EvolDir

February 1, 2012

Month in Review

Foreword

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

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

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

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Conferences

ArizonaStateU Phylomedicine Mar23-24 Deadline

Final call for submitting applications for Travel Grants

Eligibility: Students, Postdocs, and early career scientists

Support: $500 for US and $1000 for international selectees Apply by E-mail to phylomedicine@asu.edu

Attach PDF/DOC/DOCX files containing:

(1) 200 word abstract PLUS title.

(2) Your full CV, including the name of your mentor (if appropriate)

(3) Filled out Registration form (see http://www.smbe.org/phylomed/registration.php)

Deadline: January 5th, 2012

Each travel grant awardee will be required to present a poster on March 23, 2012.

http://www.smbe.org/phylomed/ SMBE Satellite Symposium on Phylomedicine (March 23-24, 2012)

Arizona State University

Tempe, Arizona, USA

s.kumar@asu.edu

Avignon PetitPoisDeride Aug28-31

Never been to Avignon? Good news: the 34th “Petit Pois DeridÃ” (Ha-pea meeting*) will take place next August 28-31, 2012, in Avignon. This a yearly meeting of the French community of evolutionary biologists, population biologists and ecologists. Emphasis is on having students and postdocs present their work and exchange with more senior scientists. The event is organized by the INRA research groups in Avignon and Sophia-Antipolis, and the University of Avignon. Book these dates! (even if you’ve been to Avignon before)

A website will open in late January with all practical facts.

The organizers * Its purpose is to bring together smooth and wrinkled... evolutionary biologists.

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Bonjour Ã tous,

Vous nâavez jamais vu le pont dâAvignon ? Super : la 34eme Ã©dition du Petit Pois DÃ©ridÃ© sera organisÃ©e par les Ã©quipes INRA de Sophia et Avignon ainsi que lâUniversitÃ© dâAvignon et des Pays du Vaucluse et se tiendra du 28 au 31 aout 2012 Ã Avignon. Bloquez ces dates sur vos agendas !

Le site internet ouvrira fin janvier avec toutes les informations pratiques.

Les organisateurs PS si vous avez dÃ©jÃ vu le pont, venez quand mÃme !

vincent.calcagno@sophia.inra.fr

ColdSpringHarbor NematodeEvolution Apr3-6

Happy New Year!

The 2012 Evolution of Caenorhabditis and Other Nematodes conference is just a few months away! Here are a few key reminders and updates...

The CSHL meeting website: http://meetings.cshl.edu/meetings/worms12.shtml Reminders:

The meeting will take place April 3-6 at Cold Spring Harbor Laboratories in New York, USA. The abstract deadline is January 27. Register for the meeting and submit abstracts at the meeting website.

Our keynote speaker is Marie-Anne Félix! Twelve other great diverse scientists in our research community are also featured as session chairs.

Abstracts will be evaluated by the meeting organizers, keynote speaker, and session chairs. We plan to review the abstracts in the weeks immediately following the abstract deadline (Jan 27). The final set of oral session themes will be decided upon after abstracts have been submitted and undergone initial evaluation. The final program details are due to CSH by March 1; we will plan to share the final program details with all meeting participants on or shortly after that date.

Please see the meeting website for additional details.

New Updates!

During the day on April 3rd, a pre-meeting satellite gathering of the NemaSym research coordination network will take place on the CSHL campus. The NSF-funded NemaSym is dedicated to the study of nematode-bacterium symbioses. For details, contact Dr. S. Patricia Stock at the University of Arizona: spstock[at]ag.arizona.edu.

The Nathan A. Cobb Foundation has generously provided funds for a partial travel award to support one graduate student who will present research on the evolution of plant- or insect-parasitic nematodes. We are still waiting to hear back from NIH and other funding inquiries for the meeting.

Cover art submissions! We invite the community to submit compelling images to be considered as cover art for the meeting?s program book. All are welcome to submit. Please send the image file as an email attachment to Dee Denver: denver[at]cgrb.oregonstate.edu. Cover art submissions must be sent to Dee by Feb 15.

See you in April!

Dee Denver & Mark Blaxter

– Dee R. Denver Associate Professor Department of Zoology Center for Genome Research and Biocomputing Oregon State University 3029 Cordley Hall Corvallis, OR 97331 PH: 541-737-3698 FX: 541-737-0501 http://denverlab.cgrb.oregonstate.edu/ denvedee@cgrb.oregonstate.edu

Dublin SMBE2012 Jun23-26 RNAi Evolution Deadline

Dear All,

A brief reminder that the closing date for abstract submissions and early registration for SMBE 2012 is January 27th.

We invite everyone working on the evolution of RNA silencing to consider submitting an abstract.

Details can be found here: http://www.smbe2012.org Best,

Justin Blumenstiel and Darren Obbard

Edinburgh QuantGenetics Jun17-22

4th International Conference on Quantitative Genetics Edinburgh 17-22 June 2012 http://-www.icqg2012.org.uk/ This is a reminder of the important deadlines coming up for abstracts for oral presentation and early registration discount for this exciting meeting:

DEADLINE FOR SUBMISSION OF ABSTRACTS FOR CONSIDERATION FOR ORAL PRESENTATION - 3 FEBRUARY 2012. DEADLINE FOR EARLY REGISTRATION DISCOUNT - 3 FEBRUARY 2012.

Polygenic variation in quantitative and other complex phenotypes underpins most important traits in human health and disease, agriculture, natural populations and evolution. This conference provides an opportunity to learn about the rapid advances in this field from the worlds leading researchers, as well as to present and discuss your own results. The meeting is being held in the impressive surroundings of the Edinburgh International Conference Centre at the heart of Scotlands historic capital.

To complement the conference, a series of courses from the Summer Institute of Statistical Genetics will be held in Edinburgh in the weeks commencing 11 June and 25 June. Further details will be posted on the Conference and University of Washington Summer Institute web sites.

Session titles, chairs and confirmed speakers are listed below. Further papers for oral presentation in these sessions will be selected from those submitted for consideration by 3rd February. There will be poster sessions and also opportunities for small symposia to be arranged by participants on Wednesday afternoon or at lunchtimes/early evening.

Sunday 17 June: Registration and evening mixer

Monday 18 am: The genetic architecture of quantitative traits

Chair: Bruce Walsh, Peter Visscher: From Galton to GWAS (and beyond): what have we learned about quantitative traits in human populations? Ed Buckler: Uniting the world's maize germplasm diversity for trait dissection and accelerated breeding Chair Veronica van Heyningen, Eric Lander: Genetics Society Mendel Lecture

Monday 18 pm: Evolutionary quantitative genetics

Chair: Derek Roff, Mark Blows: Evolution of genetic variance under selection Patrick Phillips: Gene interactions underlying the evolution of complex traits Jarrod Hadfield: (title to be confirmed)

Monday 18 early evening: Poster session

Tuesday 19 am: Variation in the genome

Chair: Greg Gibson Matt Hurles: Causes and consequences of new mutations Frank Johannes: Mapping the epigenetic basis of quantitative traits

Tuesday 19 pm: Advances from numerical methods

Chair: David Balding, John Storey: (title to be confirmed) Gustavo de los Campos: Whole-genome prediction of human complex traits using data from related and unrelated individuals Goncalo Abecasis: Computational analysis of thousands of human genomes: What do we need?

Tuesday 19 early evening: Poster session

Wednesday 20 am: Opportunities from technological advances

Chair: Bruce Weir Richard Durbin: Quantitative association genetics of high dimensional cellular traits: extending beyond expression QTLs Orjan Carlborg: Variance controlling genes and their role in the genetic architecture of complex traits Sergey Nuzhdin: Systems biology of genetic variation in Drosophila: InR/TOR

Wednesday 20 pm:

Free for arranging associated symposia Genetics Society postgraduate symposium

Thursday 21 am: Emerging areas

Chair: Marie-Anne Felix Nik Shork: Whole genome phasing and diploid variant annotations Others to be arranged as they emerge

Thursday 21 pm: Bridging the genotype-phenotype gap

Chair: Michel Georges Trudy Mackay: Systems genetics of quantitative traits in Drosophila Mark McCarthy: Diamonds in the dirt: biological and translational insights into type 2 diabetes from large-scale genetic studies.

Friday 22 am: Interactions among the individuals and with the environment

Chair: Mark Kirkpatrick Piter Bijma: The consequences of indirect genetic effects for heritable variation and response to selection Alastair Wilson:The genetics of social dominance: does competition cause constraint? Magnus Nordborg: Studying the genotype-phenotype map in Arabidopsis

Friday 22 pm: Genomic information in prediction

Chair: Theo Meuwissen Ben Hayes: (title to be confirmed) Chris-Carolin Schoen: Genome-based prediction in highly structured plant populations Pak Sham: (title to be confirmed)

Friday 22 evening: Banquet at Dynamic Earth

To receive further information about the conference and to note interest (pre-registration), please go to http://www.icqg2012.org.uk/ We look forward to seeing you in Edinburgh in June 2012.

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Edinburgh QuantGenetics Jun17-22 reminder

4th International Conference on Quantitative Genetics Edinburgh 17-22 June 2012 http://www.icqg2012.org.uk/ REMINDER: DEADLINE 3 FEBRUARY 2012 for submission of abstracts for consideration for oral presentation and for early registration discount

Abstracts for poster presentation only can be submitted up to 6 April 2012

Organising Committee

Loeske Kruuk <Loeske.Kruuk@ed.ac.uk>

Glasgow ParasiteEvolution Apr2-5 Deadline

Early bird registration for the British Society for Parasitology spring meeting 2012: DEADLINE IS SUNDAY 29 JANUARY.

Registration and abstract submission can be found here:

http://live.bsp.netxtra.net/news-and-events/news/-register-for-bsp-2012/

Registration include lunches, coffee and tea breaks. Ordinary member - Â£200

Student members - Â£110

Non-members - Â£280

Conference Gala dinner - Â£50

The BSP is celebrating its 50 year anniversary and has a diverse and exciting program, including an evolutionary ecology theme with sessions on:

- The ecology of microbial infections (Keynote: Brit Koskella, Oxford University, UK) - Molecular ecology of infection (Keynote: Steve Paterson, University of Liverpool, UK) - Integrating evolution and ecology into epidemiology (Keynote: Sebastian Bonhoeffer, ETH, Switzerland) - The role of host and parasite behaviours in infection (Keynote: Jaap de Roode, Emory University, USA) - and the first BES Parasites & Pathogens special interest group session on Ecology Meets Medicine (Keynote: Les Real, Emory University, USA).

Abstracts are now invited for contributed talks to the above sessions.

In addition to the evolution and ecology theme, the BSP 2012 has a broad scientific programme including the biannual Trypanosome and Leishmania seminar, Malaria, Helminth Immunology, Molecular Helminthology, Veterinary Parasitology, Mapping and Imaging Parasitology themes and much more.

The Spring Meeting opens with annual Public Understanding of Science lecture by Professor Mike Barrett followed by a civic reception at Glasgow City Chambers on the 2nd April and a Gala dinner at the world famous Kelvingrove Museum.

We hope you will join us and especially support the ecology sessions.

Dr Sarah Reece Centre for Immunity, Infection & Evolution. Institutes of Evolution, Immunology and Infection Research, School of Biological Sciences, Ashworth Laboratories, University of Edinburgh, Edinburgh EH9 3JT Scotland, UK

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sarah reece <sarah.reece@ed.ac.uk>

IST Austria HumanEvolution May7

Announcing the launch of the first IST Austria Young Scientist Symposium on the topic of human evolution on Monday May 7th 2012.

Human evolution is a topic that lends itself to a variety of approaches, such as genetics, cognition, the evolution of language and palaeontology, including extensive informatic applications. With this symposium we aim to bring together people from diverse academic backgrounds and give participants the opportunity to hear about research that they would perhaps not normally experience.

We are pleased to announce the following confirmed speakers: Bence Viola (MPI Leipzig, DE) Bill Sellers (Manchester, UK) Eörs Szathmáry (Budapest, HU) Daniel Nettle (Newcastle, UK) Johannes Krause (Tübingen, DE) Gil McVean (Oxford, UK)

This one-day event is organised by the students and postdocs of IST Austria, and will take place on the IST Austria 18km North of Vienna. Registration is free and includes lunch, and a shuttle bus will be provided too and from Vienna free of charge. There will also be an opportunity for a campus tour if you wish to take a look at the rest of what goes on at IST Austria

We are especially keen to give scientists at the start of their career the opportunity to interact with top scientists, and as the day will also include a question and answer session with the speakers at the end of the day on the future of human evolution, so that students can pitch their questions directly to the experts. Students are especially encouraged to register!

For more information and to register for this event, please see the following website: http://www.ist.ac.at/-young-scientist-symposium-2012 Note that registration is strictly limited to 140 people. Unfortunately as this is a free event, we are unable to provide funding for travel for delegates or assist with VISAs or accommodation.

Tom Ellis Am Campus 1 Institute of Science and Technology Austria A-3400 Klosterneuburg Austria

0043 (0) 2243 9000 3008

tom.ellis@ist.ac.at

KansasCity 2012ArthropodGenomics May30-Jun2 2

Registration is OPEN for the Arthropod Genomics Symposium and i5k Workshop, May 30-June 2, Kansas City. Please register online today at: http://www.k-state.edu/agc/symp2012/register.html !

<Dowload this announcement as a PDF: http://www.k-state.edu/agc/symp2012/images/-Announcement#3.pdf >

--*-*-* Sixth Annual Arthropod Genomics Symposium*-*-*-*-*- MAY 31, 2012 (Thursday evening) to JUNE 2, 2012

Marriott on the Country Club Plaza, Kansas City Symposium website: http://www.k-state.edu/agc/-symp2012 Keynote Speaker: + Gene E. Robinson, Entomology and Institute for Genomic Biology, University of Illinois at Urbana-Champaign; Understanding the Relationship between Genes and Social Behavior: Lessons from the Honey Bee

Featured Speakers (confirmed): + William E. Browne, Biology, University of Miami + Angela E. Douglas, Entomology, Cornell University; From Metagenomes to Function in Animal-Microbial Symbioses + Giles E. Duffield, Biological Sciences and Eck Institute for Global Health, University of Notre Dame; Circadian and Light Regulation of the Mosquito Transcriptome + Miodrag Grbic, Biology, The University of Western Ontario, London, Canada and Research Center of Vine- and Wine-related Science, LogroÃ±o, Spain;The Genome of the Two Spotted Spider Mite Tatranychusurticae: New Model for Plant-pest Interactions + Marc S. Halfon, Biochemistry, University at Buffalo-State University of New York and NY State Center of Excellence in Bioinformatics & Life Sciences; Regulatory Element Discovery in Sequenced Insect Species + Michel R. Kanost, Biochemistry, Kansas State University; Initial Insights from the Manducasexta Genome + Karl Kjer, Entomology, Rutgers University;Bernhard Misof, Zoological Research Museum Alexander Koenig, Bonn, Germany; Xin Zhou, BGI, Shenzhen, Guangdong Province, China; The 1KITE Insect Transcriptomics Initiative + S. R. Palli, Entomology, University of Kentucky; Functional Genomics of Juvenile Hormone Action + Jason L. Rasgon, Entomology, The Pennsylvania State University + David W. Severson, Eck Institute for Global Health and Department of Biological Sciences, University of Notre Dame; “Dengue Virus Vector Competence and Functional Genomics in Aedes aegypti” + Additional speakers will be announced soon!

The symposium focuses on new insights gleaned from analyzing arthropod genomes and is designed for scientists interested in genomic studies of Arthropods, both model organisms and those of agricultural or health relevance. The program will include platform presentations, a welcome reception, a bioinformatics-related workshop and arthropod genomics-related poster sessions. A few poster abstract submissions will be selected for oral platform presentations. Postdoctoral, graduate, and undergraduate students are also encouraged to attend.Sessions conclude Saturday evening, followed by an optional Kansas City Barbecue banquet.

--*-*-* New this year: i5k Community Workshop*-*-*-*-*- MAY 30, 2012 (Wednesday morning) to MAY 31, 2012 (Thursday afternoon)

i5k Community Workshop:An international effort to sequence 5,000 of the worlds key arthropod species.The Workshop will aim to bring together biologists, informaticists, and policy-makers to discuss and contribute to advance planning for the i5k initiative. Plans for the i5k Workshop include presentations by top genomics and bioinformatics researchers and representatives from the primary sequencing centers, followed by training and breakout sessions focused on i5k and other successful insect genome projects. The Workshop will conclude with a discussion of white papers and programmatic steps needed to enact i5k projects.<Download Flyer at http://arthropodgenomes.org/w/images/b/bd/i5kFlier122011.pdf >.

POSTER ABSTRACT DEADLINES IN 2012: Wednesday, February 29 If you DO wish your poster abstract to be considered for a General Session talk. Friday, March 30 - If you do NOT wish for your poster abstract to be considered for oral presentation during the General Session.

TENTATIVE PROGRAM for SYMPOSIUM & i5k WORKSHOP Wednesday, May 30 i5k Community Workshop 7:15-8:15 am Registration 8:30 am -5:30 pm Speaker sessions 7:30 pm-10:00 pm Poster session Thursday, May 31, 8:30 am-5:00 pm i5k Workshop continues with breakout groups, common session, and report-backs Thursday evening, May 31, 7:30 pm Arthropod Genomics Symposium begins with keynote presentation and welcome reception Friday, June 1 Arthropod Genomics Symposium Platform and Poster Sessions 5:30-7:30 pm - Symposium Workshop Evening, June 1 Dinner on your own

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Lisbon BehavioralEvolution Apr12-13 DEADLINE Jan15

We are pleased to announce that the next conference of the Portuguese Ethology Society will take place on 12-13 April 2012 in Lisbon, at the Faculty of Sciences and is organized by the Centre for Environmental Biology.

This meeting will bring together contributions from several related fields - Ecology, Evolution, Development, Physiology and Neuroscience - and several animal groups - unicellular, invertebrates, vertebrates, mammals, humans. The meeting aims to provide an integrative vision of the study of animal behaviour, to provide an updated overview of the research being conducted in Portugal in this field and to promote the interaction between researchers and students.

DEADLINE FOR ABSTRACT SUBMISSION: 15 of JANUARY 2012

For more information (including invited speakers) see:

http://spe2012.fc.ul.pt/EN/index.html Hope to see you there!

The organizing committee

Joana Jordão, CBA, FCUL

Rita Covas, CiBio, UP

Rita Ponce, CBA, FCUL

Sara Hagá, FP-UL

Susana Varela, CBA, FCUL

anaritaponce@gmail.com

LundU BehaviourEvolution Aug12-17

Dear evolutionary biologists,

On behalf of the organisers, we welcome you to to the International Behavioural Ecology Congress (ISBE) that will take place between August 12 and August 17 in Lund (Sweden). We have an exciting scientific programme and hope to see many of you in Lund this summer!

The registration for the meeting is now open here:

http://www.isbe2012lund.org/registration/ NOTE: Deadline for Abstract submission is March 15, 2012.

Also, note that we accept proposals also for “Post-conference” symposia. These one-day symposia take place on August 18, 2012. Deadline for submissions of proposals for post-conference symposia is January 31, 2012. Please find more information here:

http://www.isbe2012lund.org/post-conference-symposia/ Sincerely yours,

Erik Svensson & Anders Hedenström (Scientific committé of ISBE)

Erik Svensson Professor (Evolutionary Ecology) Department of Biology, Lund University SE-223 62 Lund SWEDEN

Phone: +46 46 222 38 19 Fax: +46 46 222 47 17 E-mail: erik.svensson@zooekol.lu.se

Webpage: http://www.lu.se/o.o.i.s/26007 Lab blog: http://svenssonresearchlaboratory.blogspot.com/ Researcher ID: http://www.researcherid.com/rid/E-8324-2010 Erik Svensson <Erik.Svensson@biol.lu.se>

Miami Biogeography Jan9-13

First announcement for the 6th Biennial Conference of the International Biogeography Society

Kovens Convention Center, Miami, Florida, USA

January 9th-13th, 2013

Registration, abstract submission for symposia and contributed papers will open in July 2012.

The core of the meeting will be four successive symposia on broad foundational and cutting-edge topics and approaches in biogeography and macroecology, each with a suite of leading international scientists as well as openings for contributed papers - Beyond Bergmann: New perspectives on the biogeography of traits - Island Biogeography: new syntheses - Predicting species and biodiversity in a warmer world: are we doing a good job? - Conservation paleobiology: using knowledge of past ecosystems to inform conservation priorities

The meeting also will have 12 sessions of contributed papers on key topics including and not limited to: (i) Neotropical biogeography, (ii) Climate change biogeography, (iii) Paleo-biogeography, (iv) Phylogeography, (v) Marine biogeography (vi) Disturbance regimes and biogeography, and (vii) Global biogeography

Schedule: 9th January: Workshops and fieldtrips 10th - 11th January: Symposia and poster sessions 12th January: Contributed papers 13th January: Post-conference field trips

A keynote lecture will be given by the Alfred Russel Wallace Award winner, recognizing a lifetime of outstanding contributions to biogeography.

On the day just before and after the conference (9th and 13th January), there will be arranged field excursions to a number of protected natural areas including Everglades National Park. In addition, on 9 January, several workshops will be held (topics currently in development).

Preliminary information on the venue and lodging is available on the International Biogeography website: http://www.biogeography.org/html/Meetings/-2013/index.html The International Biogeography Society (IBS; http://www.biogeography.org/) is a non-profit organization, founded in 2000, with the mission to:

Foster communication and collaboration between biogeographers in disparate academic fields. Increase both the awareness and interests of the scientific community and the lay public in the contributions of biogeographers. Promote the training and education of biogeographers so that they may develop sound strategies for studying and conserving the world's biota.

Michael N Dawson mdawson@ucmerced.edu

dawson.mn@gmail.com

Montpellier MathEvolBiol Jun18-22 registration

SECOND ANNOUNCEMENT REGISTRATION WILL BE CLOSED BY THE END OF FEBRUARY

Mathematical and Computational Evolutionary Biology June 18-22, 2012, Hameau de l'Etoile (France) http://www.lirmm.fr/mceb2012/ The subject is evolution, which is considered at different scales, from genes to populations. The focus is on the mathematical and computational tools and concepts, which form an essential basis of evolutionary studies. The meeting will bring together researchers originating from various disciplines: mathematics, computer science, phylogenetics and population genetics. Ten keynote speakers will introduce a field of research and discuss their own work in this field. Afternoon will be for short presentations and posters, with plenty of time for discussions, hiking and visits. The number of attendees will be limited (˜60) to favor exchanges.

The meeting will take place at Hameau de l'Etoile, in the Montpellier region (France). The dates are June 18-22, that is, just before SMBE 2012 that starts June 23 in the evening at Dublin (Ireland). Conference fees including accommodation (4 nights, 18 to 22), meals, coffee breaks, buses, etc., will range from ˜300 to ˜425 depending on the room type. Some financial support will be available for local fees of PhDs and postdocs

Keynote speakers:

* Michael Blum (CNRS - TIMC, FR). Approximate Bayesian Computation: theory, algorithms and applications.

* Oliver Eulenstein (Iowa State University, US). Supertrees and phylogenomics.

* Arnaud Estoup (INRA - CBGP, FR). ABC (Approximate Bayesian Computation) methods to make inference about population history from molecular data: principles and applications.

* Vincent Moulton (University of East Anglia, UK). Recent progress on phylogenetic networks.

* Rasmus Nielsen (Berkeley, US). Models and methods to reveal molecular adaptation.

* Noah Rosenberg (University of Michigan, US). Models and methods at the intra/inter species frontier.

* Alexandros Stamatakis (Heidelberg, DE). High Performance Phylogenetics.

* Mike Steel (University of Canterbury, NZ). Probabilistic models of evolutionary trees.

* Edward Susko (Dalhousie University, CA). Testing phylogenies.

* Simon TavarÃ© (Cambridge University, UK). From evolutionary biology to development and cancer.

Organizers: Olivier Gascuel and Jean-Michel Marin

See the web site for more details and pre-registration (before Feb 25)

Gascuel Olivier <gascuel@lirmm.fr>

Oleron France Wolbachia Jun7-14 registration

The 7th Wolbachia conference and the EU COST FA0701 final meeting will be held at Oleron Island France from June 7 (arrival day) to June 14 (departure day). The island is on the Atlantic coast of France, facing La Rochelle. It is connected to the main land with a road bridge. La Rochelle can be reached by train (TGV) or by plane.

Details on registration, shuttle organization, accomodations etc... are available on the Wolbachia2012 website < http://wolbachia2012.conference.univ-poitiers.fr/ >

It might be useful to bookmark this website, where further information will also be provided.

The deadlines are: - Abstract Submission = April 1st - Registration = April 15th - Shuttle organization upon arrival = May 1st

See you soon in Oleron Island,

For the Wolbachia and COST committees, Didier Bouchon and Kostas Bourtzis

– Pr. D. Bouchon

Universite de Poitiers Ecologie et Biologie des Interactions, UMR CNRS 7267 equipe Ecologie Evolution Symbiose 40 avenue du Recteur Pineau F-86022 POITIERS Cedex tel : +33 (0)5 49 45 38 95 fax : +33 (0)5 49 45 40 15 http://ecoevol.labo.univ-poitiers.fr/ http://pbildb3.univ-lyon1.fr/endosymbart/ Didier Bouchon <didier.bouchon@univ-poitiers.fr>

Ottawa Evolution Jul6-10 InfluentialSymbionts

Dear Evoldir Community

Wolfgang Miller and I (David Hughes) are convinced that symbionts generally thought of as benign may play an important role in altering host behavior. We are all becoming more familiar with the increasing studies on parasites adaptively controlling host behavior. It is easy to see why they evolved and it will be fun to figure out how they do it. But what of the many other selfish genetic elements from transposable elements to virus to bacteria that cohabit in animal bodies. How much do they impact behavior?

We think it is an interesting challenge to look for such manipulators or therefore are organizing a symposium at Ottawa entitled Influential symbionts: Master manipulators of adaptive host behavior

We have two slots left and since our whole symposia is about finding things you didn't really know you were looking for we thought to again throw the net out to catch someone. Are you working on any aspect of symbiosis (frankly that is everyone) that affects behavior?

Please let us know if you are interested.

dhughes@psu.edu wolfgang.miller@meduniwien.ac.at

David Hughes Department of Entomology and Biology Penn State http://ento.psu.edu/directory/dhughes http://www.cidd.psu.edu/people/dph14 dhughes@psu.edu

David Hughes <dph14@psu.edu>

Ottawa JointCongressEvolutionaryBiol Jul6-10

1st Joint Congress on Evolutionary Biology July 6-10, 2012; Ottawa, Canada www.evolution2012.org The 1st Joint Congress is a merging of the traditional 'Evolution meeting' (the annual meeting of the American Society of Naturalists, the Society for the Study of Evolution, and the Society of Systematic Biologists) with the annual meeting of the Canadian Society for Ecology and Evolution, and the meeting of the European Society for Evolutionary Biology.

REGISTRATION, TALK/POSTER SUBMISSION, AND ACCOMMODATION BOOKING WILL ALL BE OPENING IN EARLY FEBRUARY (a reminder will be sent at that time)

DEADLINE FOR EARLY REGISTRATION DISCOUNT: 30 APRIL 2012

Highlights - The meeting will be held at the state-of-the-art, newly opened Ottawa Convention Centre situated in the heart of downtown Ottawa. - Childcare will be available onsite at the congress venue. - Affordable residence accommodation at the University of Ottawa, only a short walk from the congress venue, and an array of hotel options. - A plenary address and two symposia sponsored by each society. - With the joint participation of the CSEE and the ASN, we welcome, and look forward to, increased participation by our ecologists. - Various optional pre- and post-congress workshops/symposia, along with the iEvoBio satellite conference (July 10-11). - Final congress dinner and farewell party (no speeches) at the spectacular Canadian Museum of Civilization. - Travel support available for graduate students and for researchers working in countries with low GDP (Note: deadlines imminent for the latter).

For more details, visit www.evolution2012.org . We look forward to seeing you in July.

Conference organizers:

Howard Rundle (uOttawa) Andrew Simons (Carleton University)

Howard D. Rundle, Associate Professor Department of Biology, 30 Marie-Curie Priv. University of Ottawa, Ottawa, ON, K1N 6N5, CANADA Ph: +1 613-562-5800 x2835; Fax: +1 613-562-5486 Skype: howarddrundle http://www.science.uottawa.ca/~hrund050 http://www.evolution.uottawa.ca howard.rundle@uottawa.ca

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Perth EvolPlantSignalling Sep16-21 Abst Mar1

Dear all,

Submission of abstracts for the 1st Symposium on Plant Signalling & Behaviour (September 16th-21st 2012 in Perth, Western Australia) is NOW OPEN!

We invite everyone conducting exciting research in the field of plant physiology, evolutionary biology and behavioural ecology - from the world of molecules to the broad processes underlying species interactions and co-evolution - to consider submitting an abstract to this inaugural meeting.

The Symposium will cover themes such as Plant Cell Biology & Signalling, Plant Sensory & Behavioural Ecology, and Theoretical Botany.

Featured speakers (confirmed):

* Sonia Sultan (Evo-devo in plants - Wesleyan University, USA)

* Corne' Pieterse (Plant-Microbe Interactions - Utrecht University, Netherlands)

* Pamela Lyon (Evolution of embodied cognition in plants - University of Adelaide, Australia)

* Rick Karban (Plant behaviour ecology - University of California Davis, USA)

* Frantisek Baluska (Plant cell biology - University of Bonn, Germany)

* Stefano Mancuso (Plant electophysiology - University of Florence, Italy)

More details can be found here: http://spsb2012.com/ ...and keep checking the site as there is much more to come!!

We hope you will join us!

Monica Gagliano SPSB2012 Convenor

Monica Gagliano <monica.gagliano@uwa.edu.au>

Prague PolyploidyBiodiversity May7-10 reminder

Hello all,

As a member of the Scientific Committee for the International Conference on Polyploidy, Hybridization, and Biodiversity taking place in Pruhonice (near Prague), Czech Republic on 7-10 May 2012, I am writing to remind potential attendees to submit their abstracts in time for the early registration deadline of 31 January, 2012. Abstracts from all relevant areas are encouraged, but we are particularly interested in abstract submissions from studies involving animal, fungal, or microbial systems.

You can learn more about the conference at the official website: http://icphb2012.ibot.cas.cz/index.html Please email me (maurine-neiman@uiowa.edu) or the main conference organizers (http://-icphb2012.ibot.cas.cz/contacts.html) with any questions.

Sincerely, Maurine Neiman

Maurine Neiman Assistant Professor Department of Biology University of Iowa 143 BB, Iowa City IA, 52242, USA maurine-neiman@uiowa.edu http://-www.biology.uiowa.edu/neiman/ "Neiman, Maurine" <maurine-neiman@uiowa.edu>

Roscoff France EvolutionaryGenomics Mar31-Apr4 3

A Jacques Monod Conference entitled "Theoretical and empirical advances in evolutionary genomics" will take place at Roscoff (Brittany, France) from March 31 to April 4, 2012.

!!!Deadline for registration is JANUARY 10TH 2012!!!

Jacques Monod Conferences, organized by CNRS, are known for the high scientific quality of the talks and discussions, in a relaxed atmosphere, in a beautiful site. The conference will cover topics in population genomics, evolutionary genomics, and evolutionary systems biology. The list of invited speakers is given below. Information about the conference and how to register is available at http://www.cnrs.fr/-insb/cjm/cjmprog_e.html The organizers: Juliette de MEAUX (Muenster University, juliette.de.meaux@uni-muenster.de) and Xavier VEKEMANS (University Lille 1, xavier.vekemans@univ-lille1.fr) Co-organizers: Guillaume ACHAZ, Laurent DURET, Oscar GAGGIOTTI, Nicolas GALTIER, Lluis QUINTANA-MURCI, Olivier TENAILLON, Renaud VITALIS

Invited speakers: BALDING David - London, UNITED KINGDOM Kinship, heritability and genetic effect sizes BELDADE Patricia - Leiden, THE NETHERLANDS Genetic and developmental mechanisms underlying the evolutionary diversification of adaptive traits BLUM Michael - Grenoble FRANCE Major axes of genetic differentiation in humans CARBONE Alessandra - Paris, FRANCE miRNA clusters and their functional organization in human chromosomes DURET Laurent - Villeurbanne, FRANCE Recombination, biased gene conversion and the evolution of the human genome DUTHEIL Julien - Montpellier, FRANCE One genome to infer them all: single-individual population genetics at the genome level EXCOFFIER Laurent - Bern, SWITZERLAND Effect of spatial processes on human diversity GLEMIN Sylvain - Montpellier, FRANCE Evolution of nucleotide landscapes in flowering plants: causes and consequences GORDO Isabel - Lisbon, PORTUGAL Fitness effects of mutations in E. coli. HEYER Evelyne - Paris, FRANCE Cultural Transmission of behaviours and genetic diversity in Human KAESSMANN Henrik - Lausanne, SWITZERLAND The evolution of mammalian tissue transcriptomes LANDRY Christian - QuÃ©bec, CANADA Evolution of Protein Interactomes LASSIG Michael - Cologne, Germany Evolutionary genomics of influenza A LOUDET Olivier - Versailles, FRANCE Decoding the complexity of quantitative natural variation for growth and response to the environment in Arabidopsis thaliana MAKSE Hernan - New York, USA Modeling the evolution of protein interaction networks. McLYSAGHT Aoife - Dublin, IRELAND Positionally biased gene loss after whole genome duplication NORDBORG Magnus - Vienna, AUSTRIA Genomic patterns of variation in Arabidopsis thaliana PATERSON Nick Boston, USA Using exact ascertainment and joint spectra to learn human genetic history PETROV Dmitri - Stanford, USA Genomic studies of adaptation in Drosophila and humans QUINTANA-MURCI Lluis - Paris, FRANCE Modes of subsistence and the landscape of African genomes ROCHA Eduardo - Paris, FRANCE Population genomics of prokaryotes SCHMID Karl - Stuttgart, Germany Genomics of local adaptation in the model plant Arabidopsis thaliana SCHMITT Johanna - Providence, USA Mapping local adaptation in Arabidopsis thaliana SUNYAEV Shamil R. - Boston, USA Title to be specified TENAILLON Olivier - Paris, FRANCE The diversity of adaptive convergence in experimental bacterial populations WHEAT Christopher W. - Helsinki, FINLAND Functional genomics of dispersal and fitness variation in the wild WITTKOPP Trisha - Michigan, USA Genomic sources of regulatory variation

Prof. Dr. Juliette de Meaux Plant Molecular Evolution Institute for Evolution and Biodiversity Hüfferstr. 1 48149 Münster

Tel: +49(0)251 83 21 095

juliette.de.meaux@uni-muenster.de

Juliette de MEAUX <juliette.de.meaux@uni-muenster.de>

Roscoff France EvolutionaryGenomics Mar31-Apr4 Deadline Jan10

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Rovaniemi Finland RodentEvoDevo Jul16-20

The 13th Rodens et Spatium

International conference on rodent biology

It will take place in Rovaniemi (Finland), July 16-20, 2012.

All fields in rodent biology are welcome. For more details on program, travel, registration and accommodation, please, visit our web site at

http://www.metla.fi/rs13

Symposium announcement

Evolution and development in small mammals

Montuire Sophie1,2 & Renvoisé Elodie3

1Biogeosciences laboratory (UMR CNRS 5561), University of Burgundy, 6 Bld Gabriel 21000 Dijon, France

2Paleodiversity and Evolution laboratory, Ecole Pratique des Hautes Etudes, 6 Bld Gabriel 21000 Dijon, France

3Evolutionary and Development laboratory, Institute of Biotechnology, University of Helsinki, P.O. Box 56 (Viikinkaari 9), 00014 Helsinki, Finland

A strong connection between phenotypic evolution and developmental mechanisms (gene regulation, protein interactions, mechanical constrains) of rodents is increasingly used to describe and explore the links between micro- and macroevolution. The classical mouse model is no longer the single best-suited model for explaining the evolution and development of rodent phenotypes (skulls, bones, teeth). Hence, the diversity of small mammals used, both by paleontologists and developmental biologists, is increasing: Cricetidae (Cricetus, Microtus, Myodes), Muridae (Mus, Apodemus), Soricidae (Sorex, Crocidura)... This symposium seeks to enable both paleontologists and biologists to share their cutting-edge experience and knowledge of small mammal evolution and development. We hope to increase interactions between these two group of researchers through their combined interests in the fast evolving rodents.

Pr. Sophie Montuire EPHE & UMR CNRS 5561 Biogéosciences Université de Bourgogne 6 Bld Gabriel 21000 Dijon Tél.: 33. (0)3.80.39.63.47 Fax : 33. (0)3.80.39.63.87 Sophie.Montuire@u-bourgogne.fr http://www.u-bourgogne.fr/BIOGEOSCIENCE/ http://www.ephe.sorbonne.fr Paleontological database http://transtyfipal.u-bourgogne.fr/ Sophie Montuire <sophie.montuire@u-bourgogne.fr>

ULiverpool EvolutionaryEcol Mar29-30

NEYEES : North Of England Young Evolutionary Ecologists Symposium 2012

University of Liverpool 29-30th March 2012

Dear Colleagues,

We would like to invite all non-tenured (post-grad - fellow) researchers currently working in the North of England to a one-off symposium held at the Institute for Integrative Biology, University of Liverpool. NEYEES aims to bring together early career researchers working in the Evolutionary Ecology field in order to promote the sharing of ideas and approaches between neighbouring institutions.

The symposium will span 2 days, with a total of 20 talks. As a guideline, sessions will be divided up into 5 themes; Molecular Evolution, Symbiont Evolution, Sex and Life Histories, Population Biology and Adaptation to changing environments

These themes are guidelines however, and any talks not fitting into these subjects will not be disadvantaged.

Confirmed speakers: Chris Wilson (Imperial College London) Kayla King (University of Liverpool) Penny Haddrill (University of Edinburgh)

All attendees are invited to submit an abstract, and registration and abstracts should be submitted by the 19th February. To register and for more details, please visit http://pcwww.liv.ac.uk/~eharriso/ We have capped attendance at 25 people to make sure that we maintain an intimate atmosphere, so be sure to register early to be sure there is space!

We hope to see you there

Ellie Harrison and Ewan Minter

ellie.harrison@liverpool.ac.uk

UStrathclyde EvolutionParasites Apr2-5

Early bird registration for the British Society for Parasitology spring meeting 2012: DEADLINE IS SUNDAY 29 JANUARY.

Registration and abstract submission can be found here:

http://live.bsp.netxtra.net/news-and-events/news/-register-for-bsp-2012/

Registration include lunches, coffee and tea breaks. Ordinary member - £200

Student members - £110

Non-members - £280

Conference Gala dinner - £50

The BSP is celebrating its 50 year anniversary and has a diverse and exciting program, including an evolutionary ecology theme with sessions on:

- The ecology of microbial infections (Keynote: Brit Koskella, Oxford University, UK) - Molecular ecology of infection (Keynote: Steve Paterson, University of Liverpool, UK) - Integrating evolution and ecology into epidemiology (Keynote: Sebastian Bonhoeffer, ETH, Switzerland) - The role of host and parasite behaviours in infection (Keynote: Jaap de Roode, Emory University, USA) - and the first BES Parasites & Pathogens special interest group session on Ecology Meets Medicine (Keynote: Les Real, Emory University, USA).

Abstracts are now invited for contributed talks to the above sessions.

In addition to the evolution and ecology theme, the BSP 2012 has a broad scientific programme including the biannual Trypanosome and Leishmania seminar, Malaria, Helminth Immunology, Molecular Helminthology, Veterinary Parasitology, Mapping and Imaging Parasitology themes and much more.

The Spring Meeting opens with annual Public Understanding of Science lecture by Professor Mike Barrett followed by a civic reception at Glasgow City Chambers on the 2nd April and a Gala dinner at the world famous Kelvingrove Museum.

We hope you will join us and especially support the ecology sessions.

sarah.reece@ed.ac.uk

Vancouver EVOWIBO2012

Registration is now open for EVO-WIBO 2012 at http://www.zoology.ubc.ca/evowibo . EVO-WIBO is a scientific meeting for the evolutionary biologists of the Pacific Northwest. Every other year, between 120 and 140 scientists, primarily from Washington, Idaho, British Columbia, and Oregon, meet to share ideas.

This years conference is generously sponsored by the American Society of Naturalists, the Canadian Society for Ecology and Evolution, and the Biodiversity Research Centre at UBC. Students who are members of either ASN or CSEE will receive substantial discounts (greater than annual membership fees) for the meeting.

Registration will be open until March 21, 2012. Accommodation (and to some extent talk slots) will be allocated by order of registration. Payment needs to be by check to the address given on the web-page (or by internal payment for UBC attendees). Please register soon.

There is a small downloadable poster at the web-site. If you feel that others at your institution would like to hear about this meeting, please consider posting the poster or forwarding this e-mail to the appropriate local mailing lists.

We hope to see you at EVO-WIBO 2012!

Thanks,

Michael Whitlock <whitlock@zoology.ubc.ca>

GradStudentPositions

Duesseldorf PlantEvolutionaryGenetics

PhD position in Duesseldorf, Germany: Plant evolutionary genetics

A PhD position is available in the lab of Prof. Laura Rose at Heinrich Heine University in Duesseldorf. In my lab, we are investigating the molecular evolution of wild tomatoes. A PhD position, funded by the German Science Foundation (DFG), is available immediately to work on this project. This project has both experimental and computational components and will involve next generation sequencing of two sibling species of wild tomatoes. Applicants should have a Master's degree or equivalent in biology or a related field. Previous laboratory experience and coursework in evolutionary biology and genetics are desirable.

The lab is located in Düsseldorf at Heinrich Heine University (www.populationsgenetik.hhu.de/unser-team). Here you will have access to state-of-the-art research facilities and the added benefit of joining the newly established plant biology graduate program (www.igrad-plant.uni-duesseldorf.de/People). The working language of the research group is English.

