EvolDir

July 1, 2011

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

Adelaide Barcode 2

Latest News on the Adelaide Conference * [1]Registration is now open for the Fourth International Barcode of Life conference in Adelaide, Australia! + Register before _15 September_ to benefit from the Early Bird discounted rate. + Register for the Pre-Conference Training Event, 28-29 November. + Secure specially-discounted conference rates on hotels and [2]half-day excursions. * The [3]Exhibitor Form is now available. Organisations should apply soon for one of the limited number of exhibition booths. * Your organization or project can be highlighted at the conference through one of the [4]Sponsorship Opportunities. * Have you [5]submitted your abstract yet? Be sure to do so before the [6]new deadline. Links:

For all links see http://barcodeoflife.us1.list-manage2.com View of the [7]South Australia Museum along North Terrace, near the University of Adelaide, site of the Adelaide Barcode Conference.

Adelaide Barcoding 3 AbstractDeadline

Latest News on the Adelaide Conference * Race to [1]submit your abstract before the _June 15 deadline_– only a week to go! * You can submit your abstract for consideration in: + Plenary Sessions + Poster Sessions + Taxonomic Sessions + Thematic Sessions * Take a look at the [2]number of abstracts already submitted for session topics. * Conference chairman Prof. Andrew Lowe offers his comments on: + The [3]Adelaide Barcode Conference + [4]Registering now for an 'Early Bird' discount + [5]Submitting your abstract online * Be sure to read up on the _Session Spotlight_ series, new on the [6]Adelaide Conference Blog. Links: 1. http://barcodeoflife.us1.list-manage.com/track/click?u=2bbe5896b006a03d890d38ac4&id=0bc1487ff1&e=c160c09eb4 2. http://barcodeoflife.us1.list-manage.com/track/click?u=2bbe5896b006a03d890d38ac4&id=2584603e6f&e=c160c09eb4 3. http://barcodeoflife.us1.list-manage.com/track/

click?u=2bbe5896b006a03d890d38ac4&id=ce1aeefd20&e=c160c09eb4 4. http://barcodeoflife.us1.list-manage1.com/track/click?u=2bbe5896b006a03d890d38ac4&id=a41aa14b61&e=c160c09eb4 5. http://barcodeoflife.us1.list-manage.com/track/click?u=2bbe5896b006a03d890d38ac4&id=13a6538dc8&e=c160c09eb4 6. http://barcodeoflife.us1.list-manage.com/track/click?u=2bbe5896b006a03d890d38ac4&id=c1ff7988fd&e=c160c09eb4 The Santos Tour Down Under passes through the landscape surrounding Adelaide Pictures by [7]0ystercatcher, [8]iansand and [9]ArthurChapman Links: 7. http://barcodeoflife.us1.list-manage.com/track/click?u=2bbe5896b006a03d890d38ac4&id=33b9ddf042&e=c160c09eb4 8. http://barcodeoflife.us1.list-manage.com/track/click?u=2bbe5896b006a03d890d38ac4&id=a469023db4&e=c160c09eb4 9. http://barcodeoflife.us1.list-manage.com/track/click?u=2bbe5896b006a03d890d38ac4&id=6561023678&e=c160c09eb4 Adelaide Barcode Conference Organizers <jettk@si.edu>

Belfast Systematics Jul4-8 AbstractDeadline

NB: the final deadline for Oral presentations and Poster abstracts for the meeting is this Sunday, 19th of June. Registration is open until the start of the meeting.

There is an exciting programme that includes both plenaries and thematic symposia, as well as contributed sessions. Scheduled symposia include:

- Next Generation Systematics - Studying Evolution and Diversity in an Era of Ubiquitous Genomics - Arthropod Systematics: are Morphology, Palaeontology and Molecules Coming Together - Algal Systematics: Where Next? - Advances in Using Museum Specimens and Ancient DNA in Systematics Research

Plenary speakers include:

Max Telford, University College London Ralf Sommer, Max Planck Institute for Developmental Biology Debashish Bhattacharya, Rutgers University Des Higgins, University College Dublin

Symposia will include a mixture of talks from invited speakers and other contributions. The Biennial also presents excellent opportunities for contributed papers on any aspect of systematics and is a great forum for students and young researchers to present their work. For further details, please see http://www.systass.org/biennial2011/ .

Juliet Brodie, President James Cotton, Programme Officer Peter Olson, Treasurer Christine Maggs, Local Organiser

Sponsors: The Linnean Society of London, British Phycological Society, Cambridge University Press, Genetics Society, Queen's University Belfast

– The Wellcome Trust Sanger Institute is operated by Genome Research Limited, a charity registered in England with number 1021457 and a company registered in England with number 2742969, whose registered office is 215 Euston Road, London, NW1 2BE.

james.cotton@sanger.ac.uk

Belfast Systematics Jul4-8 EarlyRegistrationCloses

HURRY TO TAKE ADVANTAGE OF EARLY BIRD REGISTRATION

8TH SYSTEMATICS ASSOCIATION BIENNIAL QUEEN'S UNIVERSITY BELFAST 4-8 JULY 2011

***** EARLY REGISTRATION CLOSES TODAY - WEDNESDAY 1ST JUNE 2011 *****

*****ABSTRACTS: 1ST JUNE 2011*****

Dear Colleagues,

To take advantage of discounted registration, you need to register by close of Wednesday 1st June 2011. NB: You can still register after that time.

There is an exciting programme that includes both plenaries and thematic symposia, as well as contributed sessions. Scheduled symposia include:

- Next Generation Systematics - Studying Evolution and Diversity in an Era of Ubiquitous Genomics - Arthropod Systematics: are Morphology, Palaeontology and Molecules Coming Together? - Algal Systematics: Where Next? - Advances in Using Museum Specimens and Ancient DNA in Systematics Research

Symposia will include a mixture of talks from invited speakers and other contributions. The Biennial also presents excellent opportunities for contributed papers on any aspect of systematics and is a great forum for students and young researchers to present their work. For further details, please see http://www.systass.org/biennial2011/ < https://webmail.nhm.ac.uk/exchweb/bin/redir.asp?URL=3Dhttp://www.systass.org/biennial2011/ > .

On behalf of the conference organisers, we look forward to see you there!

Juliet Brodie, President James Cotton, Programme Officer Peter Olson, Treasurer Christine Maggs, Local Organiser

Sponsors: The Linnean Society of London, British Phycological Society, Cambridge University Press, Genetics Society, Queen's University Belfast

james.cotton@sanger.ac.uk

Biddeford Maine EvolutionaryGenomics Jul10-15

Upcoming GRC on Ecological and Evolutionary Genomics, July 10-15, 2011, College of New England, Biddeford, Maine

The Gordon Conference on Ecological and Evolutionary Genomics is fast approaching! There is still time to register! We have a few slots remaining if you would like to attend.

The 2011 conference will present cutting-edge research on using genomics approaches to study adaptation of organisms to changing environments, genome evolution and population genetics, as well as the evolution of complex phenotypes. A diversity of sessions will highlight recent results from natural as well as experimental populations, and will cover both non-model and model species. There will be an exciting balance between ecologists using genomics to study adaptation in rapidly evolving systems, as well as genomicists using large-scale sequence, expression and functional assays to study variation among populations and species.

We have a great slate of speakers.ââFor more details on the program, see http://www.grc.org/programs.aspx?year=2011&program=ecolevo We hope to see you in Biddeford!

Loretta Johnson (Johnson@ksu.edu), Chair Gretchen Hofmann (hofmann@lifescie.ucsb.edu), Vice-Chair

Loretta Johnson Associate Professor Co-Director Ecological Genomics Institute http://ecogen.ksu.edu/ Division of Biology Kansas State University Manhattan KS 66506-4901 Office: 785-532-6921 www.ksu.edu/johnsonlab

Loretta Johnson <johnson@k-state.edu>

Cairns CoralAdaptation July

ICRS mini-symposium "Genomic approaches to coral reef biology" Reply-To: "Christian R. Voolstra" <christian.voolstra@kaust.edu.sa> X-Mailer: Apple Mail (2.1084)

Dear colleagues,

We would like to draw your attention to the mini-symposium "Genomic approaches to coral reef biology" at the 2012 International Coral Reef Symposium, which will take place in Cairns in July 2012 (http://www.icrs2012.com). The abstract is below.

We very much look forward to your contribution and to eventually seeing you in Cairns! If you have any questions with respect to this mini-symposium, please do not hesitate to contact any of us!

With best regards,

Christian R. Voolstra <christian.voolstra@kaust.edu.sa>

David Miller <david.miller@jcu.edu.au>

Monica Medina <mmedina@ucmerced.edu>

Tim Ravasi <timothy.ravasi@kaust.edu.sa>

Sylvain Foret <sylvain.foret@anu.edu.au>

MINI-SYPOSIUM ABSTRACT:

Coral reefs are disturbed on a global scale by means of human-induced environmental changes including global warming and progressive rise of sea surface temperatures as well as increases in carbon dioxide that lead to ocean acidification. Although the last decade has seen a lot of progress in our understanding of the responses and adaptation of the coral and its symbionts to these environmental changes, still little is known about the molecular mechanisms that underlie these responses. Mostly, because to date there have been only few efforts to apply systems biology and genomic approaches to the holistic understanding of the biology of coral reefs.

An important goal for the mini-symposium is to provide crash course introductions to some of the latest achievements in coral genomics and systems biology approaches to coral reef biology. Another purpose is to promote research in this direction and to promote interaction between coral reef researchers from different areas. The speakers will present both the wide scope of the topic and important new results. The mini-symposium will be an excellent opportunity to shed light on this new systems biology and genomics era for coral reef biology.

OPENING DATE FOR SUBMISSION OF ABSTRACTS: 1 July 2011

CLOSING DATE FOR SUBMISSION OF ABSTRACTS: 1 October 2011

IMPORTANT: Please send your submission through the ICRS website, and not directly to us.

Regards, Chris

– Christian R. Voolstra Assistant Professor of Marine Science Coral Reef Ecological Genomics, Red Sea Research Center King Abdullah University of Science and Technology (KAUST) 23955-6900 Thuwal, Kingdom of Saudi Arabia Phone: +966 5 44 7000 87 E-mail: christian.voolstra@kaust.edu.sa Web: http://faculty.kaust.edu.sa/sites/christianvoolstra/-Pages/home.aspx "Christian R. Voolstra" <christian.voolstra@kaust.edu.sa>

Flagstaff AZ PathogenEvolution Jul24-26

FINAL ANNOUNCEMENT for INCDNCM 2011 - ABSTRACT DEADLINE EXTENDED to JULY 1, 2011

Have you signed up for INCDNCM yet? The conference is coming up soon, but we are still accepting abstracts and early registration. Please join us July 24-26 in Flagstaff, AZ for the 66th International Conference on Diseases in Nature Communicable to Man The final deadline for REGISTRATION and ABSTRACT submission has been extended to July 1, 2011. Please see the conference website for details and the registration form (http://www.mggen.nau.edu/INCDNCM/-index.html).

We apologize for problems with the website last week - we are up and running again! Thank you for your patience while we worked out some kinks.

We are very pleased to announce our guest speakers for this year's conference. Dr. Paul Keim from Northern Arizona University will be our opening keynote speaker, and will focus on molecular genetic analyses of pathogens, with examples from the "Amerithrax" investigation. Dr. Joseph Hinnebusch, the Plague Section Chief of NIAID Rocky Mountain Laboratories in Hamilton, MT, will be our R.R. Parker Memorial speaker, and will speak on zoonotic pathogens.

INCDNCM (http://sites.google.com/site/incdncm/-Home) has been held annually since 1946 and has a long history of fostering collaborations among universities, health institutions, and other public agencies. A strength of this conference is the broad variety of topics its participants share each year. This includes surveys of pathogens in wildlife, evolution of virulence, vector and pathogen ecology, control efforts, host shifts, emerging infectious diseases, pathogen genetics and genomics, and much more. Student presentations are encouraged.

Don't miss your chance to join us in Flagstaff!!

Dave Wagner Dave.Wagner@nau.edu

Dave Engelthaler dengelthaler@tgen.org

Joseph Busch Joseph.Busch@nau.edu

Joseph Dominic Busch <Joseph.Busch@nau.edu>

Glasgow ConservationBiol Aug28-Sep1

Dear Colleagues,

The 3rd European Congress of Conservation Biology will be held in Glasgow, Scotland, from 28 August to 1 September 2012, and is organised by the Society for Conservation Biology -Europe Section and the University of Cumbria's National School of Forestry. The Call for symposia, workshops and training sessions is now open with a deadline for proposals of 30 September 2011. Details are posted on the congress website:www.eccb2012.org . This cornerstone international event will bring academics, students, policy makers, natural resource managers and NGO representatives from all over Europe to address all aspects of conservation biology from research to application, from terrestrial to marine issues. Already three renowned plenary speakers confirmed their participation, Ian Boyd, Ilkka Hanski and Peter Vitousek.

I do hope that the conference is of interest to you; please distribute this letter for other interested parties.

Kind regards,

The Organisers – András Báldi PhD DSc Animal Ecology Research Group, HAS, Hungarian Natural History Museum Chair, Scientific Committee, 3rd European Congress of Conservation Biology http://eccb2012.org/ http://euroconbio.blogspot.com/ http://www.nhmus.hu/~baldi/ Postal address: Baross u. 13. Budapest, Hungary, 1088

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Judit Vörös PhD Collection of Amphibians and Reptiles Hungarian Natural History Museum 1088 Budapest Baross u. 13. Tel: +36/1-267-71-00 Fax: +36/1-267-34-62

Judit Voros <jvoros@nhmus.hu>

IPasteur Paris HostGenetics Sep28-30

3rd EMBO Conference on Host Genetic Control of Infectious Diseases Institut Pasteur, Paris, France - September 28-30, 2011

http://www.pasteur.fr/hostgenetic2011 The deadline for submission of abstracts and early registration is *July 1st, 2011*.

The third EMBO conference on host genetic control of infectious diseases will be held on September 28-30, 2011 at the Institut Pasteur, Paris. Advances in hygiene and medical care in parallel with the development of antibiotics and mass vaccination in the second half of the 20th century created the belief that humanity will soon overcome the death-causing burden of infectious diseases both in developed and in developing countries. This was however an illusion. The outburst of the HIV pandemics, the spread of antibiotics resistant strains of many common infectious bacteria, the high rate of acquired infections in hospitals, the burst or re-appearance of viral epidemics, such as Influenza or SARS, the appearance of drug resistant parasitic infections etc, demonstrate that infectious diseases remain and even are amplified as a major health problem for humanity.

The subjects will be include:

*- Primary immune-deficiencies - **Host control of viruses and prions infections - **Host control of bacterial infections - Fungi and parasites - Model systems -** Human * * Evolutionary genetics

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

Tel: +33 1 40 61 34 43 Fax: +33 1 45 68 86 39 e-mail: quintana@pasteur.fr

Lluis QUINTANA-MURCI <quintana@pasteur.fr>

Jyvaskyla Coevolution Oct4-7

Symposium on CoEvolution 4th - 7th October 2011, Jyväskylä, Finland

We are pleased to announce a special symposium on Coevolution in Jyväskylä, Finland (October 4th 7th, 2011).

Our keynote speakers will be Dr. Sheena Cotter from Queens' University (Belfast), Dr. Mario Vallejo Marín from University of Stirling (Scotland) and Dr. Dagmar Voigt from University of Kiel (Germany) in addition to contributions from local professors.

We are accepting oral presentations and posters covering all aspects of coevolution with emphasis on the following themes:

1. Mutualism 2. Insect-plant interactions 3. Predator-prey interactions 4. Multitrophic interactions 5. Sexual conflict 6. Virulence evolution 7. Gene-gene interactions

Please go to https://www.jyu.fi/bioenv/en/divisions/eko/coeevolution/coevolution-symposium for more information and online registration or contact as at coevo.symposium@jyu.fi. Registration deadline is August 31st and deadline for abstract submission is July 31st.

The symposium is organized by the post-docs of the Centre of Excellence in Evolutionary Research and the Division of Ecology and Evolutionary Biology from the University of Jyväskylä. We are particularly keen to give postdocs a chance to present and discuss their work on coevolution together with other interested researchers.

Looking forward to meeting you in Jyväskylä!

On behalf of the organising committee.

Dr. Sandra Varga Postdoctoral Researcher Department of Biological and Environmental Science PO Box 35, FI-40014 University of Jyväskylä Finland

http://users.jyu.fi/~savarga/ http://-

jyu.academia.edu/SandraVarga Sandra Varga <sandra.varga@jyu.fi>

Lund Sweden EvolutionInsectFlight Aug29-30 Deadline

Symposium âInsect Flightâ, 29-30th August 2011 in Lund, Sweden

Deadline approaching! Please register by July 15th

Animal flight has evolved only four times in history, in pterosaurs, birds, bats and insects. To date, insects constitute a majority of the worldâs life forms, and flight appears to have contributed to this inordinate evolutionary success story.

Because flight links a series of fundamental processes within both the physical and biological sciences we aim to provide a plenum for scientists from various fields (evolutionary ecology, morphology, physiology, behaviour, biomechanics) to present insight into the different aspects and implications of insect flight and to combine aspects from biology and engineering to an integrated view on insect flight.

Information about CAnMove and the preliminary programme can be found at our homepage: http://canmove.lu.se/node/715 Registration: Attendance of the symposium is free, if you want to attend, please register by filling in our online-registration form. The deadline for applications is July 15th

We especially encourage Ph.D. students to present and discuss their work here. Should you have any questions regarding the symposium please do not hesitate to contact Sophia Engel (sophia.engel@biol.lu.se).

Local organisers: Sophia Engel, Erik Svensson and Anders Hedenström

CAnMove Centre for Animal Movement Research Lund University, Sweden

Sophia Engel <Sophia.Engel@biol.lu.se>

Mexico Biodiversity Jul23-26

The annual symposium of the American Genetic Association, publisher of Journal of Heredity, will be held from July 23-26 in Irapuato and Guanajuato, Mexico. The theme for 2011 is “Genomics and Biodiversity” and we have a star-studded speaker list. The venue is world class - come see for yourself the stunning new National Laboratory of Genomics and Biodiversity (http://www.langebio.cinvestav.mx/) in Irapuato and the World Heritage Town of Guanajuato. Registration continues but the deadline for presenting a poster is fast approaching and rooms in the most convenient hotel are going fast. Go to:

http://www.theaga.org/2011/ Registration is $150 (USD) for faculty and postdocs and $75 for graduate students. Small travel grants will be available to student registrants through the web site. Regular attendees are encouraged to present posters and the web site allows submission of abstracts for the conference book. This meeting promises to be a landmark gathering of researchers using next-gen and other approaches to study the evolution of life, from bacteria to humans. We hope to see you there!

For more information, please email Scott Edwards, AGA President, at sedwards@fas.harvard.edu or Anjanette Baker, at AGAJOH@oregonstate.edu

sedwards@fas.harvard.edu

Norman Evolution2011 Jun17-21 EvolutionaryMedicine

SSE and NESCent are pleased to sponsor two opportunities to learn more about evolutionary medicine at Evolution 2011. On Sunday, June 19, a full day symposium will explore recent research in evolutionary medicine. Participants will have an opportunity to discuss this emerging field with the speakers during a sponsored lunch. More information is available under “SSE Symposia”: http://www.evolution2011.ou.edu/symposia.html On Saturday, June 18, a workshop will explore ways to teach with evolutionary medicine examples. Lunch will be provided for workshop participants. More information is available under “Outreach Workshop”: http://www.evolution2011.ou.edu/workshops.html Register for the symposium lunch and the workshop by June 10.

Sign up to join the symposium speakers for lunch here: http://tinyurl.com/3qgohsk Sign up to participate in the workshop here: http://tinyurl.com/6bpw565 Kristin Jenkins, PhD Education and Outreach Program

National Evolutionary Synthesis Center 2024 W. Main Street, Suite A200 Durham, NC www.nescent.org Cell 919.260.7369 Office 608.203.5390

Kristin Jenkins <kjenkins@nescent.org>

Norman iEvoBio Jun21-22 BirdsOfAFeather

In anticipation of the 2011 conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio), we solicit all attendees to propose and discuss Birds-of-a-Feather gatherings. See below for details.

Birds-of-a-Feather gatherings (BoFs) are informal, ad-hoc, focused face-to-face discussion groups that form around a shared interest. BoFs can also take the form of a hands-on software tutorial on using a tool, or on programming an API. BoFs have a leader (usually, but not necessarily, the proposer) who initiates or moderates the discussion. The topics of BoFs can range widely, including general cultural or computational infrastructure issues, or narrower questions such as how to make the best use of a particular software tool or how to solve a particular computational challenge.

Anyone willing to lead such a group can propose a BoF. iEvoBio will provide space that can accommodate up to 8-10 BoFs. Sign-up sheets will be provided on-site on the first day of the conference where attendees can propose a BoF or sign up for one proposed by someone else. BoFs will be about 1-1.5 hours in duration and take place in the afternoon of the second day of the conference.

In line with their informal nature, there is no official prior call for or submission of BoFs. However, we encourage those intending to propose one to sound out or rally potential attendees ahead of time. We suggest to employ Twitter (http://twitter.com) for this, using the #ievobioBof tag to mark BoF proposals and comments. Similarly, users interested in seeing a hands-on tutorial BoF about their favorite tool are encouraged to use similar means to give tool developers a sense of the community interest in a tutorial BoF, and what common usage (or programming) questions are.

Birds-of-a-Feather gatherings are only 1 of 5 kinds of contributed content that iEvoBio will feature. The other 4 are: 1) Full talks (closed), 2) Lightning talks, 3) Challenge entries, and 4) Software Bazaar entries. All Calls except for Full Talks remain open (see http://ievobio.org/ocs/index.php/ievobio/2011/) .

More details about the program and guidelines for contributing content are available at http://ievobio.org. You can also find continuous updates on the conference's Twitter feed at http://twitter.com/iEvoBio . iEvoBio is sponsored by the US National Evolutionary Synthesis Center (NESCent) in partnership with the Society for the Study of Evolution (SSE) and the Society of Systematic Biologists (SSB). Additional support has been provided by the Encyclopedia of Life (EOL).

The iEvoBio 2011 Organizing Committee: Rob Guralnick (University of Colorado at Boulder) (Co-chair) Cynthia Parr (Encyclopedia of Life) (Co-chair) Dawn Field (UK National Environmental Research Center) Mark Holder (University of Kansas) Hilmar Lapp (NESCent) Rod Page (University of Glasgow)

hlapp@nescent.org

Norman iEvoBio Jun21-22 DeadlineExtended

The deadline for submitting entries to the Challenge held by conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio) has been extended by one week to June 20, 2011.

The iEvoBio Challenge is a competition to create a new software tool, or add a new feature or features to an existing platform. Entries to the Challenge need to respond to its theme, which for 2011 is "Data Integration".

Further information on the nature of challenge entries and how to submit them can be found on the iEvoBio website at http://ievobio.org/challenge.html . Selected candidates will make short oral presentations to demonstrate their work in a "Challenge session" at the conference, and if suitable will automatically be entered into the Software Bazaar track of the conference. The winning entries will be selected by a vote of the iEvoBio meeting participants, and will be awarded cash prizes.

Challenge entries are only 1 of 5 kinds of contributed content that iEvoBio will feature. The other 4 are: 1) Full talks (closed), 2) Lightning talks, 3) Software Bazaar entries, and 4) Birds-of-a-Feather gatherings. All tracks except Full Talks remain open(see http://ievobio.org/ocs/index.php/ievobio/2011/) .

More details about the program and guidelines for contributing content are available at http://ievobio.org. You can also find continuous updates on the conference's Twitter feed at http://twitter.com/ iEvoBio , or subscribe to the low-traffic iEvoBio announcements mailing list at http://groups.google.com/group/-ievobio-announce iEvoBio is sponsored by the US National Evolutionary Synthesis Center (NESCent) in partnership with the Society for the Study of Ecolution (SSE) and the Society of Systematic Biologists (SSB). Additional support has been provided by the Encyclopedia of Life (EOL).

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hlapp@nescent.org

Townsville QLD AustralasianEvolutionSociety Sep24-27

The Australian Section of the IUSSI will hold a joint meeting with the Australasian Evolution Society in Townsville, QLD in September 2011. At this time of year the weather can only be described as perfect.

The Conference will be held at the Rydges Convention Centre in Townsville, situated within the heart of the restaurant and hotel region of the town and only a short walk to the beach and ferry to Magnetic Island. Pre-conference drinks and registration start on the evening of Saturday September 24, with presentations on Sunday Sept 25, Monday Sept 26 and Tuesday Sept 27.

Conference dinner to be held on the Monday evening. Registration details to follow.

Please attend our meeting, and advertise this conference as widely is possible. Our website is:

http://aes.eriophora.com.au/events/evolution11/ Thanks,

Mathew Vickers.

Mathew.Vickers@csiro.au

UCaliforniaDavis OakGenomicsJun24

Symposium and Round Table Discussion

Title: Using Genomic Tools to Manage Healthy North American Oak Populations

Date: Friday, 24 June 2011, Davis, CA 1-5 PM Venue: UC Davus: Alpha Gamma Rho Room, Buehler Alumni and Visitor Center

in collaboration with: the Conifer Translational Genomics Network and the International Symposium on Genomics-Based Breeding in Forest Trees (June 22-24, UC Davis)

Organizers: Jessica Wright and Victoria Sork on behalf of the the North American Oak Genomics Working Group*

Symposium Presenters:

Sally Aitken, University of British Columbia. Using genomics to understand forest responses to climate change.

Richard Dodd, University of California, Berkeley. Potential use of genomic tools for hybridization studies of oaks

Susan Frankel, USDA- Forest Service, Pacific Southwest Research Station. Overview of current threats to Oaks in the West

Victoria Sork, University of California, Los Angeles. Genomics as a conservation tool for oak management

Jessica Wright, USDA-Forest Service, Pacific Southwest Research Station. Using transcriptomics to study oak pathogens

Round Table Discussants:

Susan Frankel- USDA- Forest Service, Pacific Southwest Research Station Sudden Oak Death Program

Brendan ONeil- California State Parks, District Environmental Scientist

Rick Sandiford- UC Berkeley Extension, Forest Management Specialist

Ray Sauvajot- National Park Service, Chief, Natural Resources Program

No registration fee. No-host dinner, Friday evening

RSVP by June 10 2011. jessicawwright@fs.fed.us (phone: 530-759-1742)

*Please email vlsork@ucla.edu if you want to join the North American Oak Genomic Working Group.

"Sork, Victoria" <vlsork@ucla.edu>

UGroningen MathModelsEcolEvol Aug17-19 2

Mathematical Models in Ecology and Evolution 2011

After two successful meetings in Britain (Sussex 2007 and Bristol 2009), the third biannual MMEE conference is going to make the jump to the continent, and will be organised by the University of Groningen in the Netherlands, from 17 to 19 August, 2011. Following the tradition of the previous meetings, we aim to show the latest developments of mathematical modelling in evolution and ecology by presenting a programme including keynote talks and thematic sessions. The invited speakers include:

Public lecture: . Simon Levin (Princeton University) : Evolutionary perspectives on public goods and collective behavior

Keynote lectures: . Paulien Hogeweg (Utrecht University) : Evolution of evolvability - Structuring of genomes, network and ecosystems . Chris Klausmeier (Michigan State University) : Theoretical approaches to plankton ecology . Hans Metz (University of Leiden) : The geometry of meso-evolution . Sally Otto (University of British Columbia) : Inferring the past for traits that alter speciation and extinction . Corina Tarnita (Harvard University) : Limitations of inclusive fitness theory . Andreas Wagner (University of Zurich) : The origins of evolutionary innovations

More information, the latest updates and the registration form are to be found on our website: www.mmee2011.evobio.eu .NOTE: The extended deadline for registration is June 10, 2011.

We hope to see you in Groningen this summer! Joke Bakker, Rampal Etienne, Bob Planque, Franjo Weissing

Organising Committee Mathematical Models in Ecology and Evolution 17 -19 August 2011 University of Groningen, the Netherlands mmee2011@rug.nl www.mmee2011.evobio.eu joke.bakker@rug.nl

UMunich MetazoanPhylogeny Oct11-14 Registration2

Dear colleagues,

this is just a friendly reminder that *registration and abstract submission* for the âDeep Metazoan Phylogeny 2011 â new data, new challenges“ conference, to be held from October 11-14, 2011 at the University of Munich (Germany) *closes on July 1, 2011, midnight CEST (UTC + 2)!* (about 14 days from now!)

Full list of confirmed keynote speakers can be found at < www.palmuc.de/dmp2011 >, and you can register and submit your abstract directly here: < https://www.conftool.com/dmp2011/ >!

We look forward to welcoming you in Munich in October!

for the organizing team

Gert Wörheide

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UOxford Biogeography Sep23-25

CONFERENCE: Early Career Conference "Advances in Biogeography" & symposium on "Biodiversity conservation beyond protected areas" http://www.biogeography.org/html/Meetings/2011Oxford/index.html The International Biogeography Society is pleased to announce its upcoming Early Career Conference "Advances in Biogeography", 23-25 September

2011, at the University of Oxford, UK. A special opportunity exists for attendees to also join Oxford University's Biodiversity Institute Symposium on "Biodiversity conservation beyond protected areas" (21st - 22nd September) which immediately precedes the IBS Early Career Conference.

The Early Career Conference will focus on postgraduate students and those who have recently completed their doctorates (up to five years) interested in biogeography. The aim is to provide a forum in which early career biogeographers have an opportunity to present and discuss their work through formal presentations (oral and posters), and to encourage the formation of informal peer-to-peer networks. Evening mixer events will be attended by IBS board members and other senior biogeographers.

Registration is now OPEN for the meeting, For more information about the conference & symposium, and to register, please visit http://www.biogeography.org/html/Meetings/2011Oxford/index.html If you have any questions, please write to the organizing committee at ibsearlycareerconference@gmail.com

SCHEDULE (September 2011): Friday 23rd September - evening mixer Saturday 24th & Sunday 25th - contributed oral presentations and posters, keynote addresses, and evening mixers

Keynote addresses: Lawrence Heaney - Oceanic Island Biogeography: Emerging Perspectives and Questions Catherine Graham - Untangling the Mechanisms Influencing Hummingbird Assemblages: New Tools to Answer Old Questions Ken Feeley - Advances in predicting the impacts of climate change on tropical forests Michael Dawson - Advances in Marine Biogeography

Free workshop: "Communicating Biogeography: Science writing, practical and ethical issues of collaborative working, and the peer review process" led by Robert J. Whittaker, Editor-in-Chief for the Journal of Biogeography

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.

mdawson@ucmerced.edu

Michael N Dawson <dawson.mn@gmail.com>

UStAndrews Phylogeny June16

Dear Evoldir,

Final reminder -

The first meeting of the Scottish Phylogeny Discussion Group will be at the University of St Andrews, UK, on 16th June 2011, 1 PM to 5:30 PM.

Professor Dannie Durand (Carnegie Mellon University) will talk on "Detecting incomplete lineage sorting and gene duplication in non-binary species trees".

Her talk will be followed by several presentations by researchers based more locally.

Attendance is free, but please register in advance. For registration and further details, please see:

http://biology.st-andrews.ac.uk/cegg/spdg Thank you,

Daniel

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

db60@st-andrews.ac.uk

UWashington ForensicGenetics Jul19-21

The final program for ICFIS 2011 is now posted at www.icfis2011.org For the past 20 years, population and evolutionary genetics have been playing a role in forensic science. Some of the recent applications include the FBI investigation of the 2001 Anthrax Mailings, the determination of geographic origin of seized elephant tusks, and discussions of the way to assess the strength of matching Y-STR profiles that have not previously been seen. In July of this year, these and related topics will be discussed by population geneticists, statisticians and forensic scientists at the 8th International Conference on Forensic Inference and Statistics. The conference will be held at the University of Washington, July 19-21.

You are invited to attend to learn about this interesting field, or to present any work you have done in the field. Abstracts for contributed posters are still being accepted.

Bruce Weir

Bruce Weir <bsweir@u.washington.edu>

WestVirginia MalariaEvolution Aug5-7

International Meeting on Malaria and Related Haemosporidian Parasites of Wildlife

Friday August 5th V Sunday August 7th, 2011

National Conservation Training Center, Shepherdstown, West Virginia

Sponsored by the NSF Research Coordination Network for Haemosporida of Terrestrial Vertebrates*

DEADLINE for registration, accommodation onsite, and abstracts is 30 JUNE 2011.

Organized by: Robert Fleischer and Ellen Martinsen, Smithsonian Institution Ravinder Sehgal, San Francisco State University

Dear Colleagues,

The NSF-sponsored Research Coordination Network for Haemosporida of Terrestrial Vertebrates invites you to participate in a three-day meeting on Malaria and Related Haemosporidian Parasites of Wildlife (http://malariarcn.org/conference). The meeting includes a Plenary address by Dr. Andrew Read, and invited Keynote talks by Drs. Jane Carlton, Sarah Knowles, Robert Ricklefs, and Gediminas Valkiunas. There will also be general paper and poster sessions, plus a taxonomy training session and roundtable discussions.

Topics for the meeting center around the Haemosporida of wildlife and include: haemosporidian systematics and genomics, species limits and definitions, generalist versus specialist parasites, evolution of virulence, geographic distribution of vectors and hosts, host shifts and emerging infectious diseases, parasite ecology, and vector-parasite relationships.

The meeting will commence on Friday morning, August 5th, with an optional half-day training session on haemosporidian classical taxonomy. Keynote talks and general paper and poster sessions will follow on Friday afternoon, Saturday, and Sunday morning. The meeting will end on Sunday afternoon, August 7th, with optional roundtable discussions on Limits in the Haemosporidians and Parasite Databases.

All food, lodging and meeting events will take place at the US Fish & Wildlife Services National Conservation Training Center in Shepherdstown, West Virginia, a site easily accessible through Washington, DC, area airports (closest is Dulles). Some support for accommodation is potentially available for students, postdocs, and others in need - see registration form for details, but please get registration forms and abstracts in asap if this support is requested.

Details, including conference logistics, an overview of events, the program of invited speakers, and the call for abstracts are available at http://malariarcn.org/conference. Further information can also be obtained from the meeting organizers (email: MalariaRCNMeeting@gmail.com).

*The Research Coordination Network for Haemosporida of Terrestrial Vertebrates (RCN), sponsored by the U. S. National Science Foundation and funded through 2015 at the University of Missouri-St. Louis, was established to promote communication among researchers working on the ecology and evolution of haemosporidian parasites of vertebrate wildlife populations (website: www.malariarcn.org).

“Fleischer, Robert” <FleischerR@si.edu>

GradStudentPositions

ArizonaStateU InsectSystematics

Starting the Fall semester of 2011, teaching and research assistantships will be available at the School of Life Sciences, Arizona State University (http://sols.asu.edu/), for graduate students (M.Sc. or Ph.D.) who are interested in insect systematics. A desire to work with weevils would be great but other taxon interests will receive full consideration. ASU-SoLS offers a wide range of learning and research opportunities (e.g. http://sols.asu.edu/grad/index.php; http://species.asu.edu/; http://sustainability.asu.edu/index.php), and is close to fascinating insect habitats. Interested candidates should contact me via e-mail with a statement of interest and CV.

Nico M. Franz, Ph.D. School of Life Sciences (starting Fall '11) PO Box 874501 Arizona State University Tempe, AZ 85287-4501

E-mail: nico.franz@yahoo.com http://academic.uprm.edu/~franz/ nico.franz@upr.edu

CarletonU SexualSelection

I am looking for two or three new PhD students join my lab either in September 2011 or January 2012. I want strong students who are interested in sexual selection, the evolution of acoustic mate attraction signaling, the evolution of mate choice, quantitative genetics of sexually selected traits, or quantifying mating preference functions within and across species. My laboratory works with field crickets as model organisms. Details of some of the ongoing research in my lab can be found at www.carleton.ca/~sbertram. Please contact me directly prior to applying to Carleton's PhD program. Please include a CV, a short discussion about why you are interested in joining my laboratory, transcripts (can be unofficial) and contact information for at least two people who would be willing to provide a letter of recommendation. At this time I am limited to hiring Canadian citizens or permanent residents (landed immigrants). Further, students need to be ready to enter a PhD program; due to an upcoming sabbatical I will not be able to hire MSc students until September 2013.

Regards, Sue Bertram, PhD Associate Professor of Biology Carleton University Ottawa, Ontario, Canada K1S 5B6 Sue_Bertram@carleton.ca

Sue_Bertram <Sue_Bertram@carleton.ca>

Ecuador Biodiversity

As the previous editions, the Master's Degree Program "Biodiversity in Tropical Areas and its conservation" is a one-year MSc program (75 ECTS) offered jointly by the International University Menendez Pelayo (UIMP, Ministry of Education, Spain) and the Spanish National Research Council (CSIC, Ministry of Science, Spain). The program is fully funded by the CSIC, with a strong emphasis on fellowships for Latinamerican students; the title is an official European MSc degree conceded by the UIMP. The program will be taught in Ecuador, with an emphasis on practical studies in natural reserves. The program is international, with a minimum of 15 and a maximum of 30 students.

ROUTE TO PhD DEGREE.- Qualified graduates from the MBATC program have the possibility to continue their PhD studies in CSIC Departments (Real Jardin Botanico, Museo Nacional de Ciencias Naturales, etc.) through separate application calls opened each year. They can also apply to other programs in the Spanish science system, or to any European or American university, as this MSc title is an official European degree.

WHAT DO I NEED TO APPLY TO THE PROGRAM?.- You are eligible to apply to the program if you hold a Bachelor's degree in any suitable field, especially on biosciences: biology, forestry, or agriculture, but also in geography or economics for example.

You must be proficient in Spanish language.

FINANCIAL SUPPORT.- The CSIC offers 5 scholarships covering registration fees (1300 euros/student). Independently, the program funds at least 13 additional full scholarships for Latin American applicants.

HOW TO APPLY?.- The application period for studies starting in October 2011 is now open until 9-July-2011. You can find all the information and detailed instructions on how to apply at

http://www.masterenbiodiversidad.org/ Jesús Muñoz e-mail: jmunoz@rjb.csic.es Real Jardín Botánico (CSIC) Plaza de Murillo 2 tlf. +34 91 420 3017 E-28014 Madrid fax. +34 91 420 0157 ESPAÑA (Spain)

http://www.masterenbiodiversidad.org http://-/www.rjb.csic.es/jardinbotanico/jardin/-contenido.php?Pag=413&tipo=cien tifico&codf

KRAKEN research group (environmental modelling, data processing & analysis):

http://www.unex.es/investigacion/grupos/kraken SYNTHESYS: EU funds short visits to our institution:

http://www.synthesys.info/index.htm Jesús Muñoz <jmunoz@rjb.csic.es>

EMBL Cambridge MolecularPhylogenetics

PHD FELLOWSHIP IN MOLECULAR PHYLOGENETICS

Description: A PhD fellowship is available in Nick Goldman's research group (http://www.ebi.ac.uk/-goldman) at the EMBL-European Bioinformatics Institute. The fellowship is within the European Molecular Biology Laboratory's International PhD Programme (http://www.ebi.ac.uk/training/-Studentships/phd.html; http://www.embl.org/-training/phdprogramme/index.html) and the successful applicant will be registered at the University of Cambridge.

PhD projects can be in any area of the Group's interests, which concentrate on methods of data analysis that use evolutionary information in sequence data and phylogenies to infer the history of living organisms, to describe and understand processes of evolution, and to use this information to make predictions about the function of genomic sequence. We are particularly interested in exploiting next-generation sequencing data and have also worked on applied evolutionary studies and algorithms in sequence analysis and conservation biology. We also hope to initiate a project on large-scale phylogenies (the “Million Protein, Thousand Species Tree of Life”).

PhD candidates will typically have degree-level backgrounds in one or more of mathematics, statistics, computer science, molecular biology or similar areas. Lack of experience in some of these areas is not considered a problem, so long as candidates demonstrate aptitude and enthusiasm to learn.

Further details on application procedures etc. are available at http://www.ebi.ac.uk/training/Studentships/-phd/howtoapply.html. Please note that candidates must register with the online application system by 30 June 2011 and must complete their applications by 11 July 2011. The PhD fellowship may start in October 2011, or as soon afterwards as the successful candidate is available.

Nick Goldman tel: +44-(0)1223-492530 EMBL - European Bioinformatics Institute fax: +44-(0)1223-494468 Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK

goldman@ebi.ac.uk

ETH Zurich Bioinformatics

Ph.D. studentship is available at the Computational Biochemistry Research Group (CBRG) of Prof Gaston Gonnet, department of Computer Science at the Swiss Federal Institute of Technology (ETH Zurich), highly reputable internationally. CBRG is a member of the Swiss Bioinformatics Institute (SIB) and benefits from SIB training courses and networking.

The research will focus of developing probabilistic codon models for phylogeny inference and studies of selective pressure. Successful candidates will have a strong background in bioinformatics, computer science, statistics, and/or computational biology. Fluency in a major scripting language, and experience in software development is a must. Some background in biology is desirable, but interest in biology and bioinformatics is required.

Candidates should be highly motivated and have the ability to work independently. As the research will involve a mix of disciplines, candidates with experience in several fields will be preferred (bioinformatics, genetics, protein structure, computational science, mathematics, physics, statistics).

ETH Zurich boasts excellent facilities for studying and recreation. The working language in the laboratory is English, which is also widely used in Switzerland.

Zurich is located less than one hour from the Alps, and is a small but vibrant city offering one of the best living standards in teh world. Zurich is well connected to major European cities and has a large international community.

To apply, please send a single PDF file to maria.anisimova@inf.ethz.ch containing: - CV (with publication list if applicable) - scanned academic transcripts (list of grades in university courses) - a short statement of research interests, mentioning research topics of master/diploma theses (not exceeding two pages) - three references When applying, please mention “PhD position” in the subject of your email. The position is open until filled (quick response is recommended).

Maria Anisimova maria.anisimova@inf.ethz.ch Senior research fellow Department of Computer Science, CAB H82.2 Swiss Federal Institute of Technology (ETH Zurich) Tel: +41 44 632 6076 http://www.inf.ethz.ch/-personal/anmaria maria.anisimova@inf.ethz.ch

MaxPlanckInst AvianEvolution

Master/Diploma student position at the Max Planck Institute for Ornithology

We are looking for a highly motivated student who would like to do his Master/Diploma thesis in the Behavioural Ecology department at the Max Planck Institute for Ornithology. The student will be part of the Great tit personality group of Dr. Niels Dingemanse (more info see: http://www.orn.mpg.de/ mitarbeiter/dingemanse.html). The project may focus on investigating the link between personality and chick provisioning behaviour in great tits. Data collection will mainly consist of analyzing provisioning videos that will be collected in May-June 2011. In addition, prospective students are asked to participate in winter fieldwork and acquire experience in handling birds and screening great tits for personality. The project may start from August 2011 onwards and should last for at least 6 months.

For further information and applications please contact Ariane Mutzel: mutzel@orn.mpg.de (PhD student)

– Ariane Mutzel

Max Planck Institute for Ornithology Behavioural Ecology& Evolutionary Genetics Eberhard-Gwinner-Str. 5 82319 Seewiesen Germany

email mutzel@orn.mpg.de phone +49 (0)8157 932 324 fax +49 (0)8157 932 400

Ariane Mutzel <mutzel@orn.mpg.de>

McGillU 2 ChipmunkEvolution

We are seeking two highly motivated PhD students to join our multidisciplinary research team working on different aspects of eastern chipmunks (Tamias striatus) evolutionary ecology in Southern Quebec, Canada.

The candidates will work with researchers from McGill University (Murray Humphries), Univ. of Sherbrooke (Dany Garant and Fanie Pelletier) and UQAM (Denis Réale) on a research project investigating the factors maintaining phenotypic and genetic variation in the wild. More specifically, depending on the interests of the candidates, different projects are available integrating aspects of behaviour, ecophysiology, genetics and population dynamics of chipmunks.

The fieldwork will take place 3-4 months each summer in southern Quebec. Ideally, the candidate will have previous research and fieldwork skills (MSc in biology or equivalent), and experience in handling of small mammals would also be an advantage.

The positions are open and funded for three years as soon as September 2011. Please apply by sending your CV, including the email addresses of two referees, and a letter of motivation by 15 August 2011 to manuelle.landry-cuerrier@mcgill.ca. Candidates that are eligible to apply for scholarships from NSERC (Canada), FQRNT (Quebec) or international sources will be given priority.

Dany Garant Associate Professor Department of Biology University of Sherbrooke Sherbrooke QC J1K 2R1 Canada

Tel: (819) 821-8000 ext.63198 Fax: (819) 821-8049 Courriel: Dany.Garant@USherbrooke.ca

http://pages.usherbrooke.ca/dgarant/
dany.garant@usherbrooke.ca

McMasterU P450 Evolution

Graduate and Post-doctoral Opportunities in P450 Function and Evolution

MSc (2 year), PhD (4 year) and post-doctoral positions are available in the laboratory of Dr. Joanna Wilson at McMaster University, Hamilton, Canada. We are looking for students interested in the function and evolution of the cytochrome P450 (CYP) 1 and 3 families in fish, with development of a label free assay for CYP activity. Our lab studies the evolution and function of CYPs in fish, environmental physiology, and aquatic toxicology. Lab members have diverse backgrounds and interests including environmental sciences, toxicology, biochemistry, chemistry, molecular biology, physiology, and molecular evolution. We study several species of fish and extensively use zebrafish as a model organism. A description of the laboratorys research can be found at http://www.biology.mcmaster.ca/-faculty/jwilson/jwilson.htm Cytochrome P450 (CYP) enzymes are critical component of the chemical defensome and are highly expressed in liver. We have heterologously expressed CYP1A, CYP1B1, CYP1C1, CYP1C2, CYP1D1 and CYP3A65 from zebrafish and begun to characterize their function (Scornaienchi et al 2010 Arch Biochem Biophys and Scornaienchi et al 2010 J Endocrinol). The expressed proteins will be examined in a high throughput screening laboratory to identify possible substrates in a small molecule library. Functional characterization of the CYP1 or CYP3 families will lead to an understanding of structure-activity relationships for these enzymes as well as evolution of function within protein families. This research intersects protein family evolution, molecular biology, biochemistry and toxicology.

The successful candidate(s) will have a strong background in at least one of the key areas (evolution, molecular biology, biochemistry and toxicology) and a strong interest in interdisciplinary research. The successful candidate should have strong research skills, experience in a molecular biology laboratory, be highly motivated, and can work independently.

To be considered, please send a Curriculum Vitae in PDF format, including publication list, a statement of research interest, transcripts, and a list of three academic referees. The positions are available for a Fall 2011 or January 2012 start date. Information on graduate studies in and application procedures for the Department of Biology at McMaster University can be found online at www.biology.mcmaster.ca/-bio_grad.htm . Dr. Joanna Wilson Assistant Professor Department of Biology McMaster University

1280 Main Street West Hamilton ON L8S 4K1

Tel: 905-525-9140 ext 20075 Fax: 905-522-6066 joanna.wilson@mcmaster.ca

Joanna Wilson <joanna.wilson@mcmaster.ca>

Munchen LMU Zurich EAWAG 2 HostParasiteInteractions

Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is a Swiss-based internationally active research institute that is committed to the ecological, economical and social management of water. The Ludwig-Maximilians-University (LMU) in Munich is among the top one hundred universities in the world, and part of the German Excellence Initiative. These institutions share common goals towards education, research and technology transfer at the highest international level.

The Department of Aquatic Ecology (Eawag) and the Department of Biology (Evolutionary Ecology, LMU) seek

Two PhD students in Evolutionary Biology

Project title: Hostâparasite interactions in hybridizing

Daphnia, the role of variable environments

Both PhD students will participate in a collaborative research project with Dr. Justyna Wolinska (LMU) and PD Dr. Piet Spaak (Eawag) to study the role of variable environments on hostâparasite interactions in hybrid systems and on hybridization success per se, using Daphnia (waterfleas), which are a well-established model in both host-parasite and hybridization research. Specifically, we will study changes in parasite prevalence as well as changes in host and parasite population structure, by using collections of zooplankton samples dating back to the beginning of the last century. Then we will relate the observed patterns to experienced changes in environmental conditions (like water temperature or trophy level). Finally, by using the âresurrection ecologyâ approach (i.e. hatching Daphnia clones of known age from diapausing eggs preserved in lake sediments) we will test for adaptations of old and recent clones to certain environmental conditions.

Both students will use molecular techniques and conduct laboratory experiments. However, the position at LMU focuses on host-parasite interactions. The main methods will be qPCR, cloning, sequencing, microscopy and modeling. The position at Eawag focuses on interspecific hybridization. Here the main methods are: microsatellites, sequencing, experiments and field work.

Although the students will be primarily hosted at their given institution, the German student will spend a couple of weeks working in Switzerland and vice versa. Moreover, the external collaborators on this project are hosted in Konstanz (DE) and in Sheffield (UK), and students will have the opportunity to visit these external labs as well. The students will take part in the organized PhD programs (including attending various skills courses) of their respective organization.

For this project, financed by the Swiss and German Science Foundations (SNF & DFG), we are looking for highly motivated candidates with interests in the evolutionary ecology of host parasite interactions.

We offer a stimulating research environment in lively and social institutes in Dübendorf (near Zürich) and in Munich. At both localities, the departments host other research groups in ecology and evolution. The position will be for a period of three years, and should start as soon as possible (September 2011 or soon thereafter). The Eawag PhD student will be enrolled at the Swiss Federal Institute of Technology (ETH) in Zürich the German PhD student at LMU. The ideal candidate should have good molecular skills and/or a strong background in evolutionary biology or population genetics. Excellent communicational and writing skills in English, good work ethics, and creative thinking are desired. A Diploma or Masters degree (or equivalent) in biology or related subject is necessary for admission. The working language in the groups is English.

Applications should include 1) a letter of interest with a description of pertinent experience (it should be specified which position, LMU or Eawag, would be the first choice, 2) curriculum vitae, 3) abstract of the master/diploma thesis, 4) a list of publications (if any), 5) the names (with e-mail addresses) of three potential referees, and copies of certificates of academic qualifications.

Applications can only be submitted online through the Eawag website, using the following link http://-internet1.refline.ch/673277/0058/++publications++/-1/index.html which can be found on the Eawag home page: http://www.eawag.ch/jobs/index_EN Please submit your application by 5 August 2011. For further information, consult

Justyna Wolinska: wolinska@bio.lmu.de http:/-/www.uni-muenchen.de/index.html; http://-sci.bio.lmu.de/ecology/evol_e/people_wolinska_e.html or Piet Spaak: spaak@eawag.ch www.eawag.ch; http://www.eawag.ch/forschung/eco/index_EN Spaak Piet <Piet.Spaak@eawag.ch>

NatlU Ireland ArthropodGenomics

A Four Years Science Foundation Ireland funded PhD position will be available to work on arthropod phylogenomics and arthropod genome evolution at the Bioinformatics and Molecular Evolution Unit (http:/-/bioinf.may.ie/), The National University of Ireland Maynooth starting October/November 2011.

The project you will be working on involves the generation of transcriptome-wide EST data sets, and microRNA data sets using Next Generation Sequencing and using these data to address important, unresolved questions in arthropod evolution.

This is multidisciplinary research project. Bioinformatics knowledge (including programming in PERL or PYTHON) and strong interests in phylogenetics and animal evolution are essential. In addition you will have to learn Paleontology and a range of basic techniques in Molecular Biology.

Willingness to travel and spend time abroad is essential as several international collaborators are involved in the project. In particular the student is expected to spend few months in the laboratory of Prof. Kevin Peterson (Dartmouth College - US) to carry out microRNA work.

Please send a cv and have one or preferably two letters of reference sent to the following address: davide.pisani@nuim.ie

**** Dr. Davide Pisani The National University of Ireland Maynooth, Co. Kildare, Ireland. Email: Davide.Pisani@nuim.ie Tel: 00353-1-7086368 Fax: 00353-1-7083845 http://bioinf.may.ie/index.html Davide.Pisani@nuim.ie

UAmsterdam MycologyEvolutionCooperation

PhD position: Mutualisms in a changing world

Vacancy number: 1.2011.00124

A PhD position is available at the Department of Ecological Science, Faculty of Earth and Life Sciences, Vrije Universiteit Amsterdam.

Mutualisms - cooperative interactions between species - are central to the survival and reproduction of most organisms on earth. Despite their ubiquity, explaining the evolutionary persistence of mutualisms remains one of the greatest challenges for evolutionary biology. This PhD position will utilize the arbuscular mycorrhizal mutualism to ask how ecological context modifies the evolutionary trajectory of plant and fungal partners.

Tasks Daily tasks will involve work in greenhouses, laboratories and with fungal culturing. Student must have an excellent knowledge of spoken/written English. No prior knowledge of Dutch is required. The project will be completed with papers in scientific journals and a PhD Thesis. Our group is a multidisciplinary, international team of ecologists, evolutionary biologists and plant physiologists. The student will be primarily housed in the Institute of Ecological Science, Vrije Universiteit. Funding will be provided for the student to travel to labs of other team members (France, Switzerland, USA, etc) to learn new techniques.

Requirements Candidates should have a Master's in biology, ecology & evolution, microbiology, or related fields. Experience in molecular biology, evolutionary game theory, isotope labeling, rhizosphere studies and/or plant physiology is a plus.

Further particulars The appointment will be initially for 1 year. After satisfactory evaluation of the initial appointment, it can be extended for a total duration of 4 years. You can find information about our excellent fringe benefits of employment at www.workingatvu.nl Salary The salary will be in accordance with university regulations for academic personnel, and amounts euro 2.042,- gross per month in the first year up to euro 2.612,- in the fourth year (salary scale 8.5) based on a full-time employment.

Information For additional information please contact: prof. dr. Toby Kiers Phone number +31 (0)20 5987085

E-mail: toby.kiers@falw.vu.nl

Application Applicants are requested to write a letter in which they describe their abilities and motivation, accompanied by a curriculum vitae and one or two references.

It is possible to apply by e-mail. Send applications to: falw-vacatures@falw.vu.nl

Please cc: toby.kiers@vu.nl

Please mention the vacancy number in the e-mail header

toby.kiers@vu.nl

UBern PopulationGenomics AdaptiveRadiation

Two PhD positions: UBern Population Genomics of Adaptive Radiation

Two PhD positions are available at the University of Bern in the project "Population genomics of adaptive radiation". This project, funded by the Swiss National Science Foundation, will investigate the genomic basis of population divergence during adaptive radiation at different timescales in the progression from invasion to speciation using two of the best vertebrate models available today to study this question: East African cichlids and threespined stickleback.

We will apply high-throughput next-generation sequencing techniques using the Illumina HiSeq platform. We will address questions related to the population genomic signatures of divergent selection and reproductive isolation, and the genomic architecture of divergent adaptation and speciation at different stages along the micro- to macroevolution continuum in adaptive radiation.

We are looking for candidates strongly motivated to address cutting-edge questions in evolutionary biology, who will analyse NGS data and apply bioinformatics in an evolutionary genetics context. Candidates should possess an aptitude to work with very large data sets, strong desire to develop new analytical methods, and ability to work in team. The ideal candidates will have a strong grounding in evolutionary biology with experience in programming and genetic data processing, or in bioinformatics or computer science.

Both students will be co-advised by Prof. Ole Seehausen, Dr. Arjun Sivasundar (University of Bern and EAWAG, the Swiss Federal Institute for Aquatic Research) and Prof. Laurent Excoffier (University of Bern). The students will also be part of the new doctoral program in Population Genomics (http://www.unil.ch/pg/page75326.html) and benefit from its activities.

Both positions will be available starting immediately. Applications will be considered until the positions are filled.

Salary will be according to SNSF guidelines.

Please send an application letter, CV and contact information of two references to:

Susanne Maurer (Susanne.maurer@iee.unibe.ch)

For inquiries please write to Ole Seehausen (ole.seehausen@eawag.ch)

UBremen InsectEvolution

University of Bremen, Population Ecology and Evolutionary Ecology Group

PhD position in Insect Ecology

We are looking for a highly motivated PhD candidate to study interactions between parasitoid wasps (Fopius arisanus) and arboreal weaver ants (Oecophylla longinoda) as well as ants and Mango fruit flies within a biological control project against an invasive Mango fruit fly (Bactrocera invadens) in Eastern Africa. The project aims at clarifying the efficiency of weaver ants in disturbing oviposition in native and introduced Mango fruit flies, and to study possible effects of weaver ants on foraging of native and introduced parasitoids. The studies will be conducted at the International Centre of Insect Physiology and Ecology (icipe) in Nairobi, one of the leading research institutions for insect ecology in Sub-Saharan Africa. Time at the University of Bremen will be allotted for data analysis, paper preparation, and soft-skill courses.

The position will start on September 1, 2011 and will be paid for 3 years on a stipend basis (1024.- EUR), funded by the German Federal Ministry for Economic Cooperation and Development. The successful candidate is expected to hold a Diploma or Master degree in Biology or related field and should be highly interested in entomology and behavioural ecology. Experience with quantitative behavioural observation and statistical analysis of data would be appreciated.

Please send your electronic application in a single pdf-file until *July 1, 2011* to Prof. Dr. Thomas S. Hoffmeister, Population Ecology and Evolutionary Ecology Group, Institute of Ecology, Department of Biology /Chemistry, University of Bremen, Leobener Str. NW2, 28359 Bremen. Your application letter should be accompanied by your CV, and the names, email addresses and telephone numbers of two referees.

June 15, 2011, Thomas S. Hoffmeister

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Thomas S. Hoffmeister, Prof. Dr. Population& Evolutionary Ecology Group FB2 Biology/Chemistry, University of Bremen fon +49.421.218.62930 fax +49.421.218.62949 hoffmeister@uni-bremen.de www.popecol.uni-bremen.de Thomas Hoffmeister <tsh@uni-bremen.de>

UCapeTown AvianSexualSelection

Could you please post the advert below. Many thanks

*MSc research at the Percy FitzPatrick Institute of African Ornithology, Department of Zoology, University of Cape Town***

Project: Dominance, sexual selection and conflict resolution in a cooperative species, the sociable weaver

We invite applications for the above full-time study opportunity at the FitzPatrick Institute, a world-renowned, national Centre of Excellence (CoE) in ornithological research with a strong emphasis on postgraduate studies.

The MSc student will integrate an international group of researchers investigating cooperation in sociable weavers /Philetairus socius/ near Kimberley, South Africa.

Sociable weaver individuals cooperate to build a massive communal nest structure and to raise young. How is this cooperation achieved and how do individuals decide whether to cooperate or to defect? One explanation for cooperation is kin selection, but this unlikely explains the maintenance of 'public goods' that concern a whole group rather than just kin.

This study will investigate the role of dominance and sexual selection in cooperation and conflict resolution in the sociable weaver. We will examine two behaviours: cooperative nest building and cooperative breeding. The study will involve extensive behavioural observations to establish dominance hierarchies and whether there is social segregation or competition for access to specific communal tasks (such as helping at the nest or nest-building activities). In addition, we will investigate the role of melanin-based plumage signals in both males and females.

The successful applicant will have a BSc Honours or equivalent, relevant ornithological field experience and a demonstrated ability to work independently.The student should have a strong interest in pursuing theoretical questions in behavioural ecology and motivation for conducting demanding fieldwork. Experience in handling birds and behavioural observations are important advantages.

Funding is secured for an annual R75 000 CoE bursary for two years and for project running costs.

To apply, please send a CV (including your academic record & names and contact details of three referees) and a short motivation for why you wish to undertake this research to Hilary Buchanan at hilary.buchanan@uct.ac.za. For more information on the FitzPatrick Institute visit www.fitzpatrick.uct.ac.za For more information on the project, please contact: Dr Rita Covas (rita.covas@mail.icav.up.pt) or Dr René van Dijk (R.van.Dijk@sheffield.ac.u)

/Closing date: 1 July 2011/

UCT is committed to the pursuit of excellence, diversity and redress. Students granted an award to study at UCT are required to comply with the UCT official and approved policies on postgraduate funding.

Rita Covas <rita.covas@gmail.com>

UCapeTown WeaverSexualSelection

*Study opportunity: PhD research at the Percy FitzPatrick Institute of African Ornithology, Department of Zoology, University of Cape Town***

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Project: Dominance, sexual selection and conflict resolution in a cooperative species, the sociable weaver

We invite applications for the above full-time study opportunity at the FitzPatrick Institute, a world-renowned, national Centre of Excellence (CoE) in ornithological research with a strong emphasis on postgraduate studies.

* *

The student will integrate an international group of researchers investigating cooperation in sociable weavers /Philetairus socius/ near Kimberley, South Africa. This position was previously advertised as an MSc position, but the research can be conducted towards a PhD.

Sociable weaver individuals cooperate to build a massive communal nest structure and to raise young. How is this cooperation achieved and how do individuals decide whether to cooperate or to defect? One explanation for cooperation is kin selection, but this unlikely explains the maintenance of 'public goods' that concern a whole group rather than just kin.

This study will investigate the role of dominance and sexual selection in cooperation and conflict resolution in the sociable weaver. We will examine two behaviours: cooperative nest building and cooperative breeding. The study will involve extensive behavioural observations to establish dominance hierarchies and whether there is social segregation or competition for access to specific communal tasks (such as helping at the nest or nest-building activities). In addition, we will investigate the role of melanin-based plumage signals in both males and females.

The successful applicant will have a BSc Honours or MSc, relevant ornithological field experience and a demonstrated ability to work independently.The student should have a strong interest in pursuing theoretical questions in behavioural ecology and motivation for conducting demanding fieldwork. Experience in handling birds and behavioural observations are important advantages.

Funding is secured for an annual R100 000 CoE bursary for 3-4 years and for project running costs.

To apply, please send a CV (including your academic record & names and contact details of three referees) and a short motivation for why you wish to undertake this research to Hilary Buchanan at hilary.buchanan@uct.ac.za. For more information on the FitzPatrick Institute visit www.fitzpatrick.uct.ac.za For more information on the project, please contact: Dr Rita Covas (rita.covas@mail.icav.up.pt) or Dr René van Dijk (R.van.Dijk@sheffield.ac.uk)

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Rita Covas <rita.covas@gmail.com>

UExeter ModellingEvolution

Fully funded PhD position: Modelling evolutionary and ecological processes in the marine microbial ecosystem

http://www.exeter.ac.uk/studying/funding/award/-?id=3D821 A PhD position is available with Dr Hywel Williams in Biosciences, College of Life and Environmental Sciences at the University of Exeter (Streatham Campus, Exeter) to commence October 2011. The studentship will cover UK/EU tuition fees for three years, plus an annual stipend of £13,590pa for three years.

Microbes (prokaryotes and single-celled eukaryotes) play a central role in the marine carbon cycle, which is of key importance for global climate change. New data from genomics are linking microbial genes to environmental functions, showing that microbial ecology and evolution are tightly linked to ecosystem processes. This understanding should enable better prediction of how marine ecosystems will respond to global change. However, new approaches to modelling marine ecosystems are needed to take advantage of these insights.

We have pioneered an agent-based approach that models the marine microbial food web as a complex adaptive system in which evolutionary, ecological and environmental processes can be studied simultaneously. This method is currently being used to understand selection pressures on microbial growth in different environmental conditions, the evolutionary formation of nutrient recycling loops, and how coevolutionary dynamics of bacteria and bacteriophage affect ecosystem dynamics.

The student will join our modelling team to further develop this approach. The choice of research topic will be developed in discussion between the supervisor and the student, within the broad overall theme of the marine microbial ecosystem. The student will join an active and rapidly growing research group at the University of Exeter. The project will require a strong background in mathematics, computer science, physics, or another numerical discipline. Additional background in molecular biology, microbiology, ecology, evolution, or environmental science would be an advantage, but is not essential.

We welcome informal enquiries from prospective applicants (contact Dr Hywel Williams, University of Exeter: h.t.p.williams@exeter.ac.uk).

The closing date for applications is Thursday 30 June 2011 and we expect to hold interviews towards the end of July.

http://www.exeter.ac.uk/studying/funding/award/-?id=3D821 h.williams@uea.ac.uk

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UGuelph MarineInvertBiodiversity

Graduate Position in Marine Barcoding - University of Guelph & Department of Fisheries and Oceans Canada

We are seeking an enthusiastic Ph.D. student with an interest in applied evolutionary genetics and taxonomy to conduct a DNA barcoding study on marine invertebrates as part of a large multi-disciplinary network conducting studies on aquatic invasive species (Canadian Aquatic Invasive Species Network, CAISN). This barcoding project is a collaborative one, involving researchers at the University of Guelph, Fisheries and Oceans Canada, and University of Windsor. Excellent MSc candidates with undergraduate research experience will also be considered.

Many global invaders are marine invertebrates such as crustaceans, molluscs, and ascidians that often present taxonomic challenges, especially in early life history stages. DNA barcoding has been identified as a robust, widely applicable method that could serve as an international standard for the identification of aquatic invasive species on a global scale as it has practical advantages over classical taxonomic methods. However, its utility for this purpose needs to be validated-especially when invaders and co-occurring native species are very similar-and its usefulness is a function of the availability of validated DNA barcoding datasets.

The successful candidate will apply DNA barcoding methods to generate essential baseline data on invertebrate biodiversity in Canada's coastal waters and will then evaluate the utility of this approach for invasive species identification and detection. This project may also involve generating molecular phylogenies based on multiple nuclear markers where needed to resolve taxonomic uncertainties of important marine invaders. Species identifications will be obtained in collaboration with taxonomic experts, and the relationship between cryptic species diversity and body size will be explored using the resulting datasets.

We are looking for a highly motivated candidate who is interested in playing a substantial role in developing novel research directions for this project, using the sequence data to address exciting questions in ecology and/or evolution. Potential research topics include investigating the phylogenetic distribution of "invasiveness"; analyzing molecular evolutionary rates across different taxa; or comparing patterns of genetic diversity, species diversity, species complementarity, and invasive species prevalence among regions.

The student will be co-advised by Dr. Sarah Adamowicz (University of Guelph) and Dr. Cathryn Abbott (Department of Fisheries and Oceans Canada) and will also collaborate with other DFO and university researchers. The successful candidate will be based at the Pacific Biological Station in Nanaimo, B.C. for a portion of the studentship. This position provides the opportunity to conduct novel research in invasion biology, ecology, and evolution and will serve as an outstanding training ground for those interested in governmental, academic, or private-sector careers in biology and environmental science.

Stipend funding is available at NSERC network rates. Canadian citizens and permanent residents are preferred as there are no project funds for international student fees. The project start date is to be between May 2011 and January 2012. To be considered for this position please send your CV, a brief summary of your research interests, and the names of at least two references to <sadamowi@uoguelph.ca> sadamowi@uoguelph.ca.

Sarah J. Adamowicz, Ph.D. Assistant Professor Biodiversity Institute of Ontario & Department of Integrative Biology University of Guelph 50 Stone Road East Guelph, Ontario N1G 2W1 Canada Email: sadamowi@uoguelph.ca Phone: +1 519 824-4120 ext. 53055 Fax: +1 519 824-5703 Office: Science Complex 1458 Lab: Science Complex 1403/1404

http://www.dnabarcoding.ca/ http://www.barcodinglife.org/ http://www.uoguelph.ca/ib/people/faculty/adamowicz.shtml

sadamowi@uoguelph.ca

UIceland BirdEvolution

Evolutionary status of Icelandic subspecies of birds

A three year graduate position is available at the University of Iceland to study Icelandic subspecies of birds. Several bird species in Iceland have a subspecies status. The aim of the project is to evaluate their status and test whether it is supported by historical divergence from other related subspecies or if the divergence has been driven by recent evolutionary forces. The project will be based on analysis of DNA variation and morphological data.

The applicant should hold an M.Sc. degree in Biology. Background and interest in evolutionary biology, birds, and in application of molecular and statistical methods in biology is advantageous.

The position is for three years and is financed by the University of Iceland Research Fund. Candidates will be selected based on their education, research interest, former work and letters of recommendation.

For further information contact Snæbjörn Pálsson, snaebj@hi.is, Associate professor at the Life and Environmental Sciences (http://www.hi.is/~snaebj). The application should be sent tosnaebj@hi.is, before the June 30th.

snaebj@hi.is

UInnsbruck MolecularEcology IntegrativeBiodiversity

MOLECULAR ECOLOGY, INSTITUTE OF ECOLOGY, UNIVERSITY OF INNSBRUCK PhD position

The University of Innsbruck, Austria, seeks to hire at the PhD student level in the area of molecular ecology. The position is a 3-years position at the Molecular Ecology Group of the Institute of Ecology, starting from 1 October 2011. The Molecular Ecology Group uses the exciting opportunities offered by the advance in molecular biology, to study ecology as a snap-shot of evolving biodiversity. Data from multiple sources are integrated to enhance the success of biodiversity research. The research focuses on terrestrial animals.

Responsibilities 1. participation in an interdisciplinary and integrative biodiversity research project on Palaearctic Tetramorium ants, i.e., addressing of population genetic, phylogeographic, phylogenetic and taxonomic questions relating to the delimitation of cryptic species, and the evolution and evolutionary ecology of cryptic diversity 2. application of molecular genetic lab techniques (e.g. mtDNA but also nuclear sequence loci, following their NGS-based development) and associated inference methods (e.g. gene flow analysis, phylogenetic reconstruction, phylogeographic analysis), morphometrics and relevant statistical methods, and possibly further disciplines (e.g., near-infrared spectroscopy, ecological niche modelling) 3. preparation of manuscripts 4. participation in the PhD program of Innsbruck University 5. teaching of a maximum of 2 hours per semester, if there is demand in the faculty

Selection criteria A. completed study of biology, MSc level B. demonstrated research experience in population genetics, phylogeography, phylogenetics or taxonomy of arthropods C. keen interest in evolution and ecology, and a high level of motivation D. ability to work effectively as part of a multi-disciplinary team E. flexibility in the course of progressing research F. ability to work independently G. ability to work under pressure H. good knowledge of oral and written English

PhD supervisor Birgit C. Schlick-Steiner

Salary The annual gross salary is an all-inclusive salary of EUR 25,811.80

Further reading # Schlick-Steiner et al 2010 Annual Review of Entomology 55: 421-438 # Schlick-Steiner et al 2006 Molecular Phylogenetics and Evolution 40: 259-273 # Schlick-Steiner et al 2007 Trends in Ecology and Evolution 22: 391-392 # Steiner et al 2010 Zoologischer Anzeiger 249: 223-254 # Moder et al 2007 Journal of Zoological Systematics and Evolutionary Research 45: 82-87 # Steiner et al 2006 Myrmecologische Nachrichten 8: 175-180 # Schlick-Steiner et al 2007 Biological Journal of the Linnean Society 91: 247-255 # Klarica et al. 2011 Journal of Chemical Ecology 37: 549-552 # Steiner et al 2008 Diversity and Distributions 14: 538-545

How to apply To apply, please submit, by E-mail to <fss-technik@uibk.ac.at>, with cc to <birgit.schlick-steiner@uibk.ac.at>, and with the subject line “Chiffre: BIO-6591 - Bewerbung um ein wissenschaftliche Stelle”: a cover letter (including a reference to “Chiffre: BIO-6591”), systematic point-by-point replies as to your readiness for the responsibilities and how you meet the selection criteria, brief statement of research interests, list of relevant methods successfully applied thus far, complete curriculum vitae, complete list of publications, and facultatively up to three pdf files of published work. Also, if possible, arrange for two letters of recommendation to be sent to <birgit.schlick-steiner@uibk.ac.at> Applications must be written in German or English. The deadline for receipt of all applications is June 22, 2011. The (legally binding) announcement in German can be found at: http://www.uibk.ac.at/service/c101/-mitteilungsblatt/2010-2011/24/mitteil .pdf

The research institution and its environment The University of Innsbruck has a long-standing and internationally renowned tradition in life sciences and offers a vibrant research atmosphere. It has approx. 21,000 students and 3,000 members of staff. Innsbruck is situated in the Alps and very close to Switzerland, Germany and Italy; scenery and outdoor recreation are fantastic.

More information needed? For more information, please contact the PhD supervisor: Birgit Schlick-Steiner <birgit.schlick-steiner@uibk.ac.at>

Birgit C. Schlick-Steiner Professor of Molecular Ecology

Institute of Ecology University of Innsbruck Technikerstr. 25 A-6020 Innsbruck, Austria Phone: +43 512 507-6120 Fax: +43 512 507-6190 http://www.uibk.ac.at/-ecology/forschung/molecular_ecology.html.en
Birgit.Schlick-Steiner@uibk.ac.at

ULausanne PopulationGenomics

2 PhD positions: Evolution, Symbiosis and Population Genomics: Lausanne, Switzerland

We are seeking 2 highly motivated students with an interest in molecular biology, genomics and/or evolutionary ecology to join our group working on symbiotic mycorrhizal fungi. These important fungi form mutualistic symbioses with most plants, improving plant growth and influencing diversity of ecosystems. The fungi have a highly unusual genome organization, harbouring genetically different nuclei that are passed from one generation to the next (Hijri & Sanders, Nature 2005) and this has important consequences on plant growth (See Angelard et al. 2010 in Current Biology). The main goals of our research are to understand how the genetics and multiple genomes act on these fungi and how this can be used to create more beneficial strains of the fungi for use in sustainable agriculture and the environment.

A selection of possible projects include:

- Stability/heritability of fungal traits associated with improved growth of rice and cassava - Evolutionary genomics and population genomics / transcriptomics of the mycorrhizal symbiosis - Population genetics of mycorrhizal fungi in natural or agricultural systems - Linking quantitative changes in genetically different nuclei with important plant phenotypic traits

The candidate should be familiar with ecology and evolution or molecular biology or genomics/bioinformatics and have an interest in applying this knowledge to evolutionary & ecological questions. He/she should also be willing to interact with the other group members working on evolution and population biology of mycorrhizal fungi (see list of recent publications on our web site).

The successful candidate must have a Masters degree (MSc) or equivalent in order to qualify for our PhD program. We are located in the Department of Ecology and Evolution (DEE) at the University of Lausanne (Switzerland). The Department is situated on the shores of Lake Geneva and provides a pleasant & exciting research environment and a strong PhD program. It is also one of the largest institutions in Europe for research in ecology and evolutionary biology, comprising 17 different research groups. A genomics research centre also exists at the same site.

Ability to speak and write English is essential.

The studentships are for a period of 3 years. Starting date ideally by October 2011. Closing date for application is 16 July 2011. To apply, applicants should send a CV plus a letter of motivation by EMAIL to Ian Sanders, Dept of Ecology and Evolution, University of Lausanne, Switzerland. Email: ian.sanders@unil.ch: Tel: +41 21 692 4261.

More details can be found about our group at: http://www.unil.ch/dee/page7238.html and http://web.me.com/iansanders/personal/Welcome.html Ian R. Sanders Professor of Evolutionary Biology Dept. of Ecology & Evolution University of Lausanne Biophore Building 1015 Lausanne Switzerland

Tel (direct): +41 21 692 4261 Tel (Secretary): +41 21 692 4260 Fax: +41 21 692 4265 Email: ian.sanders@unil.ch

http://www.unil.ch/dee/page7238_en.html **See my new website**

http://web.me.com/iansanders/personal/Welcome.html Ian Sanders <Ian.Sanders@unil.ch>

ULyon GenomeEvolution

PhD fellowship in evolutionary genomics

A PhD fellowship is available with Dr Benedicte Lafay (www.ampere-lyon.fr/spip.php?article351) to study the evolution of multipartite genome in procaryotes employing the tools of bioinformatics. The primary objective of the project is to investigate the setting up of coordinated processes implicated in the transmission of genetic information (multiple chromosome replication, partition and segregation), using comparative genomics and complete genome sequences available from public databases. A further objective is to build a generalized molecular model of these processes to help in the numerical modeling of these phenomena. This project offers the opportunity to work in a multidisciplinary team including evolutionary biologists, molecular microbiologists, mathematicians and complex systems engineers.

Applications are sought from suitably qualified candidates to undertake doctoral research at the University of Lyon, France (lyon-university.org). The ideal candidate will have a strong background in genetics, molecular biology, bio-mathematics, bioinformatics or similar areas, as well as a keen interest in evolutionary biology and molecular evolution. Lack of experience in some of these areas is not considered a problem, so long as candidates demonstrate aptitude and enthusiasm to learn. Knowledge of microbiology may help but is not necessary.

No nationality restriction applies to this fellowship.

Please note that applications must be received by 25 June 2011.

Contact: Benedicte Lafay

Laboratoire AmpÃre - CNRS UMR5005 - UniversitÃ© de Lyon Ecole Centrale de Lyon 36, avenue Guy de Collongue F-69134 Ecully

+33 (0)4 72 18 60 95

benedicte.lafay@ec-lyon.fr

ULyon NuclearReceptorEvolution

A three-year PhD fellowship is available at the University of Lyon (IGFL, ENS Lyon) to study the evolutionary plasticity of nuclear receptors.

The candidate should have interest and a good background in evolutionary biology, molecular evolution, genetics and bioinformatics

Contact: * François Bonneton: francois.bonneton@ens-lyon.fr * Vincent Laudet: vincent.laudet@ens-lyon.fr

Subject: Canalisation, which allows the maintenance of a phenotype despite genetic or environmental variability, influences the emergence of evolutionary innovations. On the physiological level, homeostasis may be seen as a form of canalisation that depends on externally induced signals that circulate inside the internal milieu and regulate target genes. In animals, nuclear receptors are major actors of this regulation, being both ligand receptors and transcription factors. The function of a nuclear receptor is determined by allosteric changes of the structure, which can be induced by DNA binding, ligand binding, phosphorylation or interactions with other proteins. The aim of this PhD project is to understand the constraints that determine plasticity and robustness of nuclear receptors during the evolution of animals. The three main questions are: 1) Molecular dynamic and evolutionary dynamic: Is there a link between the structural constraints and the evolutionary constraints that act on nuclear receptor? 2) Geometry of ligand-binding pocket: Is it possible to define a specific morphology for the pocket of the four different types of nuclear receptors: hormone receptors, nutritional sensors, receptors with a constitutive activity and true orphans? 3) Evolution of DNA-binding: What is the origin and evolution of DNA-binding domains and response elements of nuclear receptors?

François BONNETON

François BONNETON, Maître de conférences (Senior lecturer) IGFL, ENS Lyon, 46 Allée d'Italie, 69364 LYON cedex 07, France http://igfl.ens-lyon.fr/-Members/fbonneto/index_html/research E-mail : Francois.Bonneton@ens-lyon.fr Phone : (33) 04 72 72 86 45 Fax : (33) 04 72 72 89 92

François Bonneton <Francois.Bonneton@ens-lyon.fr>

UNebraska PlantInsectInteractions

I am seeking a student interested in studying the adaptations that enable herbivorous insects to cope with the defenses mounted by their host plants. In the lab we mostly focus on leaf beetles (Chrysomelidae) as a study system but research need not be limited to this group. There will be opportunities to work with high throughput sequencing, proteomics and RNA interference to characterize the genes and gene products that contribute to the insect's counter-defenses. A long term aim of this research is to understand the degree to which herbivorous insects are able to optimize their counter-defense strategies, particularly when comparing species with generalist versus specialist feeding habits.

Support is available in the form of a graduate assistantship that provides a stipend, tuition and partial funding of health insurance. The assistantship is open to individuals wishing to pursue a PhD. or Masters degree. Priority will be given to candidates with prior research experience.

For more information or to apply, please send a CV and contact details of at least two referees to:

Nick Miller

Department of Entomology 12BA Entomology Hall University of Nebraska-Lincoln Lincoln Nebraska 68583-0816 USA

+1 402-472-6200

nmiller4@unl.edu

USussex SocialBees

NERC/School of Life Sciences-funded PhD studentship at Sussex University

Environmental and genetic components of a major evolutionary transition

We seek a student interested in understanding the transition to sociality, one of the central problems in evolutionary biology. Functional (adaptive) questions about sociality have been well-studied, but much less is known about underlying mechanisms. Sweat bees (Halictinae) are unusually valuable for elucidating social transitions. Unlike other hymenopteran lineages, which comprise entirely social taxa (e.g. honeybees, paper wasps), there are closely related non-social as well as social sweat bees, and a well-resolved phylogeny suggests that there have been many transitions in both directions between sociality and non-sociality(1). Of special interest are socially polymorphic taxa such as Halictus rubicundus, where females in warmer environments form small social groups while those in cooler environments are non-social. Such taxa provide ideal material to investigate the underlying basis of sociality. In a recent study, we directly induced transitions between sociality and non-sociality by transplanting H. rubicundus reciprocally between UK populations that normally express alternative phenotypes(2) (see also http://www.sussex.ac.uk/newsandevents/index?id=3D5828, which includes a short video of H. rubicundus). In addition to these common garden experiments in the field(2), we are developing a method for rearing sweat bees in a controlled environment. The studentship would use these and other techniques to investigate how general social plasticity is in sweat bees, and to test potential environmental cues that determine social phenotype. Note that these are small (<1cm) bees that do not sting humans and live in colonies of <10 individuals. See our website (http://www.sussex.ac.uk/lifesci/fieldlab/) for more details of the research group. Possible foci for the research include:

(1) Social plasticity in UK sweat bees. Our previous findings(2) suggest that instead of representing repeated evolutionary gains and losses of the traits underpinning sociality, transitions between sociality and non-sociality might represent plasticity. The ability to express either sociality or non-sociality in response to environmental conditions might then be cryptic but widespread. This could be tested by carrying out common garden experiments with other UK sweat bees.

(2) Test for plasticity in North American populations of H. rubicundus. H. rubicundus has a holarctic distribution. There is significant mitochondrial differentiation between US populations expressing the two social phenotypes(3), whereas there is no such differentiation among British and Irish populations(4). This suggests that in the US, social phenotype might be genetically fixed rather than flexible. These and other differences between US and UK bees could also be examined.

(3) Environmental cues that sweat bees use to determine which social phenotype to express are currently unknown. The effect of cues such as daylength, temperature and mating status(5) could be investigated.

The balance between these aims will depend on initial results and the developing interests of the student. My group is collaborating with that of Prof Rob Paxton, a molecular ecologist at University of Halle in Germany. Prof Paxton's group is currently annotating the transcriptome of H. rubicundus. Although it would not be the main focus, it is possible that towards the end of the study, the PhD student could be involved in RNA expression work using H. rubicundus samples collected during the studentship.

References: (1) Danforth, B.N., Conway, L., and Ji, S.Q. (2003). Phylogeny of eusocial Lasioglossum reveals multiple losses of eusociality within a primitively eusocial clade of bees (Hymenoptera : Halictidae). Syst Biol 52, 23-36.

(2) Field, J., Paxton, R.J., Soro, A. & Bridge, C. (2010). Cryptic plasticity underlies a major evolutionary transition. Current Biology 20:2028-31. [see also commentary on this paper in Current Biology 20:R977-9, 2010]

(3) Soucy, S.L., and Danforth, B.N. (2002). Phylogeography of the socially polymorphic sweat bee Halictus rubicundus (Hymenoptera : Halictidae). Evolution 56, 330-341.

(4) Soro, A., Field, J., Bridge, C., Cardinal, S.C. & Paxton, R.J. (2010). Genetic differentiation across the social transition in a socially polymorphic sweat bee, Halictus rubicundus. Molecular Ecology 19:3351-3363.

(5) Yanega, D. (1989). Caste determination and differential diapause within the first brood of Halictus rubicundus in New York (Hymenoptera: Halictidae). Behavioural Ecology and Sociobiology 24, 97-107.

REQUIREMENTS: a student with an interest in behavioural/evolutionary

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UZurich EvolutionaryBiology

PhD thesis in experimental or computational evolutionary biology

A three-year Ph.D. studentship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. We are looking for a researcher to study innovation in biological systems that range from molecules to large genetic networks. Ongoing projects involve laboratory evolution of yeast, E. coli and fruitflies, as well as in vitro evolution of ribozymes (e.g., Hayden et al., Nature 474, 92-95, Dhar et al., J. Evol. Biol 5 92-95). A sample of the laboratoryâs research can be found at http://www.ieu.uzh.ch/wagner/. Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and lifeâs fundamental organizational principles.

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

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

To be considered, please send a single (!) PDF file merged from the following parts to jobs_aw@bioc.uzh.ch: CV including publication list, a statement of research interests not exceeding three pages, and three academic references. A brief sketch of an experimental evolution project is also desirable. Please include the word âEXPPHD11â in the subject line. The application deadline is August 15, 2011. The position is available in the fall of 2011.

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

annette.schmid@ieu.uzh.ch

UZurich EvolutionaryMorphology

Open PhD position in Evolutionary Morphology and Palaeobiology in Zürich

The Evolutionary Morphology and Palaeobiology of Vertebrates group at the Palaeontological Institute of the University of Zürich invites applications for a PhD position (3 years funding, with potential extension). The successful candidate will work in a Swiss National Science Foundation supported research project about life history evolution in mammals, involving skeletal and dental evolution in extant and extinct forms, under the supervision of Prof. Marcelo SÃnchez. The PhD project will build upon an existing research program (http://www.msanchezlab.net/) and includes museum visits world wide and extensive lab work. Those interested should check our website for our publications and current research projects. Details about the PhD project will be discussed upon interviews with the best-qualified applicants and the candidate is expected to co-develop her/his project.

The ideal candidate will be a highly-motivated zoologist with neontological or palaeontological background. Previous participation in research activities and excellent writing skills in English are required, knowledge of speaking German is desirable but not mandatory. Perspective students are expected to have received their Master's degree or equivalent by the start of the Ph.D. program. The selected candidate will be expected to help in teaching and writing a proposal for funding.

HOW TO APPLY: Send the following by email to: Prof. Marcelo SÃnchez: I) a one- to two-page application letter addressing, but not limited to the following questions: a) Why are you interested in a PhD in this research area? b) What are your career goals? II) A detailed curriculum vitae, including a list of lab, field, analytical, and linguistic skills, presentations at scientific meetings, and publications (if applicable); III) A copy of your undergraduate and graduate academic records; IV) two or three letters from your academic advisors addressing: your intellectual and academic skills; your dedication to science and your ability to work cooperatively in a team. Please, follow the directions carefully. âSoftâ DEADLINE FOR APPLICATION: 15. August, 2011. If needed, the position will remain open until a suitable candidate is found. STARTING DATE: late Fall of 2011 (negotiable).

The University of Zürich is one of the top comprehensive institutions in Europe and Zürich, in close proximity to the Alps, offers the conditions for an excellent quality of life. With a critical mass of researchers in Palaeontology and Evolutionary Biology at the University and the neighbouring Swiss Federal Institute of Technology (ETH Zürich), Zürich offers an exceptional academic environment for research and study. The Institute of Palaeontology of the University of Zürich offers state-of-the-art research facilities in an international and stimulating academic environment.

Please send enquiries and applications by email to Prof. Marcelo SÃnchez (e-mail: m.sanchez@pim.uzh.ch)

– Marcelo SÃnchez Paläontologisches Institut und Museum Universität Zürich Karl Schmid-Strasse 4 CH-8006 Zürich Switzerland Phone: +41 (0)44 634 23 42

Fax +41 (0)44 634 49 23 For deliveries (please add): Raum KO2 E63e Email: m.sanchez@pim.uzh.ch

Personal website: http://www.pim.uzh.ch/de/-Institut/Mitarbeitende/index.php?show4 Lab website: http://www.msanchezlab.net/ Evolutionary Biology in Zürich: http://www.bioc.uzh.ch/evobiozh/ Marcelo SÃnchez <m.sanchez@pim.uzh.ch>

UZurich MaternalEffects

PhD Position in Evolutionary Ecology University of Zurich, Switzerland

A fully-funded 3-year PhD position is available in Barbara Tschirren's group at the University of Zurich, Switzerland, to work on the genetic and epigenetic basis of maternal investment in birds.

The environment a mother provides for her offspring before birth can have significant and long-lasting consequences for her offspring's morphology, physiology and behaviour later in life. Prenatal maternal effects are therefore considered to be an important mediator of phenotypic plasticity and a major source of variation in evolutionary fitness. Yet, we still know very little about why mothers differ in the quality and quantity of resources they provide to their young and how different maternal investment strategies evolve.

In this project, we will establish breeding lines with Japanese quails (Coturnix japonica) and use molecular techniques to tackle the genetic basis of maternal investment. Furthermore, by manipulating environmental conditions experienced by mothers before reproduction, we will measure long-term consequences of environmental maternal effects on the reproductive investment of the subsequent generations (i.e. daughters and grand-daughters). The studies on captive quails will be complemented by work on wild-living passerines that takes place in our group. The project is funded by the Swiss National Science Foundation.

The ideal candidate for this project is fascinated by evolutionary questions, highly motivated, independent and creative. She / he has a background in evolutionary biology, behavioural ecology, (epi-)genetics or animal breeding (or a related field). Previous experience with molecular techniques, experimental design, and / or statistics is a plus. A MSc (or equivalent) in Biology is required. The starting date is January 1 2012.

The successful applicant will be based at the Institute of Evolutionary Biology and Environmental Studies of the University of Zurich, providing ample opportunities for collaborations and interactions with researchers working in related and complementary fields (http://-www.ieu.uzh.ch/index.html). The research groups are very international and the working language is English.

Zurich is a beautiful city that consistently ranks amongst the cities with the highest quality of life. While it offers all the pleasures of living in a bigger city, thanks to it's central location and excellent public transport connections, it is very easy to get out of the city and head for the mountains for outdoor activities such as hiking, climbing or skiing.

Applications should include 1) a cover letter outlining your motivation to work on this project as well as relevant experience, 2) a detailed curriculum vitae, 3) copies of academic qualifications, 4) the contact details of two academic referees, and 5) a 1-page description of your MSc project. Send the above as a single .pdf file to barbara.tschirren@ieu.uzh.ch

Review of applications will start on August 1 2011, but candidates will be considered until the position is filled. For more information, feel free to contact me!

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Barbara Tschirren, PhD Assistant professor SNF Institute of Evolutionary Biology and Environmental Studies University of Zurich Winterthurerstrasse 190 8057 Zurich Switzerland

Tel: +41 44 635 47 77 Fax: +41 44 635 68 18 Email: barbara.tschirren@ieu.uzh.ch http:/-/www.ieu.uzh.ch/staff/professors/tschirren.html barbara.tschirren@ieu.uzh.ch

Jobs

AustralianNatlU AvianResAssist Coevolution

Avian Field Research Assistant: Cuckoo - host coevolution Research School of Biology, Australian National University Salary: AU$49,501 - $65,086 Duration: 18 months, full or part-time (please indicate your preference), with possible extension. Closing Date: 30 June 2011

This position is available from 1 September 2011 to join Dr Naomi Langmore (ANU), Prof. Robert Heinsohn (ANU) and Dr Rebecca Kilner (UCambridge) in a long-term study of the impact of climate change on interspecific interactions and biodiversity, using cuckoo - host interactions as a model system. Primary responsibilities include mist-netting, banding, nest searching, insect surveys and supervision of assistants and research students at our study site in Canberra. For further information and how to apply, please see: http://jobs.anu.edu.au/PositionDetail.aspx?p=2103 Informal enquiries to: naomi.langmore@anu.edu.au

– Dr Naomi Langmore ARC Australian Research Fellow Evolution, Ecology and Genetics Bldg 116 Daley Road Research School of Biology Australian National University Canberra ACT 0200

Ph. 02 61258436 Fax. 02 61255573

naomi.langmore@anu.edu.au

Berlin EvolutionaryBiometrician

Job advertisement

The Leibniz Institute for Zoo and Wildlife Research (IZW) in Berlin is Germany's premier wildlife research institute and funded by the federal government of Germany and the German states ("Länder"). The IZW focuses on the life histories and mechanisms of evolutionary adaptations of mammals and birds and their conservation in natural and anthropogenically influenced environments. The institute operates within the fields of evolutionary ecology, evolutionary genetics, wildlife diseases, reproduction biology and reproduction management, has excellent facilities and is currently expanding its research programme (http://www.izw-berlin.de). For this purpose the institute is seeking to appoint

1 statistician / biometrician (position 11/2011)

to conduct research on topics important to life scientists such as non-parametric procedures, analysis of longitudinal data, Bayesian approaches to the analysis of genetic, geographic or behavioral data, or comparative methods such as phylogenetic regression; provide advice and training in biostatistical analysis and experimental design of scientists and PhD students and provide strategic guidance for the development of the institute's computer network.

You will have a PhD in (bio-) statistics, medical statistics, biometry, life sciences or natural sciences, know how to run software such as StatXact, Systat or SAS, are (very) experienced with R, enjoy developing the statistical competence of colleagues and students, relish scientific challenges in many areas, are pleased to join interdisciplinary teams from evolutionary geneticists or behavioural ecologists to infection biologists, reproduction biologists or veterinary scientists and preferably know how to program (in C++, Fortran, Python or similar languages).

The position is a tenure-track position, initially limited to three years, and available after 01 October 2011. The IZW is determined to increase the proportion of women in successful scientific careers and particularly encourages female scientists to apply. Applications will be considered until the positions are filled but preferably reach us by 10 July 2011; we hope to conduct interviews on 10 August 2011. Please direct informal enquiries to Heribert Hofer (direktor@izw-berlin.de, tel +(49)-30-5168101, fax +(49)-30-5168110) and submit your CV, a letter indicating your experience and research interests, publication list, details of external grants, copies of certificates and the names and contact details of three referees in one pdf file (max 1 MB) to Roswitha Hildebrand, Leibniz Institute for Zoo and Wildlife Research, personal@izw-berlin.de, P.O.Box 601103, D-10252 Berlin, Germany; fax: +49-30-5126104.

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Stellenausschreibung

Das Leibniz-Institut für Zoo- und Wildtierforschung im Forschungsverbund Berlin e.V. (www.izw-berlin.de), ein Mitglied der Leibniz-Gemeinschaft, untersucht die Vielfalt der Lebensweisen, Mechanismen der evolutionären Anpassungen und Anpassungsgrenzen von Wildtieren und ihre Wechselbeziehungen mit Mensch und Umwelt. Das Institut erfüllt diese Aufgabenstellung durch langfristig angelegte, anwendungsorientierte, interdisziplinäre Grundlagenforschung in den Bereichen Evolutionäre Ökologie, Evolutionsgenetik, Wildtierkrankheiten, Reproduktionsbiologie und Reproduktionsmanagement. Im Rahmen des "Interdisziplinären Forschungsverbundes Biodiversität" wird voraussichtlich von der Senatsverwaltung für Bildung, Wissenschaft und Forschung ein am IZW angesiedeltes Koordinationsbüro finanziert. Dafür suchen wir für die Dauer von 3 Jahren

1 Postdoc als Projektkoordinator/in (KZ 12/2011)

1 Sachbearbeiter/in / Sekretär/in (KZ 13/2011) Ziele des Vorhabens sind die Vernetzung der Berlin/Potsdamer Forschungslandschaft im Bereich Biodiversitäts- und Evolutionsforschung, die Verbesserung der strategischen Ausrichtung interdisziplinärer Biodiversitätsforschung unter Berücksichtigung gesellschaftlicher und politischer Bedarfe, die Erhöhung der nationalen und internationalen Sichtbarkeit der Biodiversitätsforschung am Standort Berlin/Potsdam, die Entwicklung von Konzepten zur Einbeziehung der Öffentlichkeit in die Biodiversitätsforschung und die Etablierung einer Anlaufstelle für Entscheidungsträger (Politikberatung).

Voraussetzungen: Die/der Projektkoordinator/in ist vorzugsweise eine Persönlichkeit mit Interesse an strategischen Fragen und der Weiterentwicklung neuer Initiativen in der Biodiversitäts- und Evolutionsforschung, hat eine lebenswissenschaftliche Ausbildung mit Promotion, vermag selbständig zu entscheiden und zugleich teamorientiert zu denken und zu handeln, verfügt über gute Deutsch- und Englischkenntnisse in Wort und Schrift, ist kontaktfreudig, sozial kompetent und sicher im Auftreten. Erfahrungen

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ColoradoStateU LabCoordinator EvolutionaryBiol

Posted deadline is *July 1*, but we will accept applications until the position is filled.**

Department of Biology

Colorado State University

Assistant Lab Coordinator

The Department of Biology at Colorado State University seeks a Special Administrative Professional Assistant Lab Coordinator. This 9-month position supports the undergraduate teaching program. The Assistant Lab Coordinator will assist the Lab Coordinator with preparatory and supervisory tasks as related to undergraduate teaching. Must have Master's degree in Biology, Biochemistry, or Botany, with substantial training in Botany or plant science and a minimum of two years of experience, post baccalaureate, in a university biology, biochemistry or botany lab setting that includes experience in cell and molecular biology

Primary responsibilities will include: supervision, maintenance of living specimens (especially the plant collection), lab manual development and revision, and preparation of chemical solutions and media. The successful candidate will have significant training in Botany or plant science, with experience in cell and molecular biology.

For complete job description and requirements, visit: http://www.biology.colostate.edu/employment Position available August 15, 2011

For full consideration, materials must be received by

5:00 pm MST Friday, July 1, 2011; however applications will be accepted until the position is filled.

To apply, submit cover letter, resume and two letters of reference, plus names of two additional professional references, including contact information, in an MS Word, text or pdf file online only at:

https://www.natsci.colostate.edu/employment/BiologyLab/ Incomplete applications will not be considered.

Due to the nature of recruitment for this position, travel reimbursements up to $350 will be available if selected for on-campus interview.

CSU is an EO/AA employer.

Colorado State University conducts background checks on all final candidates.

Mike Antolin <michael.antolin@colostate.edu>

CornellMedSchool Bioinformatics programmer

Bioinformatics Programmer Position A bioinformatics programmer position is now open in the research laboratory of Dr. Jason Mezey (http://mezeylab.cb.bscb.cornell.edu/) within the Department of Genetic Medicine at Weill Cornell Medical College in New York City. The Mezey group focuses on the development of novel statistical and computational methods for addressing fundamental questions in computational biology and disease genomics. The duties of the position will include implementing and improving the computational speed of algorithms, building analysis pipelines, database construction and management, and software development. The group is dynamic and interactive, and most projects require close teamwork among postdoctoral associates, graduate students, and programmers. The Mezey research group has a dual appointment in the Department of Biological Statistics and Computational Biology at Cornell University (Ithaca, NY) and in the Department of Genetic Medicine at Weill Cornell Medical College (New York City), with members at both locations. We are looking for a programmer who would be located at our New York City (Weill Cornell) location. Ideal candidates will have a computer science background, proven programming skills in C/C++ and PERL, experience with relational database, basic knowledge of web programming, familiarity with probability and theoretical statistics, and experience working with next-generation sequencing and genomic data. Salary will be commensurate with experience. The position is available immediately. To apply, please send an email with a single collated pdf including: (1) CV, (2) list of skills and employment history, (3) names and contact information of at least three references, to Jason Mezey at jgm45@cornell.edu

jgm45@cornell.edu

DukeU IntroBio TeachingAssist

Great opportunity for a recent graduate who wants teaching experience before PhD/ med school/ postdoc!

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Full-time teaching/prep positions, Duke University in the Biology 102L "Genetics and Evolution" course

Position description: Work full time (40 hours/week) as a teaching assistant and laboratory prep assistant in the introductory biology program for the 2011-2012 academic year. The position has two main components, teaching and behind-the-scenes laboratory preparation.

Teaching component: The primary teaching responsibility of the position is to lead laboratory sections of up to 16 students in the Duke University Biology Department's new genetics and evolution Gateway course, Biology102L. Each Biology 102L section meets weekly for 2.5 hours for a combined hands-on laboratory/problem-based learning session. Additional teaching responsibilities include (a) attending and taking notes at all course lectures including the weekly large discussion section, (b) grading weekly student written assignments and occasional oral presentations, (c) helping with the preparation and grading of mid-semester hourly and final exams, and (d) assisting students during office hours and otherwise mentoring students as beginning biologists.

Teaching assistants should plan to come to Durham early the week of August 22, 2011, and are expected to participate in a teacher-training workshop before the fall semester begins. TAs also attend weekly prep sessions during the semester on Mondays.

Prep component: The second set of duties associated with the position is to assist in the prep. work for the teaching labs in Biology 101L, 102L, and the laboratory diversity course, Biology 106L, as determined by the Lab Administrator. Responsibilities include setting up and putting away equipment and specimens for laboratory exercises, maintaining supplies in lab rooms between sections, cleaning glassware, assisting with field collection of live specimens, and helping to care for a diverse collection of invertebrate animals in salt-water aquaria. The lab prep workload is likely to require occasional evening (until 10 PM) and/or early morning (8 AM) work.

Salary: The projected salary for the position is $18,000 for 8.5 months. Employment begins on August 22, 2011 and ends May 6, 2012 with payment made in 9 equal amounts on the 25th of each month starting in September and ending in May. Full-time teaching/prep employees are eligible for health plans made available by the University.

Qualifications: Applicants should have a strong, varied background in biology, especially genetics and evolution, with a superior science GPA. US citizenship and fluency in English are also required. A very important attribute is a high level of energy and an enthusiasm for teaching genetics and evolution. Prior enrollment in Introductory Biology, Molecular Biology & Genetics, and Ecology & Evolution, or the equivalents, are highly desirable; experience tending Drosophila is a plus. Teaching assistants in Biology 102L are expected to be actively engaged with their students in all aspects of the course and to serve as role models and mentors. Because they are a vital part of the introductory biology teaching team both in the classroom and behind the scenes, full-time assistants must be willing to commit themselves fully to the responsibilities of the position described above and as determined by the faculty members in charge of the Gateway course.

Interviews and Application Process: Formal interviews are planned to begin after June 17, 2011. Hiring decisions will be made on a rolling basis thereafter, continuing as necessary.

Interested applicants should provide (a) a cover letter, (b) a transcript, and (c) a resume with the names of two references to Julie Noor. These may be emailed to jkfnoor@duke.edu (preferred), or mailed to her at the Department of Biology, Box 90338, Duke University, Durham, NC 27708-0338 USA. To be assured of consideration, applications should be submitted by June 17, 2010.

For more information contact Julie Noor by phone at 919-599-8047 or e-mail at jkfnoor@duke.edu

Mohamed A. F. Noor noor@duke.edu Professor & Associate Chair Tel: 919-613-8156 Biology Department Lab: 919-613-8193 Box 90338 FAX: 919-660-7293 Duke University Durham, NC 27708 USA http://www.biology.duke.edu/noorlab/ noor@duke.edu

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EAWAG Switzerland EvolutionaryBiology

Dear Colleagues, (sorry for cross posting)

2-year prestigious post doc position available in Switzerland. Profile open, come with your best idea, if you convince the committee, you will be funded to do your research in one of the top aquatic research institutes of the world.

best wishes jukka jokela

Eawag, the Swiss Federal Institute of Aquatic Science and Technology, is a Swiss-based and internationally networked aquatic research institute within the ETH domain (Swiss Federal Institute of Science and Technology). It is committed to the ecologically, economically and socially responsible management of water resources and aquatic ecosystems.

Eawag, the Swiss Federal Institute of Aquatic Science & Technology, announces a new opportunity for highly qualified individuals to apply for a 2-Year Postdoctoral Fellowship to conduct research in any field in the area of aquatic science and technology. Eawag focuses on cutting-edge research that is driven by the needs of society and leads to significant advances in the aquatic sciences. Innovative approaches and technologies for the sustainable management and use of water are developed through collaborations among natural and social scientists and engineers.

The postdoctoral fellow will be hosted within one of Eawag's 12 Research Departments (see http://www.eawag.ch/about/organisation/orgchart/index_EN). Selection of the postdoctoral fellow will be based on his or her academic record and ideas for a research project that is relevant to research activities conducted at Eawag.

The selection process will proceed in two phases. Applications will be screened in late September 2011 and short listed candidates will be invited to submit a proposal for a research project by mid-October 2011. The final selection decision will be made by mid-December 2011. It is anticipated that the starting date for the postdoctoral fellowship will be between February and May next year.

An earned Ph.D. degree is required for the postdoctoral appointment. Applications must include: a brief letter of application stating the title of the proposed postdoctoral project and identifying the Research Department that the candidate would like to host the project a curriculum vitae including a list of publications an abstract (not to exceed 1 page including references) of the proposed project names and contact information for three academic references. The deadline for applications is September 14, 2011. We look forward to receive your application.

The quickest way is to apply online. Go to http://www.eawag.ch/jobs/index_EN . Jukka.Jokela@eawag.ch

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FrenchGuiana 3yr ResAssist PlantPopGenetics

Research assistant 36-month temporary contract

Duration: 36 months

Employer: INRA

Location: Joint Research Unit ≪ EcoFoG ≫, Kourou, French Guiana

Starting date: 1st September or 1st October, 2011

A 3-year Research assistant position is available in the “Population Ecology” team of the Joint Research Unit “Ecology of Guianese Forests” under the supervision of Ivan Scotti (INRA) and Nadine Amusant (CIRAD). The grant is provided by the ANIB@ROSA project, supported by the EU-funded PO-FEDER 2007-2013 program.

The research assistant’s goals will be to (i) high-throughput sequence the transcriptome of Aniba rosaeodora (Brazilian rosewood), a commercially important tropical forest tree species; (ii) develop an array of high-throughput SNP / sequence markers for the unique identification (DNA fingerprinting) of individual plantation trees (iii) validate the identification tool on plantation and spontaneous trees (iv) assess the genome-wide distribution of genetic variation among provenances (v) evaluate the past demographic history and levels of selective pressure genome-wide and at individual gene loci, namely those coding for enzymes involved in the biosynthesis of commercially important compounds.

The research assistant will:

- Prepare cDNA libraries for high-throughput sequencing and co-operate with sequencing specialists to obtain transcriptome sequence libraries

- Annotate the above libraries

- Develop an array of 500-1000 SNP/sequence markers to be analysed by high-throughput sequencing

- Apply the markers to the fingerprinting of plantation trees

- Define the smallest set of markers allowing the unique identification of each tree

- Apply population genomics methods to the estimation of past demographic changes in natural populations of rosewood and to the identification of loci undergoing selection

- Publish scientific papers on his/her results in international peer- reviewed journals.

The appointed research assistant will have a strong background in genomics/molecular biology, bioinformatics, statistics and population genetics; will be fluent in English and in French; will be at ease with text-editing and spreadsheet software, web browsers and the R package. He or she will have a taste for scientific endeavour and technological development, engage in scientific and technical exchange with other members of the team, other project partners and the scientific community at large and will be able to make decisions autonomously and to work in tight collaboration with other scientists and staff members. The program will be executed in the Ecological Genetics laboratory of the Joint Research Unit “EcoFoG” and in other laboratories worldwide when necessary.

Candidates must file their application, along with a CV and two letters of reference, at the following e-mail addresses:

Ivan Scotti ivan.scotti@ecofog.gf

Nadine Amusant nadine.amusant@cirad.fr Interviews will take place either in person or by video call by the end of June 2011.

VISITORS TO FRENCH GUIANA MUST HOLD A VALID YELLOW FEVER VACCINE CERTIFICATE

Ivan Scotti INRA - UMR 0745 ECOFOG “Ecologie des Forêts de Guyane” / “Ecology of Guiana Forests” Team Leader ≪ Population Ecology ≫ Campus agronomique, Avenue de France BP 709 - 97387 KOUROU Cedex FRANCE Phone +594 (0)59432-9274, -9285, -9278 Fax +594 (0)59432-4302 e-mail: ivan.scotti@ecofog.gf, i.scotti.inra.kourou@gmail.com; web: http://www.ecofog.gf< http://www.ecofog.gf/ >

Ivan Scotti <Ivan.Scotti@ecofog.gf>

Helsinki ComputationalBiology

Open positions in computational sequence analysis at the Institute of Biotechnology, Helsinki, Finland

Dr. Ari Löytynoja will start as a group leader at the Institute of Biotechnology, University of Helsinki, from 1 September, 2011. He has open positions for Ph.D. students and a postdoc researcher.

The group's research interests are in evolutionary sequence analysis, both the development of advanced analysis methods and their application to biological questions of special importance. Current topics include e.g. phylogenetic sequence alignment and homology inference for evolutionary analyses, and the development of methods for comparative analysis of next-generation, high-throughput sequencing data.

An ideal candidate would be experienced with Linux/Unix systems and working with the command-line interface, and would master a scripting language such as Perl or Python. Some projects require experience on a low-level programming language such as C, C++ or Java (the current codebase is in C++). The work does not require background in biology, nor a formal training in programming or bioinformatics. The starting date is 1 September, 2011 or later.

Potential research projects are: (i) development/analysis of phylogenetic alignment methods efficiently using current computer hardware and strategies for their use on large datasets; (ii) development/analysis of phylogenetic alignment methods to account for uncertainties in the homology inference; (iii) development of methods for comparative analyses of next-generation sequencing data; (iv) evolutionary analyses of non-model organisms using next-generation sequencing data. A candidate's own project matching group's other interests can also be considered.

Information of the past work and research interests can be found from the following publications:

Löytynoja& Goldman. Science (2009), 324:1528. Löytynoja& Goldman. Science (2008), 320:1632 Löytynoja& Goldman. Phil Trans Royal Soc B (2008), 363:3913 Löytynoja& Goldman. Proc Nat Acad Sciences USA (2005), 102:10557

and from the group's homepage at http://www.biocenter.helsinki.fi/bi/loytynoja . To apply for a position, please send your CV and contact details of two referees to ari.loytynoja@helsinki.fi or to the address (valid until 31 July, 2011):

Ari Löytynoja EMBL-European Bioinformatics Institute Wellcome Trust Genome Campus Hinxton, CB10 1SD United Kingdom

– Ari Löytynoja tel:+44-(0)1223-494695 EMBL-European Bioinformatics Institute fax:+44-(0)1223-494468 Wellcome Trust Genome Campus, Hinxton, CB10 1SD, UK

ari@ebi.ac.uk

Lafayette Lousiana NMFS LabTech ConservGenetics

Molecular Technician National Marine Fisheries Service Lafayette, LA

We seek a highly motivated technician to join an active lab investigating population genetics and evolutionary histories of marine mammal species. Applicants must have extensive experience with PCR and DNA sequencing and/or microsatellite genotyping. Responsibilities include DNA extractions, sequencing and genotyping of marine mammal samples, primarily bottlenose dolphins as well as database entry and archiving.

Minimum Qualifications: Master's Degree in an appropriate field such as Biological Sciences, Molecular Biology, or Genetics, PLUS demonstrated research experience that included performing DNA extractions and PCR, and facility with standard computer software programs. Experience with microsatellite genotyping and/or gene sequencing is required. Experience amplifying from degraded, poor quality or ancient DNA samples is preferred. This is a full time 1-yr contract position open immediately. Applicants should be US citizens.

Qualified candidates should submit (via email) a letter of application describing qualifications for the position and reason for interest, CV, and letters from three references detailing the applicants level of experience with DNA sequencing and/or genotyping, and overall capabilities working in a laboratory setting to Patricia.Rosel@noaa.gov.

Patricia.Rosel@noaa.gov

LundU SystematicBiology

Lund University (Sweden) announces an opening:

Professor in Systematic Biology

Lund University is Scandinaviaâs largest institution for education and research in a broad range of disciplines, such as engineering, natural sciences, law, social science, economics, medicine, theology and the arts. The University has over 40 000 students and approximately 6 000 employees located in Lund, Malmö and Helsingborg. We have a comprehensive global network and a growing co-operation within the Ãresund University framework of Southern Sweden and Eastern Denmark.

The Department of Biology was founded on January 2010 by a fusion of the Departments of Ecology, Cell and Organism Biology (COB), Undergraduate Studies in Biology and the Biological Museums. At the same time, the building of the new Biology Centre has been completed within the North Campus, and all biology research and teaching at Lund University is now gathered together within a single site for the first time â providing unique opportunities for high quality research and innovative education within biology. The Department of Biology has ca. 300 employees, out of which ca. 80 are PhD candidates. The Biological Museums together represent one of the worldâs largest university collections (c. 12 million specimens) including, in particular, large collections of insects and vascular plants from the Nordic countries. Research at the Department is organized around research groups working within many areas of biology. We offer a range of bachelor and master teaching programmes in âBiologyâ and âMolecular Biologyâ to both Swedish and international students. Further information about the Department of Biology can be found at: http://www.lu.se/biology Basic facts regarding the position

Reference no: 2184 Closing date for applications: September 15, 2011 Date of appointment: As soon as possible Placement: Department of Biology Trades unions at Lund University: OFR, SACO and SEKO Information about the position: Christer Löfstedt, Head of Department: +46-46-222 9338, christer.lofstedt@biol.lu.se; Information about conditions of employment and the application process: Faculty Personnel Manager Gunilla Thylander, +46 -46 222 40 32, gunilla.thylander@kanslin.lu.se

Description of responsibilities The main emphasis of the position is research within systematic biology with a focus on studies of evolutionary relationships at the level of species, and/or higher taxa.

The successful candidate will be expected to play a key role in establishing a competitive word-class research programme in systematics at the Department of Biology. The candidate should take responsibility for leading a research group, and be active in the development of the collections at the Biological Museums. He/she should actively seek external funding from national research councils and other research funds in order to cover part of the salaries and operational costs for the research group. The candidate is also expected to develop collaborations with other research groups within the Department that are active in related research areas, such as evolutionary biology, molecular ecology and biodiversity research.

In addition, the successful candidate is expected to be actively engaged in teaching and development of courses (at both basic and advanced levels) within systematics, evolution and biodiversity, and in the supervision of Bachelor and Master projects, as well as PhD students.

Qualifications According to Chapter 4, Section 3 of the Higher Education Ordinance (SFS 2010:1064) a person who has demonstrated both research and teaching expertise shall be qualified for employment as a professor except in disciplines in the fine, applied or performing arts.

The successful candidate is expected to have a distinguished record of achievements in the area of systematic biology with a focus on studies of evolutionary relationships at the level of species, and/or higher taxa. Scientific qualifications will be evaluated mainly on the basis of the quality and number of scientific publications at the highest international level. Demonstrated academic leadership skills, experience of supervising undergraduate and graduate students, collaborative skills, and an ability to compete successfully for external funding are of central importance. Demonstrated ability to develop and teach undergraduate and graduate courses in systematic biology are also important merits. A demonstrated ability to establish intra- and interdisciplinary research collaborations is important for the position, and the ways in which the candidateÂs background and expertise may strengthen the research profile in evolutionary biology and biodiversity research at the new Department of Biology will be taken into consideration. Experience of curating of museum collections is regarded as a merit.

The assessment criteria for appointment as a professor, according to

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NewcastleU PheasantConservation

The World Pheasant Association is looking for a Conservation Research and Support Officer.

The Conservation Research and Support Officer will provide support to WPA's Director, based in the UK. This key role is central to our long-term objectives of developing the capabilities of in-country nationals through the implementation of important conservation projects. We believe that knowledgeable and dedicated individuals are authoritative and highly effective voices for biodiversity conservation.

The Conservation Research and Support Officer will be responsible for ensuring that WPA's research is of the highest standards and co-ordinating support to key WPA partners, especially in China, India and Brazil. This will involve: enhancing WPA's existing training programme; providing technical guidance to ongoing WPA activities; and ensuring that all new WPA activities meet appropriate scientific and conservation standards. The post holder will work with a wide variety of individuals from institutions that are leaders in research and conservation both nationally and internationally. In particular the post holder will play a key role in developing our relationship with Newcastle University's School of Biology.

The successful candidate is likely to have an advanced degree, experience of the design and execution of fieldwork projects and a passion for biodiversity conservation and training. Good communication skills and a high degree of self-motivation will be essential.

For further information and contacts:

http://www.pheasant.org.uk/jobs.aspx sent by: Kirsten Wolff

Kirsten Wolff <kirsten.wolff@newcastle.ac.uk>

NHM London ResAssist TreePopGenetics

Research Assistant for Darwin Initiative Maya Nut Project

Salary: £24,164 per annum plus benefits

Contract: 22 Month fixed term appointment

Closing date: July 4, 2011

The Natural History Museum is a world leading museum, internationally recognised as a centre of excellence in scientific research and in the presentation of natural history through exhibitions, public programmes, publications and the web.

Working on a prestigious Darwin Initiative funded project to develop tools for the sustainable harvesting of Maya-nut (Brosimum alicastrum) you will be required to assess and analyse the geographical variation within this non timber tropical forest species across Mesoamerica using DNA markers (SNPs, microsatellites or SSRs). Maya-nut tree is a non timber tropical forest food which formed an important part of pre colonial diets in Central America. The forests where they are found are degraded throughout their Mesoamerica range. Currently there is strong interest in reforestation using this species which would need to maintain in-situ genetic variation so as to maintain the ecological and the social-economic importance of this species.

You will be responsible for generating analysing and preparing results for publication in a peer-reviewed journal and so will be expected to be familiar with extracting, amplifying and assembling DNA sequence data and analysing population genetic data using software such as ARLEQUIN, GENETIX, STRUCTURE, GENECLASS2, GENEMAPPER.

An MSc (or equivalent) and proven publication experience is essential for this post. Interviews will be held between July 18 and July 22.

For a full job description and to apply online please visit the Natural History Museum website at www.nhm.ac.uk/jobs < http://www.nhm.ac.uk/jobs >

Alex Monro <a.monro@nhm.ac.uk>

NHM LosAngeles HerpetologyCurator

Assistant/Associate Curator of Herpetology

The Natural History Museum of Los Angeles County, the largest natural history museum in the western United States and a national leader in exhibitions, education and research, seeks a curator specializing in the study of amphibians and/or reptiles to oversee its extensive collection of herpetological specimens. Currently the museum is undergoing a dramatic and exciting transformation involving development of new exhibitions, outside teaching-learning gardens and a nature lab. Foremost in the museum's mission is creating experiences embodied by the phrase 'where research and collections meet the visitor experience'. The desired candidate will have high level communication skills and an innate ability to engage and enthuse the public and stakeholders through his or her work.

The museum houses and oversees a world-class collection of amphibians and reptiles, with collection strengths in plethodontid salamanders, dendrobatid and leptodactylid frogs, and anguid, teiid, and xantusid lizards of the New World, particularly Central America and the deserts of Mexico and the Southwestern United States. The collection has potential for a broad array of research and public programs both within and outside of the Natural History Museum of Los Angeles County. The successful candidate will be responsible for creating a dynamic and productive program of research to build a growing scientific and public profile, overseeing the development and curation of this important collection, maintaining and strengthening the museum's presence in key professional and governmental networks, and actively collaborating with other sections of the museum to educate and communicate with our visitors.

The successful candidate will have a Ph.D., will have a strong track record of published research with strengths in the field of evolutionary biology of amphibians or reptiles, and will be expected to build an active and publically engaging research program, develop working relationships with local universities, mentor students, and maintain research through obtaining competitive grants and/or funding from other sources. He or she must have vision and capability to enhance the herpetology program, shape the collections and research in ways that increase both their scientific and public appeal, and have collections management experience relevant to the role. A record of general publications for wider readership would be an advantage.

The ability to effectively communicate and engage with a wide variety of audiences, including the public and the museum's various stakeholders is paramount. The successful candidate will be expected to participate in a broad range of museum activities including exhibits programs, educational outreach activities, and advancement activities. He or she will interact and maintain relationships with professional associations, educators and other relevant organizations within the scientific and regional communities.

This is a full-time position with a salary commensurate with experience, plus excellent benefits. The starting date is October 1st, 2011. Review of applications begins immediately and will continue until the position is filled. Applicants should send a cover letter, resume, salary history, and the names of three referees to the Human Resources Office, Natural History Museum of Los Angeles County, 900 Exposition Blvd., Los Angeles, CA 90007, via the museum web site at: http://www.nhm.org/site/about-our-museums/working-at-nhm/jobs-nhm The Natural History Museum of Los Angeles County is an Equal Opportunity Employer

Christine Thacker Associate Curator of Ichthyology Natural History Museum of Los Angeles County 900 Exposition Blvd., Los Angeles CA 90007

Christine Thacker <thacker@nhm.org>

NHM Paris BacterialGenomics

Assistant-Professor position in Bacterial genomics and metagenomics, EPHE/Natural History Museum, Paris

A tenure-track position as an assistant professor in bacterial genomics, metagenomics and statistical genetics is available at the EPHE /Integrative Population Biology /research group (Veuille Lab) in the Natural History Museum in Paris. The lab combines large empirical datasets and computational approaches to studying microbial population genetics (see http://www.thierrywirth-lab.com/). Current work in the lab focuses on a range of topics including (i) bacterial biodiversity and connectivity in Pacific Archipelagos, (ii) the interplay of sex and virulence in bacteria (/Escherichia coli/), (iii) the evolutionary history, demography and spread of major diseases using next-generation sequencing data. Our lab benefits from an excellent background in theoretical and modern population genetics (bioinformatics, modelisation, ABC, demogenetics) as well as an interdisciplinary research environment based on national and international collaborations (Institut Pasteur, Max-Planck Institute).

The successful candidate should have a postdoctoral experience, a strong background in computer science and statistics, and a deep interest in evolutionary genetics. A strong experience in genomewide and massive parallel sequencing datasets analyses is required. Programming skills and proficiency in unix-based computational environments are essential; finally a good publication record is required. She/he will also be involved in teaching activities in the /Biology, Health and Ecology/ Master

Remark: The position concerns evolutionary genomics, therefore a background in bacteria genetics and genomics is not mandatory.

Position linkt: http://www.ephe.sorbonne.fr/-actualites/recrutement-enseignants-chercheurs-2011.html Application deadline is the 2nd of June 2011.

Informal inquiries as well as applications (including a CV, copies of relevant publications and contact information for at least two references) should be emailed to both Thierry Wirth (wirth@mnhn.fr) and Michel Veuille (veuille@mnhn.fr). The starting date can be as early as October 2011.

Prof. Thierry Wirth

Muséum National d'Histoire Naturelle - EPHE Department of Systematics and Evolution UMR-CNRS 7205 16, rue Buffon, 75231 Paris cedex 05 France tel. +33 (0) 1 4079 8036; gsm. +33 (0) 648155320 email: wirth@mnhn.fr url: http://www.thierrywirth-lab.com

UBristol ResTech 2 DrosophilaAdaptation

Two Research Technician Positions investigating limits to adaptation in rainforest Drosophila School of Biological Sciences, University of Bristol. 6 month fixed term contract Salary: £21,021 p.a.

Description: You will assist with research using quantitative genetic studies to test population genetic models of limits to adaptation at range margins. The work will focus on estimating adaptive divergence and genetic variation in Drosophila lines collected from several ecological gradients between high and low altitude rainforest in northern Queensland. Addressing these issues is crucial for assessing dangerous levels of environmental change.

The research involves collaborations with Profs Mark Blows (Queensland), Ary Hoffmann (Melbourne), as well as Nick Barton (Vienna). Training will be provided in Drosophila handling and experimental procedures, but prior experience would be a definite advantage.

Appointments are offered on a fixed-term contract of six months. It is expected that interviews will be held in early July 2011 for a start date in late July.

Further details, including a full position description and details on how to apply, can be found at http://-/www.bris.ac.uk/boris/jobs/feeds/ads?ID=97751 The closing date for this position is 9am 5th July 2011.

For informal enquiries, please contact Dr Eleanor O'Brien: eleanor.obrien@bristol.ac.uk or +44 (0)117 928 7470

– Dr. Eleanor O'Brien Postdoctoral Researcher School of Biological Sciences University of Bristol

Ph: +44 (0)117 928 7470

Eleanor O'Brien <Eleanor.OBrien@bristol.ac.uk>

UCaliforniaRiverside ResAssist SymbiosisEvolution

Job: Research Assistant II/III

The Sachs Lab at UC Riverside is seeking to hire a Research Assistant position to assist our studies of the evolutionary genetics of symbiotic bacteria. The position is available this July 2011 and will begin as soon as possible. The Research Assistant appointment is initially for a one-year period, with possible extension of another year, dependent upon satisfactory performance and presence of adequate funding. Salary is commensurate with experience and qualifications and includes full health benefits.

REQUIREMENTS FOR HIRE: i) BA or BS in Biology or related field, ii) excellent undergraduate record, iii) wet-lab experience in a research lab, iv) proficiency with accessing and manipulating data, v) two letters of recommendation from academic/scientific mentors.

PREFERRED RESEARCH SKILLS: Preference will go to applicants with some or many of the following skills. WET LAB SKILLS: Sterile bacterial culture techniques, Light Miscoscopy, Histology / Microtomography, PCR & DNA sequencing, fine dissection.

COMPUTER SKILLS: Experience with accessing and searching bioinformatic databases, experience analyzing DNA sequence data, programming skills related to DNA sequence databases, proficiency with software to design figures for publications.

APPLICATION: applicants should apply through the UCR Jobs Website: http://jobs.ucr.edu/ The position is # 201105310701

APPLICATIONS ARE DUE BY JUNE 17th

More information about UC Riverside: 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 gives every student the resources to explore, engage, imagine and excel.

At UC Riverside we celebrate diversity and are proud of our #4 ranking among the nation for most diverse universities (US News and World Report 2011). 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 ranked 41st among top public universities (US News and World Report 2011) and is an affirmative action and equal opportunity employer, with a commitment to workforce diversity.

More information about Sachs Lab Research:: Our research seeks to understand the emergence and spread of exploitative traits in symbiont populations, especially the plant symbiont Bradyrhizobium japonicum. Bradyrhizobia are bacteria that induce beneficial infections in legume plants: the bacteria form nodules on host roots and fix atmospheric nitrogen in exchange for carbon from their plant hosts. Potential projects include assisting in collections of Bradyrhizobium from wild legume populations, culturing and sequencing DNA of bacterial isolates and using computational and experimental methods to test hypotheses about the evolution of symbiosis and pathogenesis. At a broader level our lab also studies the macroevolution of symbiosis across bacteria using computational techniques that gather and analyze data from published sources. For more details see our website: www.sachslab.com Joel L. Sachs Assistant Professor Department of Biology University of California 3314 Spieth Hall Riverside, CA 92521 joels@ucr.edu Office (951) 827-6357 Fax (951) 827-4286 http://www.sachslab.com http://www.biology.ucr.edu/people/faculty/Sachs.html

joel.sachs@ucr.edu

UCollegeLondon Biodiversity

Text: Job Vacancy University College London, Department of Genetics, Evolution and Environment

Reader or Chair in Ecology and Biodiversity

Salary: UCL Reader scale, £50,902 - £55,362 per annum UCL Professorial scale: minimum salary negotiable but not less than £61,960 p.a.

Closing date: 31 July 2011

We invite applications from world class research scientists in the areas of Ecology and Biodiversity.

This appointment is part of a major initiative to strengthen and diversify research activity in evolutionary, population and environmental biology in newly refurbished laboratories within UCL. UCL has a rich history in Ecology and Evolution, including such luminaries as Robert Grant; Francis Galton; RA Fisher; Karl Pearson; JBS Haldane; and Peter Medawar, and this appointment will aim to continue this line.

The successful candidate will be expected to: play a leadership role in this initiative and promote interaction across the diverse disciplines represented in the Department, the Division of Biosciences and across UCL; coordinate efforts to respond to national and international funding initiatives; and develop existing and new postgraduate training programmes and contribute to undergraduate teaching.

For a Chair, he/she is expected to have a continuing track record of external research grant funding over a number of years, and doctoral research supervision. For a Readership, he/she is expected to have past success in obtaining external funding and experience of doctoral research supervision. At either level, candidates are also expected to have a track record in publishing high impact original research articles, experience of teaching at undergraduate or postgraduate level and excellent interpersonal, oral and written communication skills.

Further information about this post, together with application details, can be found at http://www.ucl.ac.uk/gee/jobs Informal enquiries can be made to Dr David Murrell (d.murrell@ucl.ac.uk)

NB. a second appointment in Evolutionary and Comparative Biology will also be made at the Readership/Chair level; details at same webpage.

Dr David Murrell Research Department of Genetics, Evolution and Environment, University College London, Office 108b Darwin Building Gower Street London WC1E 6BT United Kingdom

Co-Director for Biodiversity UCL Environment Institute http://www.ucl.ac.uk/environment-institute/ Associate Editor for Methods in Ecology and Evolution http://www.methodsinecologyandevolution.org/view/0/index.html And

Secretary for the British Ecological Society Specialist Interest Group in Computational Ecology

Tel: 020 7679 7268 Internal ext: 37268

Email: d.murrell@ucl.ac.uk

WEBPAGE http://www.ucl.ac.uk/slms/people/show.php?personid=3D100476 RECENT ARTICLE: http://www.esajournals.org/doi/abs/10.1890/09-0832.1 d.murrell@ucl.ac.uk

UCollegeLondon EvolutionaryBiology

Job Vacancy University College London, Department of Genetics, Evolution and Environment

Reader or Chair in Evolutionary and Comparative Biology

We invite applications from world class research scientists in the areas of Evolutionary and Comparative Biology.

This appointment is part of a major initiative to strengthen and diversify research activity in evolutionary, population and environmental biology in newly refurbished laboratories within UCL.

The successful candidate will be expected to: play a leadership role in this initiative and promote interaction across the diverse disciplines represented in the Department, the Division of Biosciences and across UCL; coordinate efforts to respond to national and international funding initiatives; and develop existing and new postgraduate training programmes and contribute to undergraduate teaching.

Further information about this post, together with application details, can be found at http://www.ucl.ac.uk/gee/jobs Closing date: 31 July 2011

NB. a second appointment in Ecology and Biodiversity will also be made at the Readership/Chair level; details at same webpage.

Max Telford Professor of Zoology Department of Genetics, Evolution and Environment, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel: +44 (0)20 7679 2554 (Internal: 32554) Fax: +44 (0)20 7679 7096 http://www.ucl.ac.uk/biology/academic-staff/telford/telford.html a new open access journal EvoDevo: http://www.evodevojournal.com/ Telford & Littlewood: Animal Evolution. OUP

Software to align Nucleotide sequence according to Amino Acid translation TranslatorX

Files and software for downloading:

Mrimpatient: If you cant wait to see latest result of MrBayes analysis. Xstem and Ystem: Software for 2y structure data in rRNA phylogenetic analyses. MtZoa and MtHydro : new amino acid substitution matrices Hacked version of MrBayes using these matrices

Xenoturbella You Tube video

The Linnean Society of London

m.telford@ucl.ac.uk

ULyon Bioinformatics

The Institut de Génomique Fonctionnelle de Lyon (IGFL) currently hosts 10 groups and is hiring 8 additional groups in line with its scientific expansion. The IGFL is run by the ENS de Lyon, CNRS, and Université Lyon 1. The Institute is relocating, early 2012, to occupy a newly commissioned 3200 m2 building, within a multidisciplinary campus. The new location will host approximately 200 scientists and staff.

Current and future research at the IGFL focuses on integrative biology, developmental biology, evolutionary sciences and bioinformatics/modeling at the genomic scale. IGFL groups will access state-of-the-art core services, including high throughput sequencing technologies, imaging, transgenic animal facilities (mouse, fish, drosophila), paleogenomics, bioinformatics, mass spectrometry, proteomics, FACS sorting, histology and electron microscopy.

The IGFL proposes three distinct calls for outstanding group leaders:

#1-2011 Non-thematic call Open call for group leaders addressing whole-organism level research, with a special focus on animal-based research falling within the scientific mission of the Institute.

#2-2011 Developmental biology In order to reinforce this research axis at the IGFL, this call targets group leaders investigating developmental mechanisms using established animal models (eg drosophila, zebrafish, mouse etc).

#3-2011 Systems biology / bioinformatics The IGFL is also seeking to recruit groups performing research on whole genome data analysis, gene regulatory networks, modeling of biological processes etc... in order to significantly contribute to our functional understanding of genome structure and evolution. These groups are highly encouraged to collaborate with experimental (wet) labs.

Applications (in English, specifying the call reference in the subject line) should include curriculum vitae, a short description of achievements and records of self-financing, a proposed research program of approx. 10 pages and contact details for 3 professional references. The deadline for applications is July 17th 2011. Please send as a single PDF named LASTNAME_IGFL_2011.pdf to direction.igfl@ens-lyon.fr Enquiries should also be directed to this address. http://igfl.ens-lyon.fr/ Joanne Burden <joanne.burden@ens-lyon.fr>

UTurku EvolutionaryInteractions

A tenure-track professorship in the field of ecological interactions is available at the University of Turku.

The full position description and application instructions can be found at:

http://www.utu.fi/faktat/tyontekijaksi/tehtavaselosteet/seloste_ekologia_ENG.pdf The deadline for applications is June 20 15:45 (Finnish time). Email application are allowed.

The University is recruiting Assistant professors in a number of fields. They will be recruited initially for a fixed-term employment relationship (of three to five years) for the tenure track, during which the work will be followed and evaluated according to defined criteria. Success in the evaluation will lead to a new fixed term employment contract (of two to four years) and the aim is to obtain tenure as a professor after an evaluation.

The minimum requirements for a person to be appointed to the tenure track are a doctoral degree, high-level academic competence, experience in managing academic research, experience of international cooperation in the field he or she represents, as well as teaching experience. When evaluating the merits of the applicant, the following factors will be taken into consideration: research and teaching merit, active participation in the academic community, success in obtaining complementary funding, as well as academic work abroad and international duties

The Department of Biology hosts three ISI Highly cited scientists and a national Center of Excellence. See http://www.sci.utu.fi/biologia/en/research/research_projects/ for more details or research projects.

Turku, Finlands 5th largest city (176 000 people), is located in the South-Western part of Finland. It has a rich cultural history and is the gateway to a beautiful archipelago. The University of Turku is one of the major multidisciplinary universities in Finland and the City of Turku was ranked third in the most recent classification of medium-sized Smart Cities (http://www.smart-cities.eu)

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Craig Primmer

Academy Professor Division of Genetics and Physiology Department of Biology (Vesilinnantie 5) 20014 University of Turku FINLAND

Office +358 2 333 5571 Mobile +358 40 1560 365 Fax. +358 2 333 6680 craig.primmer@utu.fi http://users.utu.fi/primmer Craig Primmer <craig.primmer@utu.fi>

UTurku EvolutionaryPhysiology

An ongoing, full professorship is available in the laboratory of animal physiology at the University of Turku, Finland. The formal field of the professorship is ecophysiology and ecotoxicology, but the lab has a tradition in evolutionary physiology and thus applications from researchers with a strong evolutionary background are also encouraged.

The full position description and application requirements can be found at:

http://www.utu.fi/faktat/tyontekijaksi/-tehtavaselosteet/seloste_ekofysiologia_ENG.pdf The application deadline is 15:45 (Finnish time) 15.6.2011. Email applications are allowed.

The strategy of the University of Turku for years 2010-2012 includes six fields of research strength of which two are associated with biological sciences: ecological interactions and ecological genetics, and molecular biosciences. The position to be filled aims in its part to keep the research on ecological interactions and ecological genetics at world class by increasing the focus of animal physiology and cell biology of animals towards environmental and ecotoxicological questions. Notably teaching and research on disturbances of animal function (ecotoxicological teaching and research) requires detailed understanding of normal functions of animals (ecophysiology). Thus, combination of the two in the applicants knowhow is sought . It helps in understanding environmental adaptation and combining genetic and ecological approaches to environmental biology.

The Department of Biology hosts three ISI Highly cited scientists and a national Center of Excellence (see http://www.sci.utu.fi/biologia/en/research/-research_projects/ for more details of ongoing research projects)

Turku, Finland's 5th largest city (176 000 people), is located in the South-Western part of Finland. It has a rich cultural history and is the gateway to a beautiful archipelago. The University of Turku is one of the major multidisciplinary universities in Finland and the City of Turku was ranked third in the most recent classification of medium-sized Smart Cities (http://-www.smart-cities.eu)

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Craig Primmer

Academy Professor Division of Genetics and Physiology Department of Biology (Vesilinnantie 5) 20014 University of Turku FINLAND

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Zambia FieldAssist CichlidBreeding

Field assistant to study behaviour of cooperative breeding African cichlids, Lake Tanganyika (Zambia)

The project investigates the influences of helping behavior on fitness prospects and life-history in the highly social, cooperatively breeding cichlid Neolamprologus pulcher (diving depth: 8-12m). It is part of a long term project which has been launched in 2009 attempting to follow permanently marked individuals over several years. The field assistant will carry out behavioral observations under water using Psion PDAs and Observer software of marked fish in their natural group. We search a field assistant for a diving expedition of the University of Bern in autumn 2009. The field work will last 3 months and takes place near Mpulungu, Zambia, starting end of August. Candidates must hold a SCUBA diving certificate (PADI Open Water Diver or equivalent), should have diving experience and need to have experience in behavioral observations. Experience with fish is considered an asset and a high degree of motivation is needed as field assistants will be working independently. The field team will have 7 members and support from local authorities.

Accommodation at the field site is remote and very basic, but beautifully located on the shore of Lake Tanganyika. Fieldwork and diving is physically demanding. All expenses for travel, accommodation and medical precaution are covered, but no salary can be paid.

Candidates send a statement of scientific interests and their CV to: markus.zoettl@iee.unibe.ch or arne.jungwirth@iee.unibe.ch

Further information about the working group and our institute: http://behav.zoology.unibe.ch/ Markus Zöttl & Arne Jungwirth Institute of Ecology and Evolution University of Bern Wohlenstrasse 50A 3032 Hinterkappelen Switzerland

Tel: +41 31 631 9158 Tel: +41 31 631 9160

"Zöttl, Markus (IEE)" <markus.zoettl@iee.unibe.ch>

Other

AFLP troubleshooting

Dear EvolDir members,

Recently we started to experience a drop in the number of high molecular weight bands in the AFLP profiles of our study systems (diverse alpine plants). The selective seems to work, just 20-30% of the bands are lost. This happens to fragments over 200-300 bp, and to all samples within our lab, but despite changing reagent stocks, the problem persisted. We have tried also different dillutions of res-lig and preselective reactions, but without success.

Any comments would be highly appreciated!

Thanks,

Pedro Escobar García Department of Systematic and Evolutionary Botany University of Vienna Rennweg 14, 1030 Vienna, Austria Tel. +43-1-4277/54064, Fax +43-1-4277/9541 homepage: http://www.botanik.univie.ac.at/-plantchorology/escobar.htm Pedro Escobar Garcia <pedro.escobar.garcia@univie.ac.at>

BayesTraits and EvolutionRateEstimation

Hello,

I am trying to estimate evolutionary transition rates for a multistate, non-ordinal trait that is polymorphic for several taxa (i.e., several taxa have more than one trait state).

I have a two questions about estimating these transition rates.

First, when I use either ML or MCMC in BayesTraits, for any given transition, I am encountering a wide range of rate variation across analyzes even when using the same data and the same tree. For instance, when I run a ML analysis 100 times on the same tree, for a single transition, I'll get a range of rate values from 0-33. Interestingly, I do not see a similar degree of variation in the ancestral state reconstruction.

I imagine the multistate, polymorphic nature of the trait plays a role in the variation I am observing, but it is still surprising. Is there any way I can reduce the uncertainty around these rate estimates?

Second, I am would also like to tally up the number of transitions estimated from a parsimony analysis. I can estimate ancestral states using parsimony easily enough in Mesquite. However, there are too MPRs to use the 'summarize state changes' function in Mesquite to count transitions. So I was wondering if there is a function or package in R (or elsewhere) to count state transitions across a phylogeny, given that I already have the estimated node values.

Any advice on either of these issues would be much appreciated!

Thanks! Charlie Willis

Duke University Department of Biology 125 Science Drive Durham NC 27708 CP (605) 553-1057 charlie.willis@duke.edu http://www.duke.edu/ ~ cgw6/ Charles Willis <charlie.willis@duke.edu>

Biogeography teaching exercises

Dear Evoldir,

I am designing a new course in biogeography, aimed at upper-division undergraduates. As part of the course I would like to include some simple exercises in GIS, phylogeny reconstruction, and/or phylogeography. If anybody has already developed exercises in these area and would be willing to share them with me, I would greatly appreciate it.

I am happy to post a summary of any replies I receive.

- Sarah Gilman

Sarah Gilman, Ph.D.

Joint Science Department Keck Science Center The Claremont Colleges 925 N. Mills Avenue Claremont, CA 91711

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

SGilman@jsd.claremont.edu

Biology Philosophy journal

Call for Papers: Philosophy & Theory in Biology

Philosophy & Theory in Biology is an open access, online, peer reviewed journal devoted to the interface between philosophy of science and theoretical biology. The journal is published and permanently archived by the Scholarly Publishing Office, University of Michigan Library, and is standardly indexed (e.g., PhilPapers).

The Editorial Board is composed of prominent philosophers and biologists from a variety of disciplinary backgrounds. Recently published papers include Natural Selection and Multi-Level Causation, Competition Theory and Channeling Explanation, and Beyond Inclusive Fitness? On A Simple And General Explanation For The Evolution of Altruism. We have a streamlined editorial process with efficient reviewing of manuscripts and a short time from the final acceptance of a paper to its online publication.

We are currently accepting papers in one of four general categories: a) scholarly papers on a specific aspect of philosophy of biology or theoretical biology; b) in-depth “trend” review papers on topics of current interest within the areas covered by the journal; c) extended (essay style) reviews of a book or books pertinent to the journal; d) “crosstalk” discussions - technical yet accessible articles written by biologists on topics of interest to philosophers, or by philosophers on topics of interest to biologists.

For further information please contact the Corresponding Editor, Massimo Pigliucci, at massimo@platofootnote.org, or visit us at philosophyandtheoryinbiology.org.

Massimo Pigliucci <massimo.pigliucci@gmail.com>

Deania calcea samples

Dear All,

I am requesting assistance in obtaining samples of Deania calcea (birdbeak dogfish) from the Atlantic for a population genetic study. I am part of a research consortium studying the physical and biogeochemical factors influencing the distributions and structure of deep-sea communities, focusing on the fauna of the Mid-Atlantic Ridge. I currently have samples from the Irish Sea and the Bay of Biscay but would ideally like additional samples especially from locations west of the MAR. Any help would be very much appreciated.

Thank you very much,

Laura

Dr. Laura Corrigan Molecular Ecology Group Biological and Biomedical Sciences Durham University Durham DH1 3LE UK Tel: +44 (0191) 334 1283

“CORRIGAN L.J.” <l.j.corrigan@durham.ac.uk>

Detecting population subdivision

Dear colleagues,

I am trying to detect population subdivision of metagenomic sequences. Below I described the type of data I have. I am seeking for a program / method which can measure population subdivision for my data.

This dataset is from marine metagenomics study. Basically, seawater was sampled and bacteria were filtered. Then DNA was directly sequenced from the bacterial community without culturing the bacteria. So it is difficult to trace the source organisms for the metagenomic sequences. Due to the nature of high biological diversity in the ocean ecosystem and sequencing depth coverage, the compiled sequence alignment datasets, each of which contains closely related homologous genes from a dominant bacterial population, are essentially from different but closely related organisms/lineages. For example, if there are 6 sequences in one alignment, and 8 sequences in another alignment, those 14 sequences in total are most likely from 14 individual closely related organisms/lineages.

I would greatly appreciate if you could provide some clues. Thanks!

Haiwei Luo Postdoctoral Research Associate Department of Marine Sciences University of Georgia

Haiwei Luo <hluo2006@gmail.com>

Discount registration for Evolution2011 2

$170 graduate student registration available for the Evolution conference in Norman, Oklahoma, USA, June 17-21. Normal graduate student registration is $235. If interested, please contact mniemill[AT]utk.edu

I registered for the meeting but am now unable to attend, as my father is having surgery. However, registration is transferable. mniemill@utk.edu

Matthew Niemiller <mniemill@utk.edu>

Discount registration for Evolution2011 3

Subject: Evolution 2011 registration for sale

I cannot attend the Evolution 2011 conference and I wish to sell my registration. I am asking $150 for the registration (the original cost was $235). Please contact me if you would like this registration.

Thanks

Chris

– Christopher Hamm, PhD Candidate Department of Entomology Program in Ecology, Evolutionary Biology & Behavior Michigan State University 204 Center for Integrated Plant Systems East Lansing, MI 48824

Phone (517) 432-5282 FAX (517) 353-5598 email chamm@msu.edu

http://www.msu.edu/~chamm

Chris Hamm <topher.hamm@gmail.com>

DNA isloation in plates

Dear all,

I need help with the following issue. I'm looking for a reliable kit for DNA isolation that uses slilica membrane columns in a format of 96-well plate that enables to use a standard plate centrifuge. The kits I'm aware of require centrifugation at 5000-6000xg while the maximum speed of standard plate centrifuge is around 2000-3000xg.

Many thanks advance,

Aleksandra Biedrzycka Institute of Nature Conservation Polish Academy of Sciences

biedrzycka@iop.krakow.pl

Drosophila mojavensis isofemale lines

The Drosophila Species Stock Center recently has added 40/D. mojavensis/ isofemale lines:

6 isofemale lines collected in Anza Borrego Desert, CA on April 29th, 2011 (from M. Richmond)

25 isofemale lines collected in Las Bocas, Sonora, Mexico on May 11th, 2011 (from T. Markow)

9 isofemale lines collected from Catalina Island, CA on April 12th, 2011 (from J. Kao& S. Nuzhdin)

All lines will be available until July 30th, 2011.

Details are available on the Drosophila Species Stock Center Website at https://stockcenter.ucsd.edu/info/welcome.php, or you can contact the Stock Center manager (mrichmond@ucsd.edu)

– Maxi Polihronakis Richmond, PhD Drosophila Species Stock Center University of California, San Diego 9500 Gilman Drive # 0116 La Jolla, California 92093-0116 mrichmond@ucsd.edu

Maxi Polihronakis Richmond <mrichmond@ucsd.edu>

Evolution2011 UndergraduateDiversity 2

CALL FOR MENTORS: Undergraduate Diversity at Evolution 2011

Twenty-five undergraduates will be attending the 2011 Evolution Meeting in Norman, OK with support from the NSF-funded “Undergraduate Diversity at Evolution” program (in partnership with NESCent). We invite graduate students, postdocs, and faculty members to serve as mentors to the undergraduates. Mentors take pairs of students to attend talks with them, introduce them to colleagues, network and generally make the meetings a welcoming place for them. Although costs are not covered for mentors, it is an unusually rewarding experience.

Contact Dr. Rich Kliman (rmkliman@cedarcrest.edu) if you are interested in serving as a mentor.

Jory P. Weintraub, PhD Assistant Director, Education and Outreach National Evolutionary Synthesis Center (NESCent) 2024 West Main St., Suite A200 Box 104403 Durham, NC 27705 Phone: 919.668.4578 Fax: 919.668.9198 Email: jory@nescent.org Skype: jory.weintraub Web: www.nescent.org

Jory Weintraub <jory@nescent.org>

Evolution videos

EVOLUTION ACADEMY - VIDEOS ON NATURAL SELECTION (Darwin, Matthew & Butler)

NEW SERIES. Following the introductory series of twelve 15 minute Evolution Academy videos on Evolutionary Principles, I happily present a second series of 12 videos on Natural Selection. These deal with historical aspects of Natural Selection, with special reference to the complex interactions between Charles Darwin, Patrick Matthew and Samuel Butler.

HOW TO VIEW THE VIDEO LIST. Go to web-page (http://post.queensu.ca/~forsdyke/videolectures.htm).

HOW TO VIEW THE FIRST VIDEO. This is entitled “History and Words” and may be viewed on YouTube (http://www.youtube.com/watch?v=-LPxHKPQ3SM).

The videos supplement my books on bioinformatics and biohistory, and my evolution web-pages.

Donald R. Forsdyke, Department of Biochemistry, Queen's University, Kingston, Ontario, Canada K7L3N6

forsdyke@queensu.ca

Heredity podcasts

The free Heredity podcasts have returned this year, and are available online (see below). They provide the latest research news from Heredity, in the words of the researchers themselves.

Informal interviews are used to make the science in the journal Heredity more accessible. The authors explain the basic foundations of their topic, and draw out the key findings of their paper.

The podcasts have proved popular with biology undergraduates and professionals alike.

You can listen by entering 'Heredity podcast' into your search engine clicking the link on the Heredity home page http://www.nature.com/hdy/ or by subscribing on iTunes to receive the latest episodes automatically (search for 'Heredity podcast').

Enquiries to the podcast editor r.a.nichols@qmul.ac.uk

Richard Nichols <r.a.nichols@qmul.ac.uk>

IlluminaInfinium assays and historical DNA

Dear evoldir members.

I am about to start testing Illumina SNP genotyping using Infinium assays on some historical samples (i.e., highly degraded). I am wondering if there is anyone that has had some experience with this, and may have some tips and experiences they wouldn't mind sharing. Any thoughts or suggestions would be very welcome.

Best.

Anders.

– Anders Gonçalves da Silva Postdoctoral Research Scientist CSIRO Marine and Atmospheric Research Castray Esplanade Hobart, TAS 7000 Australia

Email: anders.goncalvesdasilva@csiro.au Phone: +61 3 6232 5434

Anders.Goncalvesdasilva@csiro.au

Lab management strategies

Hi Evoldir,

I'm interested to know of different strategies people use to manage their routine molecular systematics data, namely, accessions, DNA extractions, PCRs attempted/successful, sequences, etc. I've always used Microsoft Access, which is fine for me. But it has a steep learning curve, making it hard to teach to students in the lab, and it's not available on a Mac. I know a lot of people keep everything in a Big Excel Spreadsheet, but that is not as versatile if one is accustomed to being able to run queries, etc. on a large dataset.

Perhaps there is another solution that combines ease-of-use & versatility that I'm not aware of? I will be happy to post a summary of the community's suggestions.

Cheers, Norm Douglas

– Norman A. Douglas Postdoctoral Research Associate Oberlin College Biology Department Science Center K107 119 Woodland St. Oberlin, OH 44074-1097 (440) 775-6277 norm.douglas@oberlin.edu

Norman Douglas <ndouglas@oberlin.edu>

Lab management strategies answers

Many thanks to those who replied to my query about managing lab workflows.

It seems that most respondents are currently using the Big Excel Spreadsheet method, with some groups having the spreadsheet stored "in the cloud" i.e. as a Google Doc for safety and accessibility.

Many respondents suggested using FileMaker Pro, which is a relational database (like Microsoft Access) that is a native Mac OS application. I had looked at this, and also at OpenOffice.org's Base program, which is cross-platform and open-source. Other relational databases suggested were Bento (not familiar with it, but it is made by the same company as FileMaker Pro, and seems like it might be a "lite" version) and Visual Fox Pro.

Finally, a couple of dedicated solutions were suggested (and I'm not reviewing these- just first impressions):

Lablife seems to be a web-based service with a free academic license. It seems like a very general assistant lab manager, supporting inventory, ordering, etc. with a few biology-specific features and cloning tools.

EarthCape (http://www.earthcape.com < http://www.earthcape.com/ >) seems like will be primarily a collection/accesssion management tool and not specifically oriented toward dealing with genetic data and workflows, though it may have some functionality for this.

Finally, the Moorea Biocode LIMS /(Laboratory Information Management)/ Software (http://software.mooreabiocode.org) is an add-on to the Geneious program which tracks samples and sequencing experiments within Geneious.

None of our students have had any experience with relational databases, and while some of these programs may be easier to learn & use than MS Access, it is a lot to ask of students when they are also trying to learn PCR & sequencing, etc. The Biocode LIMS looks very slick, and may be exactly what we need since our lab uses Geneious anyway.

Thanks again to all who responded! Norm

– Norman A. Douglas Postdoctoral Research Associate Oberlin College Biology Department Science Center K107 119 Woodland St. Oberlin, OH 44074-1097 (440) 775-6277 norm.douglas@oberlin.edu

Norman Douglas <ndouglas@oberlin.edu>

MrBayes convergence answers

Dear colleagues,

Thank you so much for those who responded my question about convergence issue in MrBayes tree. Below is a summary of the responses.

(1) AWTY software can be used (http://king2.scs.fsu.edu/CEBProjects/awty/awty_start.php).

(2) check the PSFR value (should approaching to 1).

(3) check the standard deviation of split frequencies (should approaching to 0, less than 0.01)

(4) Tracer software can be used (http://beast.bio.ed.ac.uk/Tracer)

Haiwei Luo University of Georiga

Haiwei Luo <hluo2006@gmail.com>

NESCent EvolutionVideoContest 3

EVOLUTION VIDEO CONTEST DEADLINE APPROACHING!

Call for entries: NESCent announces Evolution Video Contest Application deadline is one week from today: Friday June 10, 2011

Submit your best evolution-themed video for screening at this year's Evolution meeting! The National Evolutionary Synthesis Center (NESCent) invites scientists of all stripes - graduate students, postdoctoral fellows and faculty - to enter the first-ever evolution video competition.

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 top finalists will then be screened at a film festival at the 2011 Evolution meeting in Norman, OK, from 6:30 to 7:30 PM on Monday June 20th. After screening the videos, the audience will vote for their favorites. Prizes will be awarded for the top entries.

Eligibility

You do not need to attend the conference to submit an entry. All videos submitted by Friday, June 10th (5:00 p.m. ET) are eligible to win. For more information and full contest rules, please see http://evolutionvideo.wordpress.com/ or contact Dr. Jory Weintraub at jory@nescent.org, or Dr. Robin Smith at rsmith@nescent.org.

Jory Weintraub <jory@nescent.org>

PCR problems

Hello, a colleague gave me the link to your website and maybe you could help me.

For my Bachelor Thesis I work with blood samples (with EDTA) of Asian Elephants (kept in zoos) to analyse microsatellite locis. But the PCR shows no results. I tried Gradient PCR to find out the right Annealing-Temperature, but just with low success. I isolated the DNA from the samples a second time also with low results at the PCR. I also changed the conc. of the template DNA (from 0,5 to 3 μl) with no success. The analysis of mtDNA showed good results.

Ingrdients for one sample: 12,175 μl H20 3,75 μl Buffer (Mg 7,5 mM) 0,75 μl dNTPs (2 mM each) 0,5 μl Primer (10 mM) 0,075 μl Taq (5u/μl) 1 μl template DNA

I use the following Primers: La02; La03; La05; FH60; FH94; FH102; EMX02; EMX03; LafMS02; LafMS03; LafMS05.

I hope somebody who worked with EDTA blood samples and may had to do with similar problems could give me help or a hint to get some results from the samples.

with best regards,

Jens Berner

Jens Berner <jens.berner1@freenet.de>

PCR products remain in wells

Dear all,

I have a PCR phenomenon that I can find no answer to, and would like to know if anyone has an explanation. Over the course of many years (maybe too many!) of PCR reactions, typically amplifying products of between 700 - 2kb, occasionally, but only very infrequently, I have experienced samples that present what appears to be the product of the PCR reaction that has failed to migrate from the well, instead fluorescing brightly within the well. The low frequency occurrence of these events have meant that I have thought them to be curious, but largely ignored them. Looking around on various discussion threads it seems this is a phenomenon others have experienced, and there are differing opinions about what the cause is, summarized here:

1) An excessive amount of the target amplicon has been produced, and somehow this has limited its ability to migrate through the gel.

2) Too much template in the reaction.

3) The reaction failed, and what is observed in the well is the genomic template.

4) An issue related to reaction efficiency - e.g. primers are problematic.

We have a reaction where “the blob” in the well is a real issue, and we can rule out all of the above, leaving me with the question of what is actually going on? We are amplifying a 10kb mtDNA fragment in beetles. Some beetles amplify well for the fragment, while others give no band, but a blob in the well, and others may present both a faint band, and a blob in the well. So whatever is happening, the blob would seem to be the result of a reaction that is outcompeting the target amplicon for the primers and nucleotides in the reaction mix. The genomic DNA for all samples is fine, we’ve run it out to check the integrity. The primers are fine, as they work for the same set of samples (i.e. those that give the expected 10kb product, and those that yield the blob) in conjunction with other primers to amplify smaller amplicons. We’ve tried different template concentrations, and that has not solved the problem. Additionally, we can rule out that the blob is in any way related to the target amplicon, as we’ve tried sequencing the blob with a series of internal primers of known functionality, and these yield no sequences (not a trace - i.e. flat chromatagrams). Curiously, successful PCR or blobbing seems to be sample specific - i.e. samples seem to consistently amplify, or consistently blob.

All things PCR have an explanation, but this is one that I am completely at a loss to explain. Can anyone out there provide an explanation? I’m offering a pint of beer to the first person who can*.

I hope I’ve been clear, if anyone would like further details, just ask.

Best regards Brent

* postage and packaging not included.

Brent Emerson Centre for Ecology, Evolution and Conservation School of Biological Sciences e-mail: b.emerson@uea.ac.uk University of East Anglia ph: (44) 01603 592237 Norwich NR4 7TJ fax: (44) 01603 592250 ENGLAND mob: (44) 0795 121 8827 http://-

biobis.bio.uea.ac.uk/biosql/fac_show.aspx?ID=3D255

B.Emerson@uea.ac.uk

PDF 1887 article

Dear Members of Evolution directory,

Would someone be able to send me a pdf of the following article?

Dallinger, W. H. 1887. The president's address. J. Roy. Microscop. Soc., 185-199.

Thanks,

JP

jpxu@mcmaster.ca

Phyloseminar JStajich Jun29

Next up at phyloseminar.org:

Jason Stajich speaks Wednesday, June 29th at noon PST on "Fungal phylogenomics: Getting lost in the moldy forest."

Abstract: Fungi occupy diverse ecological niches in roles from nutrient cycling in rainforest floors to aggressive plant and animal pathogens. Molecular phylogenetics has helped resolve many of branches on the Fungal tree of life and enabling studies of evolution across this diverse kingdom. The genome sequences from hundreds of fungi now permit the study of change in genes and gene content in this phylogenetic context and to connect molecular evolution with adaptation to ecological niches or changes in lifestyles. I will describe our work in studies contrasting pathogenic and non-pathogenic fungi and efforts to unravel the evolution of multicellularity in fungi comparing unicellular basal fungi with multicellular mushrooms and molds.

The development of tools for data mining and use of fungal genomics is also driving the pace of molecular biology and genetics of fungi. I will highlight new approaches to make this easier and the ways data integration can inform and transform studies of functional biology of fungi.

Japan 04:00 (04:00 AM) on Thursday, June 30 New Zealand 07:00 (07:00 AM) on Thursday, June 30 West Coast USA 12:00 (12:00 PM) on Wednesday, June 29 East Coast USA 15:00 (03:00 PM) on Wednesday, June 29 England 20:00 (08:00 PM) on Wednesday, June 29 France 21:00 (09:00 PM) on Wednesday, June 29

For more details, please visit http://phyloseminar.org – Frederick "Erick" Matsen, Assistant Member Fred Hutchinson Cancer Research Center http://matsen.fhcrc.org/ phyloseminar.org

Software ChromatoGate

The program is called ChromatoGate. It performs 4 basic operations:

1. Calculation of consensus sequences (when both forward and reverse primers have worked well) 2. Generation of preliminary files (I will explain this in a while) 3. Detection of Ambiguous Characters in a multiple alignment calculated from the preliminary file 4. Detection of all polymorphic sites in a multiple alignment calculated from the preliminary file

The aim of the program is to allow for easy detection of sequencing errors in a multiple alignment.

The generation of preliminary files is basically a gathering of all the sequences generated by a sequencer into a FASTA file. Possible edge trimming according to the user's request is performed and also the reversed complement of the sequences that have been assembled with a reverse primer is calculated. This step is essential in order for the tool to remember what changes have been applied on each sequence after is was produced by the sequencer.

During the 1 and 2 operations the program stores all the information needed so that, in the 3rd and 4th operations to be able to give the exact chromatogram positions of the nucleotides responsible for polymorphisms or ambiguous characters.

The goal is to provide an alignment to chromatogram mapping in order for the user to easily check the chromatograms in order to verify whether a polymorphic site in an alignment is actually polymorphic or it is because of a sequencing error.

This is the underlying idea of the program and a paper presenting ChromatoGate and the complete framework is going to be submitted soon.

Available at http://wwwkramer.in.tum.de/exelixis/-

countChroma.php Thank you,

Nikos

– Nikolaos Alachiotis

Scientific Computing Group (Exelixis Lab) Heidelberg Institute for Theoretical Studies (HITS gGmbH)

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Skype: nikos.alachiotis WWW: http://wwwkramer.in.tum.de/exelixis/nikos/ http://www.h-its.org/english/research/sco/index.php Amtsgericht Mannheim/HRB 337446 Managing Directors: Dr. h.c. Dr.-Ing. E.h. Klaus Tschira/Prof. Dr.-Ing. Andreas Reuter

Nikos Alachiotis <n.alachiotis@gmail.com> Nikos Alachiotis <n.alachiotis@gmail.com>

Software IMgc revised

Hi,

IMgc reads recombination-rich multiple sequence alignments, and returns the largest block containing no four-gamete violations. This software was originally written to generate input datasets for the IM family of programs, a demographic inference package developed by Jody Hey. However, IMgc is useful for other purposes as well X such a creating input files for Bob Griffiths' demographic inference software, Genetree.

A software notice for IMgc was published in Bioinformatics in 2007:

Woerner, A. E., M. P. Cox, and M. F. Hammer. 2007. Recombination-filtered genomic datasets by information maximization. Bioinformatics 23:1851-1853.

IMgc is written in Perl, and the original version required a working installation of BioPerl. Over the years, this dependency has been a limiting factor for many users.

The authors announce that the BioPerl dependency of IMgc has now been removed. The new version of IMgc can be run anywhere with a basic, functioning installation of Perl. In other words, it will run as-is on OS X and most UNIX platforms, as well as under ActivePerl for Windows.

The revised code is available here:

http://massey.genomicus.com/ Alternately, a web version of IMgc is hosted here:

http://hammerlab.biosci.arizona.edu/IMGC/IMGC.html Best -Murray

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Murray Cox, Ph.D. | Senior Lecturer | Rutherford Fellow Institute of Molecular BioSciences | Massey University | New Zealand

+64-6-356 9099 x2570 | m.p.cox@massey.ac.nz | http://massey.genomicus.com/ Murray Cox <murray.p.cox@gmail.com>

Software MacClade free

MacClade free MacClade is now free to download at http://macclade.org/download.html .MacClade's PDF manual is included in the download. As we have shifted our programming efforts to Mesquite, we will only be providing limited support for MacClade.

MacClade will not work under MacOS X Lion MacClade is a program built for the older PowerPC compilers, and has been able to run on the newest Mac computers because of Apple's Rosetta, which allows PowerPC applications to run on Intel processors. However, Rosetta will no longer be included in the new version of MacOS X, 10.7 (Lion), to be released soon. For this reason, we expect that MacClade will no longer function. This will be true of all other PowerPC programs, too. Thus, if you wish to still use MacClade, you should keep a Mac running MacOS X 10.6 or before.

Open Source? We are considering opening up the source of MacClade; if you are interested in this, for example to convert it to run on the newer operating systems, please contact us. It is written primarily in Pascal.

Best wishes, David and Wayne

David R. Maddison Department of Zoology 3029 Cordley Hall Oregon State University Corvallis, OR 97331 USA

Wayne Maddison Depts. of Zoology and Botany 6270 University Boulevard University of British Columbia Vancouver, BC V6T 1Z4 Canada

http://mesquiteproject.org http://macclade.org david.maddison@science.oregonstate.edu

Software MetaPIGA

Dear all,

We are glad to announce a major release (version 2.1) of MetaPIGA now implementing PROTEIN models and multiple new features (see below). The software and its new manual are freely available at www.metapiga.org. If you own a previous version of MetaPIGA2, it will be automatically updated through the internet next time you launch the program, and the new manual will be available in the MetaPIGA -help' menu.

MetaPIGA 2.1 (BMC Bioinformatics 2010, 11: 379) is a robust implementation of the Metapopulation Genetic Algorithm (metaGA; PNAS, 99: 10516-10521 (2002)) and additional stochastic heuristics for large phylogeny inference under Maximum Likelihood. It implements complex substitution models (for protein and DNA data), discrete Gamma rate heterogeneity, the possibility to partition data, and model testing (LRT, AIC, AICc, BIC) for the selection of the model that best fits your data.

The major additional new features in version 2.1 are:

Faster processing, reduced memory requirements; Protein models (GTR20, Poisson and empirical models such as WAG, JTT, DAYHOFF, VT, BLOSUM62, CPREV, MTREV, RTREV and MTMAM); AIC (+AICc) and BIC model testing for protein data (model testing was already available for DNA data); Standard binary dataset support (GTR2: 2 states model : 0,1); Ancestral-state reconstruction using conditional likelihood values; New meta-heuristic (random-restart hill climbing); Dataset quality control for identical sequences, and for excessively divergent and/or ambiguous sequences; The possibility for automated alignment trimming using the trimAl algorithm (http://trimal.cgenomics.org' Capella-Gutierrez et al., Bioinformatics 2009 25: 1972-1973): removal of excessively gapped and/or divergent columns; Many new functionalities (multiple files -drag and drop', possibility to use FASTA files, choice of the models to compare in AIC and BIC model testing, sufficient and necessary stop conditions, extended and improved functions in the TreeViewer, ...); SourceForge support (general support, forum, bug reports, feature requests trackers, and a mailing list). Bug corrections are: Resolved “freezing” issues that could happen with multi-processors analyses; Improved consensus-tree generation; Resolved memory leak problems during model testing; Many others. Please check the -Change Log' (in the help menu) for a full list of changes.

Importantly, MetaPIGA-2.1 will make you happy if you like using a graphical user interface (GUI) BUT it should also make you happy if you hate using a GUI. Indeed, MetaPIGA provides BOTH: An extensive GUI for parameters setting, following run progress, and manipulating result trees, and High customization through manual batch files and command line processing. Furthermore, if you need to use batch files (for example, to run them on a distant server) but hate to type the commands yourself, MetaPIGA2 allows you to generate batch files through the GUI.

MetaPIGA2 uses standard formats for data sets and trees, is platform independent (Mac, Windows, and Linux), runs in 32 and 64-bits systems, and takes advantage of multiprocessor and multicore computers.

MetaPIGA2 is described in: Helaers & Milinkovitch; BMC Bioinformatics 2010, 11: 379.

The metaGA algorithm is described in: Lemmon & Milinkovitch; PNAS, 99: 10516-10521 (2002).

We hope you'll enjoy MetaPIGA-2.1 !

Michel & Raphaël.

References:

MetaPIGA2 is described in: Helaers R. & M.C. Milinkovitch MetaPIGA v2.0: maximum likelihood large phylogeny estimation using the metapopulation genetic algorithm and other stochastic heuristics BMC Bioinformatics 2010, 11: 379

The metaGA algorithm is described in: Lemmon A. R. & M. C. Milinkovitch The metapopulation genetic algorithm: an efficient solution for the problem of large phylogeny estimation PNAS, 99: 10516-10521 (2002)

Prof. Michel C. Milinkovitch Laboratory of Artificial & Natural Evolution Dept of Genetics & Evolution University of Geneva Sciences III, 30, Quai Ernest-Ansermet 1211 Genève 4, Switzerland

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www.lanevol.org

Software optiFLP

We are happy to announce optiFLP, a new member of our family of AFLP analysis software.

When using automated AFLP scoring software, having good scoring parameters is the key to achieving good binary profiles from a raw set of data. Using our earlier published tinyFLP software, it became obvious that it is not enough to test a few different parameter sets in the hope that the best one will be among them. There are thousands of possible sets, and an automated solution is needed to check all of them and identify promising parameterisations. This is the major intention of optiFLP: the user may define intervals and stepwidths for all scoring parameters, and the software will search this parameter space and perform Analysis of Ranked Similarities (ANOSIM) in order to find settings which maximise the contrast between groups of profiles.

optiFLP supports a supervised mode when it is feasible and desirable to use information on sample grouping, such as place of collection or population assignment, but also a novel unsupervised mode where no a priori information about the genetic structure of a sample has to be provided.

optiFLP will return the best parameter settings identified, a tree, results of pairwise tests between all groups of samples to identify each group's contribution to the detected signal, and outfiles that can be readily used as input for as broad range of population and phylogenetic software like MrBayes, Structure and GenAlEx. The program can be used via an interactive menu or in command line mode.

optiFLP v1.31 is available at http://sourceforge.net/projects/optiflp/ The original paper describing the software is Arthofer W., Schlick-Steiner B.C. and Steiner F.M. (2011) optiFLP: software for automated optimization of amplified fragment length polymorphism scoring parameters. Molecular Ecology Resources, doi: 10.1111/j.1755-0998.2011.03043.x.

Please note that updated versions of tinyFLP and tinyCAT are avilable at http://sourceforge.net/projects/tinyflp/ Wolfgang Arthofer Birgit C. Schlick-Steiner Florian M. Steiner

University of Innsbruck Molecular Ecology Group 6020 Innsbruck, Austria

Wolfgang Arthofer <Wolfgang.Arthofer@uibk.ac.at>

Software PHAST RPHAST

Announcing the release of a new version (v1.0) of the Phylogenetic Analysis with Space/Time models (PHAST) package, together with a package, called RPHAST, that allows much of the functionality of the PHAST libraries to be accessed within R. PHAST and RPHAST are described in detail in a recent paper in Briefings in Bioinformatics (http://bib.oxfordjournals.org/content/12/1/41).

Please send email to phast-help@cornell.edu if you have any questions about PHAST or RPHAST.

Regards, Melissa Hubisz Katie Pollard Nick Peterson Adam Siepel

Adam Siepel <acs4@cornell.edu>

Software SuiteMSA

Hi, everybody.

We are announcing our new software: SuiteMSA, a java-based application that provides unique multiple alignment (MSA) viewers. With SuiteMSA, users can directly compare multiple MSAs and evaluate where the MSAs agree (are consistent) or disagree (are inconsistent). SuiteMSA also provides a GUI for a sequence evolution simulator (indel-seq-gen version 2, iSGv2) as well as a graphical phylogeny editor/viewer.

Six main tools of SuiteMSA are: â MSA Viewer: a single MSA viewer with secondary structure and transmembrane prediction displays. â MSA Comparator: pairwise MSA comparison viewer. It also calculates statistics (e.g., sum of pair scores and column scores). â Pixel Plot: multiple MSA comparison using pixel plots showing gap patterns â iSG Simulation: sequence simulation by iSGv2 â Phylogeny Viewer: a graphic phylogeny viewer/editor â MSA reconstruction: Muscle and ClustalW2 GUI (more methods will be added soon).

SuiteMSA is available from: http://bioinfolab.unl.edu/ ˜ canderson/SuiteMSA/ BMC Bioinformatics paper on SuiteMSA has been also just published: http://www.biomedcentral.com/1471-2105/12/184 If anybody is at Evolution 2011 meeting at Norman, Oklahoma, we will be doing the demonstration of SuiteMSA during iEvoBio on June 21st: Lightning Talk (short introduction) at 2:45 pm and Software Bazaar (demo) at 3:30 pm. Please stop by. We would like to answer any questions and discuss future development personally.

If you have any questions/comments/suggestions, please email us:

Cate Anderson: anderson@cse.unl.edu Cory Strope: corystrope@gmail.com (for iSGv2) Etsuko Moriyama: emoriyama2@unl.edu

Etsuko Moriyama, PhD Associate Professor

School of Biological Sciences & Center for Plant Science Innovation University of Nebraska-Lincoln 403 Manter Hall Lincoln, NE 68588-0118

Email: emoriyama2@unl.edu Phone: 402-472-4979, Fax: 402-472-2083 (SBS business office)

Moriyama Lab web page: http://bioinfolab.unl.edu/emlab/index.html Bioinformatics at UNL: http://bioinfolab.unl.edu/unlbioinfo/index.html emoriyama2@unlnotes.unl.edu

SpeciationResearch TravelGrants

Dear colleagues,

The European Research Networking Programme “Frontiers of Speciation Research”, supported by 18 National Funding Organizations in member countries of the European Science Foundation, is inviting applications for travel grants intended to foster collaborations between European researchers working on topics related to the Programme.

Support is available for short visits (up to 2 weeks) and exchange grants (up to 3 months), with preference given to junior researchers at a graduate or postdoctoral level. Applicants will want to keep in mind that, owing to the difference in costs, applications for short visits are more likely to be successful than applications for exchange grants.

Applications are reviewed quarterly after a submission deadline of 24:00 CET on 15 March, 15 June, 15 September, and 15 December. About 4-6 weeks after each deadline, the ESF will inform applicants about the outcome of evaluations.

Further information and instructions on how to apply are available at www.iiasa.ac.at/Research/EEP/FroSpects/Travel_Grants.html .

For general information about the FroSpects Research Networking Programme, please see www.iiasa.ac.at/Research/EEP/FroSpects .

With best wishes,

Ãke Brännström & Ulf Dieckmann, on behalf of the FroSpects Steering Committee

Ulf Dieckmann Program Leader Evolution and Ecology Program International Institute for Applied Systems Analysis A-2361 Laxenburg Austria

Email dieckmann@iiasa.ac.at Phone +43 2236 807 386 Phone secretary +43 2236 807 231 Fax +43 2236 807 466 or +43 2236 71313 Web http://www.iiasa.ac.at/Research/EEP Online reprints http://www.iiasa.ac.at/˜dieckman FishACE Network http://www.iiasa.ac.at/Research/EEP/FishACE FinE Network http://www.iiasa.ac.at/Research/EEP/FinE FroSpects Network http://www.iiasa.ac.at/Research/EEP/FroSpects

dieckmann@iiasa.ac.at

SSCP company

I am having issue with finding a core facility or company that performs the SSCP (single strand conformation polymorphism) assay. Does anyone know of any institutions, whether commercial or not, that will process outsourced samples, or could connect me to someone that might be able to help me?

Please reply to: jlight2@tamu.edu

Jessica E. Light Assistant Professor and Curator of Mammals Department of Wildlife and Fisheries Sciences Texas Cooperative Wildlife Collection Texas A&M University 210 Nagle Hall, 2258 TAMUS (mailing) 320A Heep Laboratory Building (office) College Station, TX 77843 Phone: 979-458-4357 Fax: 979-845-4096 email: jlight2@tamu.edu http://wfsc.tamu.edu/lightlab Jessica Light <jlight2@tamu.edu>

Student Paper Award

Announcement: OTS Outstanding Student Paper Award

The Organization for Tropical Studies’ (OTS) Membership Committee is pleased to announce the third annual OTS Outstanding Student Paper Award. We invite nominations for a $500 cash prize for excellence in research via an outstanding publication in tropical biology written by a student.

ELIGIBILITY AND NOMINATION: At the time of the nomination deadline, the paper must be published or accepted for publication in a peer-reviewed journal and reporting work completed within the tropics. To be eligible: 1) the author must have been a student (undergraduate or graduate) when the research was completed, and, 2) satisfy at least one of the following three criteria: - nominee is an alum of an OTS course - work was completed at an OTS research station (La Selva, Las Cruces, Palo Verde) - nominee is (was) a student at an OTS member institution (Institutional members may be found here: http://www.ots.ac.cr/)

In addition, the nominee must be the first author and the paper must be published no more than 36 months before the award deadline. Self-nominations or nominations by research advisors or colleagues are invited.

SELECTION CRITERIA: Applications will be reviewed by an Awards Committee formed by a subcommittee of the OTS Assembly of Delegates. Papers will be judged upon the papers contribution to the field including originality, study design and potential impact on the field of study.

Nomination packets should consist of a single pdf document and include:

1. A nomination letter briefly describing the paper and outlining the qualification criteria from the list above. 2. A copy of the paper. 3. A brief letter from an advisor, colleague or scientist in a relevant field of study describing the impact of the paper on the field (optional, but strongly suggested). 4. A CV from the nominee

SUBMITTING APPLICATIONS: Send nomination packet electronically as a pdf to the chair of the Awards Committee, awards.ots@gmail.com

APPLICATION DEADLINE: FRIDAY OCTOBER 14, 2011 If you have questions, please email Dr. Lena Struwe (struwe@aesop.rutgers.edu). Announcement of Award Recipient will be made at March 2012 OTS Assembly of Delegates Meeting and will be recognized at the ATBC meeting.

Pdf flyer for poster and printing: http://www.ots.ac.cr/images/downloads/education/graduate/spa2011_forweb.pdf Dr. Lena Struwe | Associate Professor & Director, Chrysler Herbarium | Rutgers University | Dept of Ecology, Evolution, and Natural Resources | Dept of Plant Biology and Pathology | 237 Foran Hall | 59 Dudley Road | New Brunswick, NJ 08901 | USA | struwe@aesop.rutgers.edu | phone (732) 932-9711 x235 | fax (732) 932-9441 | www.rci.rutgers.edu/ ˜ struwe/ Lena Struwe <struwe@AESOP.Rutgers.edu>

TalkOrigins asks for donations

The TalkOrigins Archive Foundation (TOAF), a Texas 501(c)3 non-profit organization, supports keeping evolutionary science in public school science classrooms and keeping religious antievolution out. Specifically, the TOAF supports the online outreach of the TalkOrigins Archive (http://talkorigins.org), TalkDesign (http://talkdesign.org), and the Panda's Thumb weblog (http://pandasthumb.org).

In 2008, a antievolution propaganda film starring Ben Stein was released. "Expelled: No Intelligence Allowed" from the production company Premise Media was widely distributed. Since then, its claims have been critiqued in prose and in video rebuttals. Recently, Premise Media went bankrupt. The film, "Expelled", and all the production materials are now up for auction. The auction is being held online by Rosen Systems and ends on Tuesday, June 28th.

The TOAF will undertake to bid on "Expelled". We hope to serve as a way for many individuals to collaborate in this effort. If successful, we aim to give as wide and as open a release of materials from "Expelled" as will be consistent with existing contractual agreements (especially a distribution agreement in force with Vivendi) and with the aim of making the propaganda materials as little use as possible for the religious antievolutionists. We believe that the various duplicitous strategems employed by Premise Media in production of "Expelled" will be best rebutted in this fashion. While there is no guarantee that the surviving production materials will include statements linking religious motivations to the "academic freedom" label applied to the usual antievolution arguments, we believe that it is our responsibility to make an effort to obtain, archive, and publish (within the constraints outlined above) these materials. If such can be found within the "Expelled" corpus, it would link many of the prominent "intelligent design" advocates with a religious motivation in promoting their version of "academic freedom" and could be as pivotal in future court cases as the Discovery Institute's "Wedge Document" was in the 2005 Kitzmiller v. Dover Area School District case.

In order to permit the TOAF to make as large a bid as possible, we have been soliciting donations via Pay-

Pal. Because of delays in transfers, the TOAF can only commit to bid funds available on hand as of Monday, June 27th. Given the short time frame, we have not been able to seek guidance on whether donations could be refunded in the event that we are not able to make a successful high bid. Thus, we want to be clear that as things stand, donations should *not* be considered refundable, and if we do not succeed in the auction for “Expelled”, the funds would be used for the activities within the mission of the TOAF. For citizens of the USA, donations to the TOAF are tax-deductible. Again, the way I view this is to allow as many individuals as possible to band together to participate in this auction and, hopefully, preserve and expose its materials to public scrutiny.

A more complete discussion of the policy on donations to the TOAF is given by TOAF Treasurer Ken Fair at http://tinyurl.com/6aqgrqz . I have a blog post on the topic at http://pandasthumb.org/archives/2011/-06/help-talkorigin.html . Since announcing our intent to bid late on June 23rd, people have donated several thousand dollars to the TOAF. (I am not giving precise figures at the moment since that would give competing bidders too much information.) I concur with Ken Fair when he says,

“I wanted to be clear about this because I do not want anyone to donate to the Foundation if they feel uncomfortable doing so in any way. I certainly do not want anyone contributing if they feel financially strapped, or they worry about what we will do with the funds. I do recognize that people are putting their faith in us on this matter - I take that very seriously, and I deeply appreciate the response we have received thus far.”

I believe that we have an unprecedented opportunity to investigate and document a significant propaganda effort out of the religious antievolution community. I hope that you will consider supporting the TOAF in this endeavor.

Wesley R. Elsberry, Ph.D. President, TalkOrigins Archive Foundation

welsberr@baywing.net

Testing phylogeographical hypotheses using coalescent simulations

Dear all,

I am attempting to use coalescent simulations to infer recolonization scenarios for three-spine stickleback in Britain and Ireland. To do so I am using a similar approach to that suggested by Knowles & Maddison (2002) Mol Ecol implemented in Mesquite.

Therefore I am modelling genealogies constrained within hypothesis trees and then attempting to create distributions of discordance statistics between a null and an alternative hypothesis. I understand the theory, but I am having some practical problems.

Essentially I am keen to make sure I am actually conducting the coalescent analyses correctly. The bundled tutorials are useful but do not quite go far enough on testing biogeographical scenarios. I would be especially interested in any guidelines used for teaching statistical phylogeography. Does anyone have a tutorial/practical/protocol for using Mesquite in this way?

Many thanks in advance for any assistance

Mark Ravinet

Mark Ravinet PhD Student School of Biological Sciences Queen’s University Belfast Medical Biology Centre Lisburn Road Belfast BT9 7BL Tel:02890972103 Mob: 07841675863 Email: mravinet01@qub.ac.uk

mravinet01@qub.ac.uk

Thailand NatlParks

Hi all,

My name is Alyssa Stewart and I am a graduate student at UMD, studying the evolutionary ecology of Old World fruit bats. I am currently in southern Thailand to conduct a pilot study for my dissertation research, and was wondering if anyone has information, insights or connections to any national parks in the area. I am particularly interested in Thaleban National Park and Ton Nga Chang Wildlife Sanctuary. Additionally, any information about acquiring permits to conduct research in Thai national parks, or export permits to take plant samples out of Thailand, would be greatly appreciated.

Many thanks in advance, Alyssa

– Alyssa B. Stewart Behavior, Ecology, Evolution, and Systematics Graduate Program University of Maryland aly55a@umd.edu

4lyssa@gmail.com

PostDocs

CollegeCharleston ArabidopsisGenomeEvolution

Hi All,

The following postdoc ad outlines a position that would be suitable for people interested in evolution of Arabidopsis genomes and interested in mentoring UG research in evolution/ecology.

thanks, Allan

We are seeking a postdoctoral researcher/teacher to fill a central role in the NSF-supported Undergraduate Phenotyping of Arabidopsis Knowledgebase (UnPAK; see description below) project.

The successful candidate will possess a PhD in the biological sciences, have skills in database design and maintenance, be enthusiastic about teaching part-time in the College of Charleston Biology Department's ecology/evolution course sequence (details below) and mentoring undergraduate researchers. An ideal candidate will also possess additional technical skills including PCR-based methods, experience with plant growth chamber or greenhouse growing methods (ideally in Arabidopsis), and cyberinfrastructure/bioinformatics capabilities.

This position offers substantial opportunities in both research and education, and would be ideal for an individual who aspires to an academic career at an institution that embraces the teacher-scholar model. Individuals who are most successful at these institutions often bring experience in high-impact teaching and cutting-edge scholarship with them when they apply - exactly the experiences that will result from tenure as a UnPAK postdoctoral researcher.

The UnPAK postdoc will have the first chance to synthesize genetic and phenotypic data as it is collected and will be encouraged to pursue independent projects within the context of the overall research program (use of phenotypic effects of T-DNA insertion mