for three references and 2) a short proposal (2 page maximum) describing a research project fitting the theme of evolution of insect-plant interactions including preferred start date in 2015 (summer or fall preferred). (Important note: funds for new data collection will be limited, so projects should rely heavily or exclusively on existing data.)

The initial term of appointment is one year, renewable for an additional year upon satisfactory progress. Competitive salary depending on prior experience. Review of applications will begin on 7/7/2015. Outstanding candidates will be contacted for an interview.

Applications must be submitted electronically through the following application system: http://app.hireology.com/s/41990 Informal inquiries may be directed to Rick (rree@fieldmuseum.org) and/or Corrie (cmoreau@fieldmuseum.org).

Corrie Saux Moreau, Ph.D. | MacArthur Associate Curator - Insects | Integrative Research Center | Department of Science and Education | Field Museum of Natural History | 1400 South Lake Shore Drive | Chicago, IL 60605 USA | Office: (312) 665-7743 | Fax: (312) 665-7754 | Email: cmoreau@fieldmuseum.org | Moreau Lab website: http://www.moreaulab.org/ | FMNH website: http://fieldmuseum.org/users/corrie-moreau | Field Museum Women in Science: http://fieldmuseum.org/womeninscience Corrie Moreau <cmoreau@fieldmuseum.org>

FordhamU RatPopulationGenomics

Postdoctoral researcher in population genomics

Department of Biological Sciences

*Fordham University, Bronx, NY *

A postdoctoral position is available in the lab of Jason Munshi-South at Fordham University to work on a NSF-funded study examining population genomics, adaptive evolution, and global phylogeography of wild brown rats (*Rattus norvegicus*). The project aims to understand how demographic history and natural selection have influenced genomic variation in the New York City rat population since the mid 18th century. A parallel effort will investigate origins of and admixture between brown rat populations from around the world. The postdoc will also be encouraged to pursue extensions to these projects in line with their own interests.

DUTIES & RESPONSIBILITIES

The successful candidate will lead computational analyses of genome-wide SNP datasets and whole-genome sequences to investigate historical demography, selection, and phylogeography of rats. The postdoc may also be involved in museum genomics and the development of genomic technologies for rats, such as SNP chips or capture arrays. The postdoc will work with the PI and other lab members to produce manuscripts for publication, give presentations at professional meetings, and mentor graduate and undergraduate students.

QUALIFICATIONS

Required: Ph.D. in biology, bioinformatics, or similar field; experience with population genetic analysis; record of publication in peer-reviewed journals

Preferred: Research experience with population genomics, particularly demographic modeling and parameter estimation, selection scans, and admixture analyses from genome-scale datasets. Experience with SNP genotyping, SNP chip / array design, or similar. Work with genomic datasets from humans, domesticated animals, or invasive species would be particularly relevant.

SALARY & APPOINTMENT INFORMATION

The initial term of appointment is for one year, with renewal for a second year contingent on satisfactory progress. The start date is negotiable, but preferably by January 2016. The position is open until filled.

Annual salary for this position is $48,000. The successful applicant has the choice of being based out of the biology department at the Bronx campus (Rose Hill) of Fordham University, or the Louis Calder Center in Armonk, NY. The Calder Center is located 25 miles north of the Bronx, and has the advantages of an idyllic, forested setting and potential for subsidized housing. Some travel between the two sites will be necessary; Fordham provides a free shuttle.

APPLICATION PROCEDURES

To apply for this position, please send application materials as a single PDF to Jason Munshi-South at jmunshisouth@fordham.edu. A complete application will include a cover letter explaining your research interests and qualifications for the position, a CV, contact information for three professional references, and up to three PDF reprints of relevant publications. Full consideration will be given to complete applications received by *13 July 2015*.

– Jason Munshi-South, Ph.D. Associate Professor Louis Calder Center & Dept of Biological Sciences Fordham University Armonk, NY 10504 jmunshisouth@fordham.edu (914) 273-3078 ext 20 http://NYCevolution.org/ Jason Munshi-South <jmunshisouth@fordham.edu>

Georgia Tech MicrobeDynamics

Multi-scale microbial dynamics in health and disease.

The Brown lab is recruiting, with new postdoc and grad student positions available as part of an August move to the Georgia Institute of Technology (biology.gatech.edu).

I am interested in candidates with experience in either computational and/or experimental approaches that are relevant to the study of microbial dynamics:

Computational I am particularly interested in candidates with experience in statistical modeling and bioinformatics in an ecological/evolutionary context. Simulation and analytical approaches are also of interest, if coupled with experience of biological applications ÂV ideally in microbiology/ecology/evolution.

Experimental I am interested in candidates with strong backgrounds spanning molecular microbiology and ecology/evolution. Experience with Pseudomonas aeruginosa, quorum-sensing, regulatory evolution or mobile genetic elements is a plus.

Research themes Bacterial sociality, cooperation, decision-making, quorum-sensing, biofilms, microbiomes, HGT, pathogen emergence, virulence, resistance, novel therapeuticsÂK (and ecology/evolution of all the above). To learn more, take a look at our website (http://brown.bio.ed.ac.uk) and recent relevant publications:

Estrela S, Whiteley M, Brown SP. 2015. The demographic determinants of human microbiome health. Trends Microbiology 23, 134-141.

McNally L, Viana M, Brown SP 2014. Cooperative secretions facilitate host range expansion in bacteria. Nature Communications. 5, 4594.

Cornforth D, Popat R, McNally L, Gurney J, Scott-Phillips T, Ivens A, Diggle SP, Brown SP 2014 Combinatorial quorum sensing allows bacteria to resolve their social and physical environment. PNAS 111, 4280-4284.

Allen R, Popat R, Diggle SP, Brown SP 2014 Targeting virulence: can we make evolution-proof drugs? Nature Reviews Microbiology 12, 300-308.

To apply, please email a CV, brief description of research interests and how they relate to Brown lab themes (1 page) and the names and contact info for at least 3 references to Sam Brown (sam.brown@ed.ac.uk). Review of applications will begin on July 6th and continue until positions are filled. Start dates are flexible, with preference for early 2016.

– Sam Brown Centre for Immunity, Infection and Evolution University of Edinburgh West Mains Road, Edinburgh EH9 3FL http://brown.bio.ed.ac.uk/ http://ciie.bio.ed.ac.uk/ sam.brown@ed.ac.uk

<sam.brown@ed.ac.uk>

Sam Brown <sam.brown@ed.ac.uk>

IIBRRockville Maryland Phyloinformatics

Post-doctoral position in phyloinformatics

In 2012 and 2013, NESCent sponsored 2 hackathons to build a prototype “Phylotastic” [1] system with the goal of providing an open, distributed, community-owned system for efficient delivery of "Tree of Life" knowledge, so that scientists, educators, and the public can get online species trees as easily as they currently get online driving directions. NSF recently funded a 3-year collaborative project [2] to develop a production system based on this prototype.

As part of this project, a post-doc position is available with Arlin Stoltzfus at the Institute for Bioscience and Biotechnology Research (IBBR), a joint NIST-UMD-UMB institute in Rockville, Maryland, in the midst of a major biotechnology corridor in the greater Washington, DC area.

Interested individuals are encouraged to apply for this position, which provides a unique opportunity to build tools with a broad impact in spreading phylogenetic knowledge (in the scientific community and beyond). The successful applicant will become part of a distributed, collaborative team with colleagues from IBBR as well as NMSU (Enrico Pontelli), UTK (Brian O'Meara), Open Tree of Life (Karen Cranston), and Global Names (Dmitry Mozzherin).

Applications should include * A cover letter (include skills, suggested start date, and expected PhD date as needed) * A CV * A short research statement * Contact information for two references * Link(s) to repositories with examples of code you have written (or attachments including such code)

Salary is from 42000 to 46000 USD depending on experience. The desired applicant is expected to bring a scientific understanding of phylogeny use-cases into the design and testing process, and also to participate in implementation of tools where appropriate. Experience in scientific programming is required. Understanding how and why scientists use phylogenies will be extremely valuable. Knowledge of R or Python (the language of some of the prototype tools), though helpful, is not necessary. If in doubt, ask: please do not self-select yourself out from what might be a mutually beneficial position.

The University of Maryland, College Park, actively subscribes to a policy of equal employment opportunity, and will not discriminate against any employee or applicant because of race, age, sex, color, sexual orientation, physical or mental disability, religion, ancestry or national origin, marital status, genetic information, political affiliation, and gender identity or expression. Minorities and women are encouraged to apply.

Review of applications will begin on June 20th and continue until the position is filled (start dates are flexible). Presubmission inquiries are encouraged. With regards,

Arlin Stoltzfus (arlin@umd.edu) Research Biologist (NIST) Fellow (IBBR) Adjunct Associate Professor (UMD)

[1] www.phylotastic.org; see also Stoltzfus, et al., 2013, "Phylotastic! Making tree-of-life knowledge accessible, reusable and convenient" (BMC Bioinformatics 2013, 14:158), available at http://www.biomedcentral.com/-1471-2105/14/158 . [2] Arlin Stoltzfus, Enrico Pontelli, and Brian O'Meara. "Collaborative Research: ABI Development: An open infrastructure to disseminate phylogenetic knowledge."

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

IISER-TVM Kerala India PlantEvolutionaryEcol

POSTDOCTORAL POSITION IN PLANT EVOLUTION/BIOGEOGOGRAPHY AT IISER-THIRUVANANTHAPURAM, KERALA, INDIA.

A postdoctoral position in Evolutionary Ecology is available at IISER Thiruvananthapuram, Kerala, India, in the Vanasiri Evolutionary Ecology Group of Ullasa Kodandaramaiah (www.vanasiri.in)

DEADLINE: 23 June 2015

SALARY: Rs. 43,200 (Rs 36,000 + 20% Housing Rent Allowance)

DURATION: Up to 3 years (initial contract will be for 1 year, but can be extended on a yearly basis contingent on satisfactory performance).

RESEARCH AREA: The candidate is expected to play an active role in the project under which the current position is advertised, but the workload as part of project per se will be fairy light. Collaborations on other projects in plant evolutionary biology between the postdoc and our research group will be encouraged and facilitated.

The position is advertised under a collaborative project involving our group and plant taxonomists. The goal is to carry out historical biogeographic and phylogeographic analyses within a comparative biogeography framework to understand the factors affecting diversification of plants in the Western Ghats mountain system in India. The duties of the selected candidate will include some field work along with collaborators to sample plants. The major part of the work will involve DNA sequencing and phylogenetic analyses. A Junior Research Fellow will also be part of the project, and will work under the guidance of the postdoc.

Our lab has ongoing projects on plant evolutionary biology, and we would like to begin new experimental work in this area. I have several ideas in mind. However the candidate will have plenty of flexibility in designing projects, and can involve undergraduate students & interns. You are welcome to contact me informally (ullasa@iisertvm.ac.in) for discussions before sending in your formal application.

SELECTION: The advertisement for the position is at http://iisertvm.ac.in/openings/read_opening/119. The candidate should have a PhD in biological sciences, and a good publication record. Experience in phylogenetic work and familiarity with plant taxonomy will be an advantage. Independence and willingness to collaborate with the research group on other projects will be a major plus - a candidate who can bring in new expertise to the lab in this area will have a strong advantage.

LIFE IN KERALA AND THIRUVANANTHAPURAM (TRIVANDRUM): The coastal city of Thiruvananthapuram is the capital of Kerala, and has a rich cultural heritage. It is within a stone's throw away from world-famous beaches such as Kovalam and Varkala, and lovely backwater tourism areas such as Poovar. Several hill stations (e.g Ponmudi) and wildlife sanctuaries are close by. Being a major medical tourism destination, the city has excellent medical care facilities.

It is a relatively small city, and the cost of living tends to be considerably lower than in bigger Indian cities. A 2-bedroom apartment can be had for Rs 8,000 - 10,000 per month. There are plenty of options for dining out - a meal at a decent local restaurant can start from Rs 50, but a good meal with a drink even in a five-star hotel need not cost more than Rs 1000. Costs for groceries and other daily needs can be looked up here (www.kada.in). Taxis can be hired from Rs 10 per km (with a minimum fare of Rs 50), while the cost of driving your own small car (not for the faint-hearted!) is about Rs 5 per kilometer (petrol: Rs 67/litre, diesel: Rs 55/litre).

Ullasa Kodandaramaiah ullasa@iisertvm.ac.in

ISTAustria EvolutionaryGenomics

A postdoctoral position in evolutionary genomics is available in the Vicoso group at the Institute of Science and Technology, Austria. The general focus of the lab is the evolution of sex chromosomes, which we investigate using a combination of experimental and computational approaches.

Questions that motivate our research include: why do some Y/W chromosomes degenerate while other remain homomorphic? What forces drive some species to acquire global dosage compensation, while others only compensate specific genes? What are the frequency and molecular dynamics of sex-chromosome turnover?

The successful applicant will apply comparative genomics analyses to a wide variety of species, and combine them with population DNA and gene expression data, to achieve a better understanding of the evolutionary and molecular forces driving sex chromosome differentiation. Candidates wishing to work on a specific project in sex chromosome evolution are also encouraged to apply.

Applicants should have obtained, or anticipate obtaining by the start date, a PhD in biology, genetics, bioinformatics, or a related field. A strong background in one or more the following areas is highly desired: comparative genomics molecular evolution population genetics bioinformatics

The initial appointment is for two years, with the possibility of extension and a minimum salary of 49,070 Euros per year (gross).

IST Austria (www.ist.ac.at) is a young and vibrant institute dedicated to basic research, with a strong focus on evolutionary biology (other EB groups include those of Nick Barton, Jonathan Bollback, and Sylvia Cremer) and ties to several evolutionary groups in the area (www.univie.ac.at/evolvienna/). We are located on the outskirts of Vienna, and the official language of the institute is English.

To apply, send a short summary of research interests, a CV, up to three relevant publications/manuscripts, and the names and contact information for three references to Beatriz Vicoso (bvicoso@ist.ac.at). The review of applications will start on July 1st and continue until the position is filled. The start date is flexible, but an earlier start would be preferable.

More information on the lab is available at: http://ist.ac.at/research-groups-pages/vicoso-group/ Beatriz Vicoso <bvicoso@ist.ac.at>

JohnInnes UK 2 PopulationGenomics

Please distribute to anyone who might be interested. Informal enquiries are encouraged to me at lyant@oeb.harvard.edu.