The target date for applications is February 6, 2011, or when the position is filled. Applicants should send a single PDF file containing a statement of interest and previous research experience, curriculum vitae, and contact information for at least two referees to Laura.Rose@hhu.de

Prof. Dr. Laura Rose

Institute of Population Genetics Heinrich-Heine-Universität Universitätsstraße 1 40225 Düsseldorf Germany

Laura.Rose@uni-duesseldorf.de

DurhamU ArabidopsisPopGenetics

PhD project funded by the BBSRC (including a research support grant of £5,000 per year) for study at

Durham University with Prof.s Rus Hoelzel & Marc Knight.

Complete applications due by 5 February 2012

Send a copy of your c.v., a cover letter, your grade transcripts, and have two letters of reference sent to Rus Hoelzel at a.r.hoelzel@dur.ac.uk. Questions can be directed to either Rus Hoelzel or Marc Knight (m.r.knight@dur.ac.uk).

Project description:

Population genetics of key determinants of drought and freezing stress in Arabidopsis thaliana.

Different accessions of Arabidopsis thaliana from around the world have been demonstrated to have very different levels of freezing and drought stress tolerance, seemingly adapted to their local climate e.g. the Cape Verde accession is very freezing-sensitive (Cook et al., 2004; Hannah et al., 2006; Gery et al., 2011). Thus the natural distribution of Arabidopsis thaliana may reflect selective pressure for local adaptation with respect to environmental stress, which should be revealed at the genetic level.

There are already full genome sequences for almost 500 accessions of Arabidopsis thaliana, this number is planned to increase to 1000 in the next year (www.1001genomes.org). This resource is freely available, allowing the in silico mining for candidate genes and SNPs to screen in comparison with neutral loci. Loci in accessions not already sequenced will be amplified, cloned and sequenced. For instance for freezing stress, key candidates would include the CBF transcription factors (McKhann et al., 2008) (shown to be the reason for altered freezing tolerance of Cape Verde accession (Cook et al., 2004)), and for drought the DREB2 and ABF transcription factors, shown in numerous laboratory studies to be key determinants of drought stress tolerance (Kim, 2006; Qin et al., 2007; Qin et al., 2008).

Patterns of population structure at functional loci can be expected to be associated with strength of selection and influence of genetic drift (which will be related to the effective population size and pattern and extent of population connectivity).

This study will compare population genetic structure at neutral and candidate functional loci for natural Arabidopsis thaliana populations across relevant environmental gradients (from the Arctic to the equator). Signals for selection will be assessed comparing the relationship between population differentiation and diversity under neutral expectations. Initial studies will be based on assessment of allele frequency, followed by analysis of expression by real-time PCR analysis. Alleles from different accessions will be transferred by genetic transformation to validate the influence of specific alleles in different genetic backgrounds.

Key objectives will include a better understanding of the strength of selection for specific candidate gene systems related to environmental stress, and the relative importance of drift and selection in different environmental contexts. The project will also seek to determine the relative importance of each genetic determinant of freezing and drought stress in the wild, evidence for which currently only comes from controlled laboratory experiments using a limited number of accessions.

Cook, D., Fowler, S., Fiehn, O., and Thomashow, M.F. (2004). A prominent role for the CBF cold response pathway in configuring the low-temperature metabolome of Arabidopsis. P Natl Acad Sci USA 101: 15243-15248.

Gery, C., Zuther, E., Schulz, E., Legoupi, J., Chauveau, A., McKhann, H., Hincha, D.K., and Teoule, E. (2011). Natural variation in the freezing tolerance of Arabidopsis thaliana: Effects of RNAi-induced CBF depletion and QTL localisation vary among accessions. Plant Sci 180: 12-23.

Hannah, M.A., Wiese, D., Freund, S., Fiehn, O., Heyer, A.G., and Hincha, D.K. (2006). Natural genetic variation of freezing tolerance in arabidopsis. Plant Physiol 142: 98-112.

Kim, S.Y. (2006). The role of ABF family bZIP class transcription factors in stress response. Physiol Plantarum 126: 519-527.

McKhann, H.I., Gery, C., Berard, A., Leveque, S., Zuther, E., Hincha, D.K., De Mita, S., Brunel, D., and Teoule, E. (2008). Natural variation in CBF gene sequence, gene expression and freezing tolerance in the Versailles core collection of Arabidopsis thaliana. Bmc Plant Biol 8.

Qin, F., Sakuma, Y., Tran, L.S.P., Osakabe, Y., Shinozaki, K., and Yamaguchi-Shinozaki, K. (2007). An Arabidopsis Ring E3 ligase D2AIP mediates the ubiquitination and degradation of DREB2A under unstressed condition. Plant Cell Physiol 48: S241-S241.

Qin, F., Sakuma, Y., Tran, L.S.P., Maruyama, K., Kidokoro, S., Fujita, Y., Fujita, M., Umezawa, T., Sawano, Y., Miyazono, K.I., Tanokura, M., Shinozaki, K., and Yamaguchi-Shinozaki, K. (2008). Arabidopsis DREB2A-interacting proteins function as RING E3 ligases and negatively regulate plant drought stress-responsive gene expression. Plant Cell

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

Gatersleben Germany MonocotApomixis

Dear evoldir,

A 3 year phd position will begin in my laboratory this coming April (2012), as part of a newly-established graduate program here at the IPK Gatersleben.

The work will involve next-generation sequencing analysis of sexual and apomictic Poa pratensis, followed by microarray development and transcriptomal profiling of reproductive tissues in sexual and apomictic accessions. The goal will be to identify candidate genes for subsequent evolutionary and functional analyses, with possible applications to barley.

The student will be registered either at (1) the Friedrich Schiller University in Jena, as part of the IMPRS for which I am faculty member (see link below), or (2) the University of Heidelberg.

If you are interested please send me your CV and 2 to 3 references whom I could contact.

The IPK is near the Harz Mountains in central Germany, which offer great hiking and mountain biking opportunities. Berlin, Hannover, Leipzig and Halle are all within a 1 to 3 hour drive away, and there are good train connections to our institute.

Best wishes Tim

****

Dr. Tim Sharbel (sharbel@ipk-gatersleben.de) Apomixis Research Group Leader Dept. of Cytogenetics and Genome Analysis Leibniz Institute of Plant Genetics and Crop Plant Research (IPK) Corrensstraße 3, D-06466 Gatersleben Germany

Apomixis Group Webpage http://www.ipk-gatersleben.de/Internet/Forschung/CytogenetikGenomanalyse/Apomixis International Max Planck Research School (IMPRS) faculty member http://imprs.ice.mpg.de/people/Faculty_Members.htm?mp=3D12 IPK Webpage www.ipk-gatersleben.de tel: +049 (0)39482 5608 fax: +049 (0)39482 5137
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GlasgowU DiseaseEvolution

PhD studentship in Glasgow University: “Invasions of the pharynx: microbiome of infected respiratory tissue”

supervisors: Jan Lindstrom, Christopher Quince and Tom Evans

The focus of infectious disease research is most often on just one organism, the pathogen. However, when pathogens encounter a host, they do not meet a sterile environment but a pre-existing and complex multi-species microbial community that either allows, facilitates or outcompetes the newcomer and consequently determines clinical outcome. in this inter-disciplinary project, we will combine the approaches of evolutionary community ecology with metagenomics to study the composition and stability of the pharyngeal microbiome and changes that viral infection, antibiotics and immunocompromise produce. The aim is to identify key factors permitting pathogen colonization and infection to assist designing and managing interventions that maintain a pharyngeal microbial community that resists such invasion and prevents disease.

Application details can be found at: http://www.gla.ac.uk/researchinstitutes/bahcm/staff/janlindstrom/janlindstrom/ Jan Lindstrom Institute of Biodiversity, Animal Health and Comparative Medicine Graham Kerr building University of Glasgow Glasgow G12 8QQ UK

informal enquiries can be sent to any of the supervisors: jan.lindstrom@glasgow.ac.uk christopher.quince@glasgow.ac.uk tom.evans@glasgow.ac.uk

HeinrichHeineU 12 EvolutionaryNetworks

12 PhD Stipends in the Graduate Research School (Graduiertenkolleg)

Evolutionary Networks: Organisms, Reactions, Molecules (E-Norm)

at the Heinrich-Heine-University Düsseldorf, Germany

The Department of Biology, the Institute of Computer Science, and the Institute of Mathematics at the Heinrich-Heine-University of Düsseldorf (HHU) are now accepting applications for 12 PhD stipends to support advanced interdisciplinary studies at the graduate level in the field of evolutionary networks.

The central goal of the interdisciplinary Graduate Research School “Evolutionary Networks: Organisms, Reactions, Molecules” (E-Norm) is to apply the conceptual and analytical framework of networks to the investigation of biological systems, spanning several levels of biological organization: genes, genomes, biochemical pathways, organisms, behaviour, and ecology. Research will focus on the formation, function, heritable properties and evolution of networks in biological systems. The participating institutes at the HHU bring together internationally leading expertise from different disciplines (Biology, Computer Science and Mathematics). Their common goal in E-Norm is to further develop the basic science and application of networks in biology with a unifying focus on evolutionary processes.

In addition to developing specialized expertise in the application and investigation of biological networks through their scientific research, successful applicants will be receive professional career preparation and soft skill training through the iGRAD programme of the HHU-D (http://www.uni- duesseldorf.de/iGRAD/).

The E-Norm programme currently encompasses 12 research projects that fall into three broader subject areas; phylogenomics, ecology, and molecules.

1. Phylogenomic networks

- Phylogenomic networks of plants

- Reassortment in Influenza A viruses

- Trends and barriers in lateral gene transfer among prokaryotes

- Significance testing and genome data analysis

- Gene transfer, metabolic transformation, and origins of higher taxa

2. Ecological and organismal networks

- Behavior and genetic network interactions under social organization

- Behavioral and ecological dynamics in competitive pollination networks

- Past diffuse co-evolution and recent interaction networks

3. Molecular networks

- Concerted protein evolution

- Demographic and selective effects on plant genome evolution

- Networks of reactions paths - the chemical master equation

- Bacterial decision strategies - effects on microbial communities.

A short outline of each research project and information about the associated institutes can be found at http://www.hhu.de/enorm/ . The stipends are valued at 1400 per month for 3 years starting May 1, 2012. Applicants should hold an undergraduate degree in Biology, Mathematics, Computer Science, Chemistry or Physics. Applications should contain:

- a one-page cover letter stating contact information and date of availability,

- a short curriculum vitae of no more than three pages in length,

- scanned copies of undergraduate degrees received, and

- the title of up to three research projects among the 12 listed, ranked in order of interest.

Applications should be submitted electronically as a single pdf file to sek-molevol@hhu.de (the office of the coordinator, Prof. Dr. William Martin) with the subject line “E-Norm Stipend”. Deadline for applications is February 29, 2012. Selected applicants will be asked to visit for an interview. All (reasonable) travel expenses in connection with the interview will be covered.

Laura.Rose@uni-duesseldorf.de

ImperialCollegeLondon QuantGenet

Dear student or professor,

We wish to inform you about the Quantitative Biology Master in Science degree in the Department of Life Sciences at Imperial College London. We would be grateful if you would consider the course yourself (students) and also forward this information to students and other parties that may be interested. We are still accepting applicants for the course for a start date of October 2011. Bursaries to help defray costs will be available.

The Quantitative Biology MSc offers a unique training in interdisciplinary approaches to modern problems in biology. The course delivers cutting edge methodological content in mathematical, statistical and computational methods, conveyed through application to important biological problems such as the modeling of interacting ecological and evolutionary processes, predicting the impact of climate change on ecological communities and the services they provide, and coevolution of hosts and pathogens.

The program is designed for students with undergraduate degrees in either biological sciences or physical sciences (mathematics, physics, computing, engineering, etc.), who are motivated by an interdisciplinary approach to biology. More details can be found by contacting the course Director, Dr. Daniel Reuman (d.reuman@imperial.ac.uk), or on the course website: http://www3.imperial.ac.uk/lifesciences/-postgraduate/courselist/quantitative-biology . The one-calendar-year course consists of an intensive six-month taught component of instruction from mathematicians and biologists, followed by a six-month full time supervised research project. The project takes place in a laboratory of the student's choosing at Imperial College London or at one of a large number of collaborating applied and academic research institutes worldwide.

Applications can be submitted now for a start date in early October, 2011. For application information, contact the course administrator, Sarah Nolas (sarah.nolas@imperial.ac.uk).

Daniel Reuman, PhD Lecturer in Ecology and Evolution Director, MSc in Quantitative Biology

Imperial College London Ecology and Evolution Silwood Park Campus Ascot, UK SL5 7PY

d.reuman@imperial.ac.uk

Kiel Germany MateChoiceSpeciation

**** PhD position: evolution of mate choice and speciation | Helmholtz Center for Ocean Research, Kiel, Germany*****

The Helmholtz Center for Ocean Research (GEOMAR) seeks to recruit a PhD student in Evolutionary Biology. The PhD student will be funded by a German science foundation (DFG) grant, entitled "/Interactive effects of environmental change and host-parasite co-evolution on the ecological speciation of sticklebacks/".

The project:

We aim at testing experimentally the relative contribution of natural and sexual selection on the process of ecological speciation using the three-spined stickleback as model organism. Both abiotic (eutrophication) and biotic (parasitism) pressures will be manipulated in large scale mesocosm experiments and ecological (mate choice) and genomic/transcriptomic changes will be followed over generations.

The project is part of the Lead Agency Program and will be performed in strong collaboration with Dr. Blake Matthews' lab (EAWAG, Kastanienbaum, Switzerland).

The candidates should:

- Be highly motivated.

- Have a master degree (or equivalent) in Evolutionary biology, Animal biology, Genetics or any related fields.

- Be interested in host-parasite coevolution, evolution of mating strategies, speciation, genomics and evolutionary consequences of climate change.

The hosting lab:

The GEOMAR is an international research institute affiliated to the University of Kiel (Germany). The working language of the department is English. The successful student will join the junior research group of Dr. Christophe Eizaguirre, which is part of a larger department led by Prof. Thorsten Reusch.

The research activities in the department are diverse and include host-parasite interactions, conservation genetics, fishery and fishery induced evolution.

The starting date for the PhD student is flexible, but a start in mid-March, 2012 is preferred. The position is offered for 3 years and follows the standard German regulations. Potential candidates are encouraged to contact Dr. Eizaguirre before submitting a full application. Applications should include a cover letter, a CV, and names of two academic references. Copies of prior publications or theses will also be considered if made available via PDF.

The GEOMAR is an equal right employer and therefore encourages applications from all possible candidates meeting the academic prerequisites.

Please submit your application by 15th Feb 2012 as a single PDF file to Dr. Christophe Eizaguirre (ceizaguirre@ifm-geomar.de).

For further information:

please visit GEOMAR's website (http://-www.geomar.de/en/)

contact Dr. Christophe Eizaguirre (http://www.ifm-geomar.de/index.php?id=ceizaguirre&L=1)

Project summary:

How human-caused environmental change affects the ecological and evolutionary processes that create and maintain biodiversity is a pressing question in biology. The eutrophication of aquatic ecosystems is a widespread and ongoing problem that has manifold consequences for sustaining critical ecosystem services, including water quality and biodiversity. The loading of nutrients (e.g. phosphorus and nitrogen) to freshwater environments not only affects their chemical and physical condition, but also influences the nature of interactions between species such as host-parasite interactions which generate local adaptation patterns and may even lead to speciation. Pervasive effects of eutrophication can alter selection regimes and therefore, cause unexpected evolutionary changes in populations over short time scales. Here, using three-spined stickleback as a model system, we focus on how the interactive effects of nutrient loading and parasites might drive rapid evolutionary changes and breakdown of local adaptation. First, using an intensive field survey along a lake productivity gradient, we will test how lake productivity co-varies with i) parasite diversity and community composition, ii) host genotype diversity, and iii) host immune system function and gene expression- testing for local adaptation of host and parasite populations. Second, using a large scale experiment in mesocosms (42 X 1000 L), we will test how contrasting natural selection regimes, resulting from orthogonal combinations of parasites and nutrient levels, can affect phenotypically and genotypically stickleback adaptive abilities. In this experiment, we focus on phenotypic and genetic traits that have been implicated in mate selection, so that we can test if the contrasting selection regimes caused by manipulating nutrients and parasites (antagonistically) synergistically might contribute to population divergence, and play a role in (reverse) speciation. This work will shed light on how natural and sexual selection are mediated by parasites and environmental conditions, and

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London EvolutionaryEpidemiology

Measuring and Modelling Information and Disease Transmission Under Anthropogenic Change

Application deadline: 10 February 2012

Supervisory Team Dr Andrew King, ajking@rvc.ac.uk, http://sites.google.com/site/andrewjkingresearch/home, Professor Dirk Pfeiffer, dpfeiffer@rvc.ac.uk, http://www.rvc.ac.uk/Staff/pfeiffer.cfm Dr Ken Eames, ken.eames@lshtm.ac.uk, http://www.lshtm.ac.uk/aboutus/people/eames.ken Dr Jon Bielby, jon.bielby@ioz.ac.uk, http://www.zsl.org/science/ioz-staff-students/dr-jon-bielby/ Project Description

The successful applicant will use carefully designed experiments and social network theory to understand and predict the responses and adaptations of gregarious freshwater fish and amphibians to human-induced environmental change. The studentship asks how these changes influence association/contact patterns and mixing in social networks, and consequently transmission of information and diseases within micro- and macro-populations. We hypothesise that changes in the environment will indirectly affect network structures, but the consequences of this are difficult to predict. Changes could increase contact rates (e.g. increased cohesion), and so heighten disease and information transmission. Conversely, changes could reduce contact rates (e.g. reduced activity), dampening disease and information transmission. Depending on the direction and magnitude of these effects, anthropogenic change could therefore result in a net costs or benefits to populations.

The successful applicant will benefit from working within a lively research environment within the Structure and Motion Laboratory and the Veterinary Epidemiology and Public Health Group at the Royal Veterinary College Hawkshead Campus. The student will acquire diverse research skills, including field and laboratory techniques and advanced data analysis/statistical skills. The project will be supervised principally by Dr Andrew King, an expert on the structure and function of animal societies. The project will take an interdisciplinary approach and the student will work closely with Prof Dirk Pfeiffer (RVC) with expertise in analytical epidemiology, advanced multivariate techniques, spatial and temporal analysis of epidemiological data, Dr Ken Eames, a mathematical biologist based in the Centre for Mathematical Modelling of Infectious Diseases (LSHTM) who is an expert on social network analyses, and Dr Jon Bielby (Institute of Zoology, ZSL) a conservation biologist whose expertise is how life-history, ecology and threat intensity interact to determine the susceptibility of a species.

For more information, or any questions, please contact

Andrew King ajking@rvc.ac.uk

References:

1. Danchin, E., Giraldeau, L-A., Valone, T.J., & Wagner, R.H. (2004) Public Information: From Nosy Neighbours to Cultural Evolution. Science. 305, 487-491. 2. Eames, K.T. (2008) Modelling disease spread through random and regular contacts in clustered populations. Theoretical Population Biology. 73: 104-11. 3. Haddadi, H., King, A.J., Wills, A.P., Fay, D., Lowe, J., Morton, A.J., Hailes, S & Wilson, A.M.(2011) Determining association networks in social animals: choosing spatial-temporal criteria and sampling rates. Behavioural Ecology & Sociobiology. 65: 1659-1668. 4. Pfeiffer, D.U., Robinson, T.P., Stevenson, M., Stevens, K.B., Clements, A.C.A. & Rogers, D. (2008). Spatial analysis in epidemiology. Oxford University Press, Oxford, UK, 208pp.

Dr Andrew King NERC Research Fellow E-mail: ajking@rvc.ac.u Website: http://sites.google.com/site/-andrewjkingresearch/ Twitter: @SHOALgroup Skype: andrew.j.king.uk

“King, Andrew J” <ajking@rvc.ac.uk>

Madrid ForestTree EvolutionaryGenomics

We offer a four year PhD student fellowship (FPI program, 2 years scholarship + 2 years research contract) in the Center of Forest Research (CIFOR) at the National Institute of Research and Agrarian and Food Technology (INIA) in Madrid, Spain (www.inia.es). Details on the project can be found at http://sites.google.com/site/-santiagocgonzalezmartinez/adapcon The candidate will take part in a coordinated project (between CIFOR and CREAF, www.creaf.uab.es) that combines different approaches to investigate the evolutionary response of two Mediterranean conifers to selection: demographic dynamics, patterns of adaption at the phenotypic and molecular levels, and modeling of the climatic niche. More specifically, the candidate will be involved in assessing the patterns of neutral and adaptive variation of the two conifer species, Pinus pinaster and Pinus halepensis, using new sequencing and genotyping technologies.

We are looking for a highly-motivated candidate with a solid background in evolutionary genetics, and ideally with previous experience in molecular approaches (DNA extraction, PCR, nuSSR and SNP genotyping). Candidates should have:

- Citizenship or legal residence in the European Union. - Master Degree in Life Sciences, Biology or Forestry. - Excellent academic records. - Knowledge of population genetics and evolutionary biology disciplines. - Language skills (high level of written and spoken English absolutely required). - Amenability for travelling and doing research stays in different labs of Europe and North America. - Full time dedication to pursuing PhD studies at a Spanish University or an International Program recognized by the Spanish Ministry of Education.

Closing date for application, February 15th, 2012.

Applications (curriculum vitae and cover letter explaining your scientific background and experience, as well as your interests) should be sent to: Delphine Grivet (dgrivet@inia.es) and Santiago C. González-Martínez (santiago.c.gonzalez.martinez@gmail.com).

For additional information, please contact: Delphine Grivet (dgrivet@inia.es).

Delphine Grivet INIA-Center of Forest Research Carretera de la Coruña, km 7.5 28040 Madrid Spain

delphine.grivet@gmail.com

Madrid SexualSelection

PhD STUDENTSHIP IN SEXUAL SELECTION AND EVOLUTION OF SPERM TRAITS AND FUNCTION

We offer a four-year PhD studentship to study the role of sexual selection on energy metabolism and oxidative stress in mammalian spermatozoa.

The study will integrate different levels: evolutionary biology, reproductive physiology, cell biology and biochemistry. The aim is to understand whether sperm competition enhances sperm energy metabolism which, in turn, generates oxidative stress in sperm.

The study involves intensive laboratory work to analyse semen quality, sperm traits, energetic metabolism, membrane composition and oxidative stress.

We are looking for candidates with a solid evolutionary background. Previous experience in reproductive physiology and/or cell biology and biochemistry would be highly desirable. A BSc degree in Biology is the required minimum. Ideally, candidates should have a

MSc degree.

If interested please send CV to Eduardo Roldan (roldane@mncn.csic.es) with a cover letter explaining your scientific background, interests, and willingness to spend a few years in Spain.

For information about previous and ongoing projects and publications see: www.gebir.csic.es Eduardo Roldan Reproductive Ecology and Biology Group Museo Nacional de Ciencias Naturales (CSIC) Jose Gutierrez Abascal, 2 28006 Madrid, Spain

"MONTSEGK@telefonica.net" <MONTSEGK@telefonica.net>

MonashU MarineInvertEvolution

PhD Positions: The evolutionary ecology and/or quantative genetics of marine invertebrates

Two fully-funded PhD stipends are available to students interested in working on the evolutionary ecology of marine invertebrates in Dr Dustin Marshall's group. I have just transferred to a position at Monash University (www.monash.edu.au) in Victoria, Australia. The stipends include all course fees plus ˜$25,000 AU per annum tax free (the equivalent of ˜$33,000 before tax) with no teaching requirements. I can guarantee funding of project costs including the costs of attending at least one conference per year. For more information about my research and current group, please see my website (www.uq.edu.au/meeg< https://legacyexchange.uq.edu.au/owa/redir.aspx?C=904e0388737b4c77b07594bebf40ca9a&URL=http%3a%2f%2fwww.uq.edu.au%2fmeeg >). Project start dates can be any time in 2012.

Interested students should send their CVs, a brief statement of their interests and the contact details of two referees (dustin.marshall@monash.edu). To be eligible, applicants must have completed at least one year of post-graduate research and ideally a masters. Preference will be given to those with strong quantitative skills.

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

Dustin Marshall <dustin.marshall@monash.edu>

MunichU PlantSystematics

Ph.D. position in plant systematics and evolutionary biology

I am looking for a Ph.D. candidate (3 yrs) interested in the evolution of plant reproductive traits, sexual systems, or plant/animal interactions. Current research topics in our group can be found at http://www.sysbot.biologie.uni-muenchen.de/en/people/renner/website.html The student would we employed according to the standard German TV-L salary scale and would be part of Munich University's graduate program in Evolution, Ecology, and Systematics: http://www.eeslmu.de/. German language skills are not required.

Munich has a large and active research community in evolutionary biology and phylogenetics, and the city offers excellent infrastructure and beautiful surroundings.

Applications are accepted from Jan. 30 onwards and until the position is filled. Please send your application, together with a full CV, copies of publications or relevant certificates, and the names of two referees to Susanne Renner (renner@lrz.uni-muenchen.de).

Susanne Renner Research: http://www.umsl.edu/~renners/ Susanne Renner <renner@lrz.uni-muenchen.de>

NTNU Trondheim EvolutionaryBiol

NORWEGIAN UNIVERSITY OF SCIENCE AND TECHNOLOGY (NTNU)

NTNU - Innovation and Creativity The Norwegian University of Science and Technology (NTNU) in Trondheim represents academic eminence in technology and the natural sciences as well as in other academic disciplines ranging from the social sciences, the arts, medicine, architecture to fine arts. Cross-disciplinary cooperation results in innovative breakthroughs and creative solutions with far-reaching social and economic impact.

Faculty of natural science and technology - Department of Biology

PhD POSITION IN EVOLUTIONARY BIOLOGY

A PhD position in evolutionary biology focusing on effective population sizes in vertebrates is available at the Centre for Conservation Biology, Department of Biology. The fellowship is financed by an Advanced Research Grant by the European Research Council to the project Stochastic Population Biology in a Fluctuating Environment for three years with the possibility of up to four years including teaching duties to the Department of Biology. The position is within the NTNU Evolution, Ethology and Ecology group (EEE): (http://www.ntnu.no/biologi/eee)

The fellowship runs under the doctoral programme at the Faculty of Natural Sciences and Technology. The faculty is the employer, and working place is Department of Biology. The Department of Biology has 36 members of faculty (professors and associate professors), 22 research scientists and about 66 PhD students and post docs. The department has research programs in evolutionary biology, population genetics, aquatic and terrestrial ecology, conservation biology and biodiversity, ethology, molecular biology, cell biology, plant and animal physiology and ecophysiology, aquaculture, and marine biology. There is considerable collaboration between the disciplines.

More information about the Department of Biology can be found at: http://www.ntnu.no/biologi/english . Project background: Effective population size is one of the basic concepts for understanding evolutionary dynamics at the molecular and phenotypic levels. The effective size of a population, Ne, determines the expected rate of random genetic drift, increase in inbreeding coefficients, and loss of selectively neutral heterozygosity, each of which is proportional to 1/(2Ne) per generation for a diploid autosomal locus. Furthermore, Ne also interacts with selection to influence the fixation probabilities of advantageous and deleterious mutations. In real populations Ne generally is substantially smaller than N, the actual population size, often by an order of magnitude, because of uneven sex-ratio, large variance in family size (greater than the mean), and temporal fluctuations in population size. Age structure effects considerably complicate the calculation of effective population size. Formulas for effective population size with overlapping generations have been derived by several authors . However, for populations exposed to natural environments, fluctuating population size is usually the most important factor reducing Ne below the actual average size. All natural populations fluctuate due to a combination of demographic and environmental stochasticity, which generally produce fluctuations in both the age structure and total size of a population. Thus, accounting for fluctuations in population size and age structure is essential for calculating the effective size of a population with overlapping generations. The candidate will work on these problems using data from long-term study systems (e.g. house sparrows and moose) as well as being part of an international network of collaborators who can provide suitable data sets

Requirements: The position require a Master degree or similar within evolutionary biology, ecology and/or biomathematics. The applicant must be qualified for the doctoral program within these disciplines. Background in population genetics, statistics and evolutionary biology will also be considered advantageous. We are looking for a hard-working candidate, highly motivated to conduct fundamental scientific research. Ability to carry out goal-oriented work, ability to deliver, oral and written presentation of research results, and good co-operation abilities will be emphasized.

In order to be accepted as a PhD student the grades of the MSc degree has to be sufficiently high (in Norway: B/2.5, or better), or the applicant has to document a similar level through later scientific work. Candidates from universities outside Norway are requested to send a Diploma Supplement or a similar document, which describes in detail the study and grade system and the rights for further studies associated with the obtained degree: http://ec.europa.eu/education/policies/rec_qual/recognition/diploma_en.html

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QueensU Phylogeography

I am looking for a motivated doctoral student to do some genomics and transcriptomics work on the spring peeper (Pseudacris crucifer), a small, broadly-distributed, spring-breeding temperate frog. This is part of a long-term study on the phylogeographic history, secondary contact zones and evolution of the mate recognition system among divergent evolutionary lineages. We already have some great data on range wide phylogeographic patterns (references below) and more recently have been looking at some secondary contact zones, testing for the signature of reinforcement using a combination of genetics and experimentation (e.g. female phonotaxis, hybridization trials). We wish to push the project innew directions and would like to look at genome-wide patterns of genic divergence in allopatric populations of differing ages of divergence, and also gene expression profiles of hybrids within contact zones.

Queen's University is a leading research-intensive institution with a strong graduate program in Ecology and Evolution, as well as Mathematical Biology. The Biology department provides stimulating academic environment with a collegial atmosphere. Queen's Biology guarantees a minimum annual stipend of $22,500. Queen's University is committed to fostering equity and diversity in the workplace.

Applicants should have a strong academic record and demonstrated ability for independent research. I especially encourage applicants with a background in population genetics and genomics with strong quantitative skills. Please send your CV, a copy of academic transcripts and a cover letter to Steve Lougheed (steve.lougheed@queensu.ca).

Phylogeographic references

Austin, J.D., S.C. Lougheed & P.T. Boag. 2004. Discordant temporal and geographic patterns in maternal lineages of eastern north American frogs, Rana catesbeiana (Ranidae) and Pseudacris crucifer (Hylidae). Molecular Phylogenetics and Evolution 32: 799-816.

Austin, J.D., S.C. Lougheed, A.A. Chek, L. Neidrauer & P.T. Boag. 2002. Cryptic lineages in a small frog. The post-glacial history of Spring Peepers, Pseudacris crucifer. Molecular Phylogenetics and Evolution 25: 316-329.

Stephen C. Lougheed Director, Queen's University Biological Station Associate Professor, Department of Biology & School of Environmental Studies Queen's University Kingston, Ontario Canada K7L 3N6 Tel: 613-533-6128 Fax: 613-533-6617 Email: steve.lougheed@queensu.ca WebPages: http://post.queensu.ca/ ~ lough http://www.queensu.ca/qubs/ lough@queensu.ca

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RoyalVetCollege ModellingDisease

Measuring and Modelling Information and Disease Transmission Under Anthropogenic Change

Application deadline: 10 February 2012

Supervisory Team Dr Andrew King, ajking@rvc.ac.uk, http://sites.google.com/site/andrewjkingresearch/home, Professor Dirk Pfeiffer, dpfeiffer@rvc.ac.uk, http://www.rvc.ac.uk/Staff/pfeiffer.cfm Dr Ken Eames, ken.eames@lshtm.ac.uk, http://www.lshtm.ac.uk/aboutus/people/eames.ken Dr Jon Bielby, jon.bielby@ioz.ac.uk, http://www.zsl.org/science/ioz-staff-students/dr-jon-bielby/ Project Description

The successful applicant will use carefully designed experiments and social network theory to understand and predict the responses and adaptations of gregarious freshwater fish and amphibians to human-induced environmental change. The studentship asks how these changes influence association/contact patterns and mixing in social networks, and consequently transmission of information and diseases within micro- and macro-populations. We hypothesise that changes in the environment will indirectly affect network structures, but the consequences of this are difficult to predict. Changes could increase contact rates (e.g. increased cohesion), and so heighten disease and information transmission. Conversely, changes could reduce contact rates (e.g. reduced activity), dampening disease and information transmission. Depending on the direction and magnitude of these effects, anthropogenic change could therefore result in a net costs or benefits to populations.

The successful applicant will benefit from working within a lively research environment within the Structure and Motion Laboratory and the Veterinary Epidemiology and Public Health Group at the Royal Veterinary College Hawkshead Campus. The student will acquire diverse research skills, including field and laboratory techniques and advanced data analysis/statistical skills. The project will be supervised principally by Dr Andrew King, an expert on the structure and function of animal societies. The project will take an interdisciplinary approach and the student will work closely with Prof Dirk Pfeiffer (RVC) with expertise in analytical epidemiology, advanced multivariate techniques, spatial and temporal analysis of epidemiological data, Dr Ken Eames, a mathematical biologist based in the Centre for Mathematical Modelling of Infectious Diseases (LSHTM) who is an expert on social network analyses, and Dr Jon Bielby (Institute of Zoology, ZSL) a conservation biologist whose expertise is how life-history, ecology and threat intensity interact to determine the susceptibility of a species.

For more information, or any questions, please contact Andrew King ajking@rvc.ac.uk

References:

1.Danchin, E., Giraldeau, L-A., Valone, T.J., & Wagner, R.H. (2004) Public Information: From Nosy Neighbours to Cultural Evolution. Science. 305, 487-491.

2.Eames, K.T. (2008) Modelling disease spread through random and regular contacts in clustered populations. Theoretical Population Biology. 73: 104-11.

3.Haddadi, H., King, A.J., Wills, A.P., Fay, D., Lowe, J., Morton, A.J., Hailes, S & Wilson, A.M.(2011) Determining association networks in social animals: choosing spatial-temporal criteria and sampling rates. Behavioural Ecology & Sociobiology. 65: 1659-1668.

4.Pfeiffer, D.U., Robinson, T.P., Stevenson, M., Stevens, K.B., Clements, A.C.A. & Rogers, D. (2008). Spatial analysis in epidemiology. Oxford University Press, Oxford, UK, 208pp.

Dr Andrew King

NERC Research Fellow

E-mail: ajking@rvc.ac.uk

Website: SHOALgroup < http://sites.google.com/site/andrewjkingresearch/ >

Twitter: @SHOALgroup

Skype: andrew.j.king.uk

SonomaStateU PopulationGenetics

Graduate Research Opportunity in Population Genetics/Evolutionary Physiology Department of Biology - Sonoma State University

A graduate student at the M.S. level is sought to work with Dr. Nathan Rank in the Department of Biology at Sonoma State University in northern California. The successful applicant will develop a thesis research project that relates genetic variation in populations of high elevation insects to their population dynamics and ecological physiology. Summer field research will be conducted in remote parts of the Sierra Nevada mountains of eastern California near Bishop, regions that are renowned for spectacular scenery and are of great conservation value.

Applicants for this graduate position should have a strong background in field research, evolutionary principles and insect biology as well as meet the admission requirements for the Department of Biology's Graduate Program (www.sonoma.edu/biology/graduate). Experience in statistical analysis and data management is also desirable.

The application deadline for the Biology Graduate Program is January 31 for the Fall semester and October 31 for the Spring semester. Details on the procedures for applying can be found at www.sonoma.edu/biology/graduate.

Graduate students in the Department of Biology are supported in a variety of ways, including teaching assistantships, in-state tuition waivers and SSU scholarships. The National Science Foundation supports the research program, and additional support for graduate students is pending.

For more information about this opportunity, contact Nathan Rank at

rank@sonoma.edu

Spain AmphibianEvolution

A 4-year PhD position in evolutionary ecology and genomics is available under the supervision of J. M. Cano < http://www.unioviedo.es/JM_Cano > and in collaboration with researchers in other European and North American labs. The general scope of the thesis is to understand the evolutionary potential of amphibian populations to withstand rapid warming and emerging diseases. The position is associated with the project "Tracking thermal and disease induced selection on the amphibian genome" (CGL2011-23443), and the FPI Programme from the Spanish Government. A suitable candidate will have a good knowledge of molecular genetics (eg. experience in the processing and analysis of genetic markers and/or transcriptomic projects) and/or statistical analysis of generalized linear models (preferably using R software).

The position will start in the second half of 2012; the salary is approx. 1100 euros per month. The candidate will carry out her/his PhD based at the Research Unit of Biodiversity < http://www.unioviedo.es/icab/index_en.html >, Mieres, Spain, and frequent travelling to UK, Finland and USA is expected. Field-work will be performed in the Cantabrian Mountains< http://en.wikipedia.org/wiki/Cantabrian_Mountains >, northern Spain and also common-garden experiments breeding and raising amphibians in controlled laboratory conditions will be also duties of the candidate.

Instructions about the application process, general requirements and eligibility will be soon published in the BOE (official Spanish bulletin of announcements) and the Ministry web page. < http://goo.gl/y1N06 >

Prospective candidates should send an e-mail to J.M. Cano (canojose@uniovi.es), including two items (in English): 1) a statement letter about their motivation to pursue a PhD in the field of evolutionary genetics and what she/he expects from her/his PhD training period and 2) a CV detailing their academic career, experience and publications if any. Please, highlight the skills relevant to the scope of this project and provide specific examples of cases where you have used them. Applicants should have a degree in Biology/Natural Sciences/Environmental Sciences and a Master degree in equivalent subjects. Driving license is helpful but not mandatory.

Brief summary of the project:

This project merges genomic, evolutionary and ecological approaches, having an emphasis on amphibian populations in montane habitats. The model species are the common frog - Rana temporaria and common toad - Bufo bufo), which are very sensitive to rapid warming and vulnerable to the occurrence of novel pathogens (i.e. Ranavirus and Batrachochytrium dendrobatidis). The general aim is at establishing a research program to characterize biodiversity at the intraspecific level.

Multiple angles will be tackled (i.e. quantitative genetic breeding designs, population genetics, 454 transcriptome sequencing and comparative linkage/QTL-mapping), aiming at providing molecular tools to track adaptation to thermal conditions and strong disease-induced selection in the wild.

The identification and monitoring of adaptive genetic polymorphisms with respect to environmental conditions will be used in the assessment of conservation value and capacity to adapt to climate change in wild populations.

José Manuel Cano Arias <canoarias@gmail.com>

UAlberta AmphibianDiversity

We are seeking an M.Sc. candidate to conduct amphibian monitoring using eDNA. Applicants must have a strong background in ecology, while experience with molecular techniques is highly desirable. The project is a joint partnership between the University of Alberta and Alberta Conservation Association, and will require strong communication skills to work in a collaborative environment. The successful applicant will have an academic track record that qualifies for a Graduate Teaching Assistantship in the Department of Biological Sciences, or an Industrial NSERC scholarship (GPA of A- or better). For more information about graduate studies in our department see http://www.biology.ualberta.ca/programs/graduate/-prospective/index.php?Page=4783 .Interested applicants should submit a cover letter expressing your research interests, CV, and an electonic copy of your academic record to Dr. David Coltman (Dept of Biological Sciences) dcoltman@ualberta.ca by 24 February 2012. Ensure the subject line in your email reads: Amphibian Monitoring DNA Research.

dcoltman@ualberta.ca

UBasel EvolutionAlpinePlants

Open PhD position in Evolutionary Biology of Alpine Plants

A PhD postion is available in the Group of Plant Population Ecology at the Botanical Institute, University of Basel in a research project with the title: "How local adaptation and phenotypic plasticity allow plants to survive in a changing Alpine landscape: Effects of fine-grained vs. coarse-grained environmental variability".

The project is a continuation of earlier research in my lab and includes reciprocal transplantation among field sites, controlled experiments in the greenhouse and molecular work. I will contribute to a still poorly understood question of evolutionary biology: To what extend is local adaptation of alpine plants shaped by phenotypic plasticity and to what extend is it a result of fixed genotypic differences?

Genotypic variability and phenotypic plasticity are complementary mechanisms adjusting plants to environmental heterogenity. Phenotypic plasticity received increased attention because of its possible role for the colonization of new habitats or to mitigate climate change. There is a shortage of studies testing the role of phenotypic plasticity in the field. The main hypotheses to be tested in this project is, that natural selection by fine-grained environmental variability should have favored high phenotypic plasticity, while coarse-grained environmental variability should have favored fixed genotypic variability.

The successful candidate should be motivated to work on alpine evolutionary ecology. Applicants with experiences in experimental population biology and a sound background in statistics will be preferred, and skills or interest in molecular work would be appreciated. Applicants should enjoy working in the field as well as in the lab. The position is funded for three years. Preferably, work starts this spring, or by arrangement. Starting salary will be CHF 40'200.- per year.

Applications including a statement of interest, CV, and the names and addresses of 2 academic references should be send to Prof. Dr. Jürg Stöcklin, Botanical Institute, Schönbeinstrasse 5, CH-4056 Basel, Switzerland. (e-mail: juerg.stoecklin@unibas.ch) http://pages.unibas.ch/botschoen/stoecklin/index.shtml . Prof. Dr. Jürg Stöcklin Botanical Institute, Dep. of Ecology, University of Basel Schönbeinstr. 6, CH-4056 BASEL Switzerland +41 61 267 35 01, juerg.stoecklin@unibas.ch http://pages.unibas.ch/botschoen/stoecklin/index.shtml Juerg Stoecklin <juerg.stoecklin@unibas.ch>

UBristol Drosophila LifeHistoryEvolution DeadlineExt

Please could you repost this? The deadline has now been extended to 24th Feb 2012.

Many thanks

UK and UK resident EU applicants are invited for a competitively-funded BBSRC studentship to begin Sept 2012

Closing date 24th February 2012.

Divergence in life history along ecological gradients in Australian rainforest Drosophilia: how does early growth affect longevity and immunity?

Supervisors: Dr Jon Bridle (University of Bristol) and Dr Nick Priest (University of Bath)

Evolution is a multiple optimisation problem: selection to optimise one trait typically has negative effects on others. Classical trade-offs include egg size and number, development rate and competitiveness, and fecundity and longevity but we lack empirical data on how consistent these correlations are across populations of the same species. Quantifying correlations between fitness traits, especially where they act differently on different life stages or genders, is critical to understand longevity and health in natural populations.

This studentship will explore how insect life histories are shaped by local selection. We are currently testing adaptive divergence in Australian Drosophila birchii along four 2-10 km ecological gradients, and are measuring 400+ isofemale lines from different altitudes for stress resistance, female fecundity and male mating success. These lines show remarkable increases in laboratory productivity at higher altitudes, implying strong trade-offs in the field. The student will examine how these traits affect the rate of ageing and the ability to resist fungal infections. Previous analyses of such Drosophila traits have revealed consistent associations between immunity, behaviour, longevity, and temperature.

We are looking for a highly-motivated student with a passion for evolutionary biology and genetics. (S)he will receive training in life history evolution theory, quantitative genetics, and modern molecular techniques, and will measure genetic variation in life history traits in Drosophila, and (most crucially) how these correlations vary among sites. In addition, (s)he will assay genome-wide linkage disequilibria in SNPs, allowing exploration of the genomic basis for these trait correlations.

This a competitively-funded studentship; funding will only be awarded to those research projects that attract the brightest and most enthusiastic candidates.

For more details, and to apply see (in the "World Class Biosciences category"):

http://www.bristol.ac.uk/science/prospective/scienceswdtp.html

For informal enquires, please contact Jon Bridle directly (jon.bridle@bristol.ac.uk)

Jon Bridle <jon.bridle@bristol.ac.uk>

UCalgary VertebrateSkeletalEvolution

The Rolian lab at the University of Calgary is looking to recruit graduate students (MSc and PhD) who are broadly interested in vertebrate evolutionary biology, evo-devo and/or bone biology.

Current research in the lab focuses on evolutionary, developmental and functional aspects of the limb skeleton in vertebrates. The core of our research program is an artificial selection experiment targeting increases in limb bone length in a rodent model. This unique resource is being developed to study evolutionary quantitative genetics (using 3D geometric morphometrics), evolutionary developmental genetics (including transcriptomics) and functional morphology (including bone biomechanics) of the limb skeleton in mammals. Individuals with a strong background and interest in evolutionary theory, vertebrate evolutionary biology or developmental biology are particularly encouraged to apply.

The University of Calgary offers a great diversity of faculty focusing on evolutionary, developmental and skeletal biology, housed across multiple faculties and departments. Graduate students at the U of C are registered through the Faculty of Graduate Studies (FGS), and can take full advantage of interdisciplinary training and research opportunities in all departments in the FGS (e.g. Biological Sciences, Anatomy and Cell Biology, Anthropology). Funding is available through the lab, as well as through the FGS, although it is expected that students will also apply for competitive external grants to support their studies and research (e.g. NSERC). Calgary is a world-class city near the Canadian Rockies, with excellent amenities and year-round opportunities for recreation and culture.

More information on the Rolian lab can be obtained at: http://homepages.ucalgary.ca/˜cprolian Information on admission requirements to the U of C FGS can be obtained at: http://www.grad.ucalgary.ca/prospective/-howtoapply Interested candidates should email Dr. Rolian (cprolian@ucalgary.ca) with a brief description of their research interests and current studies/work. Please note that the deadline for Fall 2012 admissions varies by program, with the earliest application due February 1st 2012.

Campbell Rolian Assistant Professor Dept. of Comparative Biology and Experimental Medicine Faculty of Veterinary Medicine, University of Calgary 3330 Hospital Drive NW, Calgary AB, T2N4N1 cprolian@ucalgary.ca (403) 210-3888 http://homepages.ucalgary.ca/˜cprolian Campbell Rolian <cprolian@ucalgary.ca>

UCanberra ReptileGenomics

Fully funded PhD Project Opportunities with the Wildlife Genetics Laboratory, Institute for Applied Ecology, University of Canberra

Discovering candidate sex determining genes in a reptile with genetic and temperature dependent sex determination

We are seeking potentially TWO FULLY FUNDED PhD students with interests in genomics, genetics and reproduction, molecular cytogenetics and evolution to carry out targeted and intensive molecular and functional characterisation of candidate sex determining genes in a model reptile species.

Project Description Sex determination in vertebrates is the focus of vigorous enquiry, because of its intrinsic interest as a crucial fundamental biological process. Yet, despite decades of work, we know remarkably little, in vertebrates generally, of the processes that direct sexual development down one or the other of the male or female development pathways, and sex determining genes have been identified in only a handful of vertebrate species. Non-mammalian systems are much less well understood, partly because they have received less attention, but also because of their astonishing diversity. Reptiles, in particular have a truly impressive array of sex-determining modes, compared with the conservatism of mammals and birds. Among reptiles with genotypic sex determination (GSD), male and female heterogamety (XY and ZW) is known in turtles, female heterogamety (ZW, ZZW, or ZWW) is known in snakes and both male and female heterogamety (including XXY) are known in lizards.

The aim of this project is to carry out targeted and intensive molecular and functional characterisations of candidate sex determining genes in the model reptile, the central bearded dragon (Pogona vitticeps) in order to identify key sex determining genes in this species and to use this information to dissect evolutionary mechanisms initiating sex chromosome differentiation within reptiles.

Prospective students The prospective candidate should have experience in routine molecular genetics and cytogenetics, evolutionary genetics and genomics techniques including basic knowledge with Next Generation Sequencing approaches and analyses. The prospective candidates are expected to have demonstrated capacity to learn new techniques and skills necessary for the successful completion of the project. Candidates with previous experience in working on molecular aspects of sex determination in non model species will be advantageous but not essential.

Minimum qualifications B.Sc. with first class Honours degree or equivalent in Genetics, Genomics, Molecular Biology, comparative genomics, molecular cytogenetics.

Scholarship Funding Scholarships are available for high performing students through one off special funding which includes maintenance, tuition fees exemption and basic research funding.

Eligibility These two scholarships are open to all nationalities. However, international students need to fulfill the admission criteria set by the University of Canberra including successful completion of English language test. Please see the link below for detailed about admission at the University of Canberra. http://www.canberra.edu.au/research-students/apply . Domestic students with first class Honours are eligible for university of Canberra PhD scholarship as well as top-up scholarship offered by IAE. See the link below for IAE top up scholarship. http://www.canberra.edu.au/centres/iae/ How to Apply Prospective applicants are encouraged to make informal enquiries to Associate Professor Tariq Ezaz via email. The successful applicants are expected to start in May-June 2012, however, position will remain open until filled.

Please send your Curriculum Vitae, a summary of your written scientific work, copy of your academic transcript, and the names of three referees (one of whom should be your most recent research supervisor).

Please email above documents with a covering letter to: Associate Professor Tariq Ezaz E-mail: Tariq.Ezaz@canberra.edu.au Institute for Applied Ecology (http://www.canberra.edu.au/centres/iae/index.php) (http://www.canberra.edu.au/centres/iae/staff/ezaz/ezaz-home.php)

“Tariq.Ezaz” <Tariq.Ezaz@canberra.edu.au>

UCollegeLondon BioinformaticsNGS

Project: Bioinformatics investigation of alternative splicing and gene expression evolution utilizing next generation sequence data.

*Background: *Applications are invited to join a highly energetic and collaborative research team to investigate gene expression and alternative splicing evolution in multiple vertebrate species. The post will be jointly supervised by Dr Peter Harrison and Professor Judith Mank in the Research Department of Genetics, Evolution and Environment at University College London.

The rapid development of next generation sequencing has vastly expanded our ability to study the relationship between the genome and the phenotype, thereby creating the entirely new field of comparative transcriptomics. The successful applicant will use computational approaches to study the evolution of gene expression and alternative splicing in next generation transcriptome datasets (Illumina RNA-Seq). The post-holder will also play a key role in the broader gene expression evolution analyses conducted within the group and there will be the considerable opportunity for the candidate to develop their own research interests over the course of the studentship.The group is shortly moving to a state of the art molecular genomics laboratory at UCL with access to high performance computing resources.

Requirements: The candidate should have a first or upper second-class undergraduate degree in Biology, Genetics, Bioinformatics or related discipline.Applicants should also preferably hold or expect to obtain a masters degree in Bioinformatics, Computational Biology or have equivalent experience in this area.Experience in a programming language such as Perl, Python, Java etc. is essential.This full time post is fully funded covering tuition fees and a postgraduate stipend inclusive of London weighting available to EU or UK students.

Level: 36 month, PhD Project, starting October 2012. This full time post is fully funded covering tuition fees and a postgraduate stipend inclusive of London waiting available to EU or UK students.

Supervisors: Prof Judith Mank and Dr Peter Harrison.

Application: To apply please email a CV, contact details for at least two referees and a one-page statement of research interests and previous experience in a single PDF document to Judith.Mank@zoo.ox.ac.uk. The closing date for applications is 5pm 17th February 2012, interviews will be held in mid March at UCL. The post will start in October 2012.

Information: Further details about the post and the laboratory are available at www.zoo.ox.ac.uk/group/jmank. If you have questions please contact Prof Judith Mank (Judith.Mank@zoo.ox.ac.uk).

Judith Mank Department of Zoology University of Oxford Oxford OX1 3PS

+44 (1865) 281 312

http://www.zoo.ox.ac.uk/group/jmank/ judith.mank@zoo.ox.ac.uk judith.mank@zoo.ox.ac.uk

UExeter 2 EukaryoticEvol

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Two PhD Studentship at the University of Exeter, UK.

Modelling early eukaryotic evolution using biogeochemical data ? a systems approach.

An evolutionary fluke resulting in novel and safe drugs to protect crops and humans.

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PhD Studentship at the University of Exeter, UK.

Modelling early eukaryotic evolution using biogeochemical data ? a systems approach.

Supervisors: Dr. Mark van der Giezen (Biosciences) & Prof. Tim Lenton (Geography).

It is commonly assumed that the ancestor of all eukaryotes was aerobic and acquired a mitochondrion when oxygen first rose to significant levels in the atmosphere. However, although atmospheric oxygen concentration rose in a ?Great Oxidation? of the atmosphere around 2.4 billion years ago, it only reached 1-10% of the present level, and the deep oceans remained largely anoxic and either iron-enriched or sulphidic until 580 million years ago, when the eukaryotic radiation was well underway. This new picture could explain the widespread distribution of anaerobic biochemistry in every eukaryotic supergroup.

This project will provide training in handling large-scale datasets of various strategically-chosen anaerobic eukaryotic taxa. We have the genomes of several key organisms and proven collaborations to provide access to other key genomes which have been published, or are soon to be submitted to high impact journals. Training will also be provided to use the Proterozoic Earth system model to explore the chemical composition of the ancient ocean, with particular emphasis on availability of different trace metals. This will be matched to the anaerobic biochemical potential of representative genomes, to arrive at a novel synthesis of these interdisciplinary fields.

Lenton is an expert in the coupled evolution of life and the planet and has recently developed an Earth system model of the Proterozoic Eon in which eukaryotes evolved. This model includes a 3-dimensional ocean with sediments and many geochemical tracers that can be matched to data recorded in ancient rocks to reconstruct the environments in which eukaryotes evolved. Van der Giezen is an expert in anaerobic eukaryote biochemistry and evolution and has recently reviewed energy metabolism in anaerobic eukaryotes. This is a good time to combine our expertise on the interplay between anaerobic environments and eukaryotes through a crucial interval of Earth history. We envisage several good quality publications, given that ancient ocean redox chemistry and anaerobic eukaryotic biochemistry have both been the subject of a string of high impact papers over the last ten years or so and we have been involved in several of these.

About the award We are inviting applications to commence October 2012. For eligible students the awards will cover UK/EU tuition fees and an annual stipend (in 2011/12 this was ?13,590 for full-time students, pro rata for part-time students) for at least three years.

Entry requirements Applicants for these studentships must have obtained, or be about to obtain, a First or Upper Second Class UK Honours degree, or the equivalent qualifications gained outside the UK, in a relevant subject. The studentships are only available to UK and other EU nationals (due to funding criteria, EU nationals who have not been resident in the UK for the three years prior to the start of their studentship may be restricted to a fees-only award). The awards provide funding for tuition fees and stipend, subject to eligibility.

How to apply can be found here: http://www.exeter.ac.uk/studying/funding/award/?id=923
Application deadline: 29th February 2012

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PhD Studentship at the University of Exeter, UK.

An evolutionary fluke resulting in novel and safe drugs to protect crops and humans.

Supervisors: Dr. Mark van der Giezen & Dr. David J. Studholme.

We identified a unique and novel mechanism that can be exploited to tackle major plant pathogens such as Phytophthora. This proposal addresses the BBSRC Food Security strategic priority and will provide combined training in bioinformatics and biochemistry/cell biology.

The aims are: - Identify the novel stramenopile-specific mitochondrial transport protein by comparative genomics. - Interfere with this glycolytic transporter using substrate-analogs.

We have demonstrated that in a large group of organisms, which includes major plant pathogens such as Phytophthora and the human parasite Blastocystis, the second half of glycolysis is localized in mitochondria rather than the cytoplasm.

Mitochondrial localization of the latter half of glycolysis necessitates a novel transporter. As several genomes of related organisms are available, and both supervisors have produced additional related human and plant pathogen genomes (for example the Gatsby/FERA-funded P. ramorum sequencing project aimed at understanding the pathogen that destroys our

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UExeter HostPathogenEvolution

PhD Studenthsip on the Molecular Basis and Evolution of Host-Pathogen Interaction.

This studentship provides an exciting opportunity to involve in research towards better understanding the evolution and molecular basis of host-parasite interactions. Based in the Soyer group, the successful candidate will undertake experimental and theoretical work in collaboration with the lab of Prof. Richard Titball and the research team at DSTL.

In recent years parasite interference with host pathways has emerged as a key mechanism that ensures parasites ability to infect and reproduce in the host cell. Documented examples of parasite interference come from a variety of pathogens including Taxoplasma, Leishmania, Yersinia, and Francisella tularensis and also viruses such as herpes and HIV. In this project, we will focus on the genomic and experimental idenfitifaction of pathogen interference points in the host networks and theoretical system dynamics analysis of the corresponding host sub-networks.

Application details can be found here. http://www.exeter.ac.uk/studying/funding/award/?id=912 best regards,

Orkun S. Soyer, PhD Senior Lecturer in Systems Biology Engineering, Mathematics and Physical Sciences University of Exeter Tel: +44 (0)1392 723615 URL: http://people.exeter.ac.uk/oss203/ "Soyer, Orkun" <O.S.Soyer@exeter.ac.uk>

UHawaii Hilo PlantSpeciation

Graduate Scholarship in the Tropical Conservation Biology and Environmental Science (TCBES) M.S. Program at the University of Hawai'i Hilo.

Have you earned your B.A. or B.S. in biology or a related field? Are you interested in evolution – especially of Hawaii's native species?

Join a team that examines the mechanisms of speciation using Hawaiian Metrosideros, an endemic tree species complex that appears to capture multiple stages of the speciation process. Our studies involve field, greenhouse, and lab (molecular and microscopy) methods to examine the strengths and stages of reproductive isolation among taxa, adaptive divergence among taxa, and the molecular genetic changes that accompany divergence. The graduate scholar will receive training in field and lab methods and will contribute to the overall project, while also conducting thesis research.

The successful applicant(s) will receive $22,000 annual salary, will enroll in the TCBES Program in August 2012, and will join a vibrant research community in evolutionary genetics at UH Hilo, comprising faculty, postdoctoral researchers, and graduate and undergraduate students.

Students of Native Hawaiian, Pacific Islander, or other under-represented ancestries are especially encouraged to apply. For information on the TCBES Program and application procedures, visit: www2.hawaii.edu/~tcbes/. Please direct any questions to: Dr. Elizabeth Stacy (estacy@hawaii.edu; www2.hawaii.edu/~estacy/).

Elizabeth Stacy

Associate Professor Biology Department & TCBES Graduate Program University of Hawaii Hilo 200 West Kawili Street Hilo, HI 96720

Phone: 808-933-3153 Fax: 808-974-7693

estacy@hawaii.edu

UHawaii Hilo TropicalConservationBiol

Graduate Student Positions in the Tropical Conservation Biology and Environmental Sciences (TCBES) Graduate Program at the University of Hawaii at Hilo

http://www2.hawaii.edu/~tcbes/ Priority deadline for applications to TCBES is 1 February 2012

We are looking for highly motivated students who are interested in studying the evolution and conservation of native Hawaiian *Drosophila* Flies. These are a remarkably diverse group of insects that are endemic to the Hawaiian Islands. Students working with Dr. Donald Price (donaldp@hawaii.edu; www2.hawaii.edu/~donaldp/) will develop research projects involving the Hawaiian *Drosophila* in two general areas:

1) Adaptation to elevation and temperature gradients. We are investigating the process of adaptation of several Hawaiian *Drosophila*species along multiple elevation and temperature gradients by examining phenotypic variation of behavior and morphology, physiological adaptation, neutral genetic variation (using DNA sequencing and genotyping), and gene expression among populations.

2) The process of speciation. We are investigating the mechanisms that create species and maintain species barriers utilizing several different approaches including behavioral observations, reproductive and hybridization analyses, and neutral and adaptive genetic analyses using DNA sequencing, genotyping and gene expression techniques.

Students selected for these positions will receive approximately $22,000 annual salary and will enroll in the TCBES Graduate Program in August 2012. These students will join a vibrant research community in evolutionary genetics at University of Hawaii at Hilo, comprising faculty, postdocs, and graduate and undergraduate students.

We encourage students of Native Hawaiian, Pacific Islander, or other underrepresented ancestries to apply to the Tropical Conservation Biology and Environmental Science Graduate Program at the University of Hawai'i at Hilo and join our research team.

For information on the TCBES Program and application procedures, visit: http://www2.hawaii.edu/~tcbes/. A Bachelors degree in biology is preferred with courses or experience in ecology and evolutionary biology. Priority application deadline for the TCBES Program is 1 February 2012 with applications accepted after that time if positions are available. To discuss these positions further, please contact Dr. Donald Price (donaldp@hawaii.edu).

Donald Price Director and Professor Tropical Conservation Biology and Environmental Science Graduate Program University of Hawaii at Hilo Hilo, HI 96720

808.974.7365 Fax: 808.974.7693 donaldp@hawaii.edu

Donald Price <donaldp@hawaii.edu>

UIdaho PlasmidEvolution

PhD student opportunity at the University of Idaho

A Research Assistantship is available for a Ph.D. student to work on experimental evolution studies to determine patterns of coevolution between bacterial drug resistance plasmids and their hosts. The student will work under the direction of Dr. Eva Top (Biological Sciences) and in close collaboration with Dr. Zaid Abdo (Mathematics, Statistics). This joint experimental-theoretical project is funded by the National Institutes of Health, and is highly interdisciplinary. The successful candidate will be enrolled in the Bioinformatics and Computational Biology graduate program (http://www.uidaho.edu/cogs/bcb) or the Biology graduate program (http://www.uidaho.edu/sci/biology/academics/grad) at the University of Idaho. The PhD student will also be a member of the Institute for Bioinformatics and Evolutionary Studies (IBEST) group (http://www.uidaho.edu/research/ibest) a very dynamic and collaborative interdisciplinary research group with excellent research resources.

Qualifications: Student should be highly motivated, and have a strong background in microbiology or evolutionary biology. The successful candidate should also have a serious desire to learn statistics and mathematical biology, and preference will be given to candidates who have both a strong experimental and quantitative background.

The stipend will be $21,000-22,000 per year, and tuition, fees, and health insurance will be covered as well. In addition, funds are available to attend one conference per year.

Moscow, the home of the University of Idaho, is a city of 22,000 people, nestled between Moscow Mountain and the beautiful rolling hills of the Palouse. With a small town friendliness and safety, Moscow is referred to as the "Heart of the Arts" - with an annual international Jazz Festival, live music on the town, the Rendezvous in the Park, and summer theatre. Moscow is also a great place for those who love the outdoors, with beautiful rivers, lakes, and diverse mountains within short driving distance. The University of Idaho and Washington State University, just eight miles apart, share a large number of cross-listed courses and many collaborative programs and research activities. Moscow is 80 miles from Spokane, Washington, and an hour's flight or a 5-hour drive from Seattle.

For more information about the project and graduate school requirements at the University of Idaho please Dr. Eva Top (evatop@uidaho.edu). For more information on our plasmid research, see http://-people.ibest.uidaho.edu/ ~ etop/research.html . HOW TO APPLY: For preliminary screening, email a statement of background and interests, GRE scores (if you have them), TOEFL scores (for foreign applicants), and a copy of transcripts of academic courses taken to Dr. Eva Top (evatop@uidaho.edu), no later than February 1, or apply immediately to the BCB or Biology programs. The priority deadline for Biology was December 15 but applications are still welcome; priority deadline for BCB is February 1. The position is for Fall 2012 or Spring 2013.

Dr. Eva Top Professor Department of Biological Sciences University of Idaho 258 Life Sciences South Moscow ID 83844-3051 Phone: 1-208-885-5015 Fax: 1-208-885-7905 E-mail: evatop@uidaho.edu http://-people.ibest.uidaho.edu/~etop/ evatop@uidaho.edu

UMichigan UnderRepresented EvolBiol

-Summer research opportunity for undergraduates, ED-QUE2ST: Enhancing Diversity, Quality, and Understanding of the Ecological and Evolutionary Sciences for Tomorrow http://www.lsa.umich.edu/eeb/-undergraduates/reu/ .Application deadline January 31, 2012.

-NSF-funded Frontiers Master's Program in Ecology and Evolutionary Biology, http://www.lsa.umich.edu/-eeb/graduates/frontiers.asp. Application deadline February 1, 2012 (for students beginning summer 2012).

Bethany Christoff Grad Program Asst/Recruiter Ecology and Evolutionary Biology University of Michigan 830 N. University, Room 2019

734.764.1443 (phone) 734.763.0544 (fax)

"Christoff, Bethany" <cbethany@umich.edu>

UNorthTexas EvoDevo

University of North Texas - Graduate Students

Dr. Michael Hedrickâs Lab

http://scholar.google.com/citations?user=-nPTUk60AAAAJ Our laboratory seeks students interested in pursuing a M.S. or Ph.D. in developmental biology from an evolutionary perspective. Our lab is housed within the Developmental and Integrative Biology Cluster (http://developmentalbiology.unt.edu/) in the Department of Biological Sciences (http:/-/biology.unt.edu/). We are interested in strong applicants with a background in biological sciences who are broadly interested in the comparative and evolutionary physiology of animals. Potential graduate students interested in vertebrate comparative physiology, with an emphasis on studies of respiratory or cardiovascular physiology of ectothermic vertebrates (fish, amphibians and reptiles), as well as birds and mammals, are encouraged to apply. The main focus of the lab is examines the development of respiratory rhythm generation using an in vitro brainstem model that produces spontaneous respiratory motor output. We use amphibians as the primary model, but will expand studies to include fish, reptiles and birds in the future. Students with experience using electrophysiological techniques such as intracellular/extracellular nerve recording, patch-clamping and/or intracellular calcium measurement is desired, but not necessary. Additional ongoing studies using ectothermic vertebrates include the regulation of lymph flux, the interaction between blood pressure and breathing, cardio-respiratory limits to maximal oxygen/carbon dioxide flux and the central integration of cardiovascular and respiratory inputs. We strongly encourage applications from students that hold a M.S. in a field of biology.

Interested candidates should first email a CV and/or statement of research interests to Dr. Michael Hedrick at michael.hedrick@unt.edu

Please read about our Research Clusterâs Philosophy:

http://developmentalbiology.unt.edu/philosophy Applications to UNTâs Graduate School are reviewed on a continuous basis once they are complete. Applications are processed on a rolling admissions format. For financial support purposes, completed applications must be received in the department by the following dates:

â Fall term/semester: February 15th

â Spring term/semester: October 1st

Please familiarize yourself with the websites, below, for application to UNTâs graduate program.

http://biology.unt.edu/graduate-programs/-graduate-financial-support http://biology.unt.edu/-graduate-programs/graduate-admissions http://-/biology.unt.edu/graduate-programs/graduate-admissions/how-apply http://biology.unt.edu/-graduate-programs/graduate-admissions/application-deadlines http://biology.unt.edu/graduate-programs/-graduate-admissions/departmental-acceptance-criteria http://biology.unt.edu/graduate-programs/graduate-admissions/frequently-asked-questions John Eme, Ph.D. Postdoctoral Research Associate University of North Texas Department of Biological Sciences 1155 Union Circle #305220 Denton, TX 76203-5017 http://web.mac.com/jeme John Eme <johneme34@gmail.com>

UNorthTexas EvolutionaryDevelBiology

University of North Texas - Graduate Students Dr. Dane A. Crossley IIs Lab

http://web.me.com/dcrossle/Crossley_UNT/-Welcome.html The University of North Texas Comparative and Evolutionary Developmental Laboratory is looking for students interested in pursuing a M.S. or Ph.D. in developmental biology from an evolutionary perspective. Our lab is housed within the Developmental and Integrative Biology Cluster (http://developmentalbiology.unt.edu/) in the Department of Biological Sciences (http://biology.unt.edu/). We are interested in strong applicants with a background in biological sciences, broadly interested in the comparative and evolutionary physiology of animals. Potential graduate students interested in vertebrate comparative physiology, with an emphasis on studies of lower vertebrates (fish, amphibians and reptiles), as well as birds and mammals are encouraged to apply. Experience using molecular methods is desired. We strongly encourage applications from students that hold a M.S. in a field of biology. Accepted students will have access to our colony of hatchling alligators and turtles (hatched Aug-Sept 2011) produced from eggs incubated under chronic hypoxia or hypercapnia conditions. In addition students will have access to a large frozen turtle and alligator tissue library including heart, lung, liver and kidney from different embryonic timepoints with both to chronic hypoxia or hypercapnia as the experimental manipulation. All members of the lab are encouraged to use these animals and tissues as experimental subjects.

MOLECULAR TECHNIQUES We are particularly interested in applicants who are familiar with the molecular methodologies used to quantify gene and protein expression for cardiovascular and regulatory components (receptors and enzymes) during vertebrate development. Useful techniques that a strongly qualified applicant would posses are, mRNA quantification, Western blot analysis, 2D gel electrophoresis, real time PCR, receptor binding assays, or in situ hybridization. A background in comparative, evolutionary, developmental or reptilian biology is a plus, but is not necessary. We have compiled a large, flash-frozen library (-80C) of tissues from various embryonic timepoints for turtles and alligators exposed to chronic hypoxia or hypercapnia as embryos, including heart, lung, liver and kidney tissues. Therefore, students could be able to begin molecular work quickly.

Interested candidates should first email your CV and/or statement of research interests to Dr. Dane Crossley at Dane.Crossley@unt.edu

Please read about our Clusters Philosophy: http://-developmentalbiology.unt.edu/philosophy

Applications to UNTs Graduate School are reviewed on a continuous basis once they are complete. Applications are processed on a rolling admissions format. For financial support purposes, completed applications must be received in the department by the following dates:

Fall term/semester: February 15th Spring term/semester: October 1st

Please familiarize yourself with the websites, below, for application to UNTs graduate program. http://biology.unt.edu/graduate-programs/-graduate-financial-support http://biology.unt.edu/-graduate-programs/graduate-admissions http:/-

/biology.unt.edu/graduate-programs/graduate-admissions/how-apply http://biology.unt.edu/-graduate-programs/graduate-admissions/application-deadlines http://biology.unt.edu/graduate-programs/-graduate-admissions/departmental-acceptance-criteria http://biology.unt.edu/graduate-programs/graduate-admissions/frequently-asked-questions

thanks very much

John

John Eme, Ph.D. Postdoctoral Research Associate University of North Texas Department of Biological Sciences 1155 Union Circle #305220 Denton, TX 76203-5017 http://web.mac.com/jeme John Eme <johneme34@gmail.com>

UNottingham EvolutionaryImmunology

The University of Nottingham is advertising funded four-year PhD studentships in Biosciences for UK (fees and stipend) and EU (fees only) students. These follow BBSRC strategic priorities (http://www.bbsrc.ac.uk/-funding/priorities/priorities-index.aspx), notably (1) Molecules, cells and organisms, (2) Global Food Security and (3) Industrial Biotechnology and Bioenergy. Projects of interest to prospective evolutionary biology graduate students may well be possible under (1) and (2) (see http://www.nottingham.ac.uk/biology/-index.aspx).

In particular, Dr Andrew MacColl and Professor Jan Bradley are interested in attracting students interested in the ecological and evolutionary consequences, and genetic basis of variation in parasite resistance and immunological responses to infection in natural populations of vertebrates, including three-spined sticklebacks and small mammals (eg wood mice).

Further information is available at: http://-www.nottingham.ac.uk/graduateschool/events/-doctoral-training-partnership-in-biosciences/-index.aspx and the application form is downloadable from: http://www.nottingham.ac.uk/graduateschool/-events/doctoral-training-partnership-in-biosciences/-apply-for-dtp-funding.aspx PLEASE NOTE that applications are made to the central university graduate school, and NOT to individual supervisors, although please feel free to contact us for expansion of the research ideas above.

Deadline: 15 February 2012 (noon)

Andrew MacColl

Lecturer in Evolutionary Ecology School of Biology University of Nottingham University Park Nottingham NG7 2RD Tel: +44 115 951 3410 Fax: +44 115 951 3251 Email: andrew.maccoll@nottingham.ac.uk http://www.nottingham.ac.uk/biology/research/-animal-behaviour-and-ecology/andrew.maccoll http://ecology.nottingham.ac.uk/maccoll.html Andrew.Maccoll@nottingham.ac.uk

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UppsalaU HostMicro Coevolution

PhD position in limnology, studying coevolution between a host an its gut microbiota at Uppsala University, Sweden A PhD position is available at Limnology, the Department of Ecology and Genetics, Evolutionary Biology Centre, Uppsala University, starting spring 2012.

The PhD student will work in a project studying co-evolution and co-divergence between a host (Eurasian perch) and its gut bacteria. Individuals within a population frequently specialize on different diet items. In this project, the student will for example test the effect of diet and diet shifts on individual's gut microbiota as well as the effect of the evolutionary divergence in populations on divergence in gut bacteria

For further information regarding the position and project, please contact Assistant Prof. Richard Svanbäck, e-mail: richard.svanback@ebc.uu.se

http://www.anst.uu.se/risva021/-Richard_Svanbacks_web_pages/Home.html Read the full announcement and apply via: http://-www2.personalavd.uu.se/ledigaplatser/212PHD.html or in Swedish: http://www2.personalavd.uu.se/-ledigaplatser/212doktorand.html Richard Svanbäck Department of Ecology and Genetics, Limnology Norbyvägen 18D SE-752 36 Uppsala Sweden

email: richard.svanback@ebc.uu.se homepage: www.anst.uu.se/risva021/ richard.svanback@ebc.uu.se

UppsalaU Sexually Antagonistic Variation

Uppsala University hereby invites applications for a

Postgraduate PhD position in Animal Ecology - sexually antagonistic genetic variation

at the Department of Ecology and Genetics, Evolutionary Biology Centre (EBC) with a tentative starting date being May 1^st , 2012, or as soon as possible after this date. The Evolutionary Biology Center hosts one of the world's largest aggregations of evolutionary biologists, and is a prime research environment for a wide range of fields in evolutionary biology (see "http://www.ebc.uu.se/" for more information). The working atmosphere is very international with English as our operational language. Our graduate school offers a creative and stimulating environment and is very rich in seminars, courses and possibilities to interact with other scholars and students (see "http://www.ebc.uu.se/education/") – graduate students recently ranked Uppsala University in first place among all institutions in Europe in the subject of biology (CHE European ranking). Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated 35 minutes by train from Stockholm.

*Brief research outline: **Although males and females share much of the same genome, selection can be distinct in the two sexes. Sexually antagonistic loci are those loci where selection acts in opposing directions in the two sexes. This PhD student position is aimed at improving our emerging understanding of the **architecture of sexually antagonistic genetic variation**. Insects (seed beetles and/or fruit flies) will serve as main model systems and the research will primarily employ quantitative genetic techniques. The research will establish a series of discrete genotypes and use crosses between these to analyse, describe and understand the architecture of sexually antagonistic genetic variation. Traits in focus are sex specific measures of life history traits (especially metabolism) and integrative traits such as life-time fitness. ***

*This PhD *position forms a part of a new project on genetic conflict, funded by the European Research Council and the Swedish Research Council. The entire project will employ some 6-8 PhD students and postdocs, apart from a full time TA and the PI, and will strongly encourage interactions and collaborations within the group.

Salary and appointment: The duration of the PhD training period is four full years. The successful candidate will receive a postgraduate fellowship the first year (currently 15.500 SEK/month) and a postgraduate position year 2-4 (currently 23.300 – 26.400 SEK/month) including full social benefits.

*Eligibility:*The successful candidate should have a relevant MSc degree (or equivalent) in biology/ecology.

Qualifications and merits: We seek highly motivated candidates with a documented and strong interest in evolutionary biology and/or evolutionary genetics, preferably also with past experience of quantitative genetic analyses and an understanding of life history theory and sexual selection. Experience of laboratory work with insects is a merit as is previous experience of scientific writing and publishing. Because the holder of this position will collaborate and interact closely with other members of the group, we will put emphasis on both independence and ability to collaborate.The applicant is expected to have a good knowledge (spoken and written) of the English language.

*To apply:*Applications should include (1) personal information/background, (2) complete CV (3) a description of undergraduate training, (4) an authorized copy of the undergraduate degree and (5) the names and email addresses of three referees. Applications should be sent either by regular mail to: Göran Arnqvist, Animal Ecology, Dept. of Ecology and Genetics, Norbyv. 18D, University of Uppsala, SE-752 36 Uppsala, Sweden; or electronically as PDF files via email to: Goran.Arnqvist@ebc.uu.se. *Closing date for applications is March 20, 2012*.

*For further information*about the position, please contact the main supervisor and PI of the group: Professor Göran Arnqvist (phone +46 18 471 2645, e-mail Goran.Arnqvist@ebc.uu.se).

Prof. Göran Arnqvist Animal Ecology Department of Ecology and Evolution Evolutionary Biology Centre University of Uppsala Norbyvägen 18d SE - 752 36 Uppsala Sweden

Email: Goran.Arnqvist@ebc.uu.se Phone: +46-(0)18-471 2645 Cell phone: +46-(0)70-2935032 Fax: +46-(0)18-471 6484 NEW homepage with PDF reprints and more at: http://www.anst.uu.se/goarn789/index.html Goran.Arnqvist@ebc.uu.se

UQueensland Scholarships EvolutionaryGenetics

We have a new international PhD scholarship scheme for overseas students interested in undertaking PhDs in the School of Biological Sciences at the University of Queensland. Applicants will be considered under a new competitive, but school-specific, scheme outlined below.

We are particularly interested in recruiting students who would like to study Evolutionary Genetics. The school has strong representation in Genetics and Evolutionary Biology with more than eight independent research groups working on both theoretical and empirical problems and using both model and non-model organisms. Potential students should consult http://www.biology.uq.edu.au/research-information for specific research programmes of individual PIs. This scheme goes some way towards removing the barriers previously faced by international graduate students wishing to study evolution at an Australian University.

Many Thanks,

Steve Chenoweth

International PhD Scholarships in Biology at UQ

The School of Biological Sciences is a large and research intensive unit at the University of Queensland, one of Australias most prestigious Universities. The School has broad expertise across the disciplines of ecology and evolution, molecular and quantitative genetics, developmental biology, behaviour, plant and animal physiology, and conservation biology. Our research programs span all scales of biological organisation, from molecules and cells, to organisms, populations, species and communities, and take advantage of study animal and plant systems in a large variety of habitats (see http://www.biology.uq.edu.au/ for detailed information on our research programs). The School is very pleased to announce a new initiative that has made available a number of PhD scholarships for talented International students who enrol in our PhD program in 2012.

Qualifications Applicants should possess a Bachelors degree with Honours, Master of Science, MPhil or equivalent, and must be accepted into the PhD program at the University of Queensland. The UQ Graduate School website provides further information on the entry requirements for admission to the PhD program (http://www.uq.edu.au/grad-school/our-research-degrees).

Remuneration Living stipend (scholarship) of $23,728 per annum for 3 years which is tax free, with the possibility of a 6 month extension. International students normally pay international student fees of $29,600 per year, however individuals successful in gaining one of these scholarships will also be granted a full tuition-fee waiver.

The Application Process Interested students should identify potential supervisors within their research area of interest (http://www.biology.uq.edu.au/academic-staff) and contact them to discuss potential projects. Strong candidates will be invited to apply for entry to the PhD program, and if accepted into the program will be considered for the School of Biological Sciences International Scholarships on a competitive basis.

Enquiries For further information on the application process please contact the Postgraduate Administration Officer Gail Walter gj.walter@uq.edu.au

Steve Chenoweth, Associate Professor / Australian Research Fellow, School of Biological Sciences, The University of Queensland St Lucia, 4072, Australia

ph: + 617-3365-2188 fax: +617-3365-1655 www.chenowethlab.org Steve Chenoweth <s.chenoweth@uq.edu.au>

USalford ToxoplasmaPopulationGenomics

Disease Ecology: Parasitology

Diversity and pathogenesis of Toxoplasma gondii isolates from Africa

A new PhD position is available to work on population genomics of Toxoplasma in Prof Judith Smith's lab at the University of Salford, Manchester. Toxoplasma gondii is one of the most common zoonotic pathogens worldwide. The parasite can cause serious congenital disease in humans and animals and is potentially fatal to individuals with HIV. Prof. Smith's research group has recently isolated some of the first parasite strains from Africa revealing that they are closely related to clonal strain types (II and III) which dominate across Europe and North America and also discovering that recombination between these strains occurs in nature.

They further generated whole genome sequence for our recombinant isolate identifying over 74,000 Single Nucleotide Polymorphisms.

This analysis allowed us map regions with high levels of variation and loci under selection providing markers to investigate the diversity of strains in relation to disease phenotype. Based on these new tools we now wish to investigate the frequency of recombination and its impact on the disease virulence. The project will isolate and characterise strains from rural and urban habitats using genetic analysis to detect recombination and in vitro culture to investigate the phenotype of strains.

For more information please visit Professor Smith's research page by following this link.

Funding Notes: Prof Smith has commissioned a Grade 2 pathogen laboratory for isolation and culture of parasite strains. This allows work on the molecular and phenotypic characterization of pathogens. Support for consumables and travel is also available. The researcher would develop the project which builds on past research experience working on the diversity and environmental partitioning of parasites. The project area will fall into the remit of NERC and will pump prime a grant application in this area.

Closing date for applications: 17 Feb. 2012

For further information please contact Prof. Judith Smith (j.e.smith@salford.ac.uk). More details on the application procedure can be found at: http://www.jobs.ac.uk/job/ADV881/phd-studentship-graduate-teaching-assistant/ Dr Stefano Mariani

Reader in Wildlife Biology School of Environment & Life Sciences Peel Building, room 316 The University of Salford M5 4WT, UK ph: +44.161.2956913 fax: +44.161.2955015

Researcher.ID: A-2964-2012

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

USheffield SocialEvolution

PhDs in Social Evolution University of Sheffield - Department of Computer Science

3 year studentship

Application closing date: Wednesday 25 January 2012.

The successful applicant(s) will investigate the application of social evolution theory to understanding pro and anti-social behaviour in a biological system or systems of their choice. Social systems span all ranges of biological complexity, from populations of single-celled organisms, to multi-cellular bodies, to societies of individuals. Of particular interest for the lab is the importance of social evolution theory for understanding many aspects of disease. The successful applicants will be encouraged to empirically study their chosen systems, either developing experiments themselves or in collaboration with experimental biologists, while ensuring that any experiments are motivated by and interpreted using a good understanding of the underlying theory. A representative recent theoretical publication from the Lab in this area is http://www.sciencedirect.com/science/article/pii/S0169534711001169 The ideal candidates will be biologically-inclined physical scientists (e.g. with first degrees in mathematics, physics or computer science) or numerate life scientists. Candidates should submit an application as described below including in their application a 500 word research proposal understandable to a non-specialist, and a 250 word explanation of why their skills, experience and plans for further research or study make them a particularly suitable candidate.

Potential candidates are welcome to discuss their application informally with Dr James Marshall (james.marshall@shef.ac.uk).

The studentship will cover the candidates' fees, as well as a stipend at a level determined by the candidate's background. Applications from UK home, EU home and international students are welcomed.

About the Behavioural and Evolutionary Theory Lab: The Behavioural and Evolutionary Theory Lab is an interdisciplinary collection of individuals interested in how and why behaviours evolve. We are interested in behaviours and behavioural mechanisms, and their evolutionary function. We apply a range of theoretical approaches, from mathematics and statistics, decision theory, computer science, and physics. Particular topics of interest are currently the evolution of social behaviour, such as altruism and cooperation, and optimal decision-making mechanisms in groups, such as social insects, and in individuals.

The Lab is part of the Department of Computer Science, University of Sheffield (http://www.shef.ac.uk/dcs), and is physically based in the interdisciplinary Kroto Research Institute

Applicants should apply using the online application form at: http://www.shef.ac.uk/postgraduate/research/apply James A. R. Marshall Behavioural and Evolutionary Theory Lab Department of Computer Science and Kroto Research Institute University of Sheffield

James Marshall <James.Marshall@sheffield.ac.uk>

UStAndrews GenomicsReproductiveIsolation

PhD project available at the University of St Andrews: evolutionary genomics of social behaviour and reproductive isolation

We are seeking an enthusiastic PhD student to work on a project using two closely-related Australian field cricket species (Teleogryllus oceanicus and Teleogryllus commodus) and next-generation sequencing to identify influences of the social environment, behavioural mechanisms, and associated candidate genes that contribute to reproductive isolation. The student will work towards three goals: (1) test how variation in the social environments of T. oceanicus and T. commodus affects the expression of behaviours that impede hybridisation between the two species, (2) use genetic markers and QTL crosses to map genomic regions implicated in responses to social information and (3) identify and characterise candidate genes in those regions. The student will develop bioinformatic techniques to integrate and visualise the resulting network of genetic, mechanistic and behavioural information. Existing laboratory populations of both species and funding available for behavioural work and genetic mapping make the project feasible and will facilitate a timely finish by the postgraduate student.

The student will be based at St Andrews and will be supervised by Dr. Nathan Bailey. She or he will also benefit from co-supervision by Prof. Michael Ritchie and from a highly dynamic and stimulating intellectual environment with regular interaction between geneticists, behavioural ecologists and other evolutionary biologists. St Andrews is a leader in behavioural research, and there is a vibrant, friendly postgraduate community. For informal inquiries, contact Nathan at nwb3@st-andrews.ac.uk. Further details about the lab can be found on www.flexiblephenotype.org . The successful candidate will have a Bachelor's or Masters degree in a related field such as behaviour, evolution or genetics, and a background in, or a demonstrated ability to learn, the experimental and statistical techniques the project will entail. The starting date is September 2012.

Applications must be made through the University of St Andrews, and forms and further information can be found on the university website (http://www.st-andrews.ac.uk/admissions/pg/).

Nathan W. Bailey School of Biology Dyers Brae House University of St Andrews St Andrews Fife KY16 9TH Scotland

http://www.flexiblephenotype.org email: nwb3@st-andrews.ac.uk work phone: +44 (0) 1334 463367

nwb3@st-andrews.ac.uk

UTartu MolecularEvolution

Funded PhD position in molecular evolutionary bioinformatics in the University of Tartu

We are seeking a highly motivated PhD candidate to be supervised by Dr Gemma Atkinson within the group of Prof Tanel Tenson in the Institute of Technology, University of Tartu, Estonia.

Dr Atkinson's research addresses protein functional evolution, using bioinformatic approaches and primarily focusing on the ancient families of proteins involved in translation of mRNA to protein. Members of these families are often essential for life and predate the last common ancestor of all life on earth. Thus by studying these proteins we can gain understanding of the fundamental processes of life, and how these processes have evolved over billions of years.

The PhD project will take advantage of the thousands of whole genome sequences now available for the study of evolution of protein families from the origin of life to the present day. Work will involve sensitive sequence searching to identify the presence and absence of particular proteins across genomes, phylogenetic analyses to reconstruct their emergence and evolution, and sequence analyses to link domain- and site-specific patterns of amino acid substitution with molecular function. Specifically, the proposed PhD project will target the ABC superfamily of ATP-binding enzymes found in all domains of life. This superfamily comprises enigmatic proteins of diverse, and often unknown functions. Several ABC enzymes have recently been found to have important roles in regulation of translation such as ribosome recycling protein Rli1/ABCE1, yeast-specific elongation factor eEF3 and starvation response enzymes Gcn1 and Gcn20.

>From the results of the PhD, it is expected that enzymes with novel roles in protein synthesis will come to light as interesting targets for subsequent experimental

study. Dr Atkinson collaborates with the lab Dr Vasili Hauryliuk, also in Prof Tenson's group, for biochemical and genetic validation of in silico results. If the candidate so wishes, there is an opportunity to gain practical lab experience in Dr Hauryliuk's lab.

The candidate should have:

a Masters degree in a biological or computational discipline

a strong interest in, and enthusiasm for molecular evolution

familiarity with basic sequence and phylogenetic analyses

experience in using a programming language such as Python, Perl, Java etc

fluency in spoken and written English

Estonia has a rich culture and beautiful natural environment, with unspoiled forests, meadows and coastlines. Enjoying warm summers and cold winters, the historical city of Tartu is the intellectual capital of Estonia, and its university is the leading research and development institution in the country. The Institute of Technology is a lively, modern centre for biological and technological research.

The PhD will be funded by a monthly stipend, with additional monies available for regular attendance at international conferences and workshops, and for visiting labs abroad. Information on funding is available by request.

Applications should contain:

a full CV with detailed description of previous relevant experience

a statement of academic interests

an electronic version of the Masters thesis

the names and contact details of at least 2 referees

The candidate is expected to start at the latest September 2012. Please send applications and informal enquiries to gemma.atkinson@ut.ee

Gemma Atkinson University of Tartu, Institute of Technology Nooruse 1, 50411 Tartu, Estonia

More information about the research of Dr Atkinson can be found here: http://lepo.it.da.ut.ee/~atkinson/gem_mac/gemma_c_atkinson.html
gemma.atkinson@gmail.com

UVienna TheoreticalPopGenet

PhD Position in Theoretical Population Genetics at the University of Vienna

The mathematics and biosciences group (MaBS, homepage www.mabs.at) led by Joachim Hermisson at the University of Vienna is looking for a strong and highly motivated candidate for a PhD position in evolutionary modeling and statistical data analysis.

Project: Due to modern methods of high-throughput sequencing, huge amounts of DNA sequence data from population samples ("polymorphism data") are available today. Interpretation of these data is an important task for theoreticians. In the project, we will develop novel methods to detect so-called footprints of selection in DNA polymorphism data. These footprints can be used to describe the pattern of recent adaptations on a genome. We will particularly focus on effects of polygenic selection on genetic footprints. We will use mathematical methods based on stochastic processes (coalescent theory) and extensive computer simulations. The project is part of an international DFG-research group "Natural Selection in Structured Populations" in collaboration with groups in Evolutionary Biology at the University of Munich, and Mathematics at the University of Freiburg. This work will be conducted in collaboration with Angela Hancock, a postdoctoral researcher in the MaBS group.

Research environment: Vienna is not only one of the world's most liveable cities, but also offers an excellent research environment and is currently developing into one of the main centers in evolutionary research in Europe. The position will be located at the Max F. Perutz Laboratories, part of the Vienna Biocenter Campus, which houses a vibrant community of researchers from several institutes. As a member of the MaBS group, the student will also interact closely Magnus Nordborg and members of his group, and will be part of a larger community of evolutionary biologists and population geneticists through the activities of the Vienna Graduate School for Population Genetics (http://www.popgen-vienna.at) and EvolVienna (www.evolVienna.at).

Conditions: The position is for three years, salary is according to the FWF standard rates for PhD students in Austria. The starting date is somewhat flexible (May 2012, earlier dates negotiable, starting date before summer/fall 2012 preferred).

Application: We are looking for a candidate with a strong background in quantitative methods (analytical or computational modeling or data analysis) and interest in evolutionary research. Applicants should have a Master / Diploma degree in natural science (e.g. biology or physics), mathematics, or bioinformatics. Programming skills are highly appreciated. The working language in the group is English. German skills are not essential.

All formal applications run through the Max F. Perutz International PHD Program, see http://www.mfpl.ac.at/phd-program/ for all details. The application deadline is March 15th 2012.

For informal inquiries and further information, interested candidates are encouraged to contact us before submitting a formal application. In this case, please send a brief statement of interest and CV to

Joachim Hermisson (joachim.hermisson[AT]univie.ac.at) and Angela Hancock (angela.hancock@univie.ac.at).

– Joachim Hermisson Professor for Mathematics and Biosciences University of Vienna Department for Mathematics Nordbergstr. 15, 1090 Vienna, Austria and Max F.Perutz Laboratories Dr.-Bohrgasse 9, 1030 Vienna, Austria phone: +43 (0) 1 4277 50648 email: joachim.hermisson@univie.ac.at www.mabs.at Joachim Hermisson <joachim.hermisson@univie.ac.at>

Vienna PopulationGenetics Deadline Jan8

This is a reminder about the *upcoming application deadline for PhD positions in Population Genetics:*

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

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

Available topics include: Probabilistic models for the population genetics of molecular evolution

Inferring selection using *Drosophila* whole genome sequence data New algorithm and models to analyze population genetic massive parallel sequence data Experimental evolution in *Drosophila* Evolution of gene expression in *Drosophila* Evolution of transposable elements in *Drosophila* Natural variation in transposable element defense systems Tracing the genomic signature of hybridization between *D. mauritiana * and *D. simulans* Functionally important variation in lifespan and other life history traits in natural and experimental evolution populations Mathematical models of spatially varying selection in subdivided populations Statistical methods for detecting selective sweeps using genome-wide data Population genetic estimators from NGS data: assessing the power for methods for genome scans of selection The nature of differentiation between two closely related species of oak The footprint of adaptive gene introgression after secondary contact

Only full applications (CV, motivation letter, university certificates, indication of the two preferred topics in a single pdf) received by * 08.01.2012* will be considered. Two letters of recommendation need to be sent directly by the referees.

All information about the about the Vienna Graduate School of Population Genetics, the training program and the application procedure can be found at www.popgen-vienna.at Regards and happy new year!

Dr. Julia Hosp Vienna Graduate School of Population Genetics Coordinator www.popgen-vienna.at c/o Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 1 A-1210 Vienna

Tel: +43 1 25077 4338 Fax: +43 1 25077 4390

julia.hosp@gmail.com julia.hosp@gmail.com

WageningenU EvolutionaryGenetics

Wageningen (NL) PhD project; evolutionary genetics

Application deadline Feb 16 Additional information can be obtained from Dr. Pim van Hooft; Pim.vanHooft@wur.nl

–> evolutionary genetics / molecular ecology (job reference ESG-ECO-0072) “Genetic structure of White-fronted geese”

We are looking for an enthousiastic PhD student for the following research. The family Anser can be thought of as a well-structured group of species but equally it can be viewed as a species swarm comprised of species that are less well defined. So the Grey-lag goose is quite distinct from the White-fronted goose, but on the other hand within the Bean goose two or three species may be hardly distinguishable as cryptospecies. Since crossing is possible between all Anser species and even between Anser and Branta, much gene flow is expected between the species. Yet it is unclear under which conditions gene flow is frequent and when not. The concept of supraspecies (as we recently found for ducks) and its implications for goose evolution has to be investigated. This can be of significance both for the conservation of these geese as for the understanding of their role in disease transmission.

We ask that the selected candidate should have a Master's degree, or equivalent, in (eco-)genetics with proven abilities to interpret his/her results in an ecological context. Preferably she/he can read and speak Russian. A driving license is a necessity and so is the willingness and ability to travel independently in Eurasia. Sound statistical knowledge and proven publication skills are important.

We offer a full-time position (38 hours), initially for 18 months. If your suitability in this position is apparent, the period of employment will be extended to the remainder of your PhD-study, with another 30 months. Gross salary starts at 2042 Euro per month during the first year, increasing to 2612 Euro per month during the fourth year. Commencing as soon as possible. The candidate will be based at the Resource Ecology Group in Wageningen.

We are the Resource Ecology Group and we perform research and education in community ecology of large herbivores, with particular emphasis on the interactions between herbivores and the vegetation and their role in wildlife disease ecology. This is carried out at aggregation levels ranging from plant part to ecosystem, with a world-wide geographical focus. Our main research fields are (1) rangeland ecology of large herbivores in extensively managed ecosystems, (2) conservation genetics of large herbivores, and (3) the role of vertebrates in abundance and movements of pathogens. The research approaches include model development, model testing, and experimental hypothesis testing. The main research sites are savannas, grasslands in tropical and temperate regions, and grasslands and forests in neotropical regions. Most research is carried out by post-docs and PhD students, supported by faculty. Results have a strong bearing on nature conservation and management in tropical and temperate areas.

The department of Environmental Sciences of Wageningen University provides fundamental research and academic education on our living environment: nature, landscape, land usage, adaptation to climate change, water and ocean management, and the various competing claims on space. This also includes biodiversity and the sustainability of management and production. Wageningen University is part of the Wageningen University and Research Centre concern.

Wageningen University and Research Centre Delivering a substantial contribution to the quality of life. That's our focus - each and every day. Within our domain, healthy food and living environment, we search for answers to issues affecting society - such as sustainable food production, climate change and alternative energy. Of course, we don't do this alone. Every day, 6,500 people work on 'the quality of life', turning ideas into reality, on a global scale.

Could you be one of these people? We give you the space you need.

For further information about working at Wageningen UR, take a look at www.jobsat.wur.nl Acquisition regarding this vacancy is not appreciated.

"Hooft, Pim van" <Pim.vanHooft@wur.nl>

Jobs

Bonn Germany Curator of Mammals

The Zoologisches Forschungsmuseum Alexander Koenig (ZFMK), Bonn (http://www.zfmk.de) seeks to fill a new research and service position in the Department of Vertebrates:

Curator of Mammals

The position is available from April 2012. Potential candidates will hold a PhD in zoology or related areas, have their research focus preferably on taxonomy and systematics of Chiroptera or other small mammals, and present a substantial publication record in taxonomy, phylogenetics and/or other aspects of biodiversity research. The candidate is expected to work in these fields from a sound theoretical basis and be able to apply an array of appropriate modern methods. He/she should be able to combine collection-based work with modern phylogenetic and/or ecological approaches. The candidate is also expected to integrate into ongoing research projects at the ZFMK and teaching programs at the University of Bonn, and to obtain competitive grant funds.

As a curator, the successful candidate will be responsible for maintaining and developing the Bat Banding Center (Beringungszentrale) at the ZFMK and for editing the bat journal "Myotis". Other duties include the supervision of all scientific collections at the ZFMK following international collection standards. The position is also a central support for collection and loan management with regard to European and international regulations. Good knowledge of English and German is mandatory. He/she will also be involved in the self-administration of the institute and is expected to demonstrate commitment to community engagement in his/her field of research.

The successful candidate will be employed for an initial period of up to five years- determined on his/her experience - according to the German legislation, after which he/she will obtain tenure depending on his/her performance. Salary is according provisionally to grade TV-L/13 in the German Public Service scheme.

The ZFMK is a fellow institute of the "Wissenschaftsgemeinschaft Gottfried Wilhelm Leibniz" (WGL Science Community) and works in close cooperation with the University of Bonn. It comprises internationally important scientific collections, libraries, electron microscopy unit, and bioacoustic, histological and molecular laboratories.

The ZFMK is an equal opportunity employer. Women are therefore strongly encouraged to apply. Equally qualified handicapped applicant will be given preference.

Interested applicants should submit a CV, complete publication record, a statement of teaching experience and research funding, certificates of university degrees, and selected publications in hard copies to the following address:

Heike Lenz, Zoologisches Forschungsmuseum Alexander Koenig, Adenauerallee 160, D-53113 Bonn, Germany, by January 31 2012. E-mail inquiries: <h.lenz.zfmk@uni-bonn.de >. Please note that application documents will not be returned.

"Wägele J. Wolfgang" <W.Waegele@zfmk.de>

ColoradoCollege DeptChair

BIOLOGY, Department Chair.

Term position, approximately four years, beginning August 2012 at Colorado College.

Preference for late career or recently retired individual with previous chairing experience; other academic leadership experience highly desirable. Teaching and/or research opportunities negotiable. Colorado College is a highly selective liberal arts college with a unique one-course-at-a-time curriculum. Applicant must understand the atmosphere of a small liberal arts college, especially the role of a teacher/scholar. Preference for a cell or molecular biologist with wide appreciation for pedagogy across sub- disciplines, but other science disciplines considered. Applicant must have personal qualities that include skill in collaborative leadership and ability to work effectively with faculty, staff, and students in the department and across the institution. Colorado College is committed to increasing the diversity of its community and curriculum. Candidates are encouraged to identify the ways in which they can contribute to that goal.

Application deadline is March 15, 2012, or until position is filled.

Send letter of application describing interest in position, academic background and leadership experience, along with curriculum vitae, and names of four references to Search Committee, Department of Biology, Colorado College, 14 E. Cache la Poudre St., Colorado Springs, CO 80903. Equal Opportunity Employer: The Colorado College welcomes members of all groups and reaffirms its commitment not to discriminate on the basis of race, color, age, religion, sex, sexual orientation, gender identity, gender expression, national origin, or disability in its educational programs, activities, and employment practices.

Emilie.Gray@ColoradoCollege.edu

ColoradoMesaU EvolutionaryPhysiologist

ANNOUNCEMENT OF POSITION VACANCY

Assistant Professor of BiologyXAnimal Physiology

RESPONSIBILITIES: The Biological Sciences Department at Colorado Mesa University invites applications for a tenure-track faculty position in animal physiology beginning August, 2012. Individuals with expertise as invertebrate or vertebrate physiologists employing ecological, evolutionary, and/or cellular/molecular approaches are encouraged to apply. The successful applicant will join a dynamic department, including field, tropical, cellular, and molecular biologists, focused on excellence in undergraduate teaching and mentorship of undergraduate researchers. Responsibilities include teaching 12 credits/semester, advising students, offering research opportunities, and participating in service to the department and university. Teaching responsibilities will include lower-division majors and non-majors courses as well as the development of upper-division courses in animal physiology and within the candidates specialty. Specific teaching responsibilities will include an upper-division course in general physiology, as well as anatomy and physiology.

EDUCATION & EXPERIENCE: A Ph.D. in biology or a related field is required. Preference will be given to candidates with undergraduate teaching and postdoctoral experience. Colorado Mesa University is particularly interested in candidates who have experience working with students from diverse backgrounds and who have a demonstrated commitment to improving the levels of access and success for underrepresented students within higher education.

TYPE OF APPOINTMENT: Full-time, tenure-track appointment beginning August 2012.

SALARY: Commensurate with education and experience. Excellent health and retirement benefits package.

APPLICATION DEADLINE: Open until filled. To ensure consideration, completed application packets must be received by February 29, 2012.

APPLICATION: Submit a cover letter describing your qualifications and experience as they relate to the specific responsibilities, requirements, and preferences of this position, CV, unofficial transcripts for all degrees completed (official transcripts will be required upon hire), statement of teaching philosophy, statement of teaching interests and experience (including a list of courses you are qualified to teach), statement of research interests, three letters of recommendation, and the following completed forms:

- Applicant Authorization and Release to Conduct Reference and Background Check<

http://www.coloradomesa.edu/hr/documents/ApplicantAuthorization.ReleasetoConductReference.BackgroundCheck.pdf >

- Background Investigation Disclosure and Authorization< http://www.coloradomesa.edu/hr/documents/BackgroundInvestigationDisclosure.Authorization.pdf >

- Voluntary Affirmative Action < http://www.coloradomesa.edu/hr/documents/AffirmativeActionInformation-cmu.pdf >

Send to:

Biology Search CommitteeXAnimal Physiology

Human Resources, LHH 237

Colorado Mesa University

1100 North Avenue

Grand Junction, Colorado 81501-3122

Phone: 970 248-1820

Colorado Mesa University is committed to providing a safe and productive learning and living community. To achieve that goal, we conduct background investigations for all final applicants being considered for employment. Background investigations include reference checks, a criminal history record check, and when appropriate, a financial and/or motor vehicle history. Applicant must be able to verify U.S. employment eligibility. Colorado Mesa University is an Affirmative Action/Equal Opportunity Employer, committed to a culturally diverse faculty, staff and student body. Women and minorities are encouraged to apply.

Susan M. Longest, PhD Assistant Professor of Biology Colorado Mesa University 1100 North Avenue Grand Junction, CO 81501

Phone: (970) 248-1554

Susan Longest <slongest@coloradomesa.edu>

CornellU ResTech EvolutionaryBiology

Ecology & Evolutionary Biology Cornell University Lab Technician III Job # 16604

Research Description

We are recruiting a Research Technician for our general research program in evolutionary biology/herpetology. We use various molecular methods and field studies to understand mechanisms driving population genetic structuring and local adaptation of reptiles and amphibians. Many aspects of our research have conservation implications.

Job Description

Provide tech support for molecular systematics and comparative population genetics/genomics research. Specific responsibilities include DNA isolation, PCR, library construction, sample preparation, editing sequence data, using genomic database and searching tools, running phylogenetic and population genetic software, and data interpretation. General responsibilities include maintaining and purchasing laboratory supplies, assisting with grant proposal and manuscript preparation, and assisting with student training.

Qualifications

BS in biology-related field strongly preferred with at least one year of experience in a molecular biology or molecular systematics environment. Working knowledge of standard molecular lab protocols and basic field biology techniques. We are looking for an enthusiastic co-worker, who is self-motivated, and excited about working collaboratively as part of the research team. Neatness, attention to detail, good organizational skills and ability to be a team leader, are important. Some weekend/evening hours will be necessary for field collecting trips, and time-sensitive lab procedures.

Conditions of Appointment

Cornell staff are offered a salary according to qualifications and work experience. The range of salaries for Technician III (Band C) is $17.33-$19.57/hour. This is a full time appointment (39 hours per week) initially for a two-year term, and subject to evaluation after the first year. Endowed college employee benefits apply.

Application

Applications will be accepted through March 15, 2012. Please address any inquiries to Dr. Kelly Zamudio at krz2@cornell.edu

To apply please visit: https://cornellu.taleo.net/careersection/10164/jobsearch.ftl Job Number 16604

Located in Ithaca, NY, Cornell University is an equal opportunity, affirmative action educator and employer.

Kelly R. Zamudio Professor of Ecology and Evolutionary Biology Cornell University Ithaca, NY 14853-2701

kelly.zamudio@cornell.edu

ology, Duke University http://www.biology.duke.edu/-mitchell-olds/ mrw28@duke.edu

DukeU FieldAssist RockiesHerb

Field research opportunity in the northern Rockies

The Mitchell-Olds lab at Duke University seeks a highly motivated, detail-oriented assistant for summer field research in the northern Rocky Mountains. We are studying Boechera, a perennial herb that offers genetic tractability and ecological context. Current field experiments focus on questions related to local adaptation, speciation, plant defense, and breeding systems.

Our research sites are located in east-central Idaho and southwest Montana. Base camp is located near the beautiful town of Salmon, but travel distances between sites often necessitate overnight camping. Weather conditions in the Rockies can be severe, and assistants should expect to work in snow and rain as well as 90 degree temperatures. Regular trips are made to Missoula, Montana for groceries, supplies, and taco consumption.

Applicants must be available throughout the field season from early May or early June through mid-August, but exact start and end dates are flexible. However, ability to start May 1st is a plus. Successful applicants are expected to assist in data collection and data entry, plant care, transplanting, seed collection, and driving research vehicles. The work can be physically demanding, and the research team usually collects data 5-6 days per week. Qualifications: 1) some undergraduate education in biology, ecology, or related field, or equivalent experience; 2) experience camping and working outdoors and/or previous field research experience; 3) ability to perform repetitive tasks with a cheerful attitude and with attention to detail; 4) willingness to live and work in close proximity with six other researchers under rustic and sometimes crowded conditions; 5) a current driver's license. First aid training and/or previous experience working with plants is preferable but not required. Transportation, room with internet access, and salary will be provided.

Interested applicants should submit: 1) a short cover letter describing their qualifications as well as future academic and professional goals; 2) a rÃ©sumÃ© outlining previous work experience, relevant courses (completed or in progress), extracurricular activities; and 3) contact information of two character references. Email to:

Tom Mitchell-Olds tmo1@duke.edu Department of Biology, Duke University http://www.biology.duke.edu/-mitchell-olds/ mrw28@duke.edu

INRA France 51 Genomics

Ranked the number one agricultural institute in Europe and number two in the world, INRA (National Institute for Agricultural Research) carries out mission-oriented research for high-quality and healthy foods, competitive and sustainable agriculture and a preserved and valorised environment.

Every year, INRA seeks researchers from all disciplines to reinforce laboratory and fieldwork teams. Researchers will be heavily involved in scientific networks and tackle environmental, economic and social issues. They are expected to strive for excellence and come up with useful, concrete applications for the real world. Individual research projects will go hand in hand with group efforts in a bid to further knowledge and innovation, in order to produce sustainably, preserve the environment, and improve human nutrition.

INRA is recruiting 51 scientists through open competition and offering permanent positions.

Positions are opened to PhD (or equivalent) in a wide range of scientific disciplines such as biochemistry, biology, genetics, ecology, genomics, mathematics, physiology, microbiology, economics, forest sciences, environmental sciences, sociology, animal production sciences, computer science, chemistry, neurosciences, entomology, statistics, virology and many more.

There are 10 permanent positions in genomics and genetics: - Computational biology and bovine sequence data - Statistical genomics for genetic analysis of polygenic traits and genomic selection of crops - Methods of genomic selection and optimisation of genetic management for animal production systems based on crossbreeding - Genomic selection of cattle and sustainability of livestock production - Mining genetic diversity and wheat genomic selection - Quantitative genetics and breeding methods for forest trees - Durability of wheat resistance to fungal diseases - Evolution of populations of plant viruses in an agricultural landscape: consequences for epidemiology - Functional genomics of fish pathogenic bacteria - Genomics of beef cattle breeds

Applications are available of January 26 to February 28, 2012.

All useful information to apply are available on: www.international.inra.fr (see “Join us”) For further details: concours_chercheurs@paris.inra.fr

Sincerely.

Fabienne Giroux Assistante RH en charge de la communication sur le recrutement fabienne.giroux@paris.inra.fr

[DescriptionÂ: inra] Direction des Ressources Humaines Service recrutement et mobilitÃ© 147, rue de l’UniversitÃ© 75338 Paris Cedex 07 - France Tel 01 42 75 90 77 Fax 01 42 75 90 39

Fabienne GIROUX <Fabienne.Giroux@paris.inra.fr>

INRA Rennes PopulationDynamics

Research scientist permanent position at INRA Rennes (France)

Research field: Fish population dynamics in a changing environment

Educational background: PhD or equivalent. Candidates should have a good command of English. The successful candidates who have not yet acquired postdoctoral training will be required to do so, preferably abroad, after their probationary period (1st year) and before being eligible for promotion to an Experienced Research Scientist position (CR1).

Key activities and required skills: You will be in charge of developing research projects on the evolution of diadromous fish populations. You will have access to time series data (since the late 1970s) from surveys at the population and individual levels (runs and capture of adults, recruitment and life history traits). The project will focus on French populations but comparative approaches at the scale of distribution areas will be initiated. The aim will be to identify ecological and evolutionary mechanisms underlying the observed changes in demography and life history strategies. Data on key environmental factors (temperature, discharge, rainfall, water and habitat quality) will also be used to develop scenarios of population responses over the long-term (>50 years). Applicants should have expertise in population biology, statistical ecology, analysis of population dynamics data, and preferably have programming skills.

Person to contact before applying: Jean-Luc BAGLINIERE or Jean-Marc Roussel Tel: 02 23 48 54 44 - 02 23 48 57 75 E-mail: jean-luc.bagliniere@rennes.inra.fr E-mail: jean-marc.roussel@rennes.inra.fr

Host unit reference: Research unit: 0985 ESE Ecologie et Santé des Ecosystèmes Centre: RENNES Address: 65 Rue de Saint Brieuc 35000 RENNES

Details on the position and the procedure to apply can be found here: http://www.inra.fr/drh/cr2012/profil-cr2.php?NumProfil=CR2-2012-3-EFPA-2&langue=EN

Deadline for application is February 28th.

ITC India ComputationalBiologist

Computational Biologists Opportunity at ITC R&D Center, India

ITC is rated among the Worlds Best Big Companies, Asias Fab 50 and the Worlds Most Reputable Companies by Forbes magazine, among Indias Most Respected Companies by BusinessWorld and among Indias Most Valuable Companies by Business Today with the market capitalization of over US $22 billions. ITC R&D Center, Bangalore is seeking a highly capable Post doctoral Fellow, specialized in Bioinformatics, who can handle genome wide data sets, curate, pattern search, design markers of various types and deliver it through web-services. The role holder will work with the team of biologists and understand their customized needs and deliver products. Following are desirable qualifications.

Education : Ph.D in Bioinformatics (Desirable that the candidate has exposure/training from a global Institute of repute) Job location : ITD R&D Center, Bangalore

Experience : * Minimum of 2 years of experience in a reputed organization * A good track record of publication * Should have proven leadership skills in a multi disciplinary team. * Publicly available products in terms of software/modules/web-services. * Familiar with cluster computing Expertise : * Should have demonstrated products (software / modules / web services) * Should have clear understanding of current Bioinformatics technologies and related concepts; various sequence analysis, pattern recognition, familiar with NGS platform and related data handling; * Should have demonstrated experience in database (MySQL/PostGres/Chado); open source project management tools; server side scripting languages (PHP; PERL/Python), CVS, SVN and handling various file formats (GFF; XML. CSS). Multi-threading and Dynamic Programming.

Responsibilities: * Integration of various biological evidences on the physical map. * Development marker development pipelines * Responsible to establish and administer the web services for a various tracks of genome annotation * Key role in bridging biological data with biologists need.

Key Success Factors: * Be able to work with ambiguity * Excellent communication and presentation skills. * High energy level \ Enthusiasm * Curiosity to Experiment and Learn

The candidates will be taken as "Computational Biologist" initially for a period of 2 years, continuation depends on the candidates performance. Attractive compensation will be given depending on the experience/expertise. Interested candidates are requested to send their resume to <rajkumar.rathinavelu@itc.in>

Rajkumar Rathinavelu <Rajkumar.Rathinavelu@itc.in>

KansasStateU PlantComputational

Postdoctoral Research Scientist: Computational Modeling of Plant Gene Networks

Description of the Position A postdoctoral position is available in the department of Electrical & Computer Engineering at Kansas State University, Manhattan, Kansas. The person will work on an on-going research project funded by the NSF, âAgroecological annotation of gene function and computational analysis of gene networksâ with Dr. Stephen M. Welch (Division of Agronomy, KSU) and Dr. Sanjoy Das (Electrical & Computer Engineering, KSU) to develop analytical/computational approaches to model Arabidopsis and Brassica Rapa genetic networks.

The successful candidate should be a highly motivated individual with a Ph.D. in electrical engineering, bioinformatics, computer science, mathematics, statistics, or another closely related area. Requirements include an excellent background in analytical, computational and machine learning techniques for modeling and optimization; strong programming skills in MATLAB as well as C/C++; plus a commitment to plant genomics research.

Application Process The position will be for an initial period of 3 years, at a starting salary of $48,000 - $52,000 per annum. The candidate will report to Dr. Sanjoy Das. Review of applications will begin on March 15, 2012 and continue until the position is filled. Applicants should submit a cover letter, curriculum vitae, and a list of three references in pdf format to chassy@ksu.edu.

Further details will be available at: www.ece.ksu.edu/~sdas EEO/AA Policy Kansas State University is an equal opportunity employer and actively seeks diversity among its employees. Background check required.

Chassy Nichols '10 Project Coordinator Electrical & Computer Engineering Kansas State University 2061D Rathbone Hall Manhattan, KS Â66506 P-785-532-5601 F-785-532-1188 E-chassy@ksu.edu

Chassy Nichols <chassy@ksu.edu>

LancasterU EvolutionaryBiol

The Lancaster Environment Centre is advertising two permanent Faculty positions (one Professorial Chair and one Lecturer/Senior Lecturer) in 'quantitative natural science of the environment' and I am hoping that at least one of these will be broadly in the area of evolutionary biology, animal ecology/behaviour or theoretical ecology.

Please see the following link for more information about the posts: https://hr-jobs.lancs.ac.uk/vacancies.aspx?cat=160&type=5 Ken

Professor Kenneth Wilson Lancaster Environment Centre Lancaster University, LANCASTER LA1 4YQ United Kingdom. +44 1524 593349 / 593406 ken.wilson@lancaster.ac.uk http://www.lancs.ac.uk/staff/wilsonk4/ http://www.journalofanimalecology.org/ "Wilson, Kenneth" <ken.wilson@lancaster.ac.uk>

Netherlands EvolutionaryEcol

Tenure Track position for Behavioural or Evolutionary Ecologist at the Netherlands Institute of Ecology (NIOO-KNAW)

** The position **

The Department of Animal Ecology (AnE) of the Netherlands Institute of Ecology (NIOO-KNAW) seeks a behavioural or evolutionary ecologist for a tenure track position (vacancy number TT-AnE-012701). The research of AnE centres around the behavioural and evolutionary ecology of animals, and combines long-term population studies of hole-breeding passerines and of water birds with work in aviary and water bird facilities and with the use of avian genomic tools. AnE has an outstanding reputation within the international scientific community and was assessed as 'excellent' in the last international peer review.

** Personal profile and requirements **

We are looking for a scientist with several years of postdoctoral experience, at least two years postdoctoral experience abroad and an excellent track record in behavioural or evolutionary ecology in terms of both publications and the acquisition of research grants. (S)he is expected to build a strong research line within the department and bring in expertise complementary to the other scientists. Furthermore, (s)he sees opportunities in AnE's unique triangle of facilities of populations in the wild, amenities for studying animals under controlled conditions, and avian genomics tools. The candidate must be capable of acquiring and supervising externally funded PhD students.

The NIOO has no obligation to teach at University level, but supervision of Master's and PhD students is expected as part of normal research activity. Scientific communication is carried out in English, so knowledge of the Dutch language is not a prerequisite for this post, but a commitment to learning the language is expected in longer-term staff.

** Appointment **

The appointment is in principle for a tenure track position: the appointed scientist will be appointed on a temporary basis for a maximum of 6 years. After 3 and 5 years of employment there will be an assessment of performance based on established criteria (for criteria, see http://www.nioo.knaw.nl/en/node/2034). Based on these assessments the researcher may be promoted to the rank of senior researcher with tenure. The salary will dependent on qualifications and work experience.

** Information **

More information can be found on the NIOO website (www.nioo.knaw.nl) and from Prof. Marcel E. Visser (m.visser@nioo.knaw.nl or +31-317-473439), head of department Animal Ecology. General information on the NIOO can be found at the internet at http/www.nioo.knaw.nl . ** Applications **

Please send your application including complete curriculum vitae and three referees to vacature@nioo.knaw.nl. The closing date for application is 22 February 2012, the interviews will take place on 27 and 28 March.

Prof. Dr Marcel E. Visser Head of Department Animal Ecology Netherlands Institute of Ecology (NIOO-KNAW)

P.O. Box 50, 6700 AB Wageningen, The Netherlands Phone: +31-317-473439 E-mail: m.visser@nioo.knaw.nl Personal page: www.nioo.knaw.nl/users/mvisser
M.Visser@nioo.knaw.nl

OxfordU ResAssist AvianPop

Voluntary research assistantship in seabird behaviour & ecology Skomer Island & Oxford University

The Oxford Navigation Group (Department of Zoology, University of Oxford ,UK) are looking for an enthusiastic, hardworking young Biologist to work as a voluntary Research Assistant to help with our pelagic seabird research on Skomer Island, Pembrokeshire, Wales, in Spring and Summer 2012. The work will involve several research projects coordinated by Prof Tim Guilford (see our website oxnav.zoo.ox.ac.uk). We utilise state-of-the art tracking technologies (miniature GPS, Geolocators, & on-board video), and comprehensive automated activity monitoring systems (RFID controlled burrow-nest sensing networks), and engages several species (Manx Shearwater, Atlantic Puffin, Common Guillemot, Razorbill). Most work will involve assisting two doctoral students with the day-to-day maintenance of the burrow sensing systems, weighing and monitoring breeding birds and their chicks, and the deployment and retrieval/downloading of tracking devices. There will be some nocturnal work, since the primary study species is the Manx Shearwater, which only arrives at the colony after dark. There will also be scope for involvement in other conservation and ecological projects on the island, which is a National Nature Reserve administered by the Wildlife Trust of South and West Wales.

There is no stipend, but accommodation (shared) will be provided, as will travel to the island from within UK. However, the project is a great opportunity to gain valuable experience in modern field ornithology. Skomer is a short boat trip away from the mainland (weather permitting), has mobile coverage, and internet. There is a small community of warden, assistants and volunteers, who are involved in the running and conservation of the Nature Reserve, monitoring the seabird populations (which are spectacular), and managing the daily and over-night visitors. There may be opportunities to visit other UK island reserves during the project.

We are looking for an assistant to work with us between April and September 2012. If you are interested, please email me at tim.guilford@zoo.ox.ac.uk attaching a CV and a statement of interest. Letters of reference will also be required, and you can ask referees to send these directly to me. The application process will be open until a suitable candidate is found, but we expect to make decision by mid March.

annette.fayet@sjc.ox.ac.uk

StockholmU MicrobialMetagenomics

Posted at Stockholms universitet 2012-01-26

Ref. no. SU 619-0311-12 Dok no. 1

RESEARCH FELLOW â

metagenomic analyses of microbes in the Baltic Sea A position as researcher is open at the Department of Botany, Stockholm University. Reference number SU 619-0311-12. Deadline for application: February 20th, 2012.

Stockholm University is committed to academic excellence and is a world renowned university with about 60 000 students. The Department of Botany is within the Faculty of Science, and has about 70 employees. Teaching is oriented towards plant physiology, ecology and systematics. The plant physiology unit offers a stimulating atmosphere in well-equipped laboratories.

Position The Department seeks to employ a Researcher Fellow that will produce new essential information within the framework of an international and multidisciplinary research program: MiMeBS âMicrobial Metagenomics of the Baltic Seaâ localized at SU (www.botan.su.se/physiology). The MiMeBS program is a collaborative research effort with scientists at J. Craig Venter Institute (La Jolla, USA; www.jcvi.org) and SciLifeLab (Stockholm; www.scilifelab.se).

Focus & Expectations The focus will be on analyses of large data sets from sequenced metagenomes, transcriptomes and single cell genomes of Baltic Sea microbial populations using bioinformatic tools; and to make use of the information gained in an environmental context as means for an optimized management of the unique Baltic Sea. The Research Fellow is also expected to be in charge of the MiMeBS bioinformatic team members and act as supervisor for students and post docs.

Qualifications The position requires a person with a PhD in biology/microbiology/molecular biology/ bioinformatics, combined with a deep experience and expertise in bioinformatic tools and analyses. Eligible candidates must have a strong record of academic research demonstrated by peer-reviewed publications. Collaborative leader and innovative skills and independence are expected, as is excellence in writing and speaking English. Eligible candidates have received a PhD exam in the past 3-6 years (from the application deadline).

Terms of employment A two year full time position as researcher, starting as soon as possible.

Application The application, in English, should include and be organized as follows: a cover letter outlining your qualifications, relevant experiences and interest in the position (max 1 page) CV & publications (max 2 pages) copies of degree certificates names of two reference persons (give phone numbers and email addresses; state the relation to the reference person)

For further information, contact Professor Birgitta Bergman, telephone +46-(0)8-16 3751, bergmanb@botan.su.se

Union representatives are Bo Ekengren (SACO), Lisbeth Häggberg (ST), telephone +46-(0)8-16 2000 (switch board), and Gunnar Stenberg (SEKO), telephone +46-(0)70 316 43 41.

Applications, labeled with the Reference number SU 619-0311-12, should be posted to the address below and be postmarked no later than February 20th, 2012:

Stockholm University Registrar/PÃ SE-106 91 STOCKHOLM SWEDEN

or by e-mail to: registrator@su.se - give Reference number in the Subject head

Johan Nylander <Johan.Nylander@abc.se>

UBern FieldAssist AvianEvolution

Job: UBern.FieldAssist.AvianEvolution

Field assistants in evolutionary ecology of Great tits

(Parus major), Switzerland

I am seeking two highly motivated field assistants interested in taking part in field studies in Bern, Switzerland. Applicants will be part of the evolutionary ecology team (Institute of Ecology and Evolution, University of Bern).

The project aim to investigate the maternal effects induced by increased predation risk and is based in a forest in Bern (Switzerland)

I will require field assistants that will help with all the aspects of the work, including checking nests, ringing and taking body measures of the birds, catching adults, performing treatments, and some smaller amount of lab work. Applicants with a Msc in Biology/Ecology and/or with bird handling or field experience would have an advantage, but motivation will play a key role; the work is hard and demanding, takes place in changing weather and requires long hours at times. The study will start around the 15 of March 2012 until mid-June 2012. Fluent English, French or Italian speaking and a valid European driving license are required.

Travel expenses will be paid and accomodation will be covered; additionally, the field assistants will receive approximately 900 Swiss Francs per month to cover the expenses.

Applicants can send a letter of motivation, a CV and ask for further details or questions to:

Alessandra Basso (Institute of Ecology and Evolution, University of Bern) E-mail: alessandra.basso@iee.unibe.ch

"Basso, Alessandra (IEE)" <alessandra.basso@iee.unibe.ch>

UBristol BiologicalAdaptation

Four Lectureships available in the School of Biological Sciences, University of Bristol, UK

The School of Biological Sciences wishes to complement existing strengths with four lectureships in the areas of: behavioural biology, sensory biology, biological responses to global change, and systems approaches to water use in plants. We are also very happy to discuss the opportunities for early career scientists to apply for fellowships, or to bring them to Bristol.

These positions form part of a wider investment in the biological sciences at Bristol, and will benefit from location in the new Life Sciences Building, a £50M development to be completed in late 2013. With 13,500 square meters of accommodation and a five-storey laboratory wing, the central location and cutting-edge facilities will improve collaboration with departments across the University.

The School also benefits from being embedded in an exceptionally strong Science Faculty and having excellent collaborative links with cognate departments within other faculties. This facilitates the interdisciplinary approaches typical of innovative modern science, and creates novel research opportunities.

For further details see http://www.bristol.ac.uk/-biology/news/2012/185.html The closing date for applications is 9.00am on February 9th, 2012.

Dr Jon Bridle School of Biological Sciences University of Bristol Bristol BS8 1UD

Office B70, Lab B38/9 Tel. 0117 928 7482 Fax. 0117 331 7985

jon.bridle@bristol.ac.uk

Jon Bridle <jon.bridle@bristol.ac.uk>

UCalifornia Davis PopulationGenetics

FACULTY POSITION ANNOUNCEMENT

University of California, Davis

Assistant Professor of Animal Population/Quantitative Genomicist/Geneticist

The University of California at Davis is pleased to announce recruitment for a tenure-track faculty position in Population/Quantitative Genomicist/Geneticist. The successful candidate will join the Department of Animal Science in the College of Agricultural and Environmental Sciences (http://animal science.ucdavis.edu) at the rank of Assistant Professor. Criteria for appointment include: a Ph.D. or equivalent, a strong interest in Population or Quantitative Genetics of domestic, feral, or wild animals relevant to animal agriculture, a record of excellence in scholarly research, and demonstrable potential to establish a competitively-funded research program relevant to animal genetics, animal breeding, or population genetics of wild animals impacting the production environment. The appointee will be responsible for teaching undergraduate courses including quantitative and population genetics of domestic animals, be actively involved in undergraduate advising, curricular development and department and university service. The appointee is also expected to guide and mentor graduate students and participate in research and outreach programs consistent with the mission of the CA Agricultural Experiment Station.

Full Position Description can be found online at http://animalscience.ucdavis.edu/positions/ Inquiries can be directed to Professor J.D. Murray (jdmurray@ucdavis.edu)

Department of Animal Science, One Shields Avenue, University of California, Davis, CA 95616

Tel (530) 752-3179 <tel:%28530%29%20752-3179>

Applications should be received by April 1, 2012.

Folks-

Please contact me if you have any questions about this position.

-bernie

Bernie May, Adjunct Professor Department of Animal Science Director, Genomic Variation Laboratory 2237 Meyer Hall (office) 2403 Meyer Hall (lab) University of California Davis, CA 95616

office (530) 754-8123 <tel:%28530%29%20754-8123> , FAX (530) 752-0175 lab (530) 752-6351 <tel:%28530%29%20752-6351> , E-mail bpmay@ucdavis.edu

. For resources at our lab go to http://genome-lab.ucdavis.edu/

. For application to or information about graduate school at UCDavis go to http://-gradstudies.ucdavis.edu/homepage.htm or to the graduate groups of which I am a member

Ecology http://ecology.ucdavis.edu/, Genetics http:/-/www-ggc.ucdavis.edu/ggc/ggg/,

Bernie May <bpmay@ucdavis.edu>

UCalifornia Riverside BehaviorEvolution

Faculty Position - Assistant Professor BEHAVIORAL ECOLOGY University of California, Riverside

The Department of Biology, University of California at Riverside invites applications for a tenure-track, 9-month, academic position at the rank of Assistant Professor in the area of vertebrate behavioral ecology, starting July 1, 2012. We seek a colleague who will investigate the ecological, genetic, and/or evolutionary bases of animal behavior using an integrative approach, including a strong field component. Preference will be given to candidates who use state-of-the-art techniques to integrate behavioral studies with approaches in quantitative or molecular genetics, bioinformatics, endocrinology, sensory biology, and/or conservation biology. The successful candidate will be expected to develop a strong research program, teach at the undergraduate and graduate level, and participate in one or more graduate programs. A Ph.D. in Behavioral Ecology or a related field and at least one year of postdoctoral experience are required. The salary for this position is commensurate with the education and experience of the successful candidate.

Applications, including a curriculum vitae, separate statements of research and teaching interests, and up to three reprints must be submitted through academic jobs online (http://academicjobsonline.org). In addition, applicants should request that three letters of recommendation be submitted through this site.

Review of applications will begin on February 3, 2012.

The University of California is an Equal Opportunity/Affirmative Action employer.

Daphne J. Fairbairn, Editor-in-Chief, Evolution, Professor, Department of Biology, University of California, Riverside, California 92521 Phone: 951 827 4791

Daphne J Fairbairn <daphne.fairbairn@ucr.edu>

UFlorida EvolutionaryIntegrativeBiology

Animal Integrative Biology: Assistant Professor, tenure-track

The Department of Biology at the University of Florida is seeking applications for a tenure track faculty position beginning August 2012 at the Assistant Professor level whose work is at the interface of animal physiology and either behavior or development. We are seeking candidates who will develop an internationally recognized, externally funded research program that builds on the strengths and interconnects the departments expertise in the fields of behavior, development, evolution, ecology, genetics, systematics, morphology and physiology.

The successful candidate will be expected to contribute to the teaching of undergraduates in the areas of animal physiology and either animal behavior or developmental biology and to offer graduate seminars/courses in these or more specialized areas. A Ph.D. is required.

The Department of Biology has a strongly collegial environment that fosters collaborative interdisciplinary research and teaching that emphasizes integration of the above research areas within the framework of evolutionary principles. It enjoys strong ties with the Florida Museum of Natural History, UF Genetics Institute, UF Emerging Pathogens Institute and multiple University centers in biomedical, veterinary, environmental and agricultural sciences. For more information on the department go to http://www.biology.ufl.edu . Interested applicants must apply online at: https://jobs.ufl.edu (requisition # 0810207). For full consideration, the application should include curriculum vitae, statements of research interests and teaching philosophy (of no more than 3 pages each), a maximum of three reprints in PDF format and names of three references. For more information, please go to our website: http://www.biology.ufl.edu/jobs/aib.aspx .Review of applications will begin on January 31st 2012. Our department is committed to diversity as a component of excellence. Women, minorities and members of other underserved groups are encouraged to apply. The University of Florida is an Equal Opportunity Institution.

"Hahn,Daniel Allen" <dahahn@ufl.edu>

UHawaii Manoa ChairBotany

The Department of Botany at the University of Hawaii at Manoa will continue to accept applications for the position of Professor and Chair. The position posting is linked below:

http://www.pers.hawaii.edu/wuh/nadvert.aspx?rn=13130&si=1126637&pn=1&sn=postdate&so=desc

–

Kasey E. Barton Assistant Professor

Botany Department

University of HawaiÊ≫i at MÄnoa

3190 Maile Way, Room 101

Honolulu, HI 96822

Website http://seedlingscience.org Kasey Barton <kbarton@hawaii.edu>

ULiverpool Genomics

Faculty positions are available within the Institute of Integrative Biology, University of Liverpool, as follows:

(1) Three permanent positions at the levels of Senior Lecturer, Reader or Chair (Associate/Full Professor equivalent) http://www.liv.ac.uk/working/job_vacancies/academic/A-577068.htm (2) Two tenure track Research Fellow positions leading to permanent lectureships http://www.liv.ac.uk/working/job_vacancies/academic/A-577069.htm Closing date 20th February.

The Institute is particularly keen to attract applicants that would add to our existing strengths in Evolution, Ecology and Behaviour, and also those that use mathematical/computational approaches for understanding the behaviour of complex biological systems.

Further information on our current activity can be found on our research pages, particularly those for the research groups in Ecology, Evolution and Genomics of Infectious Disease, Evolutionary Ecology, and Mammalian Behaviour and Evolution:

http://www.liv.ac.uk/integrative-biology/research/research-groups/ http://www.liv.ac.uk/integrative-biology/research/ecology-evolution-and-gen omics-of-infectious-disease/ http://www.liv.ac.uk/integrative-biology/research/evolutionary-ecology/ http://www.liv.ac.uk/mbe The University provides a strong and supportive research environment. Particular features include: - Infectious Disease. A substantial concentration of researchers in veterinary, medical and wildlife pathogens within the University, and close links with the world-leading Liverpool School of Tropical Medicine. - Genomics. A major genomics facility within the Institute of Integrative Biology offering access to 9 next-generation sequencing machines and associated bioinformatic support. - Behaviour. Access to state-of-art animal facilities to study vertebrate behaviour, including large outdoor enclosures, video suites and breeding facilities.

Informal enquiries may be made either to our Head of Institute, Prof Andy Cossins (a.r.cossins1@liv.ac.uk), or to any of the following: Prof Mike Begon (mbegon@liv.ac.uk) Prof Jane Hurst (jhurst@liv.ac.uk) Prof Steve Paterson (s.paterson@liv.ac.uk) Prof Greg Hurst (ghurst@liv.ac.uk)

Formal applications should be made through the University website http://www.liv.ac.uk/working/job_vacancies/academic/A-577068.htm http://www.liv.ac.uk/working/job_vacancies/academic/A-577069.htm – Prof Steve Paterson Institute of Integrative Biology University of Liverpool Liverpool, L69 7ZB, UK Tel +44 151 795 4521 Fax +44 151 795 4408 s.paterson@liv.ac.uk http://www.liv.ac.uk/genomic-research/ S.Paterson@liverpool.ac.uk

UManchester EvolutionaryBiology

Evolutionary biology job opportunities in Manchester

Life Sciences in Manchester currently have both lectureships and professorial positions to offer in the areas of evolutionary and environmental biology. These four positions will be associated with our two research groupings/departments: Computational and Evolutionary Biology < http://www.manchester.ac.uk/ceb > and Environmental Research < http://www.ls.manchester.ac.uk/research/researchgroups/environmentalresearch/ >. All positions are tenured. If you're interested you can find details on how to apply here: < http://www.ls.manchester.ac.uk/recruitment/ >. Please direct informal enquires to Matthew Cobb, cobb@manchester.ac.uk, phone +44 (0)161 275 5419. Note, the lectureship positions have a closing date for applications of 27th January 2012.

– David Robertson, PhD www.manchester.ac.uk/ceb david.robertson@manchester.ac.uk

UNotreDame MolecularResTech

Molecular Research Technician, University of Notre Dame:

We seek a highly motivated person to join our workgroup as a research technician. Our group is studying the molecular detection of rare species in aquatic systems using genetic tools. The Research Technician will support the research activities of the faculty, postdocs and graduate students in the lab. This includes support for sample collecting and processing, data organization and analysis, report writing, and general lab and equipment maintenance. Applicants should have a strong interest in ecological or environmental science and possess an enthusiasm for laboratory research. Opportunities to contribute to manuscripts and proposals, build professional experience, and further training in molecular research will be provided. Responsibilities for this position include performing general molecular laboratory functions including DNA extractions, PCR, gel electrophoresis, data entry, and report writing. Additional duties include, but are not limited to ordering supplies, equipment sterilization and sample processing preparation. To apply, please visit http://jobs.nd.edu/applicants/Central?quickFind=57962 .Please apply online and do not contact hiring manager directly. Review of applications will begin on January 21, 2012 and continue until position is filled.

Crysta Gantz <Crysta.Gantz.2@nd.edu>

UNottingham HostParasite

Dear Colleagues

The School of Biology at the University of Nottingham is currently advertising for a lecturer (assistant professor) in cell/molecular biology, but there is a definite interest in appointing someone with host-parasite or pathogen interests. See:

http://www.nottingham.ac.uk/jobs/currentvacancies/ref/LC06628 Please circulate.

Best wishes Andrew MacColl

Lecturer in Evolutionary Ecology School of Biology University of Nottingham University Park Nottingham NG7 2RD Tel: +44 115 951 3410 Fax: +44 115 951 3251 Email: andrew.maccoll@nottingham.ac.uk http://www.nottingham.ac.uk/biology/research/animal-behaviour-and-ecology/andrew.maccoll http://ecology.nottingham.ac.uk/maccoll.html Andrew.Maccoll@nottingham.ac.uk

UOregon ResearchAssist MicrobialDiversity

Research Assistant Institute of Ecology & Evolution Posting: 12007 Location: Eugene Closes: Open Until Filled

The Institute of Ecology and Evolution at the University of Oregon currently has an opening for a full time Research Assistant to work on a project in the area of microbial ecology. The successful candidate will gain experience working with an interdisciplinary team developing new approaches to understanding microbial diversity in a variety of environments and habitats. The initial appointment is for one year, with the possibility of extension dependent on funding and satisfactory performance. The University of Oregon is located in Eugene, Oregon, recently rated among the top 25 $B!H(BBest Places to Live$B!I(B eugene-or.gov.

Extensive experience using molecular techniques is required, including some combination of skills in DNA/RNA extraction, PCR, cloning, next-generation DNA sequencing, bioinformatics, and phylogenetic analysis. Ability to work in a team atmosphere is a must. A Master$B!G(Bs degree in biology is desirable, but individuals with a bachelor in biology or related field and extensive experience are also encouraged to apply. The successful candidate will be responsible for conducting laboratory research under the direction of Principle Investigators Jessica Green http://biology.uoregon.edu/people/Green and Brendan Bohannan http://biology.uoregon.edu/ie2/-faculty_pages/Bohannan/. Salary will be commensurate with education and experience. We invite applications from qualified candidates who share our commitment to diversity.

Please e-mail a cover letter and current CV with names and contact information of three references to: ceebjobs@uoregon.edu. Subject: Posting 12007

Or mail to:

Posting 12007, 5289 University of Oregon, Eugene, OR 97403-5289.

To assure full consideration, applications must be received by February 15, 2012, but position will remain open until filled.

An equal-opportunity, affirmative-action institution committed to cultural diversity and compliance with the Americans with Disabilities Act.

CEEB Job Applications <ceebjobs@uoregon.edu>

UOxford Fellowships PlantEvolution

Independent Research Fellowships

Evolutionary biologists, population geneticists are encouraged to apply.

We particularly welcome enquiries by Friday 16 March, 2012 The Department of Plant Sciences at the University of Oxford is keen to hear from early career researchers who feel they have what it takes to secure a fellowship from one of the UK or international research sponsors and become an Independent Research Fellow in the Department. Fellowship opportunities include:

* BBSRC David Phillips Fellowship * Royal Society University Research Fellowship * NERC Fellowship * ERC Starting Grants.

These schemes enable the best early career researchers to establish themselves as independent research fellows with their own research groups. The fellowships are prestigious and competitive. Sponsors' eligibility criteria apply.

We can support the best candidates to apply for fellowships. We are also keen to hear from fellows who may wish to transfer a current fellowship to the Department. See www.plants.ox.ac.uk Debbie Reeves Research Coordinator Dept of Plant Sciences University of Oxford South Parks Road Oxford OX1 3RB UK

Telephone +44 1865 275053

Debbie Reeves <debbie.reeves@plants.ox.ac.uk>

Wageningen 2 EvolutionaryGenetics

Application deadline Feb 16 Additional information can be obtained from Dr. Sip van Wieren, 0317-483434; sip.vanwieren@wur.nl. 2 PhD projects:

1) evolutionary genetics / molecular ecology (job reference ESG-ECO-0072) “Genetic structure of White-fronted geese”

We are looking for an enthousiastic PhD student for the following research. The family Anser can be thought of as a well-structured group of species but equally it can be viewed as a species swarm comprised of species that are less well defined. So the Grey-lag goose is quite distinct from the White-fronted goose, but on the other hand within the Bean goose two or three species may be hardly distinguishable as cryptospecies. Since crossing is possible between all Anser species and even between Anser and Branta, much gene flow is expected between the species. Yet it is unclear under which conditions gene flow is frequent and when not. The concept of supraspecies (as we recently found for ducks) and its implications for goose evolution has to be investigated. This can be of significance both for the conservation of these geese as for the understanding of their role in disease transmission.

We ask that the selected candidate should have a Masterâs degree, or equivalent, in (eco-)genetics with proven abilities to interpret his/her results in an ecological context. Preferably she/he can read and speak Russian. A driving license is a necessity and so is the willingness and ability to travel independently in Eurasia. Sound statistical knowledge and proven publication skills are important.

2) ecology (job reference ESG-ECO-0073) “Land use changes in Russia and their impact on migrating geese”

We are looking for an enthousiastic PhD student for the following research. The breaking-up of the former USSR led to profound social and economic changes in those areas of Russia, White Russia, the Baltic Republics and Ukraine that are important to geese that migrate in winter to Western Europe. In the countryside much arable agriculture decreased (especially north of 55 degrees north but also in the steppe area in the south), livestock numbers decreased profoundly, river valleys get overgrown and hunting regimes change. The PhD student will study land use changes at the hand of sociological surveys, census outcomes and satellite imagery with the aim to understand changes in the migratory routes and population development of Barnacle geese, White-fronted geese and Bean geese, and to make well-founded predictions under different scenario developments. This has important implications for goose conservation.

We ask that the selected candidate should have a Masterâs degree, or equivalent, in ecology with proven abilities to interpret remotely sensed imageries. Preferably she/he can read and speak Russian. A driving license is a necessity and so is the willingness and ability to travel independently in the named countries. Sound knowledge of spatial statistics is important as well as proven publication skills.

For both positions:

We offer a full-time position (38 hours), initially for 18 months. If your suitability in this position is apparent, the period of employment will be extended to the remainder of your PhD-study, with another 30 months. Gross salary starts at 2042 Euro per month during the first year, increasing to 2612 Euro per month during the fourth year. Commencing as soon as possible. The candidate will be based at the Resource Ecology Group in Wageningen.

We are the Resource Ecology Group and we perform research and education in community ecology of large herbivores, with particular emphasis on the interactions between herbivores and the vegetation and their role in wildlife disease ecology. This is carried out at aggregation levels ranging from plant part to ecosystem, with a world-wide geographical focus. Our main research fields are (1) rangeland ecology of large herbivores in extensively managed ecosystems, (2) conservation genetics of large herbivores, and (3) the role of vertebrates in abundance and movements of pathogens. The research approaches include model development, model testing, and experimental hypothesis testing. The main research sites are savannas, grasslands in tropical and temperate regions, and grasslands and forests in neotropical regions. Most research is carried out by post-docs and PhD students, supported by faculty. Results have a strong bearing on nature conservation and management in tropical and temperate areas.

The department of Environmental Sciences of Wageningen University provides fundamental research and academic education on our living environment: nature, landscape, land usage, adaptation to climate change, water and ocean management, and the various competing claims on space. This also includes biodiversity and the sustainability of management and production. Wageningen University is part of the Wageningen University and Research Centre concern.

Wageningen University and Research Centre

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

Other

Advice on NSF preproposals

I wrote this piece on submitting for the new NSF preproposals for ecology and evolution. Some program officers thought it would be good to contact you to post here. Here is the link.

http://sociobiology.wordpress.com/2012/01/02/how-to-write-a-successful-nsf-preliminary-proposal/ Cheers,

Joan Joan E. Strassmann, Professor of Biology, Department of Biology, Washington University, One Brookings Drive, Campus Box 1137, St. Louis MO 63130

phone: (314) 935-3527 fax: (314) 935-4432, cell: (832) 978-5961skype: strassm, e-mail strassmann@wustl.edu

Webpage: http://strassmannandquellerlab.wordpress.com/

Blogs: http://sociobiology.wordpress.com/ http://slowbirding.wordpress.com http://goodbyehouston.wordpress.com/ Twitter: @JoanStrassmann

"Joan E. Strassmann" <strassmann@biology2.wustl.edu>

Advice on NSF preproposals 2

It may be overkill, but here is another one on preproposals. The last one got over 4000 hits, so there is a lot of interest out there.

http://sociobiology.wordpress.com/2012/01/05/are-nsf-preliminary-proposals-a-good-idea/ Cheers,

Joan Joan E. Strassmann, Professor of Biology, Department of Biology, Washington University, One Brookings Drive, Campus Box 1137, St. Louis MO 63130

phone: (314) 935-3527 fax: (314) 935-4432, cell: (832) 978-5961skype: strassm, e-mail strassmann@wustl.edu

Webpage: http://strassmannandquellerlab.wordpress.com/ Blogs: http://sociobiology.wordpress.com/

http://slowbirding.wordpress.com http://goodbyehouston.wordpress.com/ Twitter: @JoanStrassmann

"Joan E. Strassmann" <strassmann@biology2.wustl.edu>

Assignment using DNA

Dear all,

I would like to perform a population assignment test using DNA sequences (not microsatellites).

Does anybody know of a software doing this?

Thank you very much!

Best, Joaquín

(jvierna@udc.es)

Joaquín Vierna pre-doctoral researcher

Evolutionary Biology Group Universidade da Coruña – SPAIN

http://www.udc.es/grupos/gibe/

Joaquín Vierna <jvierna@udc.es>

Director CanadianInstEcolEvol

The Canadian Institute for Ecology and Evolution (CIEE/ICEE; http://ciee-icee.com/) seeks candidates for the position of Director. CIEE/ICEE is a national platform to identify and solve important problems in ecology and evolution through working groups, workshops, and other fora. In its first three years, the Institute has mounted working groups on global patterns in plankton dynamics, the application of science in implementation of the Species at Risk Act, networking of Canadian field stations and, coming this spring, the effects of rising temperatures on food web structure. The Institute also sponsors training workshops in conjunction with the Canadian Society of Ecology and Evolution, and in June will give it first graduate mini-course, Landscape Genetics. CIEE/ICEE is now poised for membership and budgetary expansion, and the new Director will provide leadership and strategic direction as CIEE/ICEE continues to grow and mature. The Director is appointed by CIEE/ICEE's Management Board (3-year, renewable term) and receives a $5000 yearly allowance. A Director can be located anywhere.

Responsibilities of the Director include:

- INSTITUTE DEVELOPMENT: The Director proposes and develops new and innovative programs and partnerships that advance the CIEE/ICEE mission. This includes the recruitment and retention of member institutions.

- PROGRAMS: The Director issues calls for proposals for CIEE/ICEE programs and, with advice from the Scientific Advisory Group, selects proposals for funding. (An Associate Director arranges practical aspects of CIEE/ICEE programs, such as travel and housing.)

- COMMUNICATIONS AND OUTREACH: The Director communicates information on CIEE/ICEE programs and accomplishments within the Institute, to relevant administrative officers at member institutions, and to the community of potential users.

- FUNDRAISING: The Director seeks financial support from governmental granting programs, universities, private donors, and other sources. The Management Board and the Associate Director assist with this responsibility.

- BUDGET: The Director (in consultation with the Associate Director) proposes a budget for approval by the Management Board.

The Directorship of CIEE/ICEE is an opportunity to have a major influence on the direction of ecological and evolutionary research, and its application, in Canada. To learn more about this opportunity, contact the Chair of the Management Board (Stephen Heard, stephen.heard@unb.ca, 506-452-6047). Applications for the directorship will be accepted immediately and until the position is filled (send a letter of interest and a CV to stephen.heard@unb.ca).

Steve Heard sheard@unb.ca Professor & Chair 506-452-6047 Dept. of Biology FAX 506-453-3583 University of New Brunswick Fredericton, NB E3B 5A3

sheard@unb.ca

Ernst Mayr Award

Society of Systematic Biologists Ernst Mayr Award (Graduate Student Award)

The Ernst Mayr Award is given to the presenter of the outstanding student talk in the field of systematics at the annual meetings of the Society of Systematic Biologists (SSB). This is SSB's premier award, and is judged by the quality and creativity of the research completed over the course of the student's Ph.D. program. The award consists of $1000, a certificate of distinction, and a two-year subscription to the journal Systematic Biology.

Eligibility: Members of the Society who are advanced Ph.D. students or have completed their Ph.D. within the last 15 months are eligible. Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to be considered (to join go to: http://systbio.org/?q=node/6). Previous Mayr award winners are not eligible.

Application Procedure: 1. To be considered for this award, you will need to submit a 400-word abstract of your talk to the Evolution Ottawa meeting website (http://www.confersense.ca/Evolution2012/index.htm) at the time of registration. Instructions for registering as a potential Mayr award contender will be given on the meeting website. 2. Abstracts should clearly indicate methods used, conclusions, and the relevance to systematics. Presentations focusing on other areas of biology (ecology, behavior, genetics, populations or molecular biology, etc.) that lack a strong systematics emphasis are not eligible. This abstract must include the title of the talk, names and institutions of the authors, and contact information for the primary author. 3. Applications for this award will be accepted only until the end of early registration (April 30, 2012). 4. At the closing of early registration, a subset of applicants will be selected by the SSB Awards Committee to present their talks in the Mayr symposium during the meeting. All applicants will be notified about selection decisions by May 15.

Judging: Based on submitted abstracts, the Mayr Awards Committee (appointed by the Awards Chair, Sydney Cameron) will select a maximum of 16 applicants for inclusion in the Mayr Award symposium.

The Mayr symposium will be held at a single venue as a continuous session. Talks will be judged on creativity, depth and excellence of research, and on quality of presentation. Competitive students are expected to be in the final stages of their doctoral program, presenting results of a major body of work.

Co-Authors: The talk may be co-authored. It is understood that the ideas, data and conclusions presented are primarily and substantially the work of the student presenter, and the intention is that the student presenter will be senior author on the published version of the paper. If a submission includes multiple authors, include a brief section below the abstract that outlines the contribution of each author to the research.

Notification of Winner: The winner of the award will be announced at the SSB business meeting in Ottawa and again during the banquet awards ceremony (complimentary ticket provided) at the conclusion of the Evolution Meetings, whereupon the winner will be given an award certificate. An announcement of the winner will be published in Systematic Biology and placed on the SSB website (see last year's winner at http://systbiol.org/).

Please see the SSB website (http://systbio.org/?q=node/10) for additional information or updates on this award.

Rhiannon Peery <ssb-apps@life.illinois.edu>

EvolutionSexGenes CallForPapers

The Evolution of Sex-Related Traits and Genes Call for Papers (International Journal of Evolutionary Biology)

Dear colleagues: Following the successful publication of our first issue on the evolution of sex-related traits and genes http://www.hindawi.com/journals/ijeb/2011/si.2/, we are pleased to announce the launching of an annual special focus issue on the topic. This issue will become the second in a series of special issues or focus issues to be published each year. We are now inviting authors to submit original research articles as well as review articles that will stimulate, contribute, and challenge our continuous effort to understand what drives the evolution of sex-related traits and genes.

For more information please visit http://www.hindawi.com/journals/ijeb/si/estg12/ Sincerely,

Alberto Civetta Jose M. Eirin-Lopez Rob Kulathinal Jeremy L. Marshall

a.civetta@uwinnipeg.ca

Fish DNA samples

Dear all,

I'm evaluating a heart regulatory element that has a very interesting evolution in fishs. To better reconstruct the genomic history inside this group I would like to check some key groups:

Acipenseridae (sturgeons) Polyodontidae (paddlefish) Amiiformes (bowfin/Amia calva) Clupeomorpha (herrings, shads, anchovies, noodlefishes) Anotophysi (milkfish)

Could someone provide me DNA samples for them?

Latimeria samples are also very welcome!!!!

Thanks in advance.

Pedro.

Pedro Edson Moreira Guimarães, PhD cel: +55 11 81880260

Google Scholar Citations: http://scholar.google.com/citations?user=3DWSADNwgAAAAJ Researcher ID: A-9715-2008 www.researcherid.com Laboratório Nacional de Biociências www.lnbio.org.br Caixa Postal 6192 Rua Giuseppe Máximo Scolfaro, 10.000 Pólo II de Alta Tecnologia CEP 13083-970 - Campinas - SP - Brazil

ninjurin@gmail.com

Genetic correlations estimates

Dear all,

I'm working on a meta-analysis involving genetic correlations (both inter-trait and intra-trait (e.g. cross-environment or cross-sex)). I would like to ask all who would be keen to contribute to this project to contact me if you have any valuable data in this matter. I'm looking especially for estimates of high genetic correlations in case of realtively low/moderate individual heritabilities as such estimates are rarely published. Also - in case of cross-sex/environment heritabilites high estimates accompanied by low heritability estimates are also desirable. But feel free to include anything you'd like to offer.

If youd like to provide any data please specify: - estimates for h2 and rG with their standard errors (if possible) + whether i's inter-trait or cross-sex/env rG - sample size used to estimate these parameters - statistical technique (e.g. animal model, full-sib analysis, half-sib analysis, parent-offspring regression etc.) - whether the data comes from wild or captive population (if the latter - whether it's from artificially selected cultivars of some kind) - any relevant information you think might be important

If you have any questions - feel free to ask. I'll try to keep all of data providers posted about progress.

Cheers, sz.

Szymon Drobniak || Population Ecology Group Institute of Environmental Sciences,Jagiellonian University ul. Gronostajowa 7, 30-387 Kraków, POLAND tel.: +48 12 664 51 79 fax: +48 12 664 69 12

www.eko.uj.edu.pl/drobniak geralttee@gmail.com

Heat sealing PCR plates

Hi all,

We have had trouble with evaporation during 10 uL PCRs run in 96-well plates. Samples on the perimeter of the plate routinely evaporate when the sealing tape opens up around the plate edges.

As a possible solution to this problem, our lab is considering the purchase of heat sealer, such as the Eppendorf PCR Plate Heat Sealer, for use with sealing foil.

Can anyone attest to the effectiveness of this method? Is evaporation completely eliminated for small volume PCR when using a heat sealer? Are there other solutions we should consider?

Thanks for any feedback,

Ivan

Ivan C. Phillipsen Postdoctoral Researcher Department of Zoology Oregon State University 3029 Cordley Hall Corvallis, OR 97331-2914 Email: philliiv@science.oregonstate.edu

phillipsen@gmail.com

Hymenoptera PloidySize

Dear All

I've been searching the literature for data about size changes (any measure of size) between diploid males and haploid males (and/or triploid workers and normal diploid workers) in the hymenoptera. I would appreciate any references people had. Especially useful would be papers that have data about these size differences in monogamous (or monogynous and lowly multiply mated) eusocial species. Thanks for your time

Eamonn

Dr. Eamonn Mallon Lab 219 Department of Biology University of Leicester Tel 01162523488

"Mallon, Eamonn B. (Dr.)" <ebm3@leicester.ac.uk>

Ingroup Mouse Rat

Hi,

Does anybody know of researchers working on Murinae species that are ingroups between mouse and rat? We would like to contact those researchers to obtain liver samples from these ingroup species.

According to Steppan et al. 2005, here is a list of ingroups in case people heard of someone working with them:

** Mus sp. Apodemus sp. (Liverpool, Edinburgh) Hylomyscus sp. Zelotomys sp. Mastomys sp. Praomys sp. Malacomys sp. Arvicanthis sp. Lemniscomys sp. Rhabdomys sp. Aethomys sp. Oenomys sp. Hybomys sp. Stochomys sp. Paratomys sp. Sudamys sp. Berylmys sp. Niviventer sp. Dacnomys sp. Maxomys sp. ** Rattus sp. * Immediate outgroups: Batomys sp. Phloeomys sp.

Thanks,

Albert Vilella, PhD. Vertebrate Genomics EMBL-EBI Cambridge, UK

Albert Vilella <avilella@ebi.ac.uk>

Ion Torrent Reviews

Hi all,

We are in the process of weighing the pros and cons of the Ion Torrent with some of the other Next-Generation Sequencing platforms, i.e. Illumina MiSeq. Specifically we would like to know: 1) What are some of the various applications where the Torrent has proven to be useful? 2) What are some of the limitations of the Ion Torrent?3) What are some of ways in the 10MB chip have been used? Any additional comments/thoughts are appreciated.

Thank you for your feedback

Carla

Carla Hurt, Ph.D. Dept. of Biology Cox science center, rm 36 1301 Memorial Dr., University of Miami Coral Gables, Fl 33146 PH# (305) 284-6566 Core Lab server access: http://zorki.bio.miami.edu/ ˜ corelab/ Carla Hurt <hurtc@bio.miami.edu>

James F Crow 1916 2012

I have just heard that James F. (Jim) Crow died peacefully in his sleep yesterday. As he was born on January 16, 1916, he was 95 years old.

Joe

Joe Felsenstein joe@gs.washington.edu Dept of Genome Sciences and Dept of Biology, Univ. of Washington, Box 5065, Seattle Wa 98195-5065

Joe Felsenstein <joe@gs.washington.edu>

Jim Crow Obituary

I often contribute to the Panda's Thumb blog, which carries responses to attacks on evolutionary biology.

I just wanted to let people know that I have written a brief obituary of Jim there. It contains two pictures of Jim (one with Motoo) that I took in 1972 in Mishima, which have not previously been circulated.

The obituary may be found here: href="http://-pandasthumb.org/archives/2012/01/james-f-crow-19.html or by feeding the words Crow Panda's Thumb into a search engine.

Joe

Joe Felsenstein joe@gs.washington.edu Department of Genome Sciences and Department of Biology, Univer-

sity of Washington, Box 355065, Seattle, WA 98195-5065 USA

Joe Felsenstein <joe@gs.washington.edu>

MaxPlanckInst Ornithology Ravens

Practical training at the Max Planck Institute for Ornithology, hand-raising of ravens (Corvus corax)

We are looking for an enthusiastic person who helps to handraise ravens (Corvus corax) from 01. April- 31. May 2012 at the Max Planck Institute for Ornithology, Seewiesen, Germany.

We seek a highly motivated, organized and reliable person who is interested in corvid behaviour and their development, likes to interact with birds and is able to monitor their behaviour.

We offer free accomodation at our guesthouse for the whole period and the opportunity to work at one of Europe's leading institutes for bird research.

For further information please contact:

Dr. Simone Pika Max-Planck-Institut für Ornithologie Research Group "Comparative Gestural Signalling" Max-Planck-Institut für Ornithologie Eberhard-Gwinner-Str. Gänsehaus D-82319 Seewiesen E-mail: spika@orn.mpg.de Webpage: www.orn.mpg.de/cgs

Simone Pika Humboldt Research Group "Comparative Gestural Signalling" Max Planck Institute for Ornithology Eberhard-Gwinner-Strasse 82319 Seewiesen Germany

Gänsehaus phone: +49 8157 932 - 237 mobile: +49 172 8872270 fax : +49 8157 932 - 259

http://www.orn.mpg.de/cgs http://www.primate-gesture-center.eu "If indeed the fish will be the last to discover water, perhaps we can help ourselves by looking at some other species" (Bruner, 1971)

Simone Pika <spika@orn.mpg.de>

MethodsEcolEvol Editor

Editor vacancy

Methods in Ecology and Evolution is a highly esteemed international journal that publishes papers with new methodological insights in any area of ecology and evolution. The Journal's mission is to facilitate the dissemination and uptake of methods by the research community, and allow papers from previously disparate subdisciplines to have a single forum.

We are seeking an Editor to strengthen and complement the current editorial team and to raise the Journal's profile worldwide. The Journal currently has one Editor who is supported by an international Associate Editorial Board, as well as by a Journal Coordinator. The two Editors will work together to determine journal strategy and to increase the reputation and quality of the Journal, in addition to being responsible for making decisions on submitted manuscripts. Further details about the Journal and its current editorial team can be found at www.methodsinecologyandevolution.org Journal page: http://www.methodsinecologyandevolution.org Further details about the position: http://www.britishecologicalsociety.org/documents/about_bes/MEE_Advert_Jan_2012.pdf Closing date: 17th February 2012

Dr Graziella Iossa

Journal Coordinator, Methods in Ecology and Evolution coordinator@methodsinecologyandevolution.org Working hours: Mon-Wedn 8-18, Thurs 8-16 GMT and Mon-Fri 8-16 GMT on alternate weeks

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coordinator@methodsinecologyandevolution.org coordinator@methodsinecologyandevolution.org

Mini-ARTS grant

The Society of Systematic Biologists is pleased to announce the availability of awards for revisionary taxonomy and systematics, modeled after the NSF Dear Colleague Letter: Advancing Revisionary Taxonomy and Systematics (ARTS) recently developed within the Systematics and Biodiversity Science Cluster. We are calling these 'mini-ARTS' grants. These awards are designed to allow SSB members (students, post-docs, and faculty) to spend a summer or semester apprenticed to an expert in a particular taxonomic group or to enhance revisionary taxonomic and systematics research in novel ways. Goals of this award program are to address constraints on our knowledge of undescribed biodiversity, assist in passing on taxonomic expertise before it is lost, increase the number of students with broad training in organismal biology and systematics, and support projects in biodiversity and taxonomy informatics as well as monographic and revisionary taxonomy. Activities can include a trip to the taxonomist's laboratory, pay for the taxonomist to visit the applicant's laboratory for a period of time, or pay for costs of computer time or development of interactive keys for electronic dissemination of systematics results. Requests for support may be in any amount up to $3,000. We will fund two or three of these awards this year.

Please visit NSF's website http://www.nsf.gov/pubs/2011/nsf11037/nsf11037.jsp for more information about their ARTS program.

How to apply A complete application includes 1) a brief description of the project, including a separate section justifying the importance of the taxon and the revisionary work, 2) an itemized budget, 3) the applicant's CV, and 4) a letter of support from the taxonomic expert or collaborator. If the applicant is a student or post-doc, please also include a reference letter from the advisor. Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications (to join go to: http://systbio.org/?q=node/6). The narrative part of the application should be no more than two pages, including the budget, but not including the curriculum vitae and letter(s).

Grant applications should be sent to the SSB Awards Committee (ssb-apps@life.illinois.edu). E-mail submissions are required, and applicants should use pdf format for all documents. In the subject line of the email, please indicate the SSB award category as 'mini-ARTS'.

Please see the SSB website (http://systbio.org/?q=node/26) for any updates or additional information about this award.

Application deadline is March 31, 2012

Rhiannon Peery <ssb-apps@life.illinois.edu>

MountainLakeBioStation Fellowships

Mountain Lake Biological Station announces Early-Career Fellowships.

The University of Virginia's, MLBS is excited to offer a limited number of fellowships to support station and residency costs for researchers to explore new projects or collect preliminary data. This is a rare opportunity to make an extended stay of up to 2 months at one of North America's premier field stations at no cost to the researcher. Preference will be given to individuals and projects with the potential to develop into long-term research activities at the Station. We especially encourage applications from individuals in the postdoctoral or early faculty phases of their careers, but will not exclude other individuals from consideration.

Interested individuals should submit a single pdf file including CV and a 2-3 pp proposal outlining the proposed research to MLBS@virginia.edu. Review of proposals will begin February 20, 2012. For more information about the fellowship program, research opportunities or Mountain Lake Biological Station (mlbs.org), please contact the Director - Butch Brodie (bbrodie@virginia.edu).

Yours,

Melissa Ivy Wender Office Manager Mountain Lake Biological Station 223 Gilmer Hall 1-434-982-5486 www.mlbs.org miw2m@eservices.virginia.edu

NESCent EvolutionVideoContest

Call for entries: NESCent announces the Second Annual Evolution Video Contest

Application deadline: Friday, June 29th, 2012

Submit your best evolution-themed video for screening at this years Evolution meeting!

The National Evolutionary Synthesis Center (NESCent)< http://www.nescent.org/ > invites scientists of all stripes X graduate students, postdoctoral fellows and faculty X to enter the second annual evolution video competition< http://filmfestival.nescent.org/ >.

To enter, submit a video that explains a fun fact, key concept, compelling question, or exciting area of research in evolution in less than three minutes. Entries may be related or unrelated to your own research, and should be suitable for use in a classroom at any level (K-12, undergraduate, graduate...your choice). Videos should be both informative and entertaining. (In other words, no taped lectures or narrated Powerpoint presentations!) Animations, music videos, and mini-documentaries are all fair game.

Selecting the winners

A panel of reviewers from both NESCent and the science video community will select the semi-finalists, who will be notified by e-mail. The semi-finalists will then be screened at a film festival at the Evolution 2012< http://www.confersense.ca/-Evolution2012/index.htm > conference in Ottawa, Ontario, Canada. After screening the videos, the audience will vote for their favorites. Prizes will be awarded for the top entries.

Eligibility

You dont need to attend the conference to submit an entry. All videos submitted by Friday June 29th (5:00 p.m. ET) are eligible to win.

For more information and full contest rules, and to see last years entrants/winners, please see filmfestival.nescent.org. For additional information, please contact Dr. Jory Weintraub at jory@nescent.org, or Dr. Robin Smith at rsmith@nescent.org

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

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

Outgroups with winclada nona

Dear Evoldir partners, First of all HAPPY 2012 for you all!

Does anybody know how to designate the outgroup(s) to use winclada/nona for parsimomy analysis?

Thanks, Rodrigo A. Torres

rodrigotorres@ufpe.br

Outlier analyses answers

Dear All,

Many thanks for all of you who have replied to my post on Evoldir last week. The responses were very useful and as many requested me to forward them the replies, I have summarised them below. For privacy’s sake I have left out people’s names.

Thank you once again,

Serinde

My original post:

I am running outlier analyses on a set of 25 markers but find discrepancies between different methods, which I find hard to explain. The dataset is comprised of both putatively neutral microsatellites and candidate SNP loci in genes of interest for divergently selected populations over 6 generations (50 individuals per population). Fdist and Schlotterer’s method are fairly consistent in the identification of outlier loci, which also correspond to patterns of allelic divergence and results obtained from exploratory analyses (AMOVA, correspondence analysis). The output from BayeScan however is very different: rather than indicating divergent selection at the loci identified by Fdist and Schlotterer’s methods (and others) other loci are identified as under balancing selection. There therefore appears to be a bias towards balancing selection rather than diversifying selection at the expected loci, which doesn’t make biological sense in the case of my data. Analysing microsatellites and SNPs independently does not radically change the findings.

I would like to know if anyone has observed similar discrepancies between BayeScan and other outlier analyses or could think of ways how such a shift (identification of different loci under balancing selection rather than the same loci under divergent selection) could be explained. Any suggestions would be extremely helpful. Thank you very much in advance.

The responses:

—–

1) The methods are really different, so you shouldn’t be shocked if they yield different results.

2) The Beaumont & Nichols FDIST/Lositan test is very intuitive and understandable, so if it does confirm likely

divergent selection at those candidate loci for which you already had biological knowledge, then that is a strong indication!

3) Consider that in most cases these tests are conducted on samples from wild populations, with large Ne and very little knowledge about them. You may have a lot of knowledge about your populations, and over 6 generations. Also if your populations are small and there is a strong genetic drift signal in your data maybe that affects the results of Bayescan. I remember some experiments on Drosophila that showed that when you have lab populations undergoing strong genetic drift, the signal of selection may not be so obvious. Maybe FDIST picks it up, and Bayescan doesn't.

4) Do you have 2 or more populations? If you have more, you could try to do tests per pairs.

5) You could also try to use multivariate ordination techniques (like PCA or FCA), separately for microsats and SNPs, and plot your individuals alongside the alleles, to see if there is any decisive pattern of association between certain alleles that you expect to be under selection and those individuals that had been exposed to said selective pressure (I suspect that if there is a real signal of selection, you should see some striking scattering).

So, these were my two-cent - good luck with your research!

—–

I saw you message on evoldir. Sorry I cant be of much use, but Id be interested in the response you get so if you dont post a summary on evoldir, perhaps you could forward the replies to me? One thought did occur. Perhaps your results are not as different from each other as they appear, it just seems that the assessment of divergent selection by BayeScan has shifted down for all loci. In that case outlier loci look like loci under ordinary drift only, and loci under drift look to be under stabilising selection. Perhaps a problem with your prior settings? Good luck in figuring out the difference and which program does the better job in your case

—–

It is a general issue that BayeScan seems to be more conservative than alternative tests (see attached if you haven't already), but be aware of the major flaw in their discussion of the hierarchical model. I don't know how large your Fst values are, but for marine fish (approx. Fst=0.0001-0.04) we do also often get candidates for balancing selection, but they're most likely false positives, and as long as the neutral background Fst is relatively low, I don't think it's possible to reliably detect true balancing selection in these types of tests. Thus, I wouldn't worry too much about that result. The lack of outliers in BayeScan may simply be due to low power in your dataset, but I guess that if you couple these observations with time series plots of Fst for the other outliers that could reinforce the results (does it make sense).

—–

How large is your Fst values over time? Does it make sense that the signal is simply too low for BayeScan to detect? A simulation trial

— / —

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

Outlier analyses question

Dear Evoldir users,

I am running outlier analyses on a set of 25 markers but find discrepancies between different methods, which I find hard to explain. The dataset is comprised of both putatively neutral microsatellites and candidate SNP loci in genes of interest for divergently selected populations over 6 generations (50 individuals per population). Fdist and Schlotterer's method are fairly consistent in the identification of outlier loci, which also correspond to patterns of allelic divergence and results obtained from exploratory analyses (AMOVA, correspondence analysis). The output from BayeScan however is very different: rather than indicating divergent selection at the loci identified by Fdist and Schlotterer's methods (and others) other loci are identified as under balancing selection. There therefore appears to be a bias towards balancing selection rather than diversifying selection at the expected loci, which doesn't make biological sense in the case of my data. Analysing microsatellites and SNPs independently does not radically change the findings.

I would like to know if anyone has observed similar discrepancies between BayeScan and other outlier analyses or could think of ways how such a shift (identification of different loci under balancing selection rather than the same loci under divergent selection) could be explained. Any suggestions would be extremely helpful. Thank you very much in advance.

Serinde van Wijk bsp609@bangor.ac.uk

Molecular Ecology & Fisheries Genetics Bangor University

serindevanwijk@gmail.com

Phyloseminar KosakovskyPond HyPhy Jan25-26

Next up at http://phyloseminar.org/: "Introduction to HyPhy: Hypothesis testing using Phylogenies" Sergei Kosakovsky Pond (UCSD)

HyPhy is an open-source software package for the analysis of genetic sequences using techniques in phylogenetics, molecular evolution, and machine learning. It features a complete graphical user interface (GUI) and a rich scripting language for limitless customization of analyses. Additionally, HyPhy features support for parallel computing environments (via message passing interface) and it can be compiled as a shared library and called from other programming environments such as Python or R.

West Coast USA: 11:00 (11:00 AM) on Wednesday, January 25 East Coast USA: 14:00 (02:00 PM) on Wednesday, January 25 England: 19:00 (07:00 PM) on Wednesday, January 25 France: 20:00 (08:00 PM) on Wednesday, January 25 Japan: 04:00 (04:00 AM) on Thursday, January 26 New Zealand: 08:00 (08:00 AM) on Thursday, January 26

– Frederick "Erick" Matsen, Assistant Member Fred Hutchinson Cancer Research Center http://-matsen.fhcrc.org/ ematsen@gmail.com

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PlantEvolution SummerInternship

Summer field research internships

Are you interested in gaining field research experience and learning about the ecology and evolution of plants and plant-animal interactions in fragmented prairie? We are looking for 3-5 summer field researchers for an NSF-funded project on habitat fragmentation of the tallgrass prairie. We are investigating how small plant population size influences inbreeding, demography, pollination, and herbivory in the purple coneflower, Echinacea angustifolia. This is a great summer internship, REU, or co-op for those interested in field biology or conservation research.

No experience is necessary, but you must be enthusiastic and hard-working. You will survey natural plant populations, measure plant traits in experimental plots, hand-pollinate plants, observe & collect insects, and assist in all aspects of research. Housing is provided and there is a stipend. Undergraduate students have the opportunity to do an independent project as an REU participant.

If you want more information or wish to apply, please visit this website http://echinaceaProject.org/-opportunities/ or contact Stuart Wagenius. Applications will be reviewed starting 29 February 2012.

Stuart Wagenius, Ph.D. Conservation Scientist Division of Plant Science and Conservation Chicago Botanic Garden 1000 Lake Cook Road Glencoe, IL 60022 phone: 847 835 6978 fax: 847 835 6975

email: echinaceaProject@gmail.com web: http://-/echinaceaProject.org/ Stuart Wagenius <SWagenius@chicagobotanic.org>

Popular culture evolution

Hello All,

I am teaching a freshman writing course on Evolution and am looking for a piece that explores the use of "evolution" in popular culture - advertising, entertainment, etc. I thought it would be easy to find such a paper but I have had no luck. I would appreciate any suggestions and will post them to the list.

Thanks very much,

Peter Wimberger Professor, Biology Director, Slater Museum of Natural History University of Puget Sound Tacoma, WA 98416 253 879-2784 http://www.pugetsound.edu/academics/academic-resources/slater-museum/ Peter H Wimberger <pwimberger@pugetsound.edu>

Queensland VolFieldAssist RainForestDrosophila

Field assistants required to study limits to adaptation in Australian rainforest Drosophila

We are looking for up to three motivated, hardworking volunteers to assist with fieldwork in northern Queensland as part of a project examining limits to adaptation in rainforest Drosophila.

The project is being carried out by researchers at the University of Bristol, UK (PI Dr Jon Bridle, postdoc Dr Eleanor O'Brien), in collaboration with researchers at the University of Queensland (Professor Mark Blows) and the University of Melbourne (Professor Ary Hoffmann). This position represents an excellent opportunity to be involved in exciting research in evolutionary biology, and would suit someone seeking direct experience of a field-based project in this area.

The role of the volunteer will be to assist with collection of Drosophila at several locations in the rainforest in northern Queensland, sort field-collected specimens, conduct mark-recapture and field fitness experiments, as well as maintain live stocks and perform other duties as required. Training will be provided in Drosophila identification and maintenance, although previous experience would be helpful.

Essential requirements: (1) BSc in evolutionary biology, genetics, ecology or a related discipline. (2) Willingness to spend long days working in the rainforest in hot, humid conditions. (3) Ability to work carefully and meticulously, with close attention to detail. (4) Enthusiasm and the ability to work as part of a team. (5) A full driving license.

Previous fieldwork experience and 4 wheel-driving experience would also be an advantage.

The volunteer must be able to spend up to 8 weeks in the field from early April - late May 2012. Full living expenses (meals and accommodation) will be paid during this period. We are also able to make a contribution of up to £400 (approx. $AU640) towards the costs of travel to the field site.

Applications should be received by the 1st February 2012, and must include a cover letter and CV, including the names of two referees.

To request further information about this position, or to apply, please contact Dr Eleanor O'Brieneleanor.obrien@bristol.ac.uk

Dr Jon Bridle Senior Lecturer in Biology School of Biological Sciences University of Bristol Bristol BS8 1UD

Office B70, Lab B38/9 Tel. 0117 928 7482 Fax. 0117 331 7985

jon.bridle@bristol.ac.uk http://www.bristol.ac.uk/-biology/research/ecological/genetics/
jon.bridle@bristol.ac.uk

Reference choice models

Dear all, I am quite new in phylogeny and I know the very bases. I know some books about phylogeny, but they all seem to present phylogeny methods and distance matrices models without explaining how to make a good choice between those methods and models (though it is interesting to compare the results from different methods).

My question is thus: do you know some interesting references (in English or in French) explaining practically how to select among phylogeny methods and models depending on your data ?

Thank you very much in advance. Regards,

Gwennaël

Gwennaël BATAILLE, PhD student - Teaching assistant

Earth and Life Institute Université Catholique de Louvain SST/ELI/ELIB Bâtiment Carnoy Croix du sud 4-5, bte L7.07.04 1348 Louvain-la-Neuve BELGIUM

gwennael.bataille@uclouvain.be

Reference choice models answers

Dear all, Thanks a lot for your answers ! Here are the main references I obtained from you on choice for phylogeny methods / models :

At first, some books : 1) Barry Hall. Phylogenetic Trees Made Easy: A How-To Manual Bellingham Research Institute ; Third Edition (Bayesian methods should be integrated in this version ;

recommended twice) : http://www.sinauer.com/hall/3e/ 2) Page & Holmes. Molecular Evolution. A Phylogenetic Approach (recommended twice) http://www.amazon.com/Molecular-Evolution-Roderick-D-M-Page/dp/0865428891/ref=sr_1_5?ie=UTF8&qid=1326723824&sr=8-5 3) Hillis, Moritz, Mable. Molecular Systematics (recommended twice)

“If you read through these three in order (or at least 1+2), you should get a solid foundation of understanding different methods and models and how to choose among them. I believe #1 has been updated to include Bayesian methods, but I’m not sure about #2+3.” [Jaret Bilewitch]

- The Phylogenetic Handbook A Practical Approach to Phylogenetic Analysis and Hypothesis Testing, by P. Lemey, M. Salemi, A.M. Vandamme (recommended twice) http://www.amazon.com/Phylogenetic-Handbook-Practical-Approach-Hypothesis/dp/0521730716/ref=pd_sim_b_1 - Phylogenetics The theory and practice of phylogenetic systematics, by E.O. Wiley,

- Inferring Phylogenies, Joseph Felsenstein : http://www.sinauer.com/detail.php?id=1775 - (in french :) Concepts et mÃ©thodes en phylogÃ©nie molÃ©culaire Collection: Collection IRIS PerriÃre, Guy, Brochier-Armanet, CÃ©line 1st Edition., 2010, XII, 250 p. http://www.springer.com/life+sciences/systems+biology+and+bioinformatics/book/978-2-287-99047-2 Then, some articles too : - Kelchner SA, Thomas MA. 2007. Model use in phylogenetics: nine key questions. Trends Ecol Evol. 22:87â94.

- Papers written by Nei and Saitou explaining advantages and disadvantages of each type of method :

Saitou N, Imanishi T (1989) Relative efficiencies of the Fitch-Margoliash, maximum-parsimony, maximum-likelihood, minimum-evolution, and neighbor-joining methods of phylogenetic tree construction in obtaining the correct tree. Mol. Biol. Evol. 6(5):514-525.

Takahashi K, Nei M (2000) Efficiencies of fast algorithms of phylogenetic inference under the criteria of maximum parsimony, minimum evolution, and maximum likelihood when a large number of sequences are used. Mol. Biol. Evol. 17(8): 1251-1258.

Tateno Y, Takezaki N, Nei M (1994) Relative efficiencies of the maximum-likelihood, neighbor-joining, and maximum-parsimony methods when substitution rate varies with site. Mol. Biol. Evol. 11(2):261-277.

- And for bayesian inference (BI) :

Douady CJ, Delsuc F, Boucher Y, Doolittle WF, Douzery EJP (2003) Comparison of bayesian and maximum likelihood bootstrap measures of phylogenetic reliability Mol Biol Evol 20(2):248-254

Alfaro ME, Zoller S, Lutzoni F (2003) Bayes or bootstrap? A simulation study comparing the performance of bayesian Markov chain Monte Carlo sampling and bootstrappingin assessing phylogenetic confidence. Mol. Biol. Evol. 20(2): 255-266.

Miscellaneous : - Workshops on phylogeny (recommended twice) : http://www.molecularevolution.org/ - In the documentation of the web server Phylemon2, the authors explain a roadmap that is normally used for phylogenetic studies and seems very interesting as a “lab protocol”: http://docs.bioinfo.cipf.es/phylemonwiki/doku.php?id=phylemon:roadmap - Two programs on model choice within algorithm : . for models of maximum likelihood (ML) or BI, there is a program called jModelTest (http://darwin.uvigo.es/software/jmodeltest.html) that lets you choose the best model that fits your data when performing the phylogenetic tree in ML or BI.

. to select between alternative substitution models, there is modelgenerator, available here (The paper is also listed there and they discuss in the paper the whole idea of comparing models) : http://bioinf.nuim.ie/modelgenerator/ Other advices : - “Talks with people, since a practical experience is sometimes needed in order to take a good decision. A secure approach remains a test of

— / —

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

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Samople request

Dear Colleagues,

We are looking for some assistance in location samples from certain taxa, to compile molecular data on a range of Arabian AND Socotran taxa. We have extensive collections of these, but are lacking in con-generic taxa from other regions. Therefore, we would be grateful to hear from anyone who could supply us with vouchered material (and DNA intact for extraction!) of the taxa in the following groups:

Cryptolepis (Apocynaceae, Asclepiadoideae)

Seddera (Convolvulaceae, especially S. evolvuloides from India)

Boswellia (Burseraceae: taxa from central and western Africa and India)

Garuga (Burseraceae)

Leucas (Lamiaceae)

Thanks very much.

Dr Alan Forrest Centre for Middle Eastern Plants RBG Edinburgh

A.Forrest@rbge.ac.uk

– The Royal Botanic Garden Edinburgh is a Charity registered in Scotland (No SC007983)

Alan Forrest <A.Forrest@rbge.ac.uk>

Software DAMBE update

Dear All,

I have uploaded a new version of DAMBE with the following improvement:

1. Tip-dating based on the least-squares criterion: Some users suggested that the input sequence name format (OTUname@Year) is not sufficient. For example, two viral sequences sampled at the end of 1999 and the beginning of 2000, respectively, could be just a few days apart instead of a whole year apart. I have added two more formats: year with decimals, e.g., OTUname@1999.98 and OTUname@DDMMYYYY.

2. Effective number of codons: some users have asked for this function, and it is added with some improvements. In particular, the original formulation handles short sequences poorly and the effective number of codons could be more than 100. I dealt with this problem by adding the option for pseudocount (which I suggest should not be greater than 1, which is also the default). There are also a few other things that I will explain in more detail if you are interested to use the function. The function is accessible by clicking 'Seq.Analysis|Codon usage|Nc: Effective number of codons'.

3. Numbering notation: After spending a part of my sabbatical in Europe (mostly in Turku, Finland), I have noticed that the European use of ',' for '.' (e.g., 1.234,56 instead of 1,234.56) affects some of DAMBE's functions. I believe that I have fixed them all. Please let me know if you experience anything unusual.

Please download the new version.

For those who do not know DAMBE, it is a comprehensive software package for extensive data analysis in molecular biology and evolution for Windows ME/2000/XP/VISTA but can be run on Intel-based Mac and Linux systems with WINE. It is freely available at

http://dambe.bio.uottawa.ca/dambe.asp You can find publications that used DAMBE by using Google scholar at:

http://scholar.google.com/scholar?as_q=3D&num=3D100&btnG=3DSearch+Scholar&as_epq=&as_oq=&as_eq=&as_occt=any&as_sauthors=Xuhua+Xia&as_publication=&as_ylo=&as_yhi=&as_sdt=1.&as_sdtp=on&as_sdtf=&as_sdts=5&hl=en
Best Xuhua

Xuhua Xia Professor, Bioinformatics and Molecular Evolution Biology Department University of Ottawa Rm 278 Gendron 30 Marie Curie, Ottawa, Ontario Canada K1N 6N5 Tel: (613) 562-5800 ext 6886 URL: http://dambe.bio.uottawa.ca Xuhua.Xia@uottawa.ca

Software raxmlGUI release

We have released raxmlGUI 1.0, an easy-to-use graphical interface for RAxML (Stamatakis, 2006) at http://sourceforge.net/projects/raxmlgui/ The following main features are available: * Perform all main RAxML phylogenetic analyses through an intuitive graphical interface: - Maximum Likelihood searches - Bootstrap (BS) analyses - Constructing consensus trees - Ancestral state reconstruction - Increase branch supports by pruning "rogue taxa" from your data (drop set function, Pattengale et al. 2011) * âBootstoppingâ function to automatically determine the necessary number of BS replicates * Analyse mixed data sets (any combination of nucleotide, amino acid, binary, and multi-state data is possible) * Convert RAxML consensus trees to be compatible with the program FigTree * A detailed manual is available in html and pdf format.

raxmlGUI is described in our application note:

Silvestro, D. & Michalak, I. (2011) raxmlGUI: A graphical front-end for RAxML. Organisms Diversity & Evolution, DOI: 10.1007/s13127-011-0056-0

Suggestions and bug reports are much appreciated.

Daniele Silvestro and Ingo Michalak

Biodiversity and Climate Research Centre (BiK-F) Senckenberg Research Institute Frankfurt/M, Germany

Daniele.Silvestro@senckenberg.de

Software SiteToSite Rate Variation

Hi folks,

We have developed a software program that might help in identifying rapidly-evolving sites without the drawback of having a starting tree.

The program is called "tiger" and it is available here: http://bioinf.nuim.ie/tiger It is written in python, the code is open source and the program should run on all platforms.

The paper describing the method and some results from our analyses using this method can be found here:

Cummins, C.A. and McInerney, J.O. (2011) A method for inferring the rate of evolution of homologous characters that can potentially improve phylogenetic inference, resolve deep divergence and correct systematic biases.Systematic Biology60 (6) 833-844. doi:10.1093/sysbio/syr064.

James.

– James McInerney, Department of Biology, NUI Maynooth, Co. Kildare, Ireland. P: +353 1 7083860 F: +353 1 7083845 W: http://bioinf.nuim.ie/james-mcinerney james.o.mcinerney@nuim.ie

Spectrophotometer question

Dear all,

Recently I've started using Jaz spectrophotometer for reflectance measurements in the field. it work fine but I'm having troubles analysing its output files (I know, there's SpectraSuite but it's missing necessary options, has very poor manual and is slow). There are several applications that were created for this - e.g. CLR an RCLR apps (they have problems reading jaz datafiles, RCLR fails to read the data correctly even after reformating it to the desired structure). And here's the question: before I start wrestling with my enemy (I've planned to write my own R/python script for handling jaz files) - have any of You, Evoldir Readers, ever encountered such problems. Maybe you know some other (free) software options that could be of help here? If so - I'd be greatful for letting me know.

Cheers, sz.

Szymon Drobniak || Population Ecology Group Institute of Environmental Sciences,Jagiellonian University ul. Gronostajowa 7, 30-387 Kraków, POLAND tel.: +48 12 664 51 79 fax: +48 12 664 69 12

www.eko.uj.edu.pl/drobniak geralttee@gmail.com

Spider samples Molecular analysis

Dear Colleagues,

We are looking for spider samples to do molecular analysis. Basically we need species (DNA, tissues or the spider) from Pisauridae, Trechaleidae, Lycosidae and Ctenidae families. Please let us know if you can help us.

Thanks in advance!

Best regards

Maria J Albo

Aarhus University

Ny Munkegade 116, Aarhus 8000

maria.albo@biology.au.dk

Maria Jose Albo <mjalbograna@gmail.com>

SSB Graduate Student Research Awards

Society of Systematic Biology Graduate Student Research Award

The Society of Systematic Biologists (SSB) announces the 2012 annual Graduate Student Research Award competition. The purpose of these awards is to assist students in the initiation (FIRST TWO YEARS) of their systematics projects and in the collection of preliminary data to pursue additional sources of support (e.g., Doctoral Dissertation Improvement Grants from the National Science Foundation) or to enhance dissertation research (e.g., by visiting additional field collection sites or museums). Applicants may be from any country, but must be members of SSB, and are advised to join the Society as soon as possible to facilitate their applications (to join go to: http://systbio.org/?q=node/6). Previous awardees may not re-apply, but previous applicants who were not selected for funding are encouraged to re-apply. Awards range between $1,200 - $2000 and approximately 10 - 15 awards will be made.

How to Apply: applicants must submit 1. a curriculum vitae (one page) 2. brief research proposal including objectives, methods, significance, and schedule (max. three single-spaced pages including literature cited and any figures and tables) 3. budget and budget justification (1 page) 4. and arrange for two reference letters; one letter must be from the student's current graduate advisor.

All application materials must be in electronic format. Applicants and those writing reference letters are required to use pdf format to minimize difficulties in file transfer. Applicants should send all materials (except reference letters) in a SINGLE pdf file. Letters of reference should be sent separately by the referees in pdf format or in the text of an e-mail; please include the FULL NAME OF APPLICANT in reference letters.

Please email all application materials and queries to SSB Awards Committee ssb-apps@life.illinois.edu. IN THE SUBJECT LINE OF THE E-MAIL, PLEASE INDICATE "Student Research" FOLLOWED BY FIRST INITIAL AND LAST NAME.

To be considered for this year's award, application materials, including letters of recommendation, must be received electronically no later than March 31, 2012.

Please see the SSB website (http://systbio.org/?q=node/22) for additional details of this award.

Rhiannon Peery <ssb-apps@life.illinois.edu>

Titanium 454 provider

Request 454 Titanium XL+ provider

Dear all

I am looking for a provider offering the longer titanium xl+ chemistry for pooled amplicon sequencing. Anyone knows a company already offering the 454 xl+ chemistry with up to 1000bp, the response so far was "planning on installing the new version" but only offers for the titanium chemistry...

Best regards

Gregor Wachter

Gregor.Wachter@student.uibk.ac.at

Titanium 454 provider answers

454 Titanium+ providers: Answers

Dear Evoldir Community,

thank you for your responses to a request about Titanium XL + providers I posted a few days ago. As several people asked me to share the results, find blow a compilation of helpful answers I received, and a list of companies which confirmed using XL+ chemistry.

best,

Gregor

—–

Xl is only available for fragment libraries. For amplicons you are stuck with gs flx titanium for the foreseeable future

P

—–

Dear Gregor,

The Centre for Genomic Research atUniversity ofLiverpool runs 2x 454xl+ machines. Both shotgun and amplicon libraries. Note that 1000bp is the absolute maximum read. Median is more like 700 - 750bp.

Contact our centre manager, Dr Christiane Hertz-Fowler, if you'd like a quote or further details.

chf@liv.ac.uk

http://www.liv.ac.uk/genomic-research/ Best wishes, Steve

—–

Dear Gregor,

I've had your request for a 454 Titanium XL+ provider passed on to me from a colleague that is on the same email list as you. We do currently offer 454 Titanium

XL+ sequencing and have for a few months now.

However, these kits are currently not supported for amplicon sequencing (only for gDNA and cDNA libraries) and Roche strongly recommends that amplicons still be run using the Titanium XLR70 kits. I have run one short amplicon library as a test for a customer with the XL+ kits and the data was not nearly as good as has been obtained for his similar libraries sequenced with the XLR70 kits. Other service providers have said the same, the XL+ kits consistently give worse results for amplicons. This is due at least in part to the software not yet being updated/optimised for longer amplicons.

I hope this you find this information helpful.

Kind regards,

Jason Koval

–

Ramaciotti Centre for Gene Function Analysis

Level 1, Biological Sciences Building (D26)

The University of New South Wales

NSW 2052

Telephone: +61 (2) 9385 1144

Facsimile: +61 (2) 9385 1277

http://www.ramaciotti.unsw.edu.au

—–

Hi,

we are in contact with LGC Genomics (through its Berlin facility) which offers at least 700 bp reads.

www.lgcgenomics.com

We have no practical experience with them yet

==List of companies:

FLX sequencing platform, Matís: www.matis.is

—–

FGCZ Sequencing Team, Zurich: sequencing@fgcz.ethz.ch

—–

Ramaciotti Centre, Sydney: http://www.ramaciotti.unsw.edu.au

—–

University ofLiverpool,Liverpool:

http://www.liv.ac.uk/genomic-research/ —–

LGC Genomics, Berlin: www.lgcgenomics.com

—–

Research and Testing, Lubbock: http://researchandtesting.com/Sequencing.html Gregor Wachter <Gregor.Wachter@student.uibk.ac.at>

Transmission Disequilibrium Test

Hi All, we are trying to run what should be a simple TDT test on a data set, but are having trouble with both an R-script and a program (PDT, Martin et al. 2000, Am. J. Hum. Genetics). Both give error messages that don't make sense, etc.

Anyone have either experience with these programs or recommendations for other software to run this test?

Thanks,

Devon

Devon Pearse <devon.pearse@noaa.gov>

Undergrad Res Experience reminder

Dear Colleagues,

Please circulate this email to to eligible undergraduates at your institutions or post this message - thank you!

The Research Experiences for Undergraduates (REU) program, funded by the U.S. National Science Foundation, offers paid summer internships for qualified undergraduate students to conduct research projects with AMNH scientists in evolutionary biology, linked to specific individual research projects. Included in the program are a general orientation to the Museum and a series of weekly meetings at which students discuss their research, present informal progress reports, and participate in discussions and seminars as well as graduate and research career opportunities. At the conclusion of the internships, students deliver oral presentations of their work and prepare publication quality research papers.

The program is open to all students who are U. S. citizens or permanent residents and who are currently enrolled in a four-year undergraduate degree program. Pending the approval of federal funding, successful applicants will receive a stipend, while dormitory housing on a nearby university campus, or an equivalent housing stipend, will be provided together with a subsistence allowance. Based on need, travel costs to and from New York City are also covered.

A description of the potential projects and more information on how to apply may be found here: http://rggs.amnh.org/pages/academics_and_research/reubio **Please note that the deadline for all application materials is February 10th, 2012**

Susan Perkins, Ph.D. Associate Curator & Professor Sackler Institute for Comparative Genomics and Division of Invertebrate Zoology American Museum of Natural History Central Park West at 79th Street New York, New York 10024 p: 212-313-7646 f: 212-313-7819 http://malaria.amnh.org http://genomics.amnh.org Blogs: Parasite of the Day: http://dailyparasite.blogspot.com Dechronization: http://treethinkers.blogspot.com Susan Perkins <perkins@amnh.org>

PostDocs

ArizonaStateU ComputEvolGenetics

POSTDOCTORAL RESEARCH ASSOCIATE OPENING

The Cartwright Lab at Arizona State University is seeking Postdoctoral Research Associates in the area of Computational Evolutionary Genetics (broadly defined). The Cartwright Lab is part of The Center for Evolutionary Medicine and Informatics (CEMI), one of 10 research centers in the Arizona State University's Biodesign Institute.

Research in the Cartwright Lab covers many different questions in population genetics and molecular evolution, at the interface of biology, statistics, and computer science. A majority of our research involves developing, implementing, and applying novel methodologies to study genomic datasets. Potential research topics for postdoctoral research associates include

* The study of mutation patterns between human families and across species, using data from next-generation sequencing. This includes both indel and point-mutation patterns. * Models of frequency-dependent selection, with applications to genomic data. * New methods for alignment and phylogeny reconstruction that take into account the uncertainty of genomic data. * New methods for simulating homologous sequences that can be optimized to mimic natural datasets.

For more information see http://scit.us/ or http://labs.biodesign.asu.edu/cartwright/ . To apply, forward one document that includes a cover letter, detailed CV, and 3 references to cartwright@asu.edu. Please put the job title in the subject line of the letter. The initial closing date is January 31, 2012, Applications will continue to be accepted and considered until the job is filled/closed. A background check is required for employment. ASU is an EO/AA employer and is committed to excellence through diversity.

See full ad at http://www.biodesign.asu.edu/jobs/postdoctoral-research-associates-2011-12-15-11-54 Contact Dr. Cartwright at cartwright@asu.edu or 480-965-9949 for more information.

– Reed A. Cartwright, PhD Assistant Professor of Genomics, Evolution, and Bioinformatics School of Life Sciences Center for Evolutionary Medicine and Informatics The Biodesign Institute Arizona State University

rcartwri@asu.edu

Barcelona Chordate EvoDevo Genomics

Department of Genetics, University of Barcelona (Spain)

Our new group on the field of Functional Evo-Devo and Genomics is looking for one CANDIDATE to apply for a POSTDOC FELLOWSHIP from the Catalan Government, Spain.

Candidates have to be enthusiastic, and need to have a competitive CV to successfully apply for fellowship. Experience in Molecular Genetics, Transgenesis and Developmental Biology, and (or) Background in Bioinformatics, and Comparative Genomics will be positively considered.

Our main research interest is to understand the impact of gene losses on the evolutionary diversification of mechanisms of development in chordates. Our work focuses on comparative approaches between vertebrates, urochordates and cephalochordates. Our main subject of study is Oikopleura dioica, a new emergent urochordate model within our own phylum, with the smallest genome size known so far in all metazoans, and with an outstanding amount of gene losses (Denoeud et al., Science, 2010).

Candidate requirements for this fellowship call: a) Date of PhD degree (thesis defense date) between Jan-1-2006 and Dec-31-2010. b) Have completed or be on a postdoctoral stage a minimum period of two years by the time the beneficiary joins our group.

The current call will be opened very soon. (Previous call information: http://www10.gencat.cat/agaur_web/AppJava/english/a_beca.jsp?categoria=3Dpostdoctorals&id_beca=17221 Interested candidates, please send a brief letter of interest and a CV in one single pdf file to Cristian Cañestro (canestro@ub.edu)

Interested candidates for future for POST- or PRE-DOCTORAL applications, please feel free to contact too.

For an outline of our group's research: http://www.ub.edu/genetica/evo-devoen/canestro.htm http://www.uoneuro.uoregon.edu/ ˜ cristian/Canestro.html oikocris@gmail.com

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Barcelona MammalianGenomics

Postdoc position in Comparative Genomics

I am looking for a highly motivated candidate that can apply for a Beatriu de Pinós postdoctoral fellowship (DGR, Generalitat de Catalunya). The aim of the project is to study the genomic structure of evolutionary genomic regions in different mammalian species. Interest in evolutionary biology, molecular biology and cell biology is required. Applicants should have a PhD in a relevant area (evolutionary biology, genomics). I am seeking for someone with a vivid interest in evolution research and a strong background in population genetics/ statistical genetics. Skills in bioinformatics and/or programming are essential.

Our group works in the fields of comparative genomics, evolution and chromosomal instability and, in particular, we are interested in the mechanisms that are driving karyotype evolution and genomic architecture in mammals. For further information please see our webpage (http://grupsderecerca.uab.cat/evolgenom/).

The Universitat Autònoma de Barcelona (UAB) is located close to the city of Barcelona and is one of the major public universities in Spain. The UAB is internationally acknowledged for its quality and innovation in research. It coordinates a potent scientific and technological centre, which comprises all the departments, science and technology services, research centres, institutes and university hospitals affiliated with the UAB.

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

Application deadline: 5th February 2012.

Aurora Ruiz-Herrera, Ph.D.

Cytology and Histology Unit Dept. Cell Biology, Physiology and Immunology Universitat Autònoma de Barcelona Efidici C E-08193 Bellaterra, Spain Phone +34935812051 Fax +34935813357 aurora.ruizherrera@uab.cat http://grupsderecerca.uab.cat/evolgenom/en Cytogenetics Group Institut de Biotecnologia i de Biomedicina Universitat Autònoma de Barcelona E-08193 Bellaterra, Spain Phone +34935811379 aurora.ruizherrera@uab.cat

"Ruiz-Herrera, A" <aurora.ruizherrera@uab.cat>

BuenosAires ConservationGenetics

Postdoctoral position Conservation Genetics and Biodiversity Group Museo Argentino de Ciencias Naturales Buenos Aires, Argentina

We are seeking a post-doctoral fellow to lead a project on ecological and phylogeographic determinants of species and populations boundaries in subterranean rodents of the genus Ctenomys. The project seeks to understand the evolutionary biology of populations and species of the genus, commonly known as tuco-tucos,in fragmented habitats in a marshland in northern Argentina. In order to generate a comprehensive picture of the evolutionary dynamics of the group, phenomena belonging to three different sources/scales will be considered: (1) A spatial approach involving comparisons of the degree of differentiation in fragmented vs. continuous populations, (2) a temporal approach, which considers comparisons of the populations before and after the fragmentation event, and (3) a model based approach, which will simulate genetic differentiation resulting from diverse scenarios of habitat isolation and fragmentation. The project is led by Dr. Patricia Mirol, from the Argentinian Natural History Museum in Buenos Aires, Argentina; Dr. Marcelo Kittlein, from Mar del Plata University, Argentina and Dr. Oscar Gaggiotti, from U. J. Fourier, Grenoble, France. The successful candidate will conduct fieldwork in Corrientes, Argentina, in order to analyze landscape genetics and ecology of the species, including demographic parameters in two model populations and measurement of dispersal using radiotelemetry; labwork to obtain genotypes of the sampled animals; and it will also work on the development of model based approaches to simulate genetic diversity under different fragmentation scenarios. The project start date is to be no earlier than April 2012 and project duration is 2 years. To be considered for this position, please send your CV to pmirol@macn.gov.ar

Dr. Patricia Mirol Conservation Genetics and Biodiversity Group Museo Argentino de Ciencias Naturales Angel Gallardo 470, C1405DJR Buenos Aires, Argentina

patricia mirol <patricia_mirol@yahoo.com.ar>

CFIA Charlottetown Bioinformatics

Visiting Fellowships in Canadian Government Laboratories V CFIA-Charlottetown Laboratory

The Visiting Fellow (postdoctoral fellow) with research background in bioinformatics and molecular phytopathology/phytobacteriology will join a research team working on genomic analysis of plant pathogens of regulatory concerns at a Canadian Food Inspection Laboratory (CFIA) laboratory in Canada. Job responsibilities include research in comparative genomics, utilization of DNAbarcode technology, and development of methods for detection and diagnosis of plant pathogenic bacteria, fungi, and nematodes. The candidate should have a strong background in bioinformatics, analyses of genomic/metagenomic sequence data, and assay development including design of real time PCRassays, and use of molecular biology tools aimed at detection and monitoring pathogens. The incumbent is expected to publish research in refereed journals and has the opportunity to contribute to extensive knowledge through CFIA and Agriculture and Agri-Food Canada.

The Visiting Fellowships in Canadian Government Laboratories (VF) Program provides promising emerging scientists and engineers with the opportunity to work with research groups or leaders in Canadian government laboratories and research institutions. Fellowships are awarded for one year with the possibility of renewal for a second and third year, depending on the funding availability (http://www.nserc-crsng.gc.ca/Students-Etudiants/-PD-NP/Laboratories-Laboratoires/index_eng.asp).

Initial funding is available for one year with renewal for a second year upon satisfactory performance. A PhD degree in bioinformatics, plant pathology, or closely related field with extensive experience in genomic analyses is desired. Submit letter of application describing research interests and professional goals, and fill the online application Form 200 at the NSERC website (http://www.nserc-crsng.gc.ca/Students-Etudiants/-PD-NP/Laboratories-Laboratoires/index_eng.asp). Additionally, please provide current CV, transcripts, and name and contact information for three references to Dr. Sean Li at Canadian Food Inspection Agency, Charlottetown Laboratory, 93 Mount Edward Road, Charlottetown, PE, C1A 5T1 (sean.li@inspection.gc.ca). The successful candidate must meet all CFIA security requirements.

Sean Li <Sean.Li@inspection.gc.ca>

Cornell ComparativeGenomics AmphibianImmunity

Postdoctoral Researcher in Comparative Population Genetics/Genomics of Amphibian Immunity.

A postdoctoral position is available in the Zamudio laboratory, Department of Ecology and Evolutionary Biology, Cornell University. This position is funded by an NSF Ecological Genetics grant to study the evolution of immunity in Central American amphibian populations recently exposed to the chytrid fungus Batrachochytrium dendrobatidis, using a combination of candidate loci assays (including MHC genes), laboratory challenge experiments, and transcriptomic analyses.

The primary responsibilities of this position include 1) conducting field and laboratory research to clone and characterize MHC genes in non-model amphibian taxa and measure selection in populations that have suffered disease-related declines, 2) overseeing challenge assays of hosts from focal populations for transcriptomic analyses of expression patterns in different populations, 3) analyzing data and writing manuscripts, 4) contributing to grant proposals for future work, and 5) contributing to mentoring and coordination of projects of undergraduate students involved in research.

For additional information about this and other research programs ongoing in our laboratory please visit our web site at http://www.eeb.cornell.edu/zamudio/-KZ_home/ * Qualifications * Required qualifications include a Ph.D. in evolution, molecular biology, or related field; demonstration of molecular laboratory experience with genetic techniques (DNA/RNA extraction, PCR, cloning); the ability to organize and lead field efforts in a foreign country (up to 6-8 weeks in Panama); strong writing skills; and the ability to work independently. Candidates familiar with animal husbandry, experience working with genomic/transcriptomic data, and a working knowledge of Spanish will be preferred.

* Terms of Appointment * Starting salary is $ 38,000 - $43,000 depending on experience, plus Cornell University Endowed College benefits. Funds are available for one year, and renewable for a second pending satisfactory progress.

* Applications * To apply, please send cover letter, CV, a statement of research interests/experiences, and names and contact information for three references that are familiar with your work. Applications should be in PDF format, e-mailed to Kelly Zamudio (krz2@cornell.edu)

Position is available starting September 2012 (negotiable). Review of applications will begin March 15, 2012, and continue until suitable candidate is found.

Cornell University Department of Ecology and Evolutionary Biology E209 Corson Hall Ithaca, NY14853-2701

Cornell University is an equal opportunity, affirmative action educators and employers. Applications from women and minorities are encouraged.

kelly.zamudio@cornell.edu

HowardU ChordateComparativeEmbryology

Postdoctoral Position in Chordate Comparative Embryology

A recent PhD or junior-level Postdoctoral Fellow is sought to join the Rui Diogo laboratory, at the Howard University College of Medicine, Department of Anatomy (Washington DC).

We are interested in a candidate that will contribute to uncover evolutionary and developmental mechanisms underlying both hard tissue (cartilages and bones) and soft tissue (mainly muscles) formation and patterning during ontogeny of a wide range of vertebrate taxa, as well as soft tissue in non-vertebrate taxa such as sea squirts. Some of the issues and broader questions in which we are particularly interested include: the parallelism between ontogeny and phylogeny, the remarkable similarity between the hard and particularly the soft tissues of the upper and lower limbs of tetrapods, the importance of evolutionary reversions/neotenic events, the study of birth defects and their implications for medicine and for the understanding of evolutionary biology, and the regeneration of hard and soft tissues in key vertebrate taxa. For more information about these subjects and about other issues being studied in the lab, please see www.ruidiogolab.com . The successful candidate will have a PhD degree with a broad experience in molecular biology and developmental biology (e.g., doing/using developmental techniques such as antibody staining, in situ, and cell tracing, among others), backed by publications in peer-reviewed journals, and also some experience in comparative anatomy. He/She will have the skills and motivation to pursue a career in research, be interested in studying and comparing a wide range of taxa and various model organisms and in discussing various evolutionary and developmental issues.

There are funds available for two years, the first contract being for one year, the second contract depending on the productivity, interest and dedication of the candidate. There are possibilities to continue being part of the lab after the two-year period of the post-doc position. The post-doc will also have the opportunity to take classes, and then to be instructor, of human gross anatomy; this will further allow him/her to also postulate for faculty positions in medical schools in the DC area (including Howard University) as well as in other regions.

Interested candidates should send a CV including research interests, a list of publications and the names and contact information for three references to Rui Diogo, at rui.diogo@howard.edu. Please write “postdoc in Diogo’s lab” followed by your last name in the email subject.

Howard University is a historical University situated in the center of Washington DC, which is a beautiful, green and enjoyable city with numerous cultural and outdoor activities. The Department of Anatomy provides a prosperous, resourceful and multidisciplinary environment for biomedical research, includes faculty with a broad experience in developmental biology, paleontology, neurobiology, comparative anatomy and medicine. We have strong ties with surrounding institutions, particularly with George Washington University, and the candidate will probably have the opportunity to do part of his/her research at those institutions and thus to expand his/her knowledge and academic connections.

Rui Diogo | Dep. Anatomy, Howard Univ. College of Medicine, 520 W St. NW, Washington, DC 20059, USAHomepage: ruidiogolab.com

Rui Diogo <rui_diogo@hotmail.com>

InstZoology London DiseaseEvolution

Disease Macroecologist

Zoological Society of London

One Year Fixed-term Contract Initially Salary: £27,106 plus London Weighting £3568

A postdoctoral position is available from 1st April 2012 to build global spatial and temporal empirical models of the interdependence of biodiversity and human health in Africa. The work will build on previous publications (see Jones et al. Nature 451:990) to examine the roles of biodiversity, land-use change, climate change and other socio-economic, demographic and environmental drivers on disease emergence and transmission.

The position requires an independent, enthusiastic and innovative researcher with a PhD in a relevant discipline interested in applying comparative macroevolutionary and macroecological approaches to understanding disease emergence and transmission and its effect on human wellbeing. Experience in environmental niche modelling, spatial statistical modelling, using and compiling global biodiversity, environmental and socioeconomic datasets would be an advantage.

The post will be based at The Institute of Zoology, Zoological Society of London, London, but will require visits to our partners in Africa. Starting date: 1st April 2012, end date: 31st March 2013 with the possibility of renewing for a further 2 years. Salary: £30,674 p.a. inclusive of London weighting.

Please see www.zsl.org/jobs for a job description.

To apply please send a CV, covering letter and contact details of three referees to: HR Dept., ZSL, Regent's Park, London NW1 4RY, or email hr@zsl.org Informal enquires can be made to kate.jones@ioz.ac.uk

Closing date for applications: 16th February 2012

Registered Charity in England and Wales: 208728

Dr. Kate E. Jones Senior Research Fellow Institute of Zoology Zoological Society of London London NW1 4RY

Tel: +44 (0)207449 6627. Fax: +44 (0)20 7586 2870 Web: www.zsl.org/katejones Help save the BBC Wildlife Fund! Sign the petition - http://www.savebbcwildlifefund.net My Phil. Trans. issue on Global Bodiversity of Mammals is out now!

http://rstb.royalsocietypublishing.org/site/2011/biodiversity_mammals.xhtml

Kate Jones <Kate.Jones@ioz.ac.uk>

IowaStateU InsectSociogenomics

A position for a postdoctoral research associate is available for a collaborative project in the labs of Amy L. Toth at Iowa State University and Robert L. Jeanne at the University of Wisconsin. The project will investigate the epigenetic, transcriptomic, and behavioral impacts of a maternal behavior during Polistes wasp caste development. We will study the influences of antennal drumming, a vibrational signal produced by foundress wasps, on development, behavior, and gene regulation in offspring with the goal of understanding how epigenetic social cues can influence the evolution of caste systems in social insects.

Postdoctoral position: This highly interdisciplinary project will involve field collections of paper wasps in Iowa, lab rearing and experimental manipulation of colonies, behavioral observations, high throughput RNA- sequencing, bisulfite-sequencing, and bioinformatic and statistical analyses.

Qualifications: Applicants should have completed the PhD before/around spring 2012. Those with previous experience in molecular biology techniques, behavior, bioinformatics, and/or entomology (especially social insects) are especially encouraged to apply.

Earliest start date: April 1, 2011. Funding is available for up to three years. Salary will be in the range of $40,000 depending on qualifications and experience.

Environment: The bulk of the work will take place at Iowa State University in Ames, Iowa. Iowa State University is a top research institution in the biological sciences. Outstanding nucleic acids, protein, microscopy, plant transformation and other biotechnology facilities are available. The diverse faculty has strengths in both basic and applied research, and strong collaborative and interdepartmental interactions. Ames, Iowa combines a relaxing, safe, clean, friendly small town environment with the intellectual stimuli expected of a world-class university community.

More information about the host department and university can be found at the following websites: http://www.eeob.iastate.edu/ http://www.iastate.edu/ Application: Send a complete CV, name and contact information for two references, and a short statement of interests (PREFERABLY IN A SINGLE PDF DOCUMENT BY EMAIL) by February 1, 2012 to:

Dr. Amy L. Toth, Department of Ecology, Evolution, and Organismal Biology, 253 Bessey Hall, Ames, IA 50011, USA, Email: amytoth@iastate.edu Web site: http://www.public.iastate.edu/ ˜ amytoth/Toth_lab/ and cc.

Dr. Robert L. Jeanne, Department of Entomology, 546 Russell Labs, 1630 Linden Drive, Madison, WI 53706, Email: rljeanne@wisc.edu, Web site: http://entomology.wisc.edu/˜jeanne/ Iowa State University is an Affirmative Action/Equal Opportunity Employer.

"Toth, Amy L [EEOBS]" <amytoth@iastate.edu>

IRSN France FukushimaBirdAdaptations

We are seeking a post-doctoral researcher with expertise in radiation studies and wildlife research to lead a funded project on the effects of the Fukushima nuclear power plant disaster on the local songbird community. Position is for 1 year (renewable for an additional year) and candidate will be expected to begin in late March or early April 2012. He/she will be based out of IRSN (LRE, Cadarache) in France and annual salary is 25-35 k per year. Ideal prior experience includes research in Chernobyl or on experimental animal research on radiation in the lab. Candidate will spend several months in Japan and duties will involve netting/trapping wild songbirds, taking morphological measurements, blood samples for physiological testing, and also include opportunities for expanding the research program in, for example, developmental, behavioral, genetic, and immunological directions. Please submit cover letter, curriculum vitae, and names of two references to Dr. Christelle Adam-Guillermin (christelle.adam-guillermin@irsn.fr); review of applications will begin immediately.

Kevin McGraw <Kevin.McGraw@asu.edu>

KansasStateU GenomeBioinformatics

Dr. Toomajian's Molecular Population Genetics Lab investigates genetic variation in natural populations of plants and fungi with an aim of understanding the genetics of adaptation. The lab spans the intersection of computational biology, evolution, and functional genomics. We are recruiting a highly motivated postdoc to help analyze Arabidopsis next-generation transcriptome sequence to characterize gene expression variation. This project is laying the groundwork for studies of the genetic control and evolution of gene expression and the integration with population genomics data. The candidate will also participate in the lab's fungal population genomics projects, and training on techniques related to all projects is available.

Toomajian lab website https://sites.google.com/site/-toomajianlab/ NSF Arabidopsis 2010 project website http://seqr-1.biology.utah.edu/NSF2010/index.html Department website www.plantpath.ksu.edu The lab interacts with K-State's Ecological Genomics Institute http://ecogen.ksu.edu/ The area of emphasis for this position will be bioinformatics and genomics. The successful candidate may develop independent projects related to the main goals of the lab. This position requires excellent independent discretion and judgment and may involve some supervision of graduate and/or undergraduate students.

Qualifications include:

PhD in a Biosciences field

Computer programming skills (i.e., C/C++, Python, PERL, Ruby, or R)

Familiarity with the UNIX/LINUX computer-operating environment and with databases

Experience in and/or knowledge of bioinformatics and statistical analysis

Other preferred qualifications include:

Previous experience with molecular biology laboratory techniques

Experience working with next-generation sequencing datasets and analysis tools

Experience analyzing RNA-Seq data

Knowledge of population genetics and/or molecular evolution

Application procedure:

See full ad with complete instructions at the Toomajian lab website.

A complete application must include: 1) a cover letter that includes timing of availability for this position and lists your research interests in working in the lab of Dr. Toomajian; 2) a curriculum vitae; 3) a statement describing your relevant educational and research experiences and how they relate to the qualifications (necessary and preferred) of the position (2 pages maximum); 4) up to 3 reprints; and 5) arrange to have 3 professional letters of recommendation sent.

All application materials may be sent as hard copies or PDF documents electronically.

E-mailed applications should be sent to plantpath@ksu.edu Use "Genome bioinformatics position" in subject line of email to ensure your application materials are received.

Deadline for applications: 02/20/2012.

Kansas State University is an equal opportunity, affirmative action employer and actively seeks diversity among its employees. Background checks required.

Christopher Toomajian Assistant Professor Kansas State University Department of Plant Pathology 4024 Throckmorton Plant Sciences Center Manhattan, KS 66506 office: (785) 532-0879 fax: (785) 532-5692 toomajia@ksu.edu http://sites.google.com/site/-

toomajianlab/ iChat A/V: christoomajian@AIM

toomajia@k-state.edu

Lyon AvianEvoDevo

*A 2-year post-doctoral position**in Evo-Devo of the Dentition in Birds***

Opening in the Team of Pr. Laurent VIRIOT

INSTITUTE OF FUNCTIONAL GENOMICS OF LYON (IGFL)

http://igfl.ens-lyon.fr/ *École Normale Supérieure de LYON (France)*

The evolution of vertebrate dentition is an area of investigation common to both developmental biology and paleontology. The Viriot team is recognized for its works on the Evo-Devo of dentition in rodents, cypriniformes fish, and crocodiles. We now wish to extend the realm of our research to *bird paleobiology*, with the aim of *investigating shape, function, renewal and loss of the dentition*. Team's major assets are (1) our expertise in dental comparative anatomy, (2) our skills in 3D imaging and morphometrics, and (3) our Evo-Devo studies of the dentition including data from the fossil record as a crucial component of our investigations.

All living birds are toothless, constituting by far the most diverse toothless vertebrate clade, and are striking examples of evolutionary success following tooth loss. In recent years, an unprecedented number of Mesozoic birds have been described, illustrating the evolution of dentition reductions. Simultaneously, major advances in experimental embryology have yielded new results concerning avian edentulism. *This post-doc proposes to investigate the evolutionary developmental biology of tooth loss in birds mostly emphasizing on developmental biology aspects*.

*Applications are invited from candidates **who have previously worked on the morphogenesis, shape and evolution of dentition in a vertebrate group, whichever their background (from paleontology to developmental biology).*

Knowledge in craniofacial anatomy, as well as skills in development biology, mineralized tissue histology, microtomography, 3D imaging and 2D/3D morphometrics will be welcomed.

Applicants should send a letter of interest and CV, as well as a list of 3 references, to:

Dr. Antoine LOUCHART and Pr. Laurent VIRIOT

Team ≪Evo-Devo of Vertebrate Dentition≫

IGFL - ENS de Lyon

46 allée d'Italie - 69364 Lyon Cedex 07, France

*E-mail: **Antoine.Louchart@ens-lyon.fr and *_Laurent.Viriot@ens-lyon.fr_*

**

Five recent publications of the team:

Gomes-Rodrigues, _Marangoni_, Sumbera, Tafforeau, Wendelen, _Viriot_. (2011). Continuous dental replacement in a hyper-chisel tooth digging rodent. *Proceedings of the National Academy of Sciences of the USA *108:17355-59.

Louchart, _Viriot_. (2011). From snout to beak: the loss of teeth in birds. *Trends in Ecology & Evolution *26:663-73/./

Charles, Hovorakova, Ahn, Lyons, _Marangoni_, Churava, Biehs, Jheon, Lesot, Balooch, Krumlauf, _Viriot_, Peterkova, Klein. (2011). Regulation of tooth number by fine-tuning levels of receptor-tyrosine kinase signaling. *Development *138:4063-73.

Pasco-Viel, _Charles_, Chevret, Semon, Tafforeau, _Viriot_, Laudet. (2010). Evolutionary trends of the pharyngeal dentition in Cypriniformes (Actinopterygii: Ostariophysi). *PLoS One* 5:e11293.

Charles, _Lazzari_, Tafforeau, Schimmang, Tekin, Klein, _Viriot_. (2009). Modulation of Fgf3 dosage in mouse and men mirrors evolution of mammalian dentition. *Proceedings of the National Academy of Sciences of the USA* 106:22364-68.

Antoine LOUCHART Chargé de Recherche CNRS Team Evo-Devo of Vertebrate Dentition Institut de Génomique Fonctionnelle de Lyon CNRS UMR 5242 UCBL ENS École Normale Supérieure de Lyon 46 Allée d'Italie 69364 LYON Cedex 07 FRANCE antoine.louchart[at]ens-lyon.fr +33 4 72 72 85 08 +33 6 75 70 73 30

Louchart Antoine <antoine.louchart@ens-lyon.fr>

Montpellier PlantEvolutionaryGenomics

A post-doc position in plant evolutionary genomics is available in Montpellier (France).

The post-doctorate scientist will participate to the ARCAD program (2009-2013), “Agropolis Resource Center for Crop Conservation, Adaptation and Diversity” (www.arcad-project.org) and will work on the project “Comparative population genomics in wild and crop plants”.

“Comparative population genomics of the evolution of GC-content in angiosperms”

The aim of the project is to analyse the evolutionary forces (mutational bias, selection, biased gene conversion) affecting GC-content dynamics in several species distributed over the angiosperm phylogeny, including several monocot and eudicot species. The candidate will analyze large polymorphism and divergence dataset issued from high-throughput sequencing of transcriptomes to test population genetics predictions (mutation bias vs selection vs GC-biased gene conversion) and to infer population genetic parameters (selection/conversion intensity, mutational bias).

Eligibility criteria of the funding agency: The applicants who not have resided or carried out his/her main activity (work, studies, etc) in France for more than 12 months in the last 3 years and who have obtained his/her PhD degree for no more than 3 years will be preferred.

Performance period: 18 months from January 2012 Location: The post-doctorate will be located both in the ISE-M lab (http://www.isem.cnrs.fr/spip.php?rubrique380&lang=en) and in the AGAP unit in Montpellier (http://www.montpellier.inra.fr/centre_et_unites/unites_et_campus/les_unites_du_centre/agap)

Salary: Commensurate with qualifications and experience, benefits included. Gross salary around 2400 euro (3600$)

Application Deadline: 31 January 2012 or until suitable a candidate is found Please send a detailed CV, a letter of motivation, and two referents' names. Contact: Sylvain Glémin and Jacques David Email : sylvain.glemin@univ-montp2.fr and jacques.david@supagro.inra.fr

Sylvain Glémin Chargé de Recherche - CNRS Institut des Sciences de l'Evolution. CC64 Université Montpellier II Place Eugène Bataillon 34095 Montpellier cedex 5 France Tel : 04 67 14 35 87 http://www.isem.cnrs.fr/spip.php?article993&lang=en glemin@univ-montp2.fr

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Paris MaizePopulationGenomics

*Genomewide characterization of the effect of modern selection on genetic diversity and identification of original genetic resources in maize * *Scientific context* : Postdoctoral position is to fill as soon as possible at beginning of 2012 for a minimum of 18 months at the Plant Genetics Moulon Lab (http://moulon.inra.fr) and at the UMR AGAP in Montpellier (South of France) . Plant Genetics Moulon Lab conducts research on the determinism of complex traits and valorization of genetic diversity in plants and is located in Paris suburb's (South of Paris 30 km) in an exceptional scientific environment. *Background:* The maize genetic resources, as for most crops, remain largely underexploited in modern breeding programs because it's very hard and time-consuming to identify in the genetic resources collections the favorable alleles for agronomic traits of interest and transfer these in elite cultivated pools. During the early twentieth century, the modern selection of maize extracted inbred lines from maize landraces (populations) to produce hybrid in a controlled manner, and then exploit the hybrid vigor (heterosis) to meet the needs of modern agriculture (homogeneity, stability). During this transition of varieties from landraces to hybrids many favorable alleles have probably been lost because of their association with unfavorable alleles and/or genetic drift. However, the effect of this transition on genetic diversity is still poorly understood. *Aims of the project: * The aims of the project are to characterize the genetic diversity between and within population landraces of maize to (i) identify genetically original populations to be used in selection and possibly identify some favorable alleles by association mapping (ii) quantify the effect of selection on the evolution of genetic diversity throughout the genome. Two case studies will be considered (i) the population landraces to hybrid evolution and (ii) recurrent selection for adaptation to drought. *Scientific program: * The selected candidate will analyze and compare the genetic diversity of 150 representative maize population landraces by using 50 000 SNPs distributed along the genome (Ganal et /al./, 2011) and a collection of 1000 populations using a subset of SNPs. The selected candidate will implement and possibly improve the statistical methods to quantify allele frequencies of the SNPs from DNA pooling of individuals belonging to each population. Based on these allele frequencies estimated at each SNPs, the selected candidate will 1) assess the contribution of different factors explaining the genetic structure of populations including the use of the spatial coordinates of these populations and/or historical information 2) compare the diversity of these populations to that present within panels of inbred lines representing the diversity presently used in breeding 3) compare the evolution of genetic diversity in four tropical populations selected for their drought tolerance, to identify possibly genomic regions under selection 4) identify most original populations among a collection of 1000 populations to be used as sources to increase the diversity of existing breeding program. The genotyping data have already been acquired on almost inbred lines (900 in total) and about half of the population and will be completed up to 150 populations at the start of the project. The selected candidate could organize/perform complementary genotyping of additional populations landraces and inbred lines if required. He will work at the UMR AGAP in Montpellier (South-East of France) where is located the maize landraces genetic resources collection and recurrent selection populations program (B. Gouesnard and A. Zanetto) and the INRA station of St. Martin de Hinx (South-West of Frances) where is located the inbred lines genetic resources collection (J. Laborde). He will also work in connection with private maize breeders. *Skills:* PhD in genetics or in plant breeding. Goods skills in quantitative and population genetics and statistics and in R programming, other (s) language (s) appreciated (s), Knowledge in plant breeding and / or genetic resources as well as modeling would be appreciated *Salary:* ~ 2200-2600euro / months depending on experiences including charges for health, unemployment and retirement insurances (~ 300-400euro / month) *Desired starting date: early 2012 * A letter summarizing experience and research interests, and a complete curriculum vitae including contact information for three references should be sent to: Stephane Nicolas (snicolas@moulon.inra.fr), Alain Charcosset (charcos@moulon.inra.fr) and Brigitte Gouesnard (Brigitte.Gouesnard@supagro.inra.fr)

snicolas@moulon.inra.fr

QueensU AvianLifeHistory

Description: We are seeking a talented and highly motivated postdoctoral associate for work on an NSF-funded study on the role of glucocorticoids in mediating life history tradeoffs in tree swallows. The successful candidate will become a member of the Department of Biological Sciences at Virginia Tech in Blacksburg, Virginia, and will work closely with Ignacio Moore and Fran Bonier. The project will require that the postdoc spend approximately 3 months at the Queen's University Biological Station in Ontario, Canada every year, from late April until late July, working with a team comprised of undergraduate field assistants, graduate students, and the PIs (Bonier, Moore, and Mark Haussmann of Bucknell University). The postdoc will coordinate field activities and supervise the field team. The project will involve large-scale field experiments (manipulations of glucocorticoids, parasites, and reproductive effort) and measurement of effects on reproductive investment, parental behavior, immune function, and markers of oxidative stress. The postdoc will have the opportunity to be involved in all aspects of the project, and thus will receive broad training in field and laboratory methods. Start date: September 2012, with some flexibility including potential for participation in the field project beginning in May 2012.

Qualifications: Must have completed a PhD in Biology or related fields prior to the start date. Previous relevant field and lab research experience and some postdoctoral experience preferred. Strong publication record, written and oral communication skills, organizational skills, teamwork, and leadership ability required.

Interested candidates should send 1) a cover letter summarizing their professional goals and research interests, 2) a cv, and 3) contact information for at least 2 professional references to Fran Bonier (bonierf@queensu.ca) by *15 March 2012*. More information about ongoing research in the Bonier lab can be found at: http://post.queensu.ca/~bonierf/, information on the Moore lab can be found at: http://www.faculty.biol.vt.edu/moore/, and information about the field station can be found at: http://www.queensu.ca/qubs/index.html . Frances Bonier, PhD Banting Postdoctoral Fellow Queen's University Biology Department Biosciences Complex 3523 Kingston, ON K7L 3N6 Canada

Research Scientist Virginia Tech Department of Biological Sciences Blacksburg, Virginia

phone: 613-533-6000 x77024 email: bonierf@queensu.ca http://post.queensu.ca/~bonierf/index.html fbonier@gmail.com

SanAntonio HelminthFunctionalGenomics

POSTDOCTORAL SCIENTIST: GENETIC ANALYSIS OF HOST SPECIFICITY IN SCHISTOSOME PARASITES

DEPARTMENT OF GENETICS TEXAS BIOMEDICAL RESEARCH INSTITUTE SAN ANTONIO, TX

We are searching for an enthusiastic Postdoctoral Scientist to work on functional genomics of an important human helminth pathogen, Schistosoma mansoni. The central goal of this project will be to understand the genetic basis of behavioral and physiological traits underlying parasite specificity to the snail intermediate host. This will be achieved using genetic crosses, next generation sequence methods, and a linkage analysis framework. The complete lifecycle of this parasitic trematode is maintained in San Antonio, and there is a developing genomic toolkit for this organism, including a genome sequence and genetic map, RNAi and transfection methods. This is a good opportunity for someone who would like to work on an important applied problem using genomic methods and an evolutionary framework. The ideal candidate will have good experimental, molecular and computer skills, together with initiative and drive. The successful candidate will work with Dr. Tim Anderson at TBRI, and collaborate with Dr Phil LoVerde at the University of Texas Health Science Center in San Antonio.

EDUCATION/EXPERIENCE/SKILLS: REQUIRED: Ph.D. in a biological science or related field. Strong motivation, good laboratory and analytical skills. PREFERRED: Ph.D. in genetics/evolutionary biology/parasitology. Experience in genetics, evolutionary biology, molecular methods and/or parasitology

POTENTIAL HAZARDS: This position will involve exposure to infectious materials (BSL-2), cryogenics, and animals (rodents). Participation in a medical monitoring and surveillance program is required. Safety training and protective clothing, equipment and supplies will be provided. Will involve extensive computer work.

OTHER: This is a full-time salaried (exempt) position. Texas Biomedical Research Institute business hours are Monday through Friday - 8:00 a.m. to 5:00 p.m.

Apply online at www.txbiomed.org , position 11-034. EOE

Tim JC Anderson Texas Biomedical Research Institute PO Box 760549 San Antonio, TX 78245-0549

Tel: (210) 258 9596 Fax: (210) 258-9131 email: tanderso@TxBiomedgenetics.org

Tim Anderson <tanderso@txbiomedgenetics.org>

StockholmU MicrobialMetagenomics

Posted at Stockholms universitet 2012-01-26

Ref. no: SU 619-0098-12 Dok no. 1

POST DOC - metagenomic analyses of microbes related to management of the Baltic Sea

A position as Post Doctor is open at the Department of Botany, Stockholm University (Reference number SU 619-0098-12). Deadline for application: February 20th, 2012.

Stockholm University is committed to academic excellence and is a world renowned university with about 60 000 students. The Department of Botany is within the Faculty of Science, and has about 70 employees. Teaching is oriented towards plant physiology, ecology and systematics. The plant physiology unit offers a stimulating atmosphere in well-equipped laboratories.

Position The Department of Botany seeks to employ a post doctor that will produce new essential information within the framework of two international and multidisciplinary research programs: BEAM âBaltic Ecosystem Adaptive Managementâ a Stockholm University Strategic Marine Environment program (www.smf.su.se/-beam) and MiMeBS âMicrobial Metagenomics of the Baltic Seaâ (www.botan.su.se/physiology). MiMeBS is a collaborative program between scientists at Department of Botany and J. Craig Venter Institute (La Jolla, USA; www.jvci.org), and at SciLifeLab, Stockholm (www.scilifelab.se).

Focus The position will be structured as a collaborative and stimulating effort with MiMeBS and BEAM team members. The focus will be on analyses of sequenced metagenomes and transcriptomes of the Baltic Sea microbial populations and on development of tools to make use of the information gained in an environmental context (via environmental data and models), in turn meant as means for an optimized management of the unique Baltic Sea.

Qualifications The post doc position requires a person with a PhD in biology/microbiology/molecular biology/ bioinformatics, preferentially with knowledge in bioinformatic analyses and ecosystem processes, combined with knowledge/interest in management of aquatic ecosystems. Eligible candidates must have a strong record of academic research demonstrated by peer-reviewed publications. Collaborative and innovative skills as well as independence are expected, as is excellence in writing and speaking English. Eligible candidates have received a PhD exam in the past 3-5 years (from the application deadline).

Terms of employment A 1.5 year (18 months) full time Post Doctoral position, starting as soon as possible 2012.

Application The application, in English, should include and be organized as follows: a cover letter outlining your qualifications, relevant experiences and interest in the position (max 1 page) CV & publications (max 2 pages) copies of degree certificates names of two reference persons (give phone numbers and email addresses; state the relation to the reference person)

For further information, contact Professor Birgitta Bergman, telephone +46-(0)8-16 3751, bergmanb@botan.su.se

Union representatives are Bo Ekengren (SACO), Lisbeth Häggberg (ST), telephone +46-(0)8-16 2000 (switch board), and Gunnar Stenberg (SEKO), telephone +46-(0)70 316 43 41.

Applications, labelled with the Reference number SU 619-0098-12, should be posted to the address below and be postmarked no later than February 20th, 2012:

Stockholm University Registrar/PÃ SE-106 91 STOCKHOLM SWEDEN

or by e-mail to: registrator@su.se - give Reference number in the Subject head

Johan Nylander <Johan.Nylander@abc.se>

UCalifornia Riverside MosquitoGenomics

POSITION DESCRIPTION

A postdoctoral position is available in the lab of Dr. Bradley White at the University of California Riverside. The long-term goal of the lab is to identify the genetic polymorphisms that control natural variation in medically and ecologically important traits of malaria mosquitoes and to characterize the evolutionary forces that create and maintain these polymorphisms.

Currently, research in the lab focuses on the two main vectors of malaria in Africa – Anopheles gambiae and Anopheles funestus. Both mosquitoes belong to species complexes composed of at least seven isomorphic sibling species. Each complex exhibits a gradient of vectorial capacity with species ranging from non-vectors to major vectors. Consequently, these two systems offer an excellent opportunity to investigate, at both the genetic and phenotypic levels, why some species transmit malaria while others do not. Moreover, due to the varying hybridization levels among sibling species this system is also useful for studying the formation and preservation of species boundaries under different degrees of gene flow. The genome of An. gambiae was sequenced in 2002 and the genome of An. funestus will be sequenced in 2012, providing an excellent platform for dissecting the genetic basis of complex traits.

Currently, three projects are ongoing in the lab including (1) the evolution of anti-malarial genes (An. gambiae), (2) the genomics of species boundaries (An. gambiae), and (3) the genetic basis of host preference (An. funestus). As this position is not directly tied to funding for a particular project, the successful candidate will have an opportunity to pursue any of the above topics and will be given the latitude to develop additional research questions. For more background please see the publications listed at:

< http://scholar.google.com/citations?user=3DbI-WIgMAAAAJ&hl=3Den >

TO APPLY

A minimum qualification is a PhD or equivalent in Biology, Computer Science, or a related discipline. Applicants should be highly motivated, intellectually curious, and possess expertise in population genomics, computational genomics, vector biology, or insect behavior. A willingness to travel to Africa is a plus, as is the ability to mentor undergraduate students and work within a collaborative framework. To apply, please send a brief description of previous research (1 page), a CV, and the names and contact information for two references to bwhite@ucr.edu. Informal inquiries are welcome.

Initial appointment will be for one year with the opportunity for renewal of additional years. Pay will be commensurate with experience.

ADDITIONAL INFORMATION

The White Lab is housed in the recently built (2002) Entomology Building at UCR. We are also members of the Institute for Integrative Biology (IIGB), allowing for access to state of the art genomic and bioinformatic core facilities. Finally, we are part of the Center for Disease Vector Research (CDVR), which is composed of a diverse and highly talented group of vector biologists.

In the Heart of Inland Southern California, UC Riverside is located on nearly 1,200 acres near Box Springs Mountain in Southern California, the park-like campus provides convenient access to the vibrant and growing Inland region. The campus is a living laboratory for the exploration of issues critical to growing communities air, water, energy, transportation, politics, the arts, history and culture.

UCR is ranked 43rd among top public universities (US News and World Report 2010). At UC Riverside we celebrate diversity and are proud of our #5 ranking among the nation for most diverse universities (US News and World Report 2010). Become part of a place that fosters success for all its constituents, students, faculty, and staff, and where work/life balance and campus culture are integral to our way of life.

UCR is an affirmative action and equal opportunity employer with a commitment to workforce diversity. AA/EOE

Bradley J. White Assistant Professor Center for Disease Vector Research Department of Entomology University of California Riverside, CA 92521

bradley.white@ucr.edu

UChicago ButterflyGenomicsBehavior

POSTDOCTORAL POSITIONS IN BUTTERFLY GENOMICS, EVOLUTION & BEHAVIOR

I am looking for one or two exceptional post-doctoral researchers to join my lab when we move to the University of Chicago in July, 2012. The work of the Kronforst lab focuses on adaptation and speciation in the wing pattern radiation of Heliconius butterflies. In particular, we are currently examining the genetic and developmental mechanisms behind wing patterning and mate preference. We also work on related questions in a variety of other taxa.

Two projects of particular interest are:

Comparative neurobiology & mate preference - This project is aimed at examining the genetic, developmental, and neural mechanisms underlying assortative mate preference in Heliconius. A strong background in neurobiology and/or developmental biology is preferred.

Population genomics of adaptive radiation - This project is focused on using genome resequencing and transcriptome data to examine the genomic consequences of adaptation and speciation in Heliconius and other butterfly groups. A firm background in methods associated with assembling and analyzing next-generation sequence data is essential.

Applications should be sent to mkronforst@cgr.harvard.edu. Please send a cover letter describing your research interests and experience, a C.V. and contact information for three references. Review of applications will begin immediately.

Please contact me with any questions or if you are interested in this work but have a different background.

The University of Chicago is an Affirmative Action / Equal Opportunity Employer.

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Marcus Kronforst Department of Ecology and Evolution University of Chicago www.kronforstlab.org mkronforst@cgr.harvard.edu

UCincinnati UGA EvolutionOfResistance PlantMatingSystem

A post-doctoral research associate position is available in the Baucom (University of Cincinnati) and Chang (University of Georgia) labs to work on a USDA-funded project investigating the influence of the mating system on the evolution of herbicide resistance. The successful applicant will be responsible for locating and collecting populations of the common morning glory across the Southeast and Midwest; designing and implementing studies to assess the contribution of gene flow and male fitness on the evolution of resistance; and aiding and collaborating with members of the Chang lab at the University of Georgia to perform herbicide resistance screens. The successful applicant will be expected to mentor undergraduate and graduate researchers and otherwise be a productive and positive member of the labs. The associate will be primarily located in Cincinnati, OH, but will need to travel across the US and spend significant time in Athens, GA in collaboration with the Chang lab. The position is available for one year initially with the potential, upon progress, to continue for up to three years.

Qualifications:

Minimum: PhD in Genetics, Biology or a related discipline and experience working with plants in the field and greenhouse; performing studies using microsatellite or SNP molecular markers; proficiency in the R and SAS statistical programming languages; a positive work ethic and the willingness to contribute scientifically to a growing research group.

Preferred: Minimum plus experience with quantitative genetics and plant mating systems.

To apply: Send a single PDF file with a brief statement (1 page or less) summarizing previous scientific work and experience, a CV and the names and contact information for three references to regina.baucom@uc.edu. The successful applicant could start as early as April or May 2012 (dependent upon formal creation of the position at UC) but no later than Sept, 2012. Review of applications will begin Feb 1, 2012.

For more information, please contact Gina Baucom (regina.baucom@uc.edu) and/or Shu-mei Chang (chang@plantbio.uga.edu).

Baucom lab: http://homepages.uc.edu/ ~ baucomra/Baucom_Lab/Home.html Chang lab: http://www.plantbio.uga.edu/ ~ chang/chang.html Regina S. Baucom Assistant Professor Dept of Biological Sciences 721 Rieveschl Hall University of Cincinnati Cincinnati OH 45221 (513) 556-9721 Baucom Lab < http://homepages.uc.edu/ ~ baucomra/Baucom_Lab/Home.html >

gina.baucom@gmail.com

UCollegeLondon EvolComputGenetics

The Balloux lab has recently relocated to the UCL Genetics Institute (UGI) at University College London and will have openings for three postdoctoral positions.

Over recent years, we have witnessed unprecedented progress in genetic sequencing technologies. As a result, we are now in a position to sequence large numbers of genomes from a variety of organisms in no time and at reasonable cost. However, genomic data in itself does little more than clog up computers.

This is where the lab fits in. Its mission statement is to harness genomic information to address important questions in evolution, epidemiology and public health, through the analysis of genomic datasets and the development of new methodological tools. The empirical work is primarily centred on humans and human pathogens (MRSA, the plague and malaria). Research in the lab also aims at overcoming the divide between fundamental and applied science. As such, the work spans a large continuum ranging from the fundamental (e.g. reconstructing the colonisation of the world by our ancestors) to the applied (e.g. tracking MRSA infections in hospital wards).

Two positions are in human evolutionary genetics and are funded by the BBSRC. The successful applicants for these posts will be involved in a long-term collaborative project between Francois Balloux and Andrea Manica at Cambridge University on the relative role of past demography and natural selection in shaping the human genomic diversity. The third position is ERC funded and its primary objective of the post holder will be to develop and apply new methodologies taking advantage of genomic data to reconstruct transmission chains in disease ("who infected whom").

Job descriptions and person specification for each post can be accessed at the following URL: https://atsv7.wcn.co.uk/search_engine/jobs.cgi. Reference numbers for the posts are 1227782 and 1228554 for the positions in human genetics and 1227745 for the one in infectious disease epidemiology. Informal enquiries should be addressed to Professor Francois Balloux f.balloux@ucl.ac.uk

UEdinburgh DiseaseEvolution

A full-time Postdoctoral Research Associate position is available in the Institute of Evolutionary Biology, University of Edinburgh, UK

A post-doctoral position is available starting on May 1, 2012 to work on dynamics of within- and between-species parasite transmission in a natural small mammal community in the UK. This will be part of a NERC funded grant led by Andy Fenton (University of Liverpool), Amy Pedersen (University of Edinburgh) and Owen Petchey (University of Zurich) to quantify host species contributions to parasite transmission and persistence across a diverse, natural multi-host-multi-parasite community. This work will involve a combination of fieldwork (small mammal trapping), large-scale ecological manipulation experiments, laboratory assays, and theoretical modelling.

The post holder will help manage the field-trapping programme, conduct laboratory assays for parasite identification, carry out data management and statistical analysis and help develop the community epidemiology models. Experience in laboratory molecular work and statistical analyses are essential, and experience in small mammal trapping, disease ecology and mathematical modelling are desirable. The post holder will have the unique opportunity to link experimental field based approaches with a theoretical ecology framework to better understand how host community composition influences parasite persistence and the success of targeted disease control programmes.

The post will be for up to 36 months and will be based within the lab of Amy Pedersen at the Institute of Evolutionary Biology & Centre of Immunity, Infection, and Evolution at the University of Edinburgh, and will be fully integrated within the wider research team from the Universities of Liverpool and Zurich. For more information on the research groups please see the following websites:

http://www.biology.ed.ac.uk/research/groups/-apedersen/ http://ciie.bio.ed.ac.uk/ http://-www.ed.ac.uk/schools-departments/biology/-evolutionary-biology http://www.liv.ac.uk/integrative-biology/staff/andrew-fenton/ http://www.ieu.uzh.ch/-petchey/index.html The salary range is £30,122 - £35,938; dependent on experience.

Applications will be accepted until February 23, 2012.

For the Postdoctoral Research Associate (Ref. #: 3015298) application and specific job description, please go to: http://-www.jobs.ed.ac.uk/vacancies/index.cfm?fuseaction=-3Dvacancies.detail&vacancy_ref=3015298 For specific information about the project, please email Amy Pedersen (amy.pedersen@ed.ac.uk) and/or Andy Fenton (a.fenton@liverpool.ac.uk).

Amy B. Pedersen, Advanced Fellow Centre for Immunity, Infection and Evolution

Institutes of Evolutionary Biology, Immunology & Infection Research School of Biological Sciences University of Edinburgh Kings Buildings Ashworth Labs, West Mains Road Edinburgh EH9 3JT, UK

amy.pedersen@ed.ac.uk +44(0) 131 650 8674

Ashworth 2 - 4.07 http://www.biology.ed.ac.uk/-research/groups/apedersen/ amy.pedersen@ed.ac.uk

UHull DNAbarcoding EcologicalNetworks

Postdoctoral Research Associate in Ecology & Evolutionary Biology. Dept Biological Sciences, University of Hull, UK

Applicants with a strong background in evolutionary biology and/or ecology are invited for the position of post-doctoral Research Associate to investigate the impacts of climate change on farmland ecological networks. The post holder will use both novel molecular approaches and ecological networks to determine how climate-driven changes affect the ecosystem service of natural biocontrol. The economic impacts of climate-driven changes will also be determined with an emphasis on how altered host-parasitoid interactions affect agricultural crop yields.

We are looking for someone who has proven ability in a molecular lab, with lots of experience of PCR, DNA barcoding, and DNA data analysis. You will develop and extend the suite of molecular tools currently deployed to accurately determine parasitism rates and identity. This will provide the highly resolved data necessary for quantitative network construction and analysis.

The successful candidate will join an interdisciplinary research group led Dave Lunt and Darren Evans (Biological Sciences) as part of the University^{1}s Centre for Adaptive Science and Sustainability (CASS).

The successful applicant will hold a PhD in evolutionary biology, ecology or a relevant subject. A proven ability in molecular ecology, DNA barcoding, and DNA data analysis is essential. The applicant will also carry out ecological network construction and analysis; knowledge of statistical modelling (preferably using R) would be advantageous. You must have excellent scientific communication, presentation and writing skills, as well as very good critical and analytical problem solving skills.

This is a full time position for a fixed term period of 24 months. The post holder will be strongly encouraged to develop fellowship applications to extend the project and appropriate mentoring will be available. Salary range £30,870 - £35,789 pa, pro rata.

You can learn more about this position and apply online at www.hull.ac.uk/jobs (vacancy ref: FS0172).

To discuss this role informally, please contact Dr. Darren Evans, T 01482 465187, E d.evans@hull.ac.uk or Dr. Dave Lunt, T 01482 465514, E d.h.lunt@hull.ac.uk

Closing date: 13th February 2012

Dr Dave Lunt Department of Biological Sciences University of Hull Hull HU6 7RX UK

d.h.lunt@hull.ac.uk +44 (0)1482 465514 http://www.hull.ac.uk/biosci http://davelunt.net http://davelunt.net/research/ D.H.Lunt@hull.ac.uk

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ULiverpool HostParasite

Postdoctoral position in Host-parasite evolutionary ecology. University of Liverpool

Inherited microbes have recently emerged as incredibly important elements of arthropod ecology and evolution, determining host features as diverse as reproductive system, susceptibility to natural enemies, and host plant usage. Despite passing maternally from a female to her progeny within species, these microbes establish regularly in new host species following host shifts events. However, the 'fit' in new host-symbiont combinations is never perfect. This project will consider two question:

a) To what extent does natural selection in the early stage of new symbioses act to produce a fit between microbe and host?

b) What microbe systems are involved in producing this fit?

We are seeking a postdoctoral scientist to join a NERC funded project examining the effects of host shift events on the tempo and mode of evolution of inherited microbes. The project will generate 'artificial' combinations of host and microbe and examine the transmission rate and fitness effects of these microbes at the point of introduction. The parasite will then be passaged through the new host and its evolution monitored both through phenotypic assays and whole genome resequencing. The latter will be used to create a view of how evolutionary rates alter on a genome scale following host shift events of different magnitudes, and also to identify the elements of the genome that are evolving in response to host shift events. This data will then be examined alongside genome sequence for natural isolates of the parasite obtained from different host species in the wild, to examine whether host shift events have driven the diversification of the pathogen that is observed in the natural environment.

The project will work use Nasonia wasps as a model host. In addition to driving the project, the postdoc will be expected to manage the daily activities of a technician in maintaining and characterizing the infections. The work will require someone who is hardworking and meticulous, and able to maintain long term experimental cultures of insects and their parasites. Quantitative skills are also important. The project will require analysis of NGS data, although training will be given in this area if necessary. The project is for 2.5 years, and is supervised by Prof. Greg Hurst, Prof. Steve Paterson, Dr. Mike Brockhurst and Dr. Kayla King at the Institute of Integrative biology at the University of Liverpool (http://www.liv.ac.uk/integrative-biology/). The appointee will join the Ecology, Evolution and Genomics of Infectious Disease Research Group (http://www.liv.ac.uk/integrative-biology/research/ecology-evolution-and-genomics-of-infectious-disease/). This research group, which comprises eight academic staff members and their individual groups, investigate host-parasite interactions at a variety of levels, with particular interests in Wildlife disease dynamics, the impact of coinfection on the ecological and evolutionary dynamics of parasites, the dynamics of coevolution between hosts and parasites, and Parasite genomics. The group is currently supported by extensive grants from the NERC, Wellcome Trust, BBSRC and MRC. Three relevant publications for this project are: Duron, O et al. 2010. Interspecific transmission of a male-killing bacterium on an ecological timescale. Ecology Letters 13: 1139-1148 Wilkes T E et al (2010) The draft genome sequence of Arsenophonus nasoniae, son-killer bacterium of Nasonia vitripennis, reveals genes associated with virulence and symbiosis. Insect Molecular Biology 19: 59-73 Paterson S, et al. (2010) Antagonistic coevolution accelerates molecular evolution. Nature 464: 275-278 Informal enquiries about this position can be made to Greg Hurst (g.hurst@liv.ac.uk). Full details of the post, and the process for application, can be found at: http://www.liv.ac.uk/working/job_vacancies/research/R-5749291.htm .Applications should be submitted on the appropriate forms to jobs@liv.ac.uk by the 3rd of February. We would hope the appointed candidate would start in April 2012, in time for a Spring Field collection.

Greg Hurst Institute of Integrative Biology University of Liverpool

G.Hurst@liverpool.ac.uk

UOslo EvolutionaryBiology

Natural History Museum, University of Oslo Postdoctoral position 1: Evolutionary Biology (Intraspecific Divergence)

The postdoc fellow will work on the project The early stages of the speciation process - prezygotic reproductive isolation and diversification in passerines, funded by the Research Council of Norway and NHM. Speciation is a fundamental evolutionary process in which lineages diverge to form new species. Understanding speciation processes is essential for understanding the evolution of biodiversity. Sexual selection may play a role in speciation processes, e.g. by promoting evolution of secondary sexual traits and preferences in allopatry, leading to divergence and premating isolation upon secondary contact. However, if sexual ornaments do not diverge in allopatry, populations may evolve deep genetic divergence but still despeciate upon secondary contact. The postdoctoral fellow will investigate cases of deep sympatric intraspecific divergences in two passerine species (common redstart and raven), using multilocus coalescence-based analyses, and explore several hypotheses for how such deep divergences have evolved. The project will require the use of a variety of analytical tools, like modern molecular genetic analyses, population genetics and coalescence analyses, and comparative statistics. The project will include comprehensive field work, both in Europe, Asia and North America.

The project team will consist of two postdocs and one field/lab technician and two senior NHM scientists: professor Jan T. Lifjeld and associate professor Arild Johnsen (project leader). The project will be performed in close collaboration with associate professor Kevin Omland (University of Maryland, Baltimore County, USA), and his research group

In order to be successful, the applicant should satisfy the following:

hold a degree equivalent to a Norwegian PhD/doctoral degree. be an evolutionary biologist with a scientific record in avian molecular systematics and phylogeography have experience with modern DNA sequencing techniques (including next generation sequencing), multilocus coalescence-based methods and comparative statistics methods

The postdoc fellow will be expected to participate in the supervision of PhD and Master students and should have good training in ornithological field methods. The postdoc fellow must be prepared to spend several months in the field during the first half of the employment period. A research stay of up to one year at University of Maryland, Baltimore County, USA, will be included in the project period. In the ranking of competent applicants, the whole breadth of their qualifications will be assessed. The employment is for three years, starting as soon as possible after 1 April 2012.

Pay Grade: 57 60 (NOK 456 100-480 900 per year depending on qualifications)

Application Deadline: 19 February 2012.

Informal inquiries to associate professor Arild Johnsen (arild.johnsen@nhm.uio.no).

For full announcement and details on how to apply, please see http://uio.easycruit.com/vacancy/675503/-71922?iso=no arild.johnsen@nhm.uio.no

UOslo EvolutionaryBiology2

Natural History Museum, University of Oslo Postdoctoral position 2: Evolutionary Biology (Reproductive Isolation)

The postdoc fellow will work on the project The early stages of the speciation process - prezygotic reproductive isolation and diversification in passerines, funded by the Research Council of Norway and UiO. Speciation is a fundamental evolutionary process in which lineages diverge to form new species. Understanding speciation processes is essential for understanding the evolution of biodiversity. Spermatozoa are the most diverse cell types in the animal kingdom, indicating that they evolve rapidly. Given the high evolvability and divergence of sperm cells, we hypothesize that sperm cells and their interaction with the female reproductive system play crucial roles in promoting speciation in passerine birds. The postdoctoral fellow will investigate the role of such postmating, prezygotic selection as mechanisms of reproductive isolation, by performing sperm motility experiments in four species/subspecies pairs with variable degree of divergence. The project will require the use of a variety of analytical tools, like invitro sperm motility analysis, proteomic analyses, and comparative statistics. The project will include comprehensive field work, both in Norway and elsewhere in

Europe.

The project team will consist of two postdocs and one field/lab technician and two senior NHM scientists: professor Jan T. Lifjeld and associate professor Arild Johnsen (project leader). The project will be performed in close collaboration with professor Glenn-Peter Sætre (CEES, UiO) and associate professor Anna Qvarnström (EBC, Uppsala University), and their respective research groups.

In order to be successful, the applicant should satisfy the following:

hold a degree equivalent to a Norwegian PhD/doctoral degree. be an evolutionary biologist with a scientific record in avian behavioural ecology and/or molecular systematics with focus on speciation processes have experience with analyses of sperm motility (Computer-Assisted Sperm Analysis), modern DNA and protein analyses, and comparative statistics methods

The postdoc fellow will be expected to participate in the supervision of PhD and Master students and should have good training in ornithological field methods. The postdoc fellow must be prepared to spend several months in the field during the first half of the employment period. A research stay of up to one year at Uppsala University will be included in the project period. In the ranking of competent applicants, the whole breadth of their qualifications will be assessed. The employment is for three years, starting as soon as possible after 1 April 2012.

Pay Grade: 57 60 (NOK 456 100-480 900 per year depending on qualifications)

Application Deadline: 19 February 2012.

Informal inquiries to associate professor Arild Johnsen (arild.johnsen@nhm.uio.no).

For full announcement and details on how to apply, please see http://uio.easycruit.com/vacancy/675379/-71922?iso=no arild.johnsen@nhm.uio.no

UppsalaU Genomics of Metabilic Rate

< http://www2.personalavd.uu.se/ledigaplatser/-67postdokENG.html >

Uppsala University hereby declares the following position to be open for application:

Postdoctoral Researcher in Evolutionary Biology (*UFV-PA 2012/68)*

at the Animal Ecology Program, the Department of Ecology and Genetics, Evolutionary Biology Centre (EBC) with starting date being May 1^st , 2012, or as soon as possible after this date. The Evolutionary Biology Center hosts one of the world's largest aggregations of evolutionary biologists, and is a prime research environment for a wide range of fields in evolutionary biology and genetics (see "http://www.ebc.uu.se/" for more information). The working atmosphere is very international with English as our operational language. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated 40 minutes with train from Stockholm.

*Brief research outline: **The holder of this position will direct research towards an evolutionary understanding of **the genomics of metabolic rate**. Insects (seed beetles) will serve as the model system. The candidate will first complete a collaborative effort to produce a /de novo/ complete genome sequence of our main model system (/Callosobruchus maculatus/) which is currently underway. The holder of this position will then concentrate on the genetics of metabolic rate using focussed genotype-phenotype matching and upon sex-specific selection on discrete genotypes using experimental genomics. This research will involve whole-organism phenotyping of metabolic rate (using a state-of-the art respirometry system) and will focus on those nuclear and mitochondrial genes that are involved in the oxphos pathway and epistatic interactions between these.*

*This post*doctoral position forms a part of a new project on genetic conflict, funded by the European Research Council and the Swedish Research Council. The entire project will employ some 6-8 postdocs and PhD students, apart from a full time TA and the PI, and will strongly encourage interactions and collaborations within the group.**

Salary and appointment: The period of initial appointment is two years, with the possibility of prolonging the contract with another two years *(i.e., 2+2 years)*. Uppsala University adopts an individual salary policy but the starting salary for postdoctoral researchers is typically about 29.000 SEK per month and includes full social benefits.

*Eligibility:*The successful candidate must have a Ph.D, or an exam which is judged comparable to a PhD, that was completed within three years of the application deadline. Applicants that received their PhD earlier than this date will be considered if special circumstances exist (such as prolonged periods of illness, parental leave, military service, union duties and others of similar character).

Qualifications and merits: The ideal candidate has a documented expertise in using genomic tools in evolutionary biology and has a documented interest in the study of phenotypic selection and/or general evolutionary theory. Experience of /de novo/ next-generation sequencing is a merit, as is experience of genotype-phenotype matching using genomic data and/or comparative genomics. Experience of laboratory work with insects and/or previous experience of work with respirometry phenotyping of metabolism will also be considered merits. Because the holder of this position will interact and collaborate closely with other members of the group, we will put emphasis on both independence and ability to collaborate. The holder of this position will be responsible for orchestrating part of the larger research project as an independent junior scientist and the ideal candidate therefore already has some postdoctoral research experience.**

*To apply:*Candidates should submit a cover letter, a curriculum vitae including a list of publications and a short (1-3 pages) description of past research accomplishments and future research ambitions. Applicants should also include names and e-mail addresses of two referees and should specify the date they will be available to start the position.

*For further information*about the position, please contact the PI of the group: Professor Göran Arnqvist (phone +46 18 471 2645, e-mail Goran.Arnqvist@ebc.uu.se). The trade union representatives are Anders Grundström, Saco (the Swedish Confederation of Professional Associations), phone +46 18 471 5380, Carin Söderhäll, TCO/ST (the Swedish Confederation of Professional Employees), phone +46 18 471 1996, and Stefan Djurström, Seko (the Union of Service and Communication Employees), phone +46 18 471 3315.

*You are welcome*to submit your application no later than *March

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

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UppsalaU Sexually Antagonistic Variation

Uppsala University hereby declares the following position to be open for application:

Postdoctoral Researcher in Evolutionary Biology (*UFV-PA 2012/67)*

at the Animal Ecology Program, the Department of Ecology and Genetics, Evolutionary Biology Centre (EBC) with starting date being May 1^st , 2012, or as soon as possible after this date. The Evolutionary Biology Center hosts one of the world's largest aggregations of evolutionary biologists, and is a prime research environment for a wide range of fields in evolutionary biology (see "http://www.ebc.uu.se/" for more information). The working atmosphere is very international with English as our operational language. Uppsala University is the oldest university in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated 40 minutes with train from Stockholm.

*Brief research outline: **The research will aim at improving our understanding of the **architecture of sexually antagonistic genetic variation**. Insects (seed beetles and/or fruit flies) will serve as main model systems and the research will primarily employ quantitative genetic techniques. The research will establish a series of discrete genotypes and use crosses between these to describe and understand the architecture of sexually antagonistic genetic variation. Traits in focus are sex specific measures of life history traits (especially metabolic parameters) and life-time fitness. ***

*This post*doctoral position forms a part of a new project on genetic conflict, funded by the European Research Council and the Swedish Research Council. The entire project will employ some 6-8 postdocs and PhD students, apart from a full time TA and the PI, and will strongly encourage interactions and collaborations within the group.

Salary and appointment: Period of appointment is two years. Uppsala University adopts an individual salary policy but the starting salary for postdoctoral researchers is typically about 29.000 SEK per month and includes full social benefits.

*Eligibility:*The successful candidate must have a Ph.D, or an exam which is judged comparable to a PhD, that was completed within three years of the application deadline. Applicants that received their PhD earlier than this date will be considered if special circumstances exist (such as prolonged periods of illness, parental leave, military service, union duties and others of similar character).

Qualifications and merits: We seek candidates with a documented expertise in quantitative genetic analyses and with a firm understanding of life history theory. Experience of laboratory work with insects is a merit as is previous experience of work with respirometry assays of metabolism. Because the holder of this position will collaborate and interact closely with other members of the group, we will put emphasis on both independence and ability to collaborate.

*To apply:*Candidates should submit a cover letter, a curriculum vitae including a list of publications and a short (1-3 pages) description of past research accomplishments and future research ambitions. Applicants should also include names and e-mail addresses of two referees and should specify the date they will be available to start the position.

*For further information*about the position, please contact the PI of the group: Professor Göran Arnqvist (phone +46 18 471 2645, e-mail Goran.Arnqvist@ebc.uu.se). The trade union representatives are Anders Grundström, Saco (the Swedish Confederation of Professional Associations), phone +46 18 471 5380, Carin Söderhäll, TCO/ST (the Swedish Confederation of Professional Employees), phone +46 18 471 1996, and Stefan Djurström, Seko (the Union of Service and Communication Employees), phone +46 18 471 3315.

*You are welcome*to submit your application no later than *March 20**,**2012 (UFV-PA 2012/67)*. Please use the link below for access to an on-line application portal:

http://www2.personalavd.uu.se/ledigaplatser/-67postdokENG.html Prof. Göran Arnqvist Animal Ecology Department of Ecology and Evolution Evolutionary Biology Centre University of Uppsala Norbyvägen 18d SE - 752 36 Uppsala Sweden

Email:Goran.Arnqvist@ebc.uu.se Phone: +46-(0)18-471 2645 Cell phone: +46-(0)70-2935032 Fax: +46-(0)18-471 6484 NEW homepage with PDF reprints and more at: http://www.anst.uu.se/goarn789/index.html Goran.Arnqvist@ebc.uu.se

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USheffield FishEvoDevo

Post-doctoral Research Associate in evolutionary developmental biology of fishes, Department of Animal and Plant Sciences, University of Sheffield, UK.

This is an ideal opportunity for an ambitious Postdoctoral Research Associate to work at the interface between evolution and developmental biology. This project explores the evolution and development of continuous tooth replacement mechanisms in non-model fishes (including the catshark, pufferfishes and cichlids). The work will be performed in a large, high profile 5* research department with a strong commitment to research-led teaching.

The position is funded by the Leverhulme Trust to study the genetics of vertebrate tooth replacement mechanisms. The overall aim of the project is to understand how continuous tooth replacement programmes are maintained for lifelong replacement and how tooth replacement mechanisms differ among diverse vertebrates.

You will have a PhD or equivalent experience in evolutionary or developmental biology of vertebrates, preferably fishes, and a track record of publishing in leading specialist or multidisciplinary journals. A strong interest and/or background in evolutionary biology would be desirable.

The post is fixed-term for 3 years.

Main Duties

Characterise gene expression and gene function associated with the maintenance of a stem-like cell niche responsible for repeated tooth replacement

Focus on alternative tooth replacement systems of non-model species including pufferfishes, cichlid fishes of Lake Malawi and the small spotted catshark

Job Reference Number: UOS003921

Application Deadline: February 22nd, 2012

Informal enquiries:

For informal enquiries about this job and department, contact: Dr Gareth Fraser on

g.fraser@sheffield.ac.uk or 0114 222 4317.

For further job details and for information on how to apply visit: www.shef.ac.uk/jobs Quoting the reference number: UOS003921

For all on-line application system queries and support, contact: e-Recruitment@sheffield.ac.uk .

http://www.shef.ac.uk/aps/staff-and-students/-acadstaff/fraser-gareth http://www.shef.ac.uk/aps/-index Gareth J. Fraser, Ph.D Lecturer in Zoology Department of Animal and Plant Sciences Alfred

Denny Building University of Sheffield Western Bank Sheffield S10 2TN UK Phone: +44(0)1142224317 Email: g.fraser@sheffield.ac.uk

Gareth J Fraser <g.fraser@sheffield.ac.uk>

UToronto PlantEvolGenomics

Post-Doctoral Position in Plant Evolutionary Genomics at the University of Toronto

We are seeking applications for a Post-Doctoral Researcher to study the evolutionary genomic consequences of plant sexual reproduction in the Department of Ecology and Evolutionary Biology (www.eeb.utoronto.ca) and the Department of Biology (www.utm.utoronto.ca/~w3bio/homepage) at the University of Toronto. This project seeks to understand how repeated transitions between sexual and functionally asexual reproduction in the evening primrose family (Onagraceae) have shaped the evolution of plant transcriptomes, including the diversity and levels of expressed genes, the strength of selection of protein coding regions, the structural evolution of proteins, and the demographic and speciation history of sexual and asexual lineages.

This project is ideally suited for individuals seeking to be productive while doing cutting edge research within a large collaborative group that includes diverse interests and expertise. The successful candidate will be an integral and leading member of a group of researchers from Canada, U.S.A., Germany, Finland, Poland and China, where the collaborators' expertise spans evolution, ecology, chemistry, physiology, cytogenetics and bioinformatics. In collaboration with the One Thousand Plant Initiative we have generated a large Illumina transcriptome dataset of 60 populations that represent over 30 species taken from a well resolved phylogeny of Oenothera, where there have been over 15 transitions between sexual and asexual reproduction.

We are interested in all outstanding post-doctoral applicants with an interest and expertise in bioinformatics OR evolutionary genomics. Candidates with expertise in computer programming and bioinformatics of large genomic or transcriptomic datasets are especially encouraged to apply. Applicants are expected to have expertise with one or more of the following skills: genome assembly, gene annotation and alignment of RNA-seq datasets, population and evolutionary genetics, and phylogenetics.

The successful candidate will work collaboratively in the labs of Profs. Marc Johnson (www.evoeco.org) and Stephen Wright (http://labs.eeb.utoronto.ca/wright) at the Mississauga and St. George campuses of the University of Toronto.

Toronto is a world class city that is culturally diverse. The city boasts an abundance of restaurants, an excellent transit system, a diversity of cultural activities (theatres, sports, bars, clubs), and an abundance of parks and water.

Starting salary: commensurate with experience

Start date: flexible

Benefits: Ontario Health Insurance Plan

Please send all applications to: marc.johnson@utoronto.ca and stephen.wright@utoronto.ca by March 1, 2012. Applications should include: i) a cover letter, ii) CV, iii) PDFs of top two publications, and iv) contact information for three references.

Cheers, Marc

marc.johnson@utoronto.ca

UToronto Speciation

The Cutter lab at the University of Toronto is seeking a postdoctoral researcher to study the genetic basis of adaptation and reproductive isolation. The Cutter lab uses Caenorhabditis nematodes related to C. elegans as a model system to investigate these problems in evolutionary genetics. In particular, we are trying to understand how evolutionary adaptation to temperature by C. briggsae manifests in terms of sequence changes to its genome, and to understand the evolution of genetic incompatibilities between C. briggsae and a close relative. To do so, we are applying and developing resources for mapping with advanced intercross recombinant inbred line (RIL) and near isogenic introgression line (NIL) strain libraries, coupled with high-throughput next-generation sequence-based genotyping and functional experiments, to determine the identity and function of quantitative trait nucleotides (QTN).

For recent publications motivating these topics, see: http://dx.doi.org/10.1111/j.1558-5646.2011.01514.x http://dx.doi.org/10.1111/j.1558-5646.2010.01110.x http://dx.doi.org/10.1016/j.tree.2011.11.004 The ideal candidate will have strong interest in genetics, and strong knowledge of and practical experience in quantitative and/or general genetics, molecular biology, statistics and computation, as well as knowledge in evolutionary biology and a track record of writing and publication. It would also be valuable to have experience working with C. elegans and next-generation sequence data. Applicants should send their CV, a 1-2 page statement of research interests and experience, and the names and contact information for 3 individuals who can speak on their behalf to asher.cutter@utoronto.ca via email.

The Cutter lab is based at the University of Toronto in the Department of Ecology & Evolutionary Biology. The University of Toronto is a leading academic institution in Canada, with exceptional depth of research in evolutionary and molecular genetics. Toronto is a vibrant and multicultural city, offering an exceptional quality of life.

For additional information about the Cutter lab and the EEB department, see: http://labs.eeb.utoronto.ca/cutter http://eeb.utoronto.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 email: asher.cutter@utoronto.ca http://www.eeb.utoronto.ca/people/faculty/cutter http://labs.eeb.utoronto.ca/cutter asher.cutter@utoronto.ca

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UTuebingen FishVisionEvolution

The Faculty of Science and the Institute of Evolution and Ecology of the Eberhard-Karls University Tuebingen invite applications for a Postdoctoral academic associate in fish visual ecology (3 + 3 years) (German federal salary scale 13 TV-L).

The successful candidate will be integrated in an ongoing research programme within the Animal Evolutionary Ecology Unit in which the function and evolution of fish fluorescent patterns is investigated using state-of-the-art equipment and infrastructure. He/she is expected to develop a high-profile own research and teaching programme. Succesful candidates should have a PhD in a relevant area in the biosciences, with an emphasis on the theoretical and empirical analysis of environmental light regimes, fish colour vision and behavioural experiments to prove existing and new hypotheses in this area. We cooperate with other groups with complementary expertises, both nationally and internationally. The teaching load is 60 h during winter and summer term each.

The University of Tübingen is an equal opportunity employer. Qualified female researchers are strongly encouraged to apply. Equally qualified severely disabled applicants will be given priority.

In order to apply, please send a single pdf to nico.michiels@uni-tuebingen.de including a motivation letter as well as a full c.v. including details on research interests and accomplishments, teaching experience, external funding plus names and email addresses of at least two referees. Application deadline is 31 January 2012.

The appointment is made by the central administration of the university.

Prof. Dr. N. Michiels, Animal Evolutionary Ecology, Institute of Evolution and Ecology, Faculty of Science, University of Tübingen, Morgenstelle 28, 72076 Tübingen, Germany (Tel. +49 7017-29 74649)

Nico Michiels, Prof. Dr. Animal Evolutionary Ecology Department of Biology Auf der Morgenstelle 28 72076 Tuebingen Germany

Tel. +49 7071 2974649 Fax +49 7071 295634 Mobile +49 170 4758003

nico.michiels@uni-tuebingen.de

www.eseb2011.de www.evoeco.uni-tuebingen.de www.eve.uni-tuebingen.de Nico Michiels <nico.michiels@uni-tuebingen.de>

UUtah MolecularEvolution

Postdoctoral Fellowship: Molecular Evolution: The Dearing lab at the University of Utah invites applications for a postdoctoral fellow to participate in a study on the evolution of detoxification enzymes in mammalian herbivores. Our preliminary data implicates the cytochrome P450 subfamily 2B as being critical in the biotransformation of plant secondary compounds, particularly terpenes. The structure and copy number of CYP2B enzymes may be key in an herbivores ability specialize on a terpene-rich diet. Future work on this project will consist of cloning and sequencing CYP2B enzymes from a variety of mammalian species and comparing predicted protein sequence with respect to degree of dietary specialization. For more information on previous research, see

http://biologylabs.utah.edu/dearing/2011/-Publications/Woodrats/mec_4171.pdf http://biologylabs.utah.edu/dearing/2011/-Publications/Woodrats/Xeno-Haley.pdf http://-biologylabs.utah.edu/dearing/2011/Publications/-Woodrats/Skopec2007.pdf The ideal candidate will have a strong interest and experience in theories and techniques of molecular evolution or molecular ecology. Knowledge of the literature on plant-mammal interactions or pharmacology desired but not required. Possible field work. The candidate should have at least one first authored publication in press and a track record of mentoring undergraduate researchers.

The position is available beginning April 2012 for up to three years contingent on annual progress. Please send a C.V., statement of research interests and career goals (2 pages), pdfs of papers, and contact information (emails and phone numbers) for at least 3 references to Dr. Denise Dearing, denise.dearing@utah.edu; please put Postdoctoral Applicant in the Subject Line.

Denise Dearing, Ph.D Professor, Department of Biology Associate Dean, College of Science University of Utah Salt Lake City, UT 84112

Phone: 801-585-1298 Fax: 801-581-2174

http://biologylabs.utah.edu/dearing/-2011/Index_New.html Denise Dearing <u0028665@utah.edu>

UWesternAustralia EvolutionaryBiol

Dear Colleagues,

Call for applications -

The Centre for Evolutionary Biology is seeking applicants for the 2012 University of Western Australia Postdoctoral Research Fellowships.

University wide, up to 3 new 3-year (full-time) or 4-year (75% research/25% teaching) University Postdoctoral Fellowships will be awarded.

Proposals will be selected where the case has been established for a postdoctoral research fellow, who will bring special new expertise together with a high level of relevant experience not otherwise available to the University. Applications must be endorsed, as detailed in the Guidelines and Conditions, by the Head of the relevant University school.

We Centre for Evolutionary Biology at UWA are keen to recruit new members through these fellowship opportunities. For further information about the Centre for Evolutionary Biology (CEB) please see http://www.ceb.uwa.edu.au/ or contact Leigh Simmons, Joseph Tomkins or another member of the Centre.

The Guidelines and Conditions are available at

http://www.research.uwa.edu.au/staff/funding/-postdoctoral-research **Please note: because there are a limited number of cases that each school can support, applications must be made through the School of Animal Biology. Last year the School was allowed to support up to 3 applicants. Potential applicants should ensure that they discuss their application with a member of the CEB (or School) and forward a CV, and a 300 word statement of their proposed research plus a 300 word strategic statement outlining what they will bring to the school in terms of expertise. These documents should be sent to Kerry Knott <kerry.knott@uwa.edu.au>. They will be assessed by the Research Committee who will select applicants to proceed to full proposal.

CVs and statements should be submitted to the Research Committee by 5pm, Friday 2nd March.

The University's closing date for applications is 5pm, Friday 13 April 2012.

For the University's administrative information regarding the position please contact:

Olivia Langensiepen olivia.langensiepen@uwa.edu.au

Cheers

Dr Joseph Tomkins Room 2.15, The Centre for Evolutionary Biology, The Zoology Building, The School of Animal Biology, The University of Western Australia, WA 6009. Australia http://www.ceb.uwa.edu.au/ http://alternativetactics.org/index.html Joseph Tomkins <joseph.tomkins@uwa.edu.au>

UWyoming ComputComparativeGenomics

Postdoctoral Position in Computational Comparative Genomics

A postdoctoral position is immediately available in the Liberles Group at University of Wyoming in the field of computational comparative genomics. The project involves developing new models to detect positive selection and for the evolution of gene duplicates and to apply new and existing models to a large Chordate comparative genomic dataset. The successful candidate will have strong skills in programming coupled to experience with databases and with genomic sequence data and/or gene family analysis. The position is grant funded and includes a competitive salary and benefits package.

University of Wyoming is located in Laramie, WY, 2 hours north of Denver in the Rocky Mountains. It is an ideal location for those with interests in outdoor activities in the mountains.

To apply, please send a CV, letter of motivation, and contact information for three references to liberles@uwyo.edu. Review of applications will continue until the position is filled.

Required disclaimer written by the University of Wyoming Office of Diversity: The University of Wyoming is committed to diversity and endorses principles of affirmative action. We acknowledge that diversity enriches and sustains our scholarship and promotes equal access to our educational mission. We seek and welcome applications from individuals of all backgrounds, experiences, and perspectives.

David Liberles <liberles@uwyo.edu>

WayneStateU EvolutionaryGenomics

Postdoctoral Position in Evolutionary Genomics at Wayne State University

A postdoctoral position is immediately available in the Hao Group at Wayne State University in the field of evolutionary genomics.

The Hao laboratory is interested in developing a better understanding of the highly dynamic processes and the corresponding functional consequences of genome evolution. To accomplish this research we conduct comparative genomic studies using next-generation sequencing, computational/bioinformatics approaches and mathematical modelling in the context of rigorous, statistical frameworks.

Current projects include: whole genome sequencing of emerging bacterial pathogens, understanding the evolution and epidemiology of bacterial pathogens, developing new models to detect/quantify fine-scale homologous recombination and horizontal gene transfer (in both prokaryotes and eukarytoes), and the birth and death of gene families.

A minimum qualification is a PhD in evolutionary biology, computational biology, genomics or related field. Applicants should be highly motivated, have strong writing skills, and have expertise with some or all of the following skills: phylogenetics, genome assembly, comparative genomics, and computational genomics.

To apply, applicants should send a curriculum vitae, a cover letter with a brief statement of research interests, PDFs of two publications, and contact information for three references. Application material should be sent by email (a single PDF file preferred) to Dr. Weilong Hao at HaoW@wayne.edu.

For more information, please contact Dr. Hao at HaoW@wayne.edu or 313-577-6450.

Wayne State University is an equal opportunity, affirmative action employer. Applications from women and minorities are encouraged.

Weilong Hao, Ph.D Assistant Professor Department of Biological Sciences 5047 Gullen Mall, #5107.1 Wayne State University Detroit, MI 48202

Phone (313) 577-6450 Fax (313) 577-6891 Email: haow@wayne.edu https://sites.google.com/site/haolabwsu haow@wayne.edu

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YaleU CancerEvolutionaryGenomics

Yale University is recruiting applications for positions in bioinformatics to be employed in a long-term collaborative project between Yale and Gilead Pharmaceuticals. Several positions are available now at the postdoctoral associate or research scientist level. Applications for faculty positions could also be considered. Research in these positions will be focused on identifying tumorigenic mutations based on extensive in-house and public tumor DNA sequencing. Applicants should be proficient at processing large next-generation sequencing datasets and should be capable of working productively with others on parallel projects at a rapid pace. Ideal candidates would have familiarity with maximum likelihood and Bayesian statistical inference, cancer biology, and in some cases transcriptomics and / or molecular evolutionary biology. Appointments may start immediately or at any time within the next nine months, and are open until filled. For full consideration, please send a CV and a list of three references with contact information to Jeffrey.Townsend@Yale.edu.

Jeffrey P. Townsend Yale University

Townsend.Yale@GMail.com

WorkshopsCourses

Florence AncientDNA Mar22

Dear Friends and Colleagues,

we are pleasure to announce a one day Workshop that will hold in Florence (Department of Evolutionary Biology, DBE) on March 22 th , title: “A day with.ancient DNA”

Speakers:

Michael Hofreiter

Johannes Krause

Carles Lalueza-Fox

Tomas Marques Bonet

Ludovic Orlando

Ermanno Rizzi

The workshop is FREE and open to any interested participants. Participation by graduate students and post-docs is particularly encouraged. Limited space is available at the Aula Magna of DBE so we ask to register asap @ http://www.unifi.it/dbalan/CMpro-v-p-166.html where you will find all other information (venue, talk title, time table and registration form).

The application deadline is on March 9th.

So save the date and ..see you in Florence,

David Caramelli, Martina Lari, Carles Lalueza-Fox.

David Caramelli Department of Evolutionary Biology Laboratory of Anthropology Molecular Anthropology/Paleogenetics Unit University of Florence Via del Proconsolo 12 50122 Florence- Italy tel +390552743021 fax+390552743038

david.caramelli@unifi.it

Germany ProgrammingForEvolutionaryBiology March17-Apr1

We announce a beginner’s programming course for evolutionary biology.

The course will take place at the University Leipzig from March 17th to April 1st 2012.

Website: http://evop.bioinf.uni-leipzig.de “Nothing in Biology Makes Sense Except in the Light of Evolution” (Dobzhansky, 1973). Today, evolutionary biology often involves the analysis of an unprecedented amount of information and supports many other disciplines, such as medicine (evolutionary medicine), behavioral biology (evolutionary psychology), ecology, and information transfer. Scientists have to analyze large datasets, which requires computational programming skills to design and apply own ideas into customized algorithms.

In this intensive 16 days course, students will learn how to survive in a Linux environment, get hands-on experience in two widely used programming languages (Perl and R), and statistical data analysis. The classes will be given by experts in the field and consist of lectures and exercises with the computer. The aim of the course is to provide the students with the necessary background and skills to perform computational analyses with a focus on solving research questions related to genomics and evolution. The philosophy of the course will be "learning by doing", which means that the computational skills will be taught using examples and real data from evolutionary biology for the exercises. During the course, students will also propose projects of their own interest and perform them as final projects in small groups under the supervision of a teaching assistant. This summer school is open for students from all countries and targeted toward PhD students and postdocs of evolutionary biology or related research fields with no or little programming experience who want to become proficient in computational evolutionary biology in a couple of weeks.

The course will take place at the University Leipzig, which is conveniently located in the center of the city. Leipzig is a modern city with many students, an international flair, and an established cultural scene. You can find here many parks and exciting night life. Leipzig is only about one hour away from Berlin and three hours away from Prague.

The deadline for application is January 31st. For more information about the course and how to apply, see: http://evop.bioinf.uni-leipzig.de This course is supported by the Volkswagen Foundation, Germany.

– Dr. Katja Nowick

Group Leader "TFome and Transcriptome Evolution" www.nowick-lab.info Universität Leipzig Härtelstrasse 16-18 04107 Leipzig Germany Phone 1: +49 341 97-16684 Phone 2: +49 341 97-16653 Fax: +49 341 97-16679

nowick@bioinf.uni-leipzig.de

Helgeland Norway FluctatingEnvir Apr23-27

WORKSHOP April 23-27, 2012 STOCHASTIC DEMOGRAPHY IN FLUCTUATING ENVIRONMENTS: THEORY AND EMPIRICAL PATTERNS

On the occasion of Professor Russell Lande's award of the Balzan Prize 2011 for Theoretical Biology or Bioinformatics, the Centre for Conservation Biology (CCB) will organize a workshop in Stochastic demography in fluctuating environments: theory and empirical patterns April 23-27, 2012. The workshop will be aimed at young scientists in the initial stages of their scientific career. The focus will be on models for describing the demography of populations in fluctuating environments, methods for estimation of parameters from data and presentations of empirical examples that illustrate the practical application of this quantitative approach for understanding dynamics of populations. Topics that will be covered are the concepts of demographic and environmental stochasticity, density-dependence in age-structured populations, techniques for estimating key parameters in age-structured models, spatial synchrony in population fluctuations, population viability analyses and community dynamics.

The workshop will be based on introductory lecturers by Prof. Steinar Engen, Prof. Russell Lande, Prof. Bernt-Erik Sæther, Prof. Jarle Tufto and Researcher Vidar Grøtan. In addition, the participants will present their own research in short talks, which will be subject for open discussion. The participants will also be involved in short group exercises on selected topics under the supervision of researchers at CCB.

The venue will be the island of Lovund at Helgeland in northern Norway (http://www.lovund.no/). Several field studies (e.g. on house sparrows) run by CCB have been located in this pristine coastal environment.

Applications. The workshop is primarily aimed at young (<37 years old) researchers (e.g. graduate students and post docs) in the beginning of their research career, but applications from more senior persons will also be considered. The stay will be free. If necessary, the organizers can also provide funding for travel costs.

The application should contain a CV, including all contact details. In addition, a summary (<200 words) of the current research interests, the three most relevant papers (if applicable), whether you need travel funds and the airport of departure for the travel to Helgeland should be included. The application should be emailed as pdf or Word files to Ingunn Yttersian (Ingunn.Yttersian@bio.ntnu.no) by February 15, 2012.

Ingunn Yttersian <ingunn.yttersian@bio.ntnu.no>

KansasStateU EnvironmentAdaptation Summer

ANNOUNCING: Summer 2012 REU Opportunities in The Ecology and Evolution of Changing Environments at Kansas State University

Kansas State University invites applicants for a 10-week REU Summer Program. The focus of the program is on the mechanistic understanding of ecological and evolutionary responses to short- and long-term responses to changing environments. Research projects will address biological patterns observed in changing environments by examining underlying genetic, developmental, physiological, or ecological mechanisms.

The program is hosted by the Ecological Genomics Institute, The Konza Prairie Biological Station, and the Division of Biology at K-State. Over 30 faculty from the Division of Biology and Departments of Entomology, Geography, and Plant Pathology, will serve as potential mentors. Participants will learn modern approaches in ecology and evolutionary biology, attend professional development seminars, travel to important ecological sites and genomic centers in Kansas and Missouri, and have two opportunities to present their research. The program covers costs of accommodations and meals. Participants will also receive a generous 10-week stipend.

The deadline for applications is the 1st of March 2012.

More information is available by visiting http://-www.ksu.edu/reu or by contacting the PIs (Dr. Bruce A. Snyder and Dr. Theodore J. Morgan) at biologyreu@ksu.edu.

Theodore J Morgan, Assistant Professor Mail: Division of Biology, 116 Ackert Hall, Kansas State University, Manhattan, KS 66506 Office: 785.532.6126, Molecular Lab: 785.532.6074, Fly Lab 785.532.6416, Fax: 785.532.6653 Email: tjmorgan@ksu.edu, Skype: morganlab.ksu, www.ksu.edu/-morganlab tjmorgan@ksu.edu

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KelloggBioStation ELME2012 Jun4-22 Applications

ELME is a summer educational program at the Kellogg Biological Station devoted to Enhancing Linkages between Mathematics and Ecology.

ELME 2012 will be a sequence of three courses covering: Week 1) Maximum Likelihood Estimation, week 2) Structural Equation Modeling, and week 3) Matrix Population Modeling. In this hands-on environment, students will learn the basics in a lecture setting and cement their knowledge with independent and collaborative modeling projects using the computer program R.

Dates: June 4-22, 2012

Hours: Mon-Fri 9-5

Instructors: Week 1) Colin Kremer (Michigan State University), week 2) Don Schoolmaster (National Wetlands Research Center / USGS), and week 3) Hal Caswell (Woods Hole Oceanographic Institute)

Target audience: 12-18 graduate students or exceptional undergraduates

Prerequisites: At least one semester of statistics, undergraduate calculus, and familiarity with basic matrix manipulations Previous exposure to theoretical ecology and R useful but not required.

Format: A mixture of lecture, guided computer labs, and independent/team projects

To apply, email elme2012@kbs.msu.edu <elme2011@kbs.msu.edu> the following:

- your CV

- a statement of research interests and why you'd benefit from the course (< 1 page)

- a statement of relevant educational/research experience, including related coursework (< 1 page)

- the name of a reference who you've asked to email a letter of support

Deadline for applications: March 15, 2012

Preference will be given to students interested in all three courses.

Financial support to cover room and board and help defray transportation costs is available. Let us know if this is not necessary. Academic credit, if desired, is available at appropriate MSU rates. Let us know if this is desired.

For more info see < http://www.kbs.msu.edu/-education/elme > or email elme2012@kbs.msu.edu <elme2011@kbs.msu.edu>.

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Elizabeth Miller W. K. Kellogg Biological Station 3700 E. Gull Lake Dr. Hickory Corners, MI 49060 Graduate Program in Ecology, Evolutionary Biology, and Behavior Department of Plant Biology Michigan State University

Beth Miller <mill1455@msu.edu>

MichiganStateU MicrobialMetagenomics Jun3-16

Microbial Metagenomics, Michigan State University, Summer Course 2012, June 3rd - June 16th

Learn state-of-the-art genomic methods to identify relationships between the structure and function of microbial communities. This intensive two-week course will provide hands-on experience with all aspects of a metagenomic study. You will formulate hypotheses and design experiments to test them. You will isolate and sequence environmental DNA. You will perform computational and statistical analyses to test your hypotheses. Your system will be an ongoing study of the effects of land use on the production of the greenhouse gas nitrous oxide at the nearby Kellogg Biological Station Long Term Ecological Research Site (http://-lter.kbs.msu.edu).

Morning lectures will discuss microbial and ecological principles underlying experiments that you will conduct during the afternoons. The wet lab sessions will include purification of DNA from soil for clone libraries and 454 pyrosequencing and for quantitative PCR. In the computer lab you will analyze your sequences and metagenomic data with a suite of contemporary programs to measure community diversity, and use multivariate analyses to relate community composition to ecosystem function.

The course will be taught primarily by Drs. Thomas Schmidt, Jay Lennon and Clegg Waldron of Michigan State University. Other researchers (from MSU and elsewhere) will be contributing their expertise in both lectures and lab sessions.

Who can attend? This course is primarily for graduate students, postdocs and faculty. Advanced undergraduates and other researchers will be considered. This year, for the first time, the course can be taken as a workshop or for credit.

What do I need to know in advance? We encourage diversity of backgrounds. The primary prerequisite is a keen interest in adding molecular methods to your research.

Where will it be held? Lectures and laboratory sessions will be held on the main campus of Michigan State University in East Lansing, Michigan, USA. Single-room accommodation is available on campus.

When do I apply? Application is open now until March 16th, 2012. Additional information and application forms are at http://metagenomics.wikidot.com/ Jay T. Lennon Assistant Professor W.K. Kellogg Biological Station Department of Microbiology & Molecular Genetics. Michigan State University 3700 East Gull Lake Drive Hickory Corners, Michigan 49060 269-671-2340 lennonja@msu.edu Lab website: http://microbes.kbs.msu.edu/ Lab wiki: http://lennonlab.kbs.msu.edu/ Jay Lennon <lennonja@msu.edu>

OceanSprings MS HerpEvolution May14-25

The Gulf Coast Research Laboratory in Ocean Springs, MS is pleased to offer the course - Coastal Herpetology - from May 14-25, 2012. The coastal plain of the Southeast boasts an outstanding diversity of amphibians and reptiles, making the region an excellent place to study these often reclusive and elusive creatures. This course will provide students with an introduction to herpetology through lectures and associated readings, discussions of original research papers, and a class project. Topics covered will include the ecology, evolution, life history, diversity, behavior, and conservation of amphibians and reptiles. There will also be many field excursions highlighting the methods and techniques for capturing and studying amphibians and reptiles. Be prepared to get wet and muddy since we will be exploring the marshes, pine woods, bayous, and other habitats as we search for and learn about the amphibians and reptiles of the northern coast of the Gulf of Mexico. College credit is available through the University of Southern Mississippi or one of many affiliated universities. For more information, visit us at www.usm.edu/-gcrl or contact the instructor, Dr. Matthew Chatfield, at mattchat@tulane.edu.

Matthew W. H. Chatfield, Ph.D. Tulane University Dept of Ecology & Evolutionary Biology 400 Lindy Boggs Building New Orleans, LA 70118 (504) 862-8289 mattchat@tulane.edu

"And the end of all our exploring will be to arrive where we started, and know the place for the first time." - T. S. Eliot

mwhchatfield@gmail.com

Smithsonian PhylogenyEstimation May20-22

Dear Colleagues,

We are writing to let you know about a workshop and symposium that we will hold on May 20-22, 2012, at the Smithsonian Institution in Washington, DC. The workshop will provide training in advanced methods for multiple sequence alignment and phylogeny estimation, and will take place on May 20 and 21; the symposium will follow immediately and will feature research presentations on the same topic. This workshop is funded by:

US NSF DEB 0733029 Large-scale simultaneous multiple alignment and phylogeny estimation Project Webpage: http://www.cs.utexas.edu/users/tandy/ATOL-MSA.html The workshop will include presentations of new methods for maximum likelihood phylogeny estimation of large sequence alignments (including GARLI and FastTree), for comparing different alignments of the same dataset, for phylogenetic analyses of datasets that include partial sequences (e.g., short reads generated in a metagenomic analysis), for supertree estimation, and for simulating sequence evolution. However, a main focus is to train participants in both basic and advanced use of the SATé software (Liu et al. 2009, Science, Vol. 324, no. 5934, pp. 1561-1564) for simultaneous estimation of alignments and trees – software available for download at

http://phylo.bio.ku.edu/software/sate/sate.html Workshop participants are expected to bring laptops with them to the workshop, so that they can perform alignment and phylogenetic tree estimations. We will provide test datasets for you to learn how to use SATé, but strongly encourage you to bring your own datasets to analyze.

Attendance at the workshop is limited to 40 participants, and registration is required. If you are interested in attending the workshop, whether or not you are requesting travel support, please fill out the Word document available at

http://www.cs.utexas.edu/users/tandy/workshop-application.doc, and return it to Laurie Alvarez (lauriea@austin.utexas.edu) by February 15, 2012. We will respond to requests for registration by March 1, 2012.

For more information on the workshop, please contact me (Tandy Warnow), at tandy@cs.utexas.edu. For more information on the Symposium, please contact Mike Braun (braunm@si.edu). We look forward to seeing you at the Smithsonian workshop and symposium!

Regards, Tandy Warnow and Mike Braun On behalf of the AToL project team:

Michael Braun, The Smithsonian Institution Mark Holder, The University of Kansas Jim Leebens-Mack, The University of Georgia Randy Linder, The University of Texas Etsuko Moriyama, The University of Nebraska Tandy Warnow, The University of Texas

emoriyama2@unlnotes.unl.edu

Sweden HymenopteraSystematics Aug5-12

To Prospective Participants:

We are pleased to announce the fourth offering of HYM Course (http://hymcourse.org/), scheduled for August 5-12, 2012 at Tovetorp Zoological Research Station, Sweden (http://www.zoologi.su.se/tovetorp/).

The main objective of HYM Course is to provide participants with knowledge and experience in identifying parasitic and predatory wasps, sawflies, wood wasps, bees, and ants. Information on natural history is also presented, and that information is reinforced with fieldwork. Techniques used to collect, rear, preserve, and curate specimens are presented in a hands-on manner to allow participants to learn directly by doing.

The course is limited to 25 participants. Applications are due March 2, 2012. Students in Sweden are eligible for financial aid through the Swedish Taxonomy Initiative. Please visit the HYM Course website (http://hymcourse.org/) for details, including information on how to apply, costs for taking the course, and logistics of travel to and within Sweden.

We look forward to seeing you in Sweden! Instructors, HYM Course 2012

Hege V??rdal Intendent Hymenoptera/Curator Hymenoptera Enheten f??r Entomologi/Department of Entomology Naturhistoriska riksmuseet/Swedish Museum of Natural History Box 50007 104 05 STOCKHOLM hege.vardal@nrm.se

Hege V??rdal <Hege.Vardal@nrm.se>

UBelgrade VirusEvolutionBioinformatics Aug27-31

17th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology

http://www.rega.kuleuven.be/cev/veme-workshop/2012 Dear colleague,

We would like to announce the "17th International Bioinformatics Workshop on Virus Evolution and Molecular Epidemiology", which will be organized August 27-31, 2012 at the University of Belgrade, Faculty of Medicine in Belgrade. The workshop provides theoretical and practical training in phylogenetic inference and evolutionary hypothesis testing as applied in virology and molecular epidemiology. Teaching is provided by a team of experts in this field, including software developers of popular analysis tools. A registration fee of 750 Euro covers lectures, practical sessions in computer classes, lunches and coffee breaks. Participation is limited to 25 scientists in each module and is dependent on a selection procedure based on the submitted abstract and statement of motivation. A limited number of grants are available for scientists who experience difficulties to attend because of financial reasons. Abstract and application deadline is 31 March.

Additional information and application forms are available at our website: http://www.rega.kuleuven.be/cev/veme-workshop/2012 We are confident that this course meets the needs of many molecular virologists and epidemiologists, and hope we can assist you in your search for training in Bioinformatics methods.

Yours sincerely,

Philippe Lemey, Organizer of the workshop

Maja Stanojevic, Co-Organizer of the workshop

Anne-Mieke Vandamme, Co-Organizer of the workshop

philippe.lemey@rega.kuleuven.be

UOxford ComputBiol Jul9-Aug17

University of Oxford

Oxford Summer School in Computational Biology 2012

>From July 9th until August 17th 2012, a project-based summer school in computational biology will take place at the University of Oxford. Applications are invited from outstanding students who have completed at least two years of undergraduate study, with a strong background in mathematics, statistics, computer science, physics or chemistry.

Students will work in teams of three for the six-week period on a cutting-edge research project in bioinformatics and computational biology, working with leading researchers from Oxford and a number of collaborators visiting from overseas.

The programme will also include a series of lectures and tutorials covering key topics in bioinformatics and genome analysis, and presentations from top researchers in the field.

Accepted students will be offered university accommodation for the duration of the programme, and will receive a stipend towards living expenses.

Applications will be assessed in two rounds, and students whose applications are received by the first deadline (27th January) may be eligible for additional funding.

For more information, and to apply, visit www.stats.ox.ac.uk/genome/summer_school Final application deadline: 5th March, 2012

Madeline Mitchell PA to Professor Jotun Hein, Professor Chris Holmes & Group Secretary, (Professor Peter Donnelly FRS FMedSci (WTCHG): PA +44 1865 287725) Department of Statistics University of Oxford 1 South Parks Road Oxford OX1 3TG tel. (0)1865 285386: fax. (0)1865 285384 email: mitchell@stats.ox.ac.uk www.stats.ox.ac.uk Madeline Mitchell <madeline.mitchell@stats.ox.ac.uk>

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.