Applications are invited for two Postdoctoral Researchers to join my lab in the Department of Cell and Developmental Biology at the John Innes Centre. We are currently moving to JIC after getting started in the Department of Organismic and Evolutionary Biology at Harvard (http://projects.iq.harvard.edu/yantlab/home).

Successful candidates will be absorbed by challenging problems in population genomics and will have demonstrated scientific success during or following their PhD. The primary research aim of these positions will be to take ownership of large-scale population genomic resequencing projects focused on scanning for selection following genome duplication and/or invasion of challenging habitats. This includes 1) performing genome resequencing of hundreds of individuals representing an array of phenotypic contrasts; 2) conducting population genomic analysis to determine patterns of demographic structure and gene flow across landscapes within and between species, and pinpointing selective sweeps underlying relevant adaptations; and 3) functional confirmation of the effects of discovered alternative alleles as part of established collaborations with partner labs in the UK and Europe.

Enthusiasm for and sound understanding of population genetics is essential, as well as skills in at least one major scripting language (Python or Perl). An affinity for programming would be beneficial. We encourage candidates with initiative, strong analytical skills, and a drive to push forward on new problems in population-level analysis. Candidates are expected to be interested in innovating, developing methods where needed. An interest in coalescent theory and modelling is highly advantageous.

Salary on appointment will be within the range Â£29,500 to Â£36,060 per annum depending on qualifications and experience. This post is for a contract of 36 months.

For further information and details of how to apply, please visit our web site https://jobs.jic.ac.uk/Details.asp?vacancyID=10751 or contact Human Resources, Norwich BioScience Institutes Partnership, Norwich Bioscience Institutes, Norwich, NR4 7UH, UK, 01603 450149 quoting reference 1002881. As a user of the of the disability symbol, we guarantee to interview all disabled applicants who meet the minimum essential criteria for this vacancy.

Positions are available to start as early as 1st September 2015; the closing date for applications will be 1st August 2015.

Levi Yant

Group Leader Organismic and Evolutionary Biology 22 Divinity Ave Room 301 Harvard University Cambridge MA 02138

(mobile) 617-852-7982

http://projects.iq.harvard.edu/yantlab/home "Yant, Levi" <lyant@oeb.harvard.edu>

Lausanne Switzerland EvolutionaryConservationBiol

Available:

Postdoc position, 3-5 years

Department of Ecology and Evolution, University of Lausanne, Switzerland

Start: September 2015 or later

Our group studies the selective forces that act on freshwater fish, i.e. the effects of human activities in interaction with natural and sexual selection. The position is financed by an new SNF project that focuses on salmonid fish (various brown trout and grayling populations) and combines different types fieldwork, labwork, and modeling. Our website: http://www.unil.ch/dee/home/menuinst/research/group-wedekind.html We are seeking candidates with a strong background in one or several of the following fields: population genetics, population management, life history, bioinformatics, evolutionary ecology

Please send your application by email (all material in one attached file please) to Claus Wedekind (claus.wedekind@unil.ch). Include your Curriculum vitae, a short description of your research interests and research experience, and contact details of two references. Review of applications will begin June 20th 2015, but applications will be accepted until the position is filled.

– Claus Wedekind Department of Ecology and Evolution, Biophore, University of Lausanne, 1015 Lausanne, Switzerland. Tel. +41 21 692 42 50, Fax +41 21 692 42 65 http://www.unil.ch/dee/home/menuinst/-people/group-leaders/prof-claus-wedekind.html Claus Wedekind <Claus.Wedekind@unil.ch>

Lusignan France PlantBreeding

Dear Member,

Postdoctoral Position in plant breeding methodology to optimise selection schemes and selection indices for the improvement of grassland species mixtures at INRA URP3F (France)

POSITION DESCRIPTION. The INRA URP3F research unit is seeking for a post-doctoral researcher to contribute to a collaborative research project (PRAISE) granted by the ANR 2013 call ÂÂBioadaptÂÂ±. PRAISE is a pluridisciplinary project at the crossroad of Quantitative and Population Genetics, Ecophysiology and Functional Ecology. It aims to identify the best genetic composition of sown grassland mixtures and to provide the bases of innovative selection methods of grassland species for their use in mixture. This post-doctoral research will develop a theoretical analyse of selection schemes designed to improve grassland species for their use in mixture and will set up a new selection index method to reach optimal compromise between directional selection on some traits and conservation of diversity on others. Theoretical analyse of selection schemes for the use of grassland species in mixtures. The usual selection scheme of grassland species is a recurrent selection scheme based on the agronomic assessment of half-sib progenies. Half-sib progenies are usually tested in pure mono-specific stands although grassland species are commonly sown in mixtures of several grass and legume species. However, previous results obtained at INRA UR P3F suggest that the agronomic value of genotypes in pure stands correlates quite poorly with their value in mixtures of two or more species. It is thus necessary to conceive selection schemes in which half-sib progenies of a species would be tested in micro-assemblages with other species. Such selection schemes can be considered as multi-species selection schemes in which several species would be simultaneously improved. At each selection cycle, half-sib progenies of a given species would be tested in factorial micro-assemblages with other species. Different factorial micro-assemblage designs can be conceived with different emphasis on the general and specific abilities for association in plurispecific mixtures (GAA and SAA, respectively). The post-doctoral research will aim to define the relative efficiency of several factorial micro-assemblage designs according to values of GAA and SAA on the basis of theoretical expectations of genetic gains. These expected genetic gains will also be compared to the correlative response of mixture performance obtained with parallel classical selection schemes based on the test of pure stands of half-sib progenies, according to the value of the correlation of pure stand performances with GAA and SAA. Finally, field assays from INRA UR P3F will provide experimental values of GAA, SAA and of their correlation with pure stand performances to practically identify the best selection design. Optimisation of selection indices. The selection methods used in plant breeding are inherently directional and reduce genetic variability. They allow maintenance of variability only for traits genetically unrelated to traits submitted to selection. Usually, the control of selection on several traits is obtained by choosing candidates to selection based on the value of an index, i.e. a linear combination of the estimated breeding values of candidates for traits being selected. The coefficients of the index are determined using a constraint system based on expectations of genetic gains. The post-doctoral fellow will complete this constraint system by applying additional constraints to maintain sufficient genetic variance of some traits and will set up an operational research script to solve this constraint system. This improved index selection method will enable to deal with the trade-off between selection on some traits and conservation of diversity on others, which is of primary importance to release improved populations of grassland species for creating species mixtures able to cope with various environmental conditions.

REQUIREMENTS. The post-doctoral fellow is expected to have a background in quantitative genetics, statistics, applied mathematics and agronomic sciences.

CONDITIONS. The post-doctoral fellow will be hosted at the INRA URP3F research unit in Lusignan (France) where he will get support from Jean-Paul Sampoux (responsible of work-package about selection methodology of PRAISE) and Isabelle Litrico (coordinator of PRAISE). The appointment is for one year duration; starting date is wished between October 1st 2015 and January 1st 2016. _HOW TO

APPLY._ Candidates can apply by sending a copy of their CV and a cover letter to J.P. Sampoux and I. Litrico (jean-paul.sampoux@lusignan.inra.fr; isabelle.litrico@lusignan.inra.fr)

best regards,

–

Isabelle Litrico INRA - URP3F Le ChÂÂo̲ne RD 150 BP 86006 86600 Lusignan

isabelle.litrico@lusignan.inra.fr

— / —

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

Lyon GrapeMolecularEvolution

Postdoc in comparative genomics and molecular evolution in grapevine, 18 months, Lyon (France)

Context: The project is part of an ANR grant (InteGrape) and consists on studying the molecular evolution of two multigenic families (P450 and terpene synthases) implicated in grapevine (Vitis vinifera) secondary metabolism and that show a remarkable expansion in the grapevine genome. The richness of grapevine metabolism and its potential for giving rise to an exceptional diversity of flavor compounds contribute greatly to the aromatic complexity of wine. The goal of the project is to decipher the evolutionary mechanisms that led to the expansion of these families, and its potential link with domestication, performing comparative analysis between grapevine varieties with different aromatic properties, domesticated and wild grapevine and more broadly within different species of the Vitaceae family. This work will extend the integrated approach used with the stilbene synthases family in Parage et al. Plant Physiol. 2012.

Skills required: bioinformatics, genome assembly and annotation, comparative genomics, dN/dS analyses, molecular phylogeny.

Salary: 2500 euros/month, health insurance included.

Host team: ≪ Sex and Evolution ≫, LBBE, CNRS/Université Lyon 1.

http://lbbe.univ-lyon1.fr/-Equipe-Sexe-et-Evolution-.html Contact: raquel.tavares@univ-lyon1.fr

—

Postdoc en génomique comparative et évolution moléculaire chez la vigne, 18 mois, Lyon.

Contexte : Le projet sinscrit dans un contrat ANR (InteGrape) et consiste à étudier lévolution moléculaire de deux familles multigéniques (terpène synthases et P450) impliquées dans le métabolisme secondaire de la vigne (Vitis vinifera) et qui ont subi une expansion notable chez la vigne cultivée. Le métabolisme secondaire chez la vigne est extrêmement diversifié et responsable, entre autres, des arômes des vins. Le but est de comprendre lhistoire évolutive de ces familles de gènes et le lien éventuel avec la domestication, via létude comparative entre cépages avec des propriétés aromatiques différentes, entre vigne domestiquée et vigne sauvage et plus largement au sein des Vitaceae. Ce travail prolongera lapproche intégrée faite pour la famille des stilbène synthases dans Parage et al. Plant Physiol. 2012.

Profil recherché : bioinformatique, assemblage et annotation de génomes, génomique comparative, analyses dN/dS, phylogénie moléculaire.

Salaire brut : 2500 euros par mois (sec sociale incluse).

Equipe daccueil : Sexe et Evolution, LBBE, CNRS/Université Lyon 1.

http://lbbe.univ-lyon1.fr/-Equipe-Sexe-et-Evolution-.html Contact : raquel.tavares@univ-lyon1.fr

Raquel TAVARES

University of Lyon- UMR CNRS 5558 Laboratoire de Biométrie et Biologie Évolutive Bat. Gregor Mendel, 16 rue Raphael Dubois 69622 Villeurbanne cedex France

Tel: (+33) (0) 4 72 43 35 83 Fax: (+33) (0) 4 72 43 13 88

Email: raquel.tavares@univ-lyon1.fr

TAVARES RAQUEL <Raquel.Tavares@univ-lyon1.fr>

MaxPlanck Tuebingen EvolDevelVariation

* Genetic mapping of evolutionary developmental variation using hybrid mouse in vitro crosses *

One postdoctoral position, one PhD position and a staff scientist position are available in the Chan Lab at the Max Planck Institute in Tübingen as part of a prestigious 1.5M EUR European Research Council grant investigating the role of gene regulatory network evolution in mice by studying "*in vitro*" genetic crosses.

The goal of our research is to adopt cutting-edge tissue culture techniques for studying evolutionary divergence in gene networks. We will generate recombinant inbred panels from mouse hybrids spanning increasing evolutionary divergence. We will assay expression and tissue phenotypes at the tissue, fitness and even organismal levels. This ground-breaking research will elucidate the gene network evolution underlying tissue function and speciation in mammals.

Postdoc position in complex trait genetics and tissue engineering

Your role: You will be the main driver in our exciting new project in studying gene network evolution using in vitro crosses of tissues from interspecific mouse hybrids. You will be responsible for the derivation of specialized embryonic stem cell and iPSC lines and the generation of recombinant inbred mapping panels from these lines. You will adopt tissue engineering techniques to assay expression and tissue phenotypes. You will analyze DNA and RNAseq data to dissect the genetic architecture of gene expression evolution in mouse tissue models. You will have the opportunity to develop independent research ideas within our mouse in vitro cross framework.

Requirements: You will have a PhD or equivalent degree in the areas of genetics, molecular biology or regenerative medicine. You should demonstrate expertise and experience in tissue engineering techniques. We are looking for a strong track-record and demonstrated excellence in creative and interdisciplinary thinking. A strong bioinformatics or statistical background will be advantageous. A background in evolutionary biology will be helpful, but not a requirement. We are interested in candidates who are keen to apply and develop new genetic tools and technologies. Passion for research, team spirit and enthusiasm are essential.

Our Team: You will work in a multidisciplinary team that focuses on mammalian EvoDevo, combining population and comparative genomics with molecular biology and tissue engineering techniques to study the evolution of gene regulatory network in mouse and its close relatives. Our research group is funded by the European Research Council (ERC) and the Max Planck Society and is located on the Max Planck Campus in Tübingen, Germany. Tübingen is one of the best locations in the world in evolutionary genomics research. Our campus hosts world-class research groups, including a Nobel laureate and 11 other ERC-funded teams. We operate state-of-the-art sequencing and other core facilities. English is the working language. All seminars and communications are in English.

Our Offer: The position is available for an initial 2 years with the possibility of extension. Salary and benefits are according to the German public service pay scale (TVöD Bund up to and including E13) and are commensurate with training and experience.

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

For more information please see: http://fml.tuebingen.mpg.de/chan-group/open-positions
To Apply: Consideration of applications will begin on June 15th 2015, and will remain open until filled. Please send your application with 1. a statement of research interests and why you have applied for this position, 2. your CV, and 3. three reference letters to Dr Frank Chan at frank.chan@tue.mpg.de or the postal address below. Incomplete applications will not be considered.

Dr. Frank Chan

Friedrich Miescher Laboratory of the Max Planck Society

Spemannstrasse 39

72076 Tübingen

Germany

Please see related posts for other positions.

–

Frank Chan Max Planck Research Group Leader Friedrich Miescher Laboratory of the Max Planck Society Spemannstrasse 39 72076 Tübingen Germany

T: +49 (0)7071 601 888 F: +49 (0)7071 601 801 @: frank.chan@tue.mpg.de http://www.fml.tuebingen.mpg.de/chan-group.html Frank Chan <frank.chan@tue.mpg.de>

MfN Berlin TheoreticalPopGenetics

Postdoctoral position in Theoretical Population Genetics

A postdoctoral position in Theoretical Population Genetics is available at the Museum of Natural History in Berlin. The postdoc will participate in research related to the Germany-wide Priority Program "Rapid Evolutionary Adaptation" funded by the German Research Foundation (DFG).

The specific project focuses on the role of polygenic selection in fast adaptation. It involves the mathematical analysis of a multi-locus model of a quantitative trait that is subject to stabilizing selection and mutation. We will study the response to selection after an environmental shift of the trait optimum. Furthermore, we construct statistical tests to detect the signatures of polygenic selection in the genome. Our recent publications on these topics include:

Stephan, W. (accepted): Signatures of positive selection: from selective sweeps at individual loci to subtle allele frequency shifts in polygenic adaptation. Molecular Ecology.

Jain, K. and W. Stephan (2015): Response of polygenic traits under stabilizing selection and mutation when loci have unequal effects. G3-Genes Genomes Genetics 5: 1065-1074.

Wollstein, A. and W. Stephan (2014): Adaptive fixation in two-locus models of stabilizing selection and genetic drift. Genetics 198: 685-697.

Pavlidis, P., D. Metzler, and W. Stephan (2012): Selective sweeps in multi-locus models of quantitative traits. Genetics 192: 225-239.

We seek a very highly motivated colleague with a strong record of accomplishments from her/his PhD work. Ideally, applicants should have a strong background in population genetics, computational biology and statistics.

The research group of Wolfgang Stephan will relocate to the Museum of Natural History (MfN) Berlin this fall. MfN is located in the middle of Berlin on a vibrant campus of bioscience institutes of the Humboldt University and various other institutions with a broad interest in evolutionary and theoretical biology.

The postdoc will receive a salary according to the German pay scale (100% E13 TV-L). Interested candidates should send a CV, statement of interest, and contact information of three potential referees as a single PDF file to Prof. Wolfgang Stephan (stephan@bio.lmu.de).

Website: http://evol.bio.lmu.de Review of applications will begin on July 30, 2015 and will continue until the position is filled.

"hutter@zi.biologie.uni-muenchen.de"

MonashU PhytoplanktonEvolution

A two year postdoc in phytoplankton biology (with an option for a further 2 years) are available in the Marshall group. See http://jobs.monash.edu.au/-jobDetails.asp?sJobIDs=536209&lCategoryID=-641%2C+640%2C+636&lBrandID=&lWorkTypeID=-&lLocationID=&stp=AW&sLanguage=en for details

Prof. Dustin Marshall School of Biological Sciences Monash University, Clayton Campus Victoria, Australia, 3800 Ph: +61 (3) 9902-4449

"dustin.marshall@monash.edu"
<dustin.marshall@monash.edu>

NatlTaiwanU FishEvolution

Post-doc research associate position on evolution of ray-finned fishes at Institute of Oceanography, National Taiwan University

One to two new post-doc (and/or research assistant) positions (one year contract; renewable for another year) are currently available in Dr. Wei-Jen Chen's lab, Institute of Oceanography, National Taiwan University. Our research group focuses on three research axes (1) Phylogeney of ray-finned fishes at both large and small evolutionary time scales; (2) Evolutionary genomics, particularly the species diversification in relation to gene duplication; (3) Biogeography (historical biogeography and comparative phylogeography) of the Indo-West Pacific fishes. We are seeking for a post-doctoral researcher with interest/expertise in these three research axes (specially, the third one). The successful applicant will involve in high throughput generation and analysis of genetic/genomic data of ray-finned fishes. Our currently confusing species/groups for the studies are from the Percomorpha, Lethrinidae (preferable), Pomacentridae, and Sciaenidae. Candidates are welcome to suggest other species or group of fishes of his/her interest as models for the study. A good knowledge on fish taxonomy will be helpful, but not very necessary for conducing the studies. The ideal candidate should have experience with molecular genomics and/or bioinformatics. However, candidates with research experience in any the following will be considered in priority: next generation sequencing; statistical phylogeography (involving coalescence theory, e.g.); applied methods in likelihood and Bayesian statistics (e.g., BEAST) to evolutionary biological studies. Finally, interested candidates should be highly motivated, organized, and independent for the lab work, and willing to board on research vessel and/or go to remote islands for conducting prospective fieldwork for taxon sampling.

Applicants should email a brief cover letter describing research interests/experiences, a CV, and the names and contact information for 2-3 references to wjchen.actinops@gmail.com. A brief research proposal and scans of candidate's diploma/certificate of working experience will be required from the final selected candidate for processing the official request of the position from the Ministry of Science and Technology, Taiwan. This process will take around 1~2 months. Review of applications will begin immediately and continue until the position is filled. The starting date (negotiable) for the positions is expected to be on the first August 2015. For more information, visit our Lab website (https://sites.google.com/site/wjchenactinops/) or contact by email.

- 02 June 2015

Wei-Jen Chen Associate Professor

Room 301 Institute of Oceanography National Taiwan University No.1 Sec. 4 Roosevelt Rd. Taipei 10617, Taiwan

Phone: 886 (0)2 3366-1630 Email: wjchen.actinops@gmail.com Web: http://sites.google.com/site/wjchenactinops/ Wei-Jen CHEN <wjchen.actinops@gmail.com>

OregonStateU EvolutionaryGenomics

The laboratory of Dee Denver in the Department of Integrative Biology at Oregon State University is seeking a new postdoctoral scholar to join our team. The position is to perform research on a NSF-funded project that examines compensatory evolutionary responses to mitochondrial dysfunction using experimental evolution approaches and next-gen sequencing in C. elegans and C. briggsae.

Initial funding is for one year, with the possibility of extension for another year. We are looking for someone with strong interest in evolutionary questions, solid bioinformatic skills, and strengths in bringing projects to completion (i.e., publication).

The job is immediately available. We are ideally looking for someone who can start by the end of summer.

Contact Dee directly by email if you are interested in the job or would like more information:

denver@cgrb.oregonstate.edu

Initial email inquiries should include a CV attachment and 1-2 paragraph about the candidate's interest in the job.

You can learn more about the Denver lab here:

http://denverlab.weebly.com/ you can learn more about OSU Integrative Biology here:

http://ib.oregonstate.edu/ – Dee R. Denver Director Molecular and Cellular Biology Program Associate Professor Department of Integrative Biology Oregon State University

"denvedee@cgrb.oregonstate.edu" <denvedee@cgrb.oregonstate.edu>

OxfordU 2 AvianEvolution

Research Fellowships on avian evolutionary biology at Oxford University Up to two Research Fellowships are available to be held at the Edward Grey Institute, Department of Zoology, University of Oxford, from October

2015. The fellowships are open to applicants from any nationality, and in any area of research using birds as a model system to address questions in the broad fields of behaviour, ecology and evolution. Preference will be given to candidates whose research integrates across two or more of these fields. Applications are invited from candidates with up to 4 years postdoctoral experience at 1 October 2015; the successful candidates will hold a PhD and research specialisation in a relevant field.

Details here: http://www.zoo.ox.ac.uk/jobs/-list#job_118386 Closing date is noon on 22 June.

Tommaso Pizzari <tommaso.pizzari@zoo.ox.ac.uk>

Oxford Vietnam InfluenzaDengueEvolution

Post-doctoral Position in the Evolutionary Epidemiology of Dengue Virus and Influenza Virus. University of Oxford. Based full-time in Vietnam.

An exciting opportunity has arisen for a Postdoctoral Mathematical Modeler or Mathematical Epidemiologist based in Vietnam working at the Oxford University Clinical Research Unit in Ho Chi Minh City. We are seeking an experienced, self-motivated, analytically-minded postdoctoral research scientist that (1) has a quantitative background in modern methods in mathematical epidemiology, disease dynamics, and model-fitting, and (2) wishes to use this opportunity to build a research team around their own research questions.

The initial parts of the research project will focus on analyzing "antibody time series" of infectious disease, which we hope to use to reconstruct the entire epidemiological and evolutionary history of dengue virus and influenza virus circulating in southern Vietnam. We have been performing continuous general-population serum collections in southern Vietnam since 2009, and microarray-based assays have begun to convert this serum collection into a time series of antibody measurements. We are currently working on the initial methods development to perform inference in this complex system, and we are seeking a posdoctoral fellow to lead parts of this effort. Candidates should have a PhD focused on mathematical modelling, quantitative biology, disease dynamics, big data analysis, statistics, biostatistics, or a related field, experience in a programming language like C++, Java, Python, or similar and proven ability to work collaboratively.

The position is available on a full-time basis for 2 years in the first instance, with a possibility for renewal for candidates that seek to use this opportunity as a jumping off point to start their own research groups.

Starting salary: $46,000 - $57,000, depending on experience (plus benefits, plus overseas allowances to cover living expenses in Vietnam)

Start date: flexible, mid-2015 to early-2016.

The candidate will work with Dr Maciej Boni's research group. See:

http://mol.ax http://www.tropicalmedicine.ox.ac.uk/-maciej-boni Official Oxford job advert is posted here:

http://j.mp/1F63wd0 Only applications received before 12.00 midday on Monday 6 July 2015 will be considered.

Contact Bethany Valentine (tropical-personnel@ndm.ox.ac.uk) or Maciej Boni (maciej.boni@ndm.ox.ac.uk).

Maciej F Boni <mboni@oucru.org>

PennState EcolEvolutionaryGenomics

Postdoc ad below. I'll be at Evolution (Brazil), ESA (Baltimore), & Plant Genome Evolution (Amsterdam in September) this summer for anyone interested in meeting in person.

A postdoc position is available in the lab of Jesse R. Lasky (laskylab.org) in the Department of Biology at The Pennsylvania State University, University Park, PA. Lab goals are to understand the processes that generate and maintain biodiversity, with a focus on spatiotemporal variation in high-dimensional systems. In particular, the lab studies genetic and ecological mechanisms of local adaptation to environment. Furthermore, the lab will pursue connections between local adaptation and community ecology, conservation, and agriculture. The primary study organisms are plants; currently including forest trees, Arabidopsis, and sorghum. Penn State University has research strengths in genomics (https://www.huck.psu.edu/-content/people/area-of-interest/Bioinformatics and Genomics), plant biology (https://www.huck.psu.edu/-content/people/area-of-interest/Plant Biology), and ecology (https://www.huck.psu.edu/content/people/-area-of-interest/Ecology) across departments and colleges. The postdoc will have freedom to develop new projects in the lab and to build collaborations with other labs.The position requires a PhD in Ecology, Evolution, Genetics, Plant Biology, Statistics, or a related field. The ideal candidate will have experience including population/landscape genomics, analysis of sequence data, GWAS methods, statistics, and computation (R, python, shell, HPC cluster). Complementary expertise in molecular biology, ecophysiology, and ecology is also of interest, but not required. Excellent communication skills, including writing, are required, as is a strong publication record. Applications must be submitted electronically at https://psu.jobs/job/58109 and include a cover letter detailing experience and research interests, a current CV, and contact information for three professional references. The position is initially funded for one year, with possibility of refunding. Anticipated start date is Fall 2015, but this is flexible. Review of applications will begin on June 15, and continue until the position is filled.

CAMPUS SECURITY CRIME STATISTICS: For more about safety at Penn State, and to review the Annual Security Report which contains information about crime statistics and other safety and security matters, please go to http://www.police.psu.edu/clery/, which will also provide you with detail on how to request a hard copy of the

Annual Security Report. Penn State is an equal opportunity, affirmative action employer, and is committed to providing employment opportunities to all qualified applicants without regard to race, color, religion, age, sex, sexual orientation, gender identity, national origin, disability or protected veteran status.

Job URL: https://psu.jobs/job/58109 "jrl35@psu.edu" <jrl35@psu.edu>

TGAC Norwich PopGenetics

To apply for this job

- Either - Download, Save and Complete a copy of the application form < http://jobs.tgac.ac.uk/-application_form.docx > using Microsoft Word Or - Prepare a copy of your CV that contains all the information requested in the application form - Submit your application document (single file in word or acrobat format) together with your Personal details, Referees and Equal Opportunities Monitoring data

---

The Genome Analysis Centre

The Genome Analysis Centre (TGAC) is a vibrant, contemporary research institute and registered charity, working in an area of rapid technological development and innovation.

TGAC is strategically funded by the BBSRC to lead the development of a skill base in bioinformatics and a genomics technology platform for UK bioscience. The Institute is located on the Norwich Research Park, together with its partners: the John Innes Centre, the Institute of Food Research, The Sainsbury Laboratory, the University of East Anglia and the Norfolk and Norwich University Hospital. The research park has an excellent reputation for research in plant and microbial sciences, interdisciplinary environmental science and food, diet and health, to which TGAC contributes strengths in genomics and bioinformatics. Close links exist between the NRP partners and new opportunities for collaboration in exciting new initiatives are under development. The NRP recently received £26M of government investment to facilitate innovation and further develop infrastructure to attract science and technology companies to the Park to enhance the vibrant environment and realise economic impact from research investment.

TGAC is a UK hub for innovative Bioinformatics through research, analysis and interpretation of multiple, complex data sets. It hosts one of the largest computing hardware facilities dedicated to life science research in Europe. This has been boosted recently by an e-Infrastructure grant to expand the data storage capacity to a multi-petabyte unit, deploying a high performance cluster and large-memory server enabling the allocation of processes requiring several terabytes of computing memory.

TGACs state of the art DNA sequencing facility operates multiple complementary technologies for data generation that provide the foundation for analyses furthering our fundamental understanding of genomes and how they function. We aim to be at the forefront of technological advances and are developing and implementing technologies to generate and analyse new types of data. We also develop novel platforms to provide access to computational tools and processing capacity for multiple academic and industrial users and promoting applications of computational bioscience. TGAC has one fully owned subsidiary, Genome Enterprise Ltd (GEL) via which it offers genomic and bioinformatics services on a trading basis and works with commercial providers on a partnership basis. TGAC also receives specific funding to enable knowledge exchange programmes which are supported across the institute teams.

< http://www.direct.gov.uk/en/DisabledPeople/-

Employmentsupport/LookingForWork/DG_4000314 >

< http://theukrc.org/ >

---

*Post Number*1002863 *Job Title*Post Doctoral Scientist *Closing Date*19 Jun 2015 *Grade*SC6 *Starting Salary*£29,500 - £32,780 *Hours per week* 37 *Project Title* Applying genomics-driven surveillance to the wheat yellow rust pathogen *Expected/Ideal Start Date* 01 Jul 2015 *Months Duration* 36 *Main purpose of the job* A postdoctoral position is available in the Saunders group at The Genome Analysis Centre in partnership with the John Innes Centre, Norwich, UK. The appointee will apply a field pathogenomics approach, which was developed in the Saunders group, to undertake comprehensive global population genetic analyses of the wheat yellow rust pathogen (Hubbard et al., Genome Biology 2015, 16:23). This pathogen poses a significant threat to wheat production in all major wheat-growing areas of the world and has recently re-emerged as a major constraint on UK agriculture. The appointee will generate next-generation sequencing datasets from infected field samples and explore associations and track pathogen dispersal on a national and international scale. This is a very exciting opportunity for the applicant to join a multi-national and multi-institutional project to address key questions in pathogen evolution, dispersal and adaptation. *Department* Genomics *Group Details* The Saunders group works on a variety of emerging and re-emerging plant pathogens using a broad array of techniques that include molecular genetics, biochemistry, cell biology, genomics, transcriptomics and data

— / —

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

---

Tokyo 10 OriginOfLife

Postdoctoral fellowships in interdisciplinary research relating to origins of life, spending 50% of time in Tokyo, Japan

The ELSI Origins Network (EON) announces the availability of post-doctoral research fellowships for research related to the Origins of Life. Ten two-year positions will be funded, to take place within the period 2016-2018.

Successful candidates will split their time between the Earth-Life Science Institute (ELSI) in Tokyo and another institution of the candidates choice, anywhere in the world. The fellowship will pay a salary for two years, which covers the time spent at both locations, as well as a generous research budget. The positions will start on or before 1st April 2016.

EON (eon.elsi.jp) is an interdisciplinary international network which seeks to foster dialogue and collaboration within the Origins of Life community to articulate and answer fundamental questions about the nature and the reasons for the existence of life on Earth, and possibly elsewhere in the Universe. Its goal is to bring together leading-edge research in all areas of the physical, mathematical, computational, and life sciences that bears on the emergence of life. ELSI is chartered as a Japanese World Premier International Research Center, to study the origin of Earth-like planets and the origin of life as inter-related phenomena. ELSI is located at the Ookayama campus of Tokyo Institute of Technology.

EON-supported research addresses three overarching questions:

1. How did life emerge on Earth?

2. How common is life in the universe?

3. What fundamental principles explain the emergence of life?

Due to the split-time nature of these fellowships, the application process requires the applicant to choose a supervisor and host institution outside ELSI who will support the proposal. EON is designed to promote collaboration across disciplinary boundaries, and host institutions in all fields are welcome.

The goal of the fellowships is cross-fertilization between specialists in Origin of Life research around the world, with a central collaborative hub at ELSI. EON aims to build a research community in which postdoctoral fellows benefit from facilities not only at ELSI but also among the centers throughout the network.

The first deadline for applications is August 1st 2015, with a second deadline on 1st October to fill any remaining places. Please check our web site for more details, including the application procedure.

Details of the fellowships are as follows, with further details available on our web site.

*Duration *- 2 years, with a start date no later than April 1, 2016.

*Salary *- USD 70,000.00/yr. (approximate equivalent, paid in JPY.)

Research Budget - USD 30,000.00/yr. (approximate equivalent, paid in JPY.)

For more details, including the application procedure, please visit *eon.elsi.jp* < http://eon.elsi.jp/ >

Bet^{1}l Kacar <betulkcr@gmail.com>

UAmsterdam PalmMacroevolution

POSTDOCTORAL RESEARCHER IN MACROEVOLUTION AND FRUGIVORY OF PALMS

Faculty of Science, Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam

A 3-year Postdoc position in macroevolution and frugivory of palms is now available in my macroecology & biodiversity lab (www.danielkissling.de) at the Institute of Biodiversity and Ecosystem Dynamics (IBED) of the University of Amsterdam. The position will be in collaboration with Jens-Christian Svenning (Aarhus University, Denmark), William Baker (Kew, UK), and Thomas Couvreur (Montpellier, France).

Applications should include a short cover letter, a detailed CV, and the names and contact addresses of two referees. Please submit applications until 26 Juli on the following page:

http://www.uva.nl/over-de-uva/werken-bij-de-uva/-vacatures/item/15-226.html The aim of this project is to investigate how frugivory-relevant plant traits (e.g. fruit size, fruit color, fruit shape etc.) are distributed within the palm family (Arecaceae), how this relates to diversification rates, and whether and how it coincides with the global biogeographic distribution of vertebrate frugivores (birds, bats, primates, etc.) and their ecological traits (e.g. diet specialization, body size, flight ability, color vision etc.).

I am looking for a talented young scientist with an interest in macroevolution and macroecology. The successful candidate should have excellent quantitative skills in phylogenetic comparative methods, plant functional traits, phylogenetic and biogeographic reconstruction, handling of large datasets, and models of trait evolution and diversification. Further background in spatial analysis, statistics and R programming is beneficial. The candidate must have a compelling publication record in international journals and an interest to work both independently and in teams.

Dr. W. Daniel Kissling Associate Professor for Quantitative Biodiversity Science Institute for Biodiversity and Ecosystem Dynamics (IBED), University of Amsterdam P.O. Box 94248, 1090 GE Amsterdam, The Netherlands Email: wdkissling@gmail.com <danielkissling@web.de> Phone: +31 (0)20 525 8423 Homepage: www.danielkissling.de Course coordinator “Biodiversity & Global Change” http://-studiegids.uva.nl/xmlpages/page/2015-2016-en/search-course/course/16029 Scientific coordinator GLOBIS-B http://www.globis-b.eu/ Subject Editor Ecography http://www.ecography.org/ wdkissling@gmail.com

---

UAntwerp EvolEcol InfectDisease Conservation

We will welcome and give full support to postdoc applications for a Marie Curie fellowship (deadline 10 september 2015) in the fields of evolutionary ecology, infectious disease ecology and conservation biology. We particularly welcome applications related to evolutionary ecology of host-parasite interactions, ecology of infectious diseases, movement ecology (dispersal, connectivity, invasive species) and landscape genomics. We are a dynamic and internationally oriented research group with three Faculty members (Herwig Leirs, Erik Matthysen, Stefan Van Dongen), several postdocs and 10-15 PhD students. Our main model systems are birds and mammals, including their parasites and infectious diseases, in both temperate and tropical systems. We combine field research with state-of-the-art modelling and molecular approaches. We are core members of two of the nine currently recognized Excellence Consortia in the University of Antwerp (Global Change Ecology and Infectious Diseases).

We will be happy to discuss possible projects and assist candidates with applications for Marie Curie funding, as well as other funding options such as FWO postdoctoral fellowships. For more information on our projects and job opportunities, see our website at www.uantwerpen.be/eveco . Erik

Prof. Dr. Erik Matthysen Evolutionary Ecology Group University of Antwerp Groenenborgerlaan 171, B-2020 Antwerpen 03 265 3464

Matthysen Erik <erik.matthysen@uantwerpen.be>

UColorado EvolutionaryBioinformatics

Postdoctoral Position Available in Evolutionary Bioinformatics / Comparative Transcriptomics

Description: A 2-year, NSF-funded postdoctoral position in Evolutionary Bioinformatics / Comparative Transcriptomics is available in the Department of Ecology and Evolutionary Biology at The University of Colorado, Boulder. The successful candidate will be expected to generate, assemble, and annotate transcriptomes from the flowers of a minimum of 48 non-model plant species, in order to investigate the genomic basis (structural, regulatory) of flower color evolution (additional research on the impacts of epigenetic mechanisms of floral color evolution may be possible pending time and funding). Specifically, this research targets evolution of the Anthocyanin Biosynthetic Pathway. Candidates should have previous experience with large-scale genome or transcriptome sequencing, proficiency in necessary programming languages (e.g., PERL, R), and experience in quantification of gene expression or co-expression networks. The candidate will be expected to contribute to supervision of lab personnel and help coordinate basic activities in the PIs lab including reagent ordering and stocking. The position will remain open until filled.

Qualifications: (1) A PhD in bioinformatics, genomics, evolutionary biology, computational biology, molecular biology, or related discipline (2) Strong publication record that includes multiple first-authored publications in the field, and overall high proficiency in scientific writing (3) Familiarity with concepts in evolutionary biology (4) Proficiency in analytical, quantitative, and computational methods with respect to management of next-generation sequence data, including programming abilities (5) Experience in both the generation of and analysis of transcriptome datasets, preferably on non-model organisms (6) Experience preparing graphical visualizations of data

Start Date: Fall or Winter 2015, with some flexibility

To Apply: Please email your cover letter, curriculum vitae, up to three publications (first author publications preferred) and names and contact information for three references to Heather Stone (heather.blair.stone@gmail.com). Please bundle all items into a single PDF. Specific questions regarding the research project should be directed to Erin Tripp (erin.tripp@colorado.edu) prior to applying.

Thanks, Erin Tripp

Assistant Professor, Department of Ecology & Evolutionary Biology Curator of Botany, Museum of Natural History (COLO Herbarium) University of Colorado, Boulder C105 Ramaley Hall, Campus Box 334 Boulder, CO 80309-0350 phone: 303.492.1862 <tel:303.492.1862> (EBIO) phone: 303.492.2462 <tel:303.492.1862> (Herbarium) fax: 303.492.0823 (or 4195 <tel:303.492.4195>)

erin.tripp@colorado.edu

UGeorgia 2 PlantGenomics

Dear All,

Two postdoctoral positions are available as part of a collaborative project between the labs of John Burke and Lisa Donovan at the University of Georgia. These positions will involve the genomic and physiological analysis of abiotic stress responses in cultivated sunflower and related wild sunflower species. The ideal candidates will have a strong background in one or more of the following areas: population/quantitative genetics, genomics, bioinformatics, plant ecophysiology, stress physiology.

Funds are anticipated to support these positions over multiple years with a preferred start date of January 2015. Review of applications will begin immediately and will continue until the positions are filled. To apply, please send your CV, a brief statement of research interests, and the names and contact information for three references to: jmburke@uga.edu and ldonovan@uga.edu. Informal inquiries are also encouraged.

For more information about the UGA Department of Plant Biology, please visit:

http://www.plantbio.uga.edu/. Information on the Burke lab can be found at:

http://www.theburkelab.org/. Information on the Donovan lab can be found at:

http://www.plantbio.uga.edu/directory/lisa-donovan .

– Lisa Donovan Professor Department of Plant Biology University of Georgia Athens, GA 30602

chasemason.evolution@gmail.com

UGeorgia ComparativeProtistGenomics

The Kissinger Research Group is seeking an energetic, organized, critical thinker to address research projects related to the evolution of apicomplexan parasites e.g. Plasmodium (the causative agent of malaria), Toxoplasma and Cryptosporidium). The position is at the post-doctoral level. Our research group is located at the University of Georgia in Athens, GA (about 60 miles outside of Atlanta). There is some flexibility associated with this position but it is expected to focus primarily on aspects of comparative genomics including population genomics, genome architecture evolution and/or the evolution of gene regulatory networks across the phylum. The group website including a listing of research interests and publications can be found at: http://mango.ctegd.uga.edu/jkissingLab/ The research group is composed of three sub-groups: staff who work on the NIH-funded Bioinformatics Resource Center EuPathDB http://eupathdb.org/eupathdb/ ; staff who work on the NIH-funded Malaria Host-Pathogen Interaction Center, MaHPIC http://www.systemsbiology.emory.edu/ ; and students from the Institute of Bioinformatics and Department of Genetics working on aspects of apicomplexan genomics. Our Research Group maintains a collaborative and supportive working environment in which we mentor and train each other. An ability to work as a part of a group and mentor others is essential.

Qualifications: A Ph.D. in a computational or biological science. An ability to program in some language (PERL, Python and/or JAVA) is required; Experience with Omics-scale analyses on some sort of genomic or functional data and an interest in molecular evolution are required. Familiarity with LINUX and R is strongly encouraged. Experience with molecular and genomic methodologies (wet lab) is a plus.

Salary: Commensurate with qualifications and not less than NIH guidelines. The position is available immediately.

Applications: Please email a completed application containing the following components to jckadmin@uga.edu: 1) CV 2) A two-page summary of your major research accomplishments with an explicit discussion of their significance and a statement of how your future research interests intersect with the interests of the Kissinger Research Group 3) The names and contact information for three references including a statement of the capacity in which they know you and your work.

The University of Georgia is an Equal Opportunity/Affirmative Action employer. All qualified applicants will receive consideration for employment without regard to race, color, religion, sex, national origin, disability, gender identity, sexual orientation or protected veteran status.

“jkissing@uga.edu” <jkissing@uga.edu>

UHelsinki EvolGenomics

Post-doc position in Evolutionary Genomics (1 year)

A 1-year post-doctoral position is available at the University of Helsinki, Finland to work in Prof. Juha Merila’s research group (Ecological Genetics Research Unit; www.helsinki.fi/biosci/egru). The research component of the position is focused on genetic differentiation in time and space using two model systems: sticklebacks and European flounders. The stickleback research aims to detect genetic responses to environmental changes in the Baltic Sea. Historical samples from museum collections will be analyzed in order to identify adaptive evolutionary changes in response to the natural and human-induced alteration of environmental conditions in the Baltic Sea. Although the three-spined stickleback is the main model, a comparative angle can be incorporated by integrating analyses of the closely related nine-spined stickleback. The flounder research aims to identify the presence and prevalence of genes associated with life history differences between the two types of flounder “demersal and pelagic” using high-throughput approaches. The work will be co-funded by Maj & Tor Nessling foundation and the University of Helsinki.

Suitable candidates are independent, adaptable and strongly committed to science. A strong background in evolutionary genetics or genomics is required. Experience with genomic methodologies (both wet-lab and bioinformatic in particular) is an advantage, as is experience with DNA extraction from museum collections.

Informal inquiries can be directed to Prof. Juha Merila (juha.merila@helsinki.fi). Formal applications including a CV, publication list and names (and contact details) of at least two referees, together with a letter of motivation (max. 2 pages) can be submitted to:

The deadline for applications is August 1 2015, with the preferred starting date being September 2015. The position is available for one year from the starting date. The salary is approx. 2800-3000 EUR per month. Most of the salary is provided by the Maj & Tor Nessling Foundation.

.More information about Helsinki, University of Helsinki, and Department Biosciences can be found from the following links: http://www.helsinki.fi/en/index.html (city) http://www.helsinki.fi/university/ (university) http://www.helsinki.fi/biosciences/ (department) http://www.helsinki.fi/intstaff/ (University of Helsinki International Staff Services)

Juha Merilä <juha.merila@helsinki.fi>

UMaryland Phylogenetics

The University of Maryland

Applications are invited for a Postdoctoral Associate position at the University of Maryland Institute for Bioscience and Biotechnology Research (IBBR).

Position Summary

Because species phylogenies (trees) are so widely used in the life sciences, there has been a major worldwide effort to determine trees for various groups and assemble them into a grand "Tree of Life" or ToL. While experts continue improving the ToL, our focus is on getting this knowledge into the hands of scientists, educators, and the general public, so that they can get online species trees as easily as they get online driving directions. In preliminary work, we organized community hackathons at which participants prototyped a web-services system, called "Phylotastic" (www.phylotastic.org), that aims to provide an open, distributed, community-owned system for efficient delivery of ToL knowledge. NSF recently funded a 3-year collaborative project to develop production system based on this prototype. Responsibilities will include participating in the design process, developing tools for specific use-cases (including educational ones), and playing a key role in software evaluation. The successful applicant will be part of a distributed, collaborative team including key personnel from IBBR, NMSU, UTK, OpenTree and GlobalNames.

Qualifications:

A Ph.D. in a relevant discipline is required. Understanding how and why scientists use phylogenies is critical. Typically this knowledge will come from research experience using phylogenies. Experience in scientific software programming is strongly preferred. Experience programming with phylogenies, or with web services, is desirable.

Salary: Commensurate with qualifications.

Applications: Applicants should send a (1) cover letter (include skills, suggested start date, and expected PhD date as needed); a (2) CV; (3) a short research statement; (4) Contact information for two references; and (5) link(s) to repositories with examples of code you have written or attachments including such code to: https://ejobs.umd.edu/postings/33884 Pre-submission inquiries are encouraged

Closing Date: Review of candidates will begin on 06/20/2015 and will continue until the position is filled.

The University of Maryland, College Park, actively subscribes to a policy of equal employment opportunity, and will not discriminate against any employee or applicant because of race, age, sex, color, sexual orientation, physical or mental disability, religion, ancestry or national origin, marital status, genetic information, political affiliation, and gender identity or expression. Minorities and women are encouraged to apply.

Rita Varela <rvarela@umd.edu>

UMissouri StLouis PlantMolecularPhylogenetics

I am looking for a postdoctoral researcher to join my lab at the University of Missouri - St. Louis. The project involves constructing a species-level phylogeny for the Neotropical genus Burmeistera (Campanulaceae) using next-generation sequencing approaches ('Hyb-Seq', targeting low-copy nuclear regions with enrichment probes and genome-skimming for plastomes). Results will be used to test the relative roles of pollinator-mediated reproductive isolation and gametic isolation (post-pollination yet prezygotic) in the diversification of Burmeistera. Candidates should have experience with plant molecular phylogenetics, including labwork and bioinformatics analysis of next-gen data, and an interest in plant speciation and/or pollination biology. Successful applicants will also be encouraged to also carry out his or her own research projects related to work done in the Muchhala Lab (see www.umsl.edu/~muchhalan). The start date for the position is flexible, from August of 2015 to January 2016. Funding is available for one year with renewal for a second year given satisfactory progress.

St. Louis is a vibrant Midwestern city that boasts an exceptional quality of life, combining a low cost of living with a variety of cultural attractions including parks, museums, and lively music and art scenes. The University of Missouri - St. Louis has strong local ties with the Missouri Botanical Garden, the Saint Louis Zoo, Washington University, St. Louis University, and the Donald Danforth Plant Science Center, and annual retreats (sleec.weebly.com) bring together ecologists and evolutionary biologists from these and other local institutions. The Department also houses the Whitney R. Harris World Ecology Center, established to promote international research, particularly in tropical regions.

Review of applications will begin on July 15th. Informal inquiries should be emailed to muchhalan@umsl.edu (I will also be at Evolution 2015 in Brazil if you want to discuss in person). Submission online at http://-www.umsl.jobs. Applicants must combine application materials, including 1) a short statement (one to two pages) on previous experience, research interest, and motivation for applying, and 2) a curriculum vitae, into a single PDF or Microsoft Word document and upload as a resume attachment. Additionally, have three recommendation letters sent to muchhalan@umsl.edu. For questions about how to apply, please call (314) 516-5258, or if you are experiencing technical problems, please email pshrsupport@umsystem.edu.

UMSL is an Equal Opportunity/Access/Affirmative Action/Pro Disabled & Veteran Employer

– Nathan Muchhala, Ph.D.

Assistant Professor Department of Biology University of Missouri -St Louis One University Blvd, R428 Research Hall St Louis, Missouri 63121 (314) 516-6672 http://-www.umsl.edu/˜muchhalan/ muchhalan@umsl.edu

---

UNAM-Mexico Bioinformatics

Postdoc Position: Bioinformatics and Evolutionary Genomics at Universidad Nacional Autonoma de Mexico

We have an opening for a postdoctoral position at the Instituto de Ecologa, UNAM, Mxico, which is granted based on academic merits and Curriculum vitae among a pool of candidates. We are seeking for a candidate with knowledge and skills in Bioinformatics and, specifically, should have proven experience with bioinformatic analyses of genomic SNPs data; also, should have the knowledge of the molecular laboratory techniques and processes needed to prepare DNA samples for SNPs development. The candidate will work in the lab of Dra. Ella Vzquez- Domnguez. In general, we work with population and landscape genetics, phylogeography and conservation of vertebrate species. The specific projects we are now developing that include SNPs data analyses involve reptile species (e.g. crocodiles and turtles) but will grow to more species. Projects include landscape genetics and adaptation questions, to be evaluated within a genomics framework.

The successful candidate will play a key role in the generation and analysis SNPs, but also: 1) participate in field work within Mexico; 2) help graduate students with software and analyses; 3) give a seminar for the Institutes community, 4) help organize and participate in Bioinformatics courses or workshops for genetic data analyses.

The postdoctoral scholarship is a UNAM grant, with a salary of approximately $1,300 US dlls per month.

Candidates need fulfill the following:

1. The postdoctoral position would start between September-October 2015, for a year with possibility of renewal for a second year pending on results.

2. The candidate must have obtained his/her PhD degree no more than five years before the starting date (i.e. if starting on 1 September, PhD must have been obtained on 1 September 2010 the earliest).

3. Should have proof of experience with published work in scientific journals

4. Communication skills in Spanish

Applications must include a complete CV, a pdf of the PhD grade, pdf of the front page of passport (if not of Mexican nationality), pdf of birth certificate, a cover letter briefly outlining the candidate's fit to the position and contact information for three references.

All information should be sent directly to Dra. Ella Vzquez-Domnguez, at evazquez@ecologia.unam.mx (deadline 30 July 2015).

Ella Vzquez Domnguez

Instituto de Ecologa, UNAM Ap. Postal 70-275 Ciudad Universitaria Mxico DF 04510 Mxico Tel +5255 5622 9015 Fax +5255 5616 1976 Email: evazquez@ecologia.unam.mx http://-web.ecologia.unam.mx/laboratorios/evazquez/
Ella Vazquez <evazquez@ecologia.unam.mx>

UNamur Belgium Bioinformatics 2

LAST CALL for a Postdoctoral bioinformatician in Evolutionary genomics, UNamur, BE

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) at the 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 and with programming skills. The position is for 3 years starting preferably in July 2015.

The closing date for applications is 10th of June 2015.

Interested applicants should send a cover letter (briefly describing research experience, interests, and career goal), curriculum vitae (with list of publications), 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/ Universit???? de Namur ASBL Rue de Bruxelles 61 - 5000 Namur Belgique

Karine Van Doninck <karine.vandoninck@fundp.ac.be>

UNorthCarolina Greensboro HoneyBeeStress

POSTDOCTORAL RESEARCH POSITION IN HONEY BEE HEALTH AND SOCIAL EVOLUTION

The collaborative team of Dr. Olav Rueppell (University of North Carolina at Greensboro), Dr. David Tarpy (North Carolina State University), and Dr. Micheline Strand (Army Research Office) is seeking a scientist to head a research project on inducible stress defenses and hormesis in honey bees. The overall project goals are to assess the potential of inducible stress defense mechanisms to improve honey bee health and to test fundamental hypotheses of social evolution. The position at the University of North Carolina at Greensboro involves advanced apicultural experiments, bioassays, molecular tests, and functional genomic studies. Thus, a combination of field and laboratory work is anticipated.

The ideal candidate will hold a Ph.D. in life sciences and exhibit outstanding research promise. In addition, demonstration of a high level of scientific productivity, technical skills in apiculture, molecular biology, and/or functional genomics, and excellent English communication and organizational skills are desired. Upon final budgetary approval, the initial appointment will be made for one year, with the possibility of a two-year extension. Salary will depend on qualifications.

To apply submit statement of interest, CV, and contact information for 3 academic references through the University of North Carolina at GreensboroÂs JobSearch site at: https://jobsearch.uncg.edu/postings/2521 EOE AA/M/F/D/V

– Dr. Olav Rueppell Professor of Biology Univ. North Carolina at Greensboro 206B Eberhart Bldg. Greensboro, NC 27403, USA Tel.: (1) 336-256-2591 Fax: (1) 336-334-5839 http://www.uncg.edu/bio/faculty/-olav_rueppell/lab/index.html orueppell@gmail.com

---

UOulu Bioinformatics

The Faculty of Humanities of the University of Oulu, Finland, announces a three-year Postdoctoral Researcher Position in bioarcheological research community to start at 1 September 2015.

Description

Bioarchaeological research community (BARC) at University of Oulu, Finland, is looking for a talented and research-oriented postdoctoral researcher. This position is for three years. The postdoctoral researcher is expected to make a contribution to multidisciplinary research of this research community by bringing in expertise in biomolecular research, more specifically bioinformatics and computational genomics.

BARC examines the effects of environmental and cultural changes on both humans and animals in northern Europe focusing on Finland and neighboring regions. The effects of neolithization, modernization and urbanization are under particularly close scrutiny. The main study materials include archaeological materials (biological and non-biological materials), museum collections and clinical samples. A broad range of methods and techniques are thus utilized from those used in archaeological and historical research to those used in bone imaging and biomolecular research. Due to this multidisciplinary research, this research community includes four research teams divided between three faculties. The four research teams are as follows:

The Post-Pleistocene Evolution of Human Skeleton (Docent Markku Niskanen, Archaeology, Faculty of Humanities) utilizes osteometric and bone imaging techniques to examine temporal and geographic variation in human body size, body shape and skeletal robusticity and how these are related to environmental and cultural changes.

Bioarchaeology of human-animal interactions: biomolecular and osteoarchaeological analyses of human and animal bones (Prof. Jouni Aspi, Biology, Faculty of Science) explores human-animal relationships through ancient DNA (aDNA), stable isotope and osteological analyses.

Material culture and the modernization of the north (Dr. Timo Ylimaunu, Archaeology, Faculty of Humanities) examines the development of society from the medieval period to the present. The focus is on examining the dynamics of modernization, globalization and consumption processes and human-environmental relationship in Northern Fennoscandia as a part of the globalizing world.

Human Biology and Comparative Anatomy (Prof. Juha Tuukkanen, Anatomy and Cell Biology, Faculty of Medicine) concentrates on functional relationship in morphology between temporally distinct populations. The main research focus is temporal trends in overall skeletal morphology, bone microstructure and biomechanical properties.

The postdoctoral researcher is expected to carry out research and participate in publishing research results in peer-reviewed journals, and to co-supervise students. It is our hope that this position would help the postdoctoral researcher to develop his/her own scientific networks through research collaboration, and that this position would be a step towards a position as a more senior and independent researcher able to develop his/her own projects.

This position will be officially based at the Faculty of Humanities, University of Oulu, Finland. In practice, the postdoctoral researcher would work in facilities, which best suit his/her actual work for the BARC.

Qualifications

The candidate must have earned his/her doctorate no more than seven years before the application deadline. This doctoral degree should be in biological anthropology, biology, biomedicine, archaeology (mainly biomolecular archaeology) or a related field. In addition, he/she should have a record of scientific achievements (e.g. peer-review publications). International mobility and experience of teaching and/or academic supervision are advantages. In addition, we appreciate ability for independent research, high motivation and efficiency, as well as ability to co-operate and work as a research team member.

We are searching for a researcher, who is familiar with bioinformatics and computational genomics. Previous experience in handling NGS data using scripts and analysis pipelines is desirable. Other highly useful skills and/or experiences include computer programming, population genetics, wet lab analysis, genome assembly and annotation.

Salary

The salary of the postdoctoral researcher will be set on levels 5ÂV6 of the national salary scale for the teaching and research staff of Finnish universities. In addition, supplementary remuneration will be given for personal achievement and performance, the sum rising to a maximum of 46.3% of the salary scale. In practice, the salary will be about 3300 ÂV 4000 euro at the start of the period.

Applications

Applications, including any attachments, should be submitted using the electronic application form by 31 July 2015.

— / —

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

---

UOulu EvolutionaryResponseRadiation

Postdoctoral position to study evolutionary response to environmental radiation

The University of Oulu is an international scientific community, with 16 000 students and approximately 3 000 employees. The strenghts of the University are wide multidisciplinary study/research interests and modern research and study environment and good cooperation with international educational and research institutes. More information http://www.oulu.fi/english/ The following job is open in the University of Oulu:

Post-doctoral researcher, Department of Genetics and Physiology

A postdoctoral position for three years is available at the University of Oulu, Finland to work with Dr Phill Watts' research group (https://wiki.oulu.fi/display/~pwatts/Phill+Watts). The project will examine the genetic and genomic consequences of exposure to ionizing radiation in small rodents (principally bank voles, Myodes glareolus) that inhabit the area surrounding Chernobyl reactor 4, Ukraine. The project's emphasis is to determine the role of DNA protection and repair pathways. While we have many samples available for analysis, there are opportunities to visit Chernobyl site to collect more samples and to conduct field experiments to assess fitness of animals with different phenotypes. The successful applicant will contribute to future design of experiments and be part of an international team who are using their diverse skills and expertise to examine the eco-evolutionary consequences of exposure to environmental radioactivity. Members of the team include: Drs Zbyszek Boratynski, Eva Kallio and Tapio Mappes and Prof Heikki Penttilä (University of Jyväskylä, Finland), Prof JiÅí Fajkus (Masaryk University, Czech Republic), Prof Tim Mousseau (University of South Carolina, USA) and Prof Anders MÃller (Université Paris-Sud XI, France). The project is funded by the Academy of Finland.

Candidate should be highly motivated and have proven molecular-genetic expertise (e.g. DNA & RNA extraction, PCR, qPCR, RT-PCR, Western blotting) and be prepared to contribute to fieldwork, and handle and collect samples from small mammals. Experience of analysis of high-throughput sequencing data is an advantage.

The salary depends on the competence of the applicant, but likely will be level 5 of the national salary scale for teaching and research staff of Finnish universities. In addition, a supplementary remuneration will be given for personal achievement and performance, the sum rising to a maximum of 46.3 % of the salary scale. (The salary is expected to be around 3,400 euro/month). The position will be filled as soon as possible. The starting date is negotiable, but preferred to be by January 2016.

Applications should consist of (1) a letter of motivation (maximum 2 pages) and (2) a CV that includes a list of publications and the contact details of at least two referees. Applications should be submitted in English using the electronic application form by August 10, 2015.

For further information please contact Phill Watts (phillip.watts[at]oulu.fi).

"P.C.Watts@liverpool.ac.uk"
<P.C.Watts@liverpool.ac.uk>

UppsalaU PalaeobiologyEvoDevo

Two year post-doc in evolutionary palaeobiology or evo-devo, Uppsala

The Department for Earth Sciences in Uppsala university covers a wide range of research topics and Uppsala University is one of the foremost centres for palaeobiological research in Europe. A two year post-doctoral position is available from the autumn of 2015 (start date negotiable).

Description of subject area: We invite applications from all areas of palaeobiology and metazoan evolution of development. However, it should be noted that internal research funds for the position are likely to be limited unless the research of the applicant is related to one of the research groups in the programme (see http://-www.geo.uu.se/research/palaeobiology).

A maximum of 20% of full time teaching can be included in a post-doc position.

Eligibility: To be eligible for a position as Post-doc, the applicant must have been awarded a PhD or equivalent by the closing date. The applicants PhD degree should not have been obtained more than three years prior to the application date unless there are special circumstances, including periods of sick leave, parental leave etc, that are deducted from the three-year period. The requirement for this position is a PhD in an appropriate geological or biological discipline.

Ranking criteria: In ranking eligible candidates, special importance will be given to scientific skills in relation to the subject area. In filling this position the university aims to recruit the person who, in the combined evaluation of competence, skills and documented qualifications, is judged most suitable to carry out and develop the work-in-hand and to contribute to a positive development of the department.

How to apply: The application should be written in English and should include a short description of the applicant and his/her research interests. It should also include a CV including a publication list and the names of two referees.

Uppsala University is an equal opportunity employer and we encourage especially women to apply for the position.

Salary: An individual salary will be negotiated, although salary suggestions are should be included in the application.

Start date: Autumn 2015 (subject to negotiation).

Employment type: time-limited two year position.ââFurther information about the position can be obtained from Prof. Graham Budd (graham.budd@pal.uu.se).Â You are also welcome to contact the heads of research groups in the programme.

Welcome to submit your application no later than June 29 th, 2015, marked UFV-PA 2015/1464. Please use the link below to access the application form:

http://www.uu.se/en/about-uu/join-us/-details/?positionId=68943 Graham E Budd <graham.budd@pal.uu.se>

UQueensland StatisticalGenomics

I came from evolutionary biology into this field just over a year ago, and we are hoping to find more evolutionary biologists who want to do evolutionary biology research using human data.

The Centre of Neurogenetics and Statistical Genomics (CNSG) is based at the Queensland Brain Institute, The University of Queensland and focuses on research towards a better understanding of psychiatric disorders and motor neuron disease and on the development of underpinning computational and statistical analysis methods. The Centre is led by an Executive Team comprising Professors Peter Visscher and Naomi Wray and A/Professor Jian Yang.

Up to 5 positions full-time, fixed term appointments at Academic level A or B for up to 36 months in the first instance, commensurate with qualification, skills and experience.

The remuneration package will be in the range of (in Australian dollars) and relocation costs:

Academic Level A - $60,829 - $82,510 p.a., plus employer superannuation contributions of up to 17% (total package will be in the range of $71,169 - $96,537 p.a.)

Academic Level B - $86,853 - $103,138 p.a., plus employer superannuation contributions of up to 17% (total package will be in the range of $101,618 - $120,671 p.a.) There are a number of research projects available, including but not limited to: 1. Multivariate whole genome estimation and prediction analysis of genomics data applied to psychiatric disorders. This project will require the development of statistical methods and computer algorithms to perform multivariate association analysis in large samples. Whilst the focus is on neurological or psychiatric disorders (e.g. schizophrenia, motor neuron diseases, Parkinson's disease and Alzheimer's disease), methods and software can be applied to other traits and disease phenotypes. The successful candidate will have a strong background in mathematics and statistics and a proven ability to code efficiently in low-level languages.

2. Develop whole-genome based methodology to estimate genetic parameters in quantitative and disease traits. This project will build on recent cutting edge research performed by CNSG for accurate estimation of genetic variance from large-scale samples. One major focus of this initiative is the development of efficient and user-friendly software, which is to be made publically available. The successful candidate will have a strong background in mathematics and statistics and a proven ability to code efficiently in low-level languages.

3. Develop methods for the analyses of âomics data. The project will build on the large amount of âomics data collected by CNSG and collaborators, including genome-wide SNPs, whole genome sequence, genome-wide gene expression, and genome-wide DNA methylation in large samples. The aim of this project is to use the integrated information from âomics data to better understand the genetic etiology of complex diseases and to achieve a higher accuracy of disease risk prediction. The successful candidate will have a strong background in quantitative genetics or bioinformatics and experience in the analysis of âomics data.

4. Analysis of genomics data of motor neuron disease (e.g. SNP, blood DNA methylation, exome sequence) from Australian and Chinese cohorts, in particular leading analyses that are informed by knowledge and understanding of the underlying biology of the disease.

see: http://jobs.uq.edu.au/caw/en/job/497548/-postdoctoral-research-fellow Applications close: 02 Aug 2015 (11:55 PM) E. Australia Standard Time

Matthew R. Robinson| Centre for Neurogenetics & Statistical Genomics| Queensland Brain Institute, University of Queensland |St Lucia, Brisbane, Australia, 4072 | t: +61 412 230 050 | w: cnsgenomics.com

Matthew Robinson <m.robinson11@uq.edu.au>

UTAustin EvolEpigenomicsBehavior

Postdoctoral opportunity: Evolutionary epigenomics of behavior, UT-Austin

The Phelps Lab at the University of Texas at Austin (phelpslab.net) is looking for a postdoctoral trainee with strong bioinformatics skills to investigate the adaptive evolution of gene regulation in non-model systems. The project seeks to identify adaptations in neuronal gene regulation associated with the emergence of monogamy in prairie voles. The successful candidate will have a publication record that indicates a solid background in evolutionary genetics, including experience with genome-wide tests of selection and comfort with standard bioinformatics methods (UNIX, R and Perl or Python). This is an excellent opportunity for a recent graduate with a background in bioinformatics, phylogenetics or population genetics looking to expand into functional measures of sequence evolution, or into neurobiology and animal behavior. Although not required, the applicant will have the opportunity to become proficient in a variety of advanced molecular methods, including ChIP-seq, meDIP, conformation capture and other techniques. UT-Austin is a wonderful place to be. There is a vibrant community of researchers working at the interface of brain, behavior and evolution, an excellent sequencing facility, and extraordinary computational resources offered through the Texas Advanced Computing Center and a variety of allied centers on campus.

The lab has two years of funding available, with the second year contingent on progress in the first year. The start date is flexible, and the position could begin as early as September 2015. Applications should include a current CV along with a cover letter that provides a short (~1 page) statement of research interests and contact information for three references. Please submit applications by email to sphelps@mail.utexas.edu, with the subject line POSTDOC APPLICATION by JULY 15, 2015. We think diversity is a component of excellence, and welcome applicants regardless of gender, ethnicity, sexuality, religious beliefs, age or disability.Thanks for your interest!

Steve Phelps Associate Professor, Department of Integrative Biology Director, Center for Brain, Behavior and Evolution University of Texas at Austin Austin, TX 78712, USA Phone: 512 475 6304

Steve Phelps <sphelps@mail.utexas.edu>

UToronto EvolutionaryBiol

The department of Ecology & Evolutionary Biology at the University of Toronto invites applications for the prestigious Banting Postdoctoral Fellowship. These awards include a $70,000 annual stipend for 2 years and are available to excellent junior scientists from any country to conduct postdoctoral research in Canada.

The University of Toronto is a leading academic institution in Canada with over 60 faculty members specializing in ecology and evolution. Strong links exist between the Department of Ecology and Evolutionary Biology and the Royal Ontario Museum, the Centre for Global Change, the School of the Environment, and the Faculty of Forestry. The University owns a nearby field station dedicated to ecological research (the Koffler Scientific Reserve, www.ksr.utoronto.ca). The department also has a partnership with the Ontario Ministry of Natural Resources that helps provide access to infrastructure, including lab facilities in Algonquin Provincial Park (www.harkness.ca), funding, and long-term data sets. Genomic analyses are supported by the Centre for the Analysis of Genome Evolution and Function (www.cagef.utoronto.ca).

To apply, applicants should first contact and obtain the agreement of a faculty advisor (or co-advisors) who is a member of EEB's graduate faculty; the faculty member(s) must agree to support the application. Please see this list for eligible faculty members: http://www.eeb.utoronto.ca/people/-G-faculty.htm Applications are due to the EEB department by July 16, 2015, with further details of the application process available on the EEB department website: http://www.eeb.utoronto.ca/about-us/-employment/postdocs/eebbanting.htm For full information on the Banting Postdoctoral Fellowships, including eligibility, please see this website: http://-banting.fellowships-bourses.gc.ca –

Asher D. Cutter Associate Professor and Canada Research Chair in Evolutionary Genomics Department of Ecology and Evolutionary Biology University of Toronto 25 Willcocks St. Toronto, ON, M5S 3B2

tel: 416-978-4602 email: asher.cutter@utoronto.ca http://labs.eeb.utoronto.ca/cutter
"asher.cutter@utoronto.ca" <asher.cutter@utoronto.ca>

UToronto UrbanEvolutionaryEcol

Post-Doctoral Position in Urban Evolutionary Ecology - University of Toronto at Mississauga (with Profs. Marc Johnson and Deep Saini)

We are seeking applications for a Post-Doctoral Researcher to study Urban Evolutionary Ecology in the Department of Biology (www.utm.utoronto.ca/~w3bio/-homepage) at the University of Toronto - Mississauga (UTM). This project seeks to understand how plants adapt to urban landscapes by examining species that occur along urban-rural gradients. We are presently studying white clover (Trifolium repens) but there are opportunities to expand this work to other systems depending on the successful candidate's interests and background. The post-doctoral researcher is expected to integrate experiments, molecular, chemical and statistical approaches to understand how the combined effects of natural selection and gene flow influence adaptation to urban landscapes. This project is ideally suited to individuals seeking to perform productive cutting edge research while connecting with an international network of scientists and the public. We are interested in all outstanding post-doctoral applicants with an interest and expertise in plant evolutionary biology or ecology. Additional expertise in molecular biology, genomics, chemistry, statistics and theory would be an asset.

The post-doctoral researchers will also be expected to take a leading role in outreach activities. This will involve organizing a conference on Urban Environmental Science, be actively involved on social media, help to launch a new centre in urban environmental science, and potentially interact with the public and media. Strong social and public speaking skills will be an asset to applicants, as well as a proven record at multitasking.

The UTM campus boasts excellent facilities for research, housing, and 225 acres of fields, forests, many trails and a wild salmon/trout river for recreation. Toronto and Mississauga are world-class cities that are interconnected and culturally diverse. They boast an abundance of restaurants, excellent transit systems, a diversity of cultural activities (theatres, sports, bars, clubs), and an abundance of parks and water.

Starting salary: $40,000 + benefits (health and dental)

Start date: flexible, but no later than January 1, 2016

Duration: 2 years (conditional on favourable annual performance review)

Application Deadline: July 1, 2015 (search will continue until a successful candidate is found)

The successful candidate will work collaboratively with Prof. Marc Johnson (www.evoeco.org) and Prof. Deep Saini (http://www.utm.utoronto.ca/biology/people/-saini-hargurdeep). Please send all applications to: marc.johnson@utoronto.ca by July 1, 2015? The search for a successful candidate will continue until the position is filled. Applicants must have earned a Ph.D. in a field related to the ad before starting the position.

Applications should include: i) a cover letter, ii) CV, iii) PDFs of top three publications, and iv) contact information for three references.

Employment as a Postdoctoral Fellow at the University of Toronto is covered by the terms of the CUPE 3902 Unit 5 Collective Agreement. Post date: June 7, 2015

“marc.johnson@utoronto.ca”
<marc.johnson@utoronto.ca>

UTurku SalmonEvolGen

A 3 year post-doctoral position, including a 25% teaching component, is available at the University of Turku, Finland to work in Prof. Craig Primmer's research group (http://users.utu.fi/primmer). The research component of the position is a part of a research consortium that aims at integrating evolutionary genetics, ecological modelling and environmental sociology to understand the external drivers of life history changes in a heavily fished Atlantic salmon population complex and to advance sustainable use of these aquatic natural resources. This project has been recently funded as a part of the Finnish Academy Arctic Research program (http://-www.aka.fi/arktiko)

The post-doc will be responsible for conducting and co-supervising research investigating the genetic basis of life-history traits such as age at maturity (e.g. Johnston et al. 2014) and repeat spawning, as well as conducting genome scans for identifying genes involved in adaptation to local environmental conditions. Teaching will involve giving lectures and computer classes on topics related to the position.

Suitable candidates will have a strong background in evolutionary genetics/genomics and/or quantitative genetics research (in any species). Experience with the methodologies for analysis of large-scale SNP and high-throughput sequencing data is an advantage, as is an interest in conservation genetics and fisheries management. Undergraduate teaching experience is also advantageous.

Informal inquiries should be directed to Prof. Craig Primmer (craig.primmer@utu.fi). Formal applications should include a CV (with names and contact details of at least two referees), a publication list, an academic portfolio and a max. 2 page letter of motivation and can be submitted at http://www.utu.fi/en/university/university-as-an-employer/open-vacancies/Pages/home.aspx. The deadline for applications is August 3, with the preferred starting date being January 2016 or earlier. The position is available until the end of 2018. The starting salary is approx. 3140 - 3500 EUR per month, depending on the previous relevant research and teaching experience of the candidate.

Turku, Finland's 5th largest city (176 000 people), is located in the southwestern Finland. It has a rich cultural history and is the gateway to a beautiful archipelago. The University of Turku is one of the major multidisciplinary universities in Finland and is ranked in the top 5% of universities in the world.

Johnston et al. (2014) Genome-wide SNP analysis reveals a genetic basis for sea-age variation in a wild population of Atlantic salmon (Salmo salar). Molecular Ecology 23: 3452-3468

–

Craig Primmer, Academy Professor Division of Genetics and Physiology Department of Biology, University of Turku, FINLAND

Room 7004, 7th floor, Pharmacity Itäinen pitkäkatu 4, 20520 Turku

Office +358 2 333 5571 Mobile +358 40 1560 365 craig.primmer@utu.fi http://users.utu.fi/primmer Twitter: @Craig_Primmer

“craig.primmer@utu.fi” <craig.primmer@utu.fi>

UWisconsin Madison MicrobialEvolution

Postdoctoral position in Microbial Evolution

Postdoctoral position is available in the laboratory of Kalin Vetsigian at the University of Wisconsin-Madison to study ecological and evolutionary dynamics in multispecies microbial communities. The postdoc will deploy novel high-throughput methodologies to quantitatively characterize microbial interactions and their evolution in laboratory communities. The lab is located in the highly interdisciplinary environment of the Wisconsin Institute for Discovery as part of the Systems Biology Theme and is also closely affiliated with the Department of Bacteriology.

We are looking for candidates with a background in Biology and/or quantitative background in Math, CS, Physics or Engineering. Previous experience with any of the following is a plus but not required: microbial ecology, evolutionary biology, actinomycetes, secondary-metabolism, next gen sequencing, genetic engineering, computer programming, mathematical modeling. The postdoctoral position will prepare candidates for a career in the rapidly expanding fields of Evolutionary Systems Biology and Synthetic Microbial Ecology.

The position is for two years with the potential for extension upon satisfactory performance. Start day is negotiable.

To apply, please send one document that includes a cover letter, CV, and statement of research accomplishments to kalin@discovery.wisc.edu. Also, arrange for 3 letters of recommendation to be e-mailed directly to the above address.

Kalin Vetsigian Assistant Professor of Bacteriology http://wid.wisc.edu/research/sysbio/labs/vetsigian-lab/ Wisconsin Institute for Discovery Systems Biology Theme, Room 3116 330 N. Orchard Street

“Kalin@discovery.wisc.edu”
<Kalin@discovery.wisc.edu>

Vienna DrosophilaExperimentalEvolution

Experimental Evolution in Drosophila

A postdoctoral position is available at the Institute of Population Genetics, Vetmeduni Vienna (Austria). The research focus of the Institute of Population Genetics is on understanding the genetics of adaptation. This central question in evolutionary biology is being tackled using up-to-date methods and a variety of approaches, including experimental evolution, quantitative genetics, functional genetics, empirical population genetics, bioinformatics and statistics.

The successful candidate will be part of a team of scientists studying adaptation of experimental Drosophila populations to temperature stress. Since our experimental evolution study is performed under controlled environmental conditions with a high level of replication we have a powerful system to successfully employ a combination of DNA sequencing, RNA-Seq and Chip-Seq to characterize the architecture of adaptation in an out-crossing species. With some of our populations having already evolved up to 100 generations, this project provides the opportunity to follow adaptive trajectories through time.

We are looking for a candidate with a good quantitative training and experience in handling large data sets. A background in population genetics and/or experience with the analysis of RNA-Seq and Pool-Seq data are a bonus.

The positions are available for at least two years starting August 2015, but the exact starting date is negotiable. The application should be emailed to christian.schloetterer@vetmeduni.ac.at as a single pdf containing CV, list of publications, a statement of research interests, and the names of three references with contact details. While the search will continue until the position is filled, applications should be received by 1.7.2015 to ensure full consideration.

Background:

1: Franssen, S.U.*, et al.* (2015) Patterns of linkage disequilibrium and long range hitchhiking in evolving experimental *Drosophila melanogaster* populations. *Molecular Biology and Evolution* 32, 495-509

2: Orozco-terWengel, P.*, et al.* (2012) Adaptation of

Drosophila to a novel laboratory environment reveals temporally heterogeneous trajectories of selected alleles. *Molecular Ecology* 21, 4931-4941

3: Schlötterer, C.*, et al.* (2015) Combining experimental evolution with next-generation sequencing: a powerful tool to study adaptation from standing genetic variation. *Heredity* 114, 431-440

4: Schlötterer, C.*, et al.* (2014) Sequencing pools of individuals - mining genome-wide polymorphism data without big funding. *Nature Reviews. Genetics* 15, 749-763

5: Tobler, R.*, et al.* (2013) Massive habitat-specific genomic response in* D. melanogaster* populations during experimental evolution in hot and cold environments. *Molecular Biology and Evolution* 31, 364-375

Christian Schlötterer Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 1 1210 Wien Austria/Europe

phone: +43-1-25077-4300 fax: +43-1-25077-4390 http://www.vetmeduni.ac.at/en/population-genetics/ Vienna Graduate School of Population Genetics http://www.popgen-vienna.at SMBE 2015 in Vienna *http://smbe2015.at* Christian Schlötterer <christian.schloetterer@vetmeduni.ac.at>

WashingtonStateU EvolutionaryGenomics

Postdoc Position: Evolutionary Genomics at Washington State University

A postdoctoral position is available in the laboratory of Dr. Joanna Kelley, in the School of Biological Sciences at Washington State University in Pullman, WA (kelleylab.wordpress.com). The research goals of the laboratory are to use genomic and computational methods to understand the genomic basis of adaptation to extreme environments. We are interested in understanding how genetic and environmental variation interact to drive population differentiation and adaptive evolution in several fish species. We study mollies, Antarctic eel pouts and mangrove rivulus. The School of Biological Sciences at Washington State University has a strong research presence in evolution and ecology research and there are many opportunities for interaction and collaboration. We welcome applications from candidates with diverse educational backgrounds.

Applicants will be expected to develop and lead projects. Candidates are required to have a Ph.D. in Genetics, Genomics, Computational Biology (bioinformatics, systems biology), Statistics, Computer Science, or related disciplines. A computing background is required, especially experience with Unix, and knowledge in one or several programming languages (Perl, Python, C/C++, R/BioConductor, etc). Additional experience with high-throughput sequencing data is highly necessary. Candidates should demonstrate a strong track record of publication; have strong organizational, written, and oral communication skills; and be able to work both independently and as part of a collaborative team.

The appointment is for one year with the possibility of renewal based on satisfactory performance. Funding is available for two years. Salary is competitive and commensurate with experience, and benefits are included.

Applicants should email Joanna Kelley at joanna.l.kelley@wsu.edu and include curriculum vitae, cover letter that includes a statement of research interests that explicitly describes your professional qualifications for the position, and contact information for three references. Start time is flexible, with a desired start in Fall 2015. Applications will be accepted through July 15th.

Joanna L. Kelley, PhD Assistant Professor, School of Biological Sciences Member, Center for Reproductive Biology Washington State University joanna.l.kelley@wsu.edu

"joanna.l.kelley@wsu.edu" <joanna.l.kelley@wsu.edu>

WorkshopsCourses

AMUPoznan Poland BioinformaticsRNA Jul6-10

Dear colleagues,

We are extremely happy to announce 11th edition of Poznan Summer School of Bioinformatics. This meeting takes place at Adam Mickiewicz University in Poznan (Poland) from 6th to 10th July 2015.

This year's course will cover modern approaches to RNA analyses, including subjects like:

1. Introduction to RNA biology 2. Applications of next-generation sequencing in RNA studies 3. Transcriptome sequencing, assembly and gene expression estimation 4. Identification and analysis of microRNAs and other small RNAs 5. long non-coding RNAs 6. Secondary and tertiary structures of RNAs

The course is suitable both for beginners and for those who already have some basic knowledge in computational biology and find it necessary and interesting to learn more about bioinformatic applications in RNA studies. Our school consists of lectures and hands-on - this combination should fit best your needs as you have a chance to try out the discussed methods yourself.

The deadline for REGISTRATION is July 1st.

For further information please visit our website: http://bioinformatics-school.pl Please forward this announcement to anyone who might be interested. Best regards, PSSB Organizing Committe Contact: genomics@amu.edu.pl

Bioinfo School <genomics@amu.edu.pl>

Baltimore DryadLab Aug9

REMINDER: Deadline to apply is this Friday, June 5!

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? Questions should be directed via email to Samantha Swauger, the DryadLab project manager, at samswauger@gmail.com. project manager, at samswauger@gmail.com.

Barcelona AnalysisR Jan18-22

Dear Colleagues,

Registration is open for the course MULTIVARIATE DATA ANALYSIS FOR ECOLOGY AND EVOLUTION IN R.

Date: January 18-22, 2016.

Course webpage: http://www.transmittingscience.org/courses/stats/multi-ecol-evol-in-r/ Instructors: Dr. Dean Adams (Iowa State University, USA) and Dr. Antigoni Kaliontzopoulou (Centro de InvestigaçÃ£o em Biodiversidade e Recursos Genéticos (CIBIO), Portugal).

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 Transmitting Science< http://www.transmittingscience.org/ >

Finland PlanktonEvolution Oct5-8

Dear all,

We are pleased to announce a four-day workshop Plankton resting stages: ecological, evolutionary and geological perspectives, held at the Tvärminne Zoological Station, Hanko Peninsula, Finland, on Oct 5-8, 2015.

The workshop brings together researchers who study phyto- and zooplankton resting stages in the fields of evolutionary biology, genetics, ecology, paleoecology, environmental science, and geology. The workshop will discuss the status of knowledge in the respective research fields, and bring forward joint targets for development and interest. The program involves three thematic components (note that the final workshop sessions will take shape based on the research themes of the registered participants):

- Resting stages and geology: Long-term archives and indicators of change - Resting stages and ecology: Environmental cues and ecological significance - Resting stages and evolution: Living archives and evolutionary significance

Register by July 31st, 2015.

http://www.planktonrestingstages.org . Register early, the space is limited.

Cheers on behalf of the organizing committee, Maija Heikkilä, Anke Kremp, Sanna Suikkanen and Anu Vehmaa

"anu.vehmaa@helsinki.fi" <anu.vehmaa@helsinki.fi>

FrenchAlps PopGen Sept7-11

Dear colleagues,

It is our pleasure to announce that the second edition of the SSMPG summer school (Software and Statistical Methods for Population Genetics) will take place in Aussois (Savoie, France) from September 7 to September 11, 2015.

The aim of the summer school is to provide a comprehensive overview on software and statistical methods for detecting genes involved in local adaptation. Lecture notes and software demos will be given during the summer school. In addition to software demos, we plan to set up a contest to promote learning. Participants will work in groups and will be asked to analyse simulated datasets. The objective will be to find adaptive loci using the different software presented at the summer school.

More details about the summer school are available online: http://ssmpg2015.imag.fr/ The deadline for pre-registration is July 05, 2015.

The scientific organizing committee Michael Blum (Univ. Grenoble) and Renaud Vitalis (INRA Montpellier)

mblum <michael.blum@imag.fr>

GTPB Portugal PopulationGenetics Jul6-9

ANNOUNCEMENT / REMINDER

Dear EVOLdir subscriber

Applications are open for

PGDH15 Population Genetics and Demographic History: model-based approaches

with Mark Beaumont, Lounes Chikhi, Willy Rodriguez and Barbara Parreira

IMPORTANT DATES for this Course Deadline for applications: June 28th 2015 Latest notification of acceptance: July 1st 2015 Course date: July 6th - July 9th 2015

Details are available at: http://gtpb.igc.gulbenkian.pt/bicourses/PGDH15/ Course description Genetic data are increasingly used by ecologists and evolutionary biologists in general. It has thus become important for many biologists with different levels of experience to produce and analyse genetic (and genomic) data. In this course we will take a practical approach to the analysis of genetic data, but we will also provide some of the theoretical background required to understand the outputs of the software used. This course will be organised so as to mix lectures where important notions are introduced with practicals where freely available software will be used. While this will not be the focus of the course, we will also introduce and discuss genealogical (coalescent-based) simulation methods and those based on forward-in-time simulations. Altogether this will allow to discuss the potentialities and limitations of the tools available to the community.

In this four-day course we will introduce the main concepts that underlie many of the models that are frequently used in population genetics. We will focus on the importance of demographic history (e.g. effective sizes and migration patterns) in shaping genetic data. We will go through the basic notions that are central to population genetics, insisting particularly on the statistics used to measure genetic diversity and population differentiation. The course will also cover a short introduction to coalescent theory, Bayesian inference in population genetics and data simulation, as they are connected to what makes landscape genetics today on the basis of multilocus data. We will also introduce two methods that have been recently developed to analyse genomic data. The PSMC of Li and Durbin reconstructs the demographic history of a species or population with the genome of a single individual. The Rehh package is an R implementation of the Extended Haplotype Homozygosity (EHH) test for selective sweeps and looks for signals of selection based on the analysis of genomic regions.

Most theory will be put into practice in practical sessions, analyzing real and/or simulated datasets. In these sessions, we will look at measures of genetic diversity and differentiation and use methods to detect population structure as implemented in the program STRUCTURE and discuss related programs such as FastSTRUCTURE. We will learn how to perform coalescent simulations of genetic data (using SPAms and ms). Some exercises will make use of R scripts (R being a freely available statistical program). Basic R knowledge is a pre-requisite but we will provide a short introduction to R. The R statistical package is a very powerful tool to analyse data outputs from many population genetics software, and can also be used to simulate genetic data under simple demographic scenarios.

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 Research mailing list Research@igc.gulbenkian.pt https://lists.igc.gulbenkian.pt/mailman/listinfo/research
Pedro Fernandes <pfern@igc.gulbenkian.pt>

Hannover LifeHistory Jul13-16 Oct14-16

Dear PhD students and PostDocs,

we seek six highly motivated young researchers to actively contribute to two workshops on the topic Towards a general theory of the pace-of-life syndrome, which will take place in Hannover (Germany) from October 14 to 16, 2015 and July 13 to 16, 2016. The workshops are fully funded by the Volkswagen Foundation (Ref: 89905).

With these workshops will revisit a broad heuristic concept suggesting that life-history characteristics, among-individual differences in behaviour (i.e. personality) and a suite of physiological traits have coevolved in response to environmental conditions forming the pace-of-life syndrome (POLS). This concept has generated much research interest because it provides an extraordinary opportunity for organismal biologists to extend fundamental principles of life-history theory to a whole set of ecologically relevant physiological and behavioural traits. However, we still lack a general theory explaining the (co)evolution and maintenance of links between life-history, physiological and behavioural traits in a general ecological framework as well as specific models predicting links between multiple traits at the different levels of variation (i.e. individual, population, species). In the workshops we will unite the expertise of 40 empiricists from various fields (behaviour, ecology, evolutionary biology, psychologists) and theoreticians to intensively work at the development of a general theory of the pace-of-life syndrome. We aim at (1) refining the general theoretical concept, (2) building specific quantitative models, (3) developing guidelines on study design and statistical analyses for empiricists, (4) initiating the creation of a public data base containing information on life-history, physiology and behaviour of species and populations in various ecological conditions, (5) using this date base to run comparative analyses to test the effect of broad-scale environmental conditions on covariation of the POLS traits, and (6) exploring the predictive potential of the POLS for species range shifts as a result of global change.

If you are interested to actively participate in these two workshops, please send a CV and a letter of motivation, explaining why you think the workshop will be interesting for you and how you can contribute to the specific objectives of the workshops. Please send your application electronically, all documents combined into a single pdf, named as your last name (e.g. Myname.pdf) to melanie.dammhahn@uni-potsdam.de. The deadline for application is July 20th, 2015.

For more details about the workshops please contact melanie.dammhahn@uni-potsdam.de

The organizing committee

Melanie Dammhahn (University of Potsdam, Germany)

Denis Réale (Université du Québec Ã Montréal, Canada)

Petri Niemelä (LMU Munich, Germany)

Niels Dingemanse (Max Planck Institute for Ornithology, Germany)

Melanie Dammhahn <melanie.dammhahn@uni-potsdam.de>

Manchester Morphometrics Nov2-Dec11

Dear colleagues

I am pleased to announce this year's morphometrics course from the University of Manchester. This year's course will run in the six weeks from 2 November to 11 December 2015.

The course information can be found on the following we site: http://www.flywings.org.uk/MorphoCourse Course content: * Data acquisition: the kinds of data and the equipment used to collect them. * Definitions of size and shape * Geometric methods to characterise shape from a configuration of landmark points (Procrustes superimposition) * Statistics of variation, scatter plots, basic multivariate statistics * Principal component analysis * Measurement error and outliers * Shape transformations and 'warping' – the thin plate spline * Analysis of outline shapes * Distinguishing between groups (taxonomy, clinical diagnosis, etc.) * Allometry and size correction * Influence of external factors on shape (ecomorphology, dose-response studies) * Symmetric forms and measurement of asymmetry. * Morphometric inferences on developmental processes * Morphological integration and modularity * Genetics of shape: analyses of resemblance between relatives, QTL analyses. * Phylogeny: reconstructing the evolution of shape

Practice examples: As far as possible, practical exercises are provided to accompany the course content. These practice exercises consist of data sets and explanations on how to run the respective analyses using the MorphoJ software (http://www.flywings.org.uk/-MorphoJ_page.htm). Participants who already have their own data are encouraged to use those and to discuss them as part of the course. I hope there will be a bit of a 'workshop' feel to the course unit.

Group work: Participants will work in small groups to prepare web presentations of possible morphometric studies (wikis prepared by the groups). This activity stimulates discussion and provides a broad overview of the broad range of questions that can be addressed with morphometric methods.

The fee for the course is GBP 330.00.

All prospective participants need to pre-register for the course. The deadline for this is the *30 September 2015*.

For further details and the pre-registration form, see the course web page: http://www.flywings.org.uk/-MorphoCourse Best wishes, Chris

Christian Peter Klingenberg Faculty of Life Sciences The University of Manchester Michael Smith Building Oxford Road Manchester M13 9PT United Kingdom

Telephone: +44 161 275 3899 Fax: +44 161 275 5082 E-mail: cpk@manchester.ac.uk Web: http://-www.flywings.org.uk Skype: chris_klingenberg

"cpk@manchester.ac.uk" <cpk@manchester.ac.uk>

Montana ConGen Aug31-Sep5

We are pleased to announce and invite you to the 7th 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 still open V but space is limited!

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 (see: Andrews and Luikart 2014).

Who should apply: Ph.D. students, post-docs, faculty, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. 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/ Field trip dinner with instructors in Glacier National Park

"Luikart, Gordon" <gordon.luikart@mso.umt.edu>

Montana ConGen Aug31-Sep5 2

Few places are still open to attend the 7th Population Genomic Data Analysis Course

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

Instructors include: Fred Allendorf, Tiago Antao, Jeff Good, Brian Hand, Paul Hohenlohe, Joanna Kelly, Gordon Luikart, Mike Miller, Jonathan Pritchard, Mike Schwartz, Jim Seeb, Lisa Seeb

(1-2 more instructors pending)

Applications for 2015 edition are still open V but space is limited!

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 (see: Andrews and Luikart 2014, Molecular Ecology, 23:1661-7. doi: 10.1111/mec.12686).

Who should apply: Ph.D. students, post-docs, faculty, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. 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/ “Luikart, Gordon” <gordon.luikart@mso.umt.edu>

Montana ConGen Aug31-Sep5 3

Few places are still open to attend the 7th Population Genomic Data Analysis Course (see attached flier)!

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

Instructors include: Fred Allendorf, Tiago Antao, Steve Amish, Jeff Good, Brian Hand, Paul Hohenlohe, Joanna Kelly, Gordon Luikart, Mike Miller, Jonathan Pritchard, Mike Schwartz, Jim Seeb, Lisa Seeb, Robin Waples

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 (see: Andrews and Luikart 2014, Molecular Ecology, 23:1661-7. doi: 10.1111/mec.12686).

Who should apply: Ph.D. students, post-docs, faculty, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. 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/ “Luikart, Gordon” <gordon.luikart@mso.umt.edu>

Rovereto Italy InsectBehaviour

“Workshop: Rovereto(Italy). Insect models of Behaviour. Sep4”

First announcement: We are happy to announce the programme of the Workshop “Insect models of Behaviour: ecology, genetics, evolution, pest management” that will take place in Rovereto (Italy) on 4th September. Beside talks of the invited speakers we will host a poster session with a prize for the best poster presented by a young investigator (up to postdoc level). The meeting is free to attend but a registration is required. We will communicate soon the details of the website for the registration, in the meantime enjoy the programme and for further questions please write to elisabetta.versace@unitn.it :

When: 4th September 2015 Where: Fondazione Museo Civico, Borgo Santa Caterina 41, Rovereto (Trento), Italy. Organizing committee: Elisabetta Versace, Anna Eriksson (University of Trento); Gianfranco Anfora (Fondazione Edmund Mach, San Michele all’Adige); Gionata Stancher (Fondazione Museo Civico Rovereto) Programme Workshop “Insect Models of Behaviour: Ecology, genetics, evolution, pest management”

9:00-9:15 Opening 9:15-10:15 Benjamin Prud’homme (Centre national de la recherche scientifique, Marseille, France) The evolution of egg laying behavior in Drosophila suzukii. 10:15-11:00 Paul Becher (Swedish University of Agricultural sciences, Alnarp, Sweden) Chemical stimuli, basic drives and behavioural responses: understanding some aspects of Drosophila chemical ecology

11:00-11:20 Coffee break

11:20-12:00 Donato Grasso (University of Parma, Italy) Ants as mutualists: from basic to applied science 12:00-12:40 Anna Eriksson, Elisabetta Versace (University of Trento, Italy): Olfactory responses in Drosophila melanogaster and Drosophila suzukii: studies on ecological specialization

12:45 Final remarks on the morning session

12:45-2:30 Lunch break

2:30-4:30 Poster session. The best poster presented by a young investigator (up to postdoc level), as judged by the Organizing committee and Invited speakers, will be announced at 4 pm.

We look forward seeing you in Rovereto.

Elisabetta Versace, PhD

Center for Mind/Brain Sciences University of Trento ACN lab - Animal Cognition and Neuroscience Laboratory Piazza della Manifattura 1, 38068 Rovereto (TN), Italy Phone: +39 0464 808658 Mobile: +39 349 8744279

@so_evolutionary

“Elisabetta.Versace@unitn.it” <Elisabetta.Versace@unitn.it>

Stellenbosch SouthAfrica EvolutionTreeInvasion Nov9-10

The Centre of Invasion Biology (CIB) is pleased to announce its international workshop “Evolutionary dynamics of tree invasions: drivers, dimensions, and implications for management” that will be held between 9th and 10th November 2015 in Stellenbosch, South Africa.

BACKGROUND INFORMATION:

An extensive body of research suggests that invasive plant populations often undergo phenotypic and ecological divergence from their native sources. These changes can result due to selective pressures in the new range or through demographic stochasticity during introduction. Given the life-history traits of trees that gives them long lifespans and generation times, it is not surprising that the evolutionary dynamics of invasive trees are still comparatively poorly understood and that their invasion potential has been often underestimated. Invasive trees have significant impacts worldwide and these are increasing rapidly in many parts of the world.

Several cases are known where invasive tree populations show differences in morphological or physiological traits or altered ecological interactions (e.g. mutualistic relationships) compared to their native sources. Despite such evidence, the understanding of the drivers and the extent of these changes remains sketchy compared to other plant forms, such as annual herbs.

The first aim of this workshop is to synthesize our current knowledge on the key processes underlying tree invasions worldwide by investigating the role of different potential drivers, including pre-adaptation, artificial selection/selective breeding, polyploidy, hybridization, reduced enemy pressure, new mutualistic interactions, and novel selection pressures, in facilitating evolutionary change. A second aim is to elucidate the dimensions of these processes to better understand across which temporal, spatial and taxonomic scales such changes can occur. This includes, for example, findings on how certain drivers are represented across different taxa, how rapidly divergence from native sources can develop and/or if a species invasion success across wide geographical ranges can be the result of different drivers. Further, we aim to explore how such processes may bias management and control approaches and how research could reduce such biases, thereby increasing our general knowledge of, and ability to manage, tree invasions.

FURTHER INFORMATION:

Please visit the workshop homepage for more information (e.g. application, directions, accommodation): http://academic.sun.ac.za/cib/workshops/-20151109/index.asp We are looking forward to receive your application and to see you in Stellenbosch, South Africa.

Centre of Invasion Biology Department of Botany & Zoology Stellenbosch University South Africa

http://academic.sun.ac.za/cib/index.asp heidihirsch71@googlemail.com

---

SwissAlps Social Interactions Jul6-9

— LAST CALL —

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. MichaÃ«l 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 taking 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=3D3D1128&id=3D2242 Queries: ecologie-evolution@cuso.ch

"Caroline.Betto-Colliard@unil.ch" <Caroline.Betto-Colliard@unil.ch>

Vairao Portugal Morphometrics Oct5-9

International Workshop "An Introduction to Geometric Morphometrics using R"

October 5-9, 2015 @ CIBIO-InBIO, Vairao, Portugal

The analysis of organismal shape is central to many questions in ecology and evolution. This workshop aims at providing an introduction to the theory and methods of geometric morphometrics for analyzing variation in shape and its covariation with other variables. It will provide an overview of the theory underlying the quantification of shape using landmark methods, and a practical guide to data acquisition, standardization for obtaining shape variables, statistical treatment of shape variation, and visualization of the results in the R language for statistical programming.

R knowledge is a requirement for the course and it will be assumed that all participants are fluent for data manipulation and basic operations in the R environment.

Click here [http://cibio.up.pt/workshops–courses/-details/introduction-to-geometri c-morphometrics-using-r] to see the PROGRAMME for this course.

COURSE INSTRUCTORS

Prof. Dean C. Adams [http://www.public.iastate.edu/-~ dcadams/homepage.html] Dr. Michael Collyer [https://www.wku.edu/biology/staff/michael_collyer] Dr. Antigoni Kaliontzopoulou [http://cibio.up.pt/-people/details/akaliont] REGISTRATION DEADLINE

Deadline for registration is July 31, 2015.

To know more about this course, please visit CIBIO-InBIO's website [http://cibio.up.pt/-workshops–courses/details/introduction-to-geometri c-morphometrics-using-r] or contact us at GM2015@cibio.up.pt.

CIBIO DivulgaçÃ£o

Wageningen GbyEInteraction Oct19-23

In October (19-23), the Animal Breeding and Genomics Centre of Wageningen UR, ABGC, is organizing a PhD-course on genotype by environment interaction, uniformity and stability. We will focus on quantitative genetics and statistical modeling from a broad perspective: animal breeding, plant breeding and natural populations.

This course will be given on the Wageningen Campus. Maximum number of participants is 40; the minimum is 15. The registration deadline is September 30th. Note that registration is not final until you have received confirmation from the course organizers that you can participate.

Course Details:

Genotype by environment interaction, uniformity and stability

Dates : 19 to 23 October 2015

Teachers : Han Mulder, Piter Bijma, Marcos Malossetti and Phillip Gienapp

Credits : 1.5 ECTS

Minimum participants: 15 Maximum participants: 40

Final Registration date: September 30, 2015

Provisional day-to-day program:

Monday: Genotype by environment interaction: concepts and implications

Tuesday: Statistical modeling of genotype by environment interaction in animal and plant breeding

Wednesday: Quantitative genetics of variability

Thursday: Statistical modeling of variability and stability

Friday: Costs and benefits of stability, plasticity and uniformity (until 12.00h)

For more course details and to register see the website:

http://www.wageningenur.nl/nl/activiteit/Indepth-Course-Genotype-by-environment-interaction-uniformity-and-stability.htm or contact Han Mulder (han.mulder@wur.nl)

"p.gienapp@nioo.knaw.nl" <p.gienapp@nioo.knaw.nl>

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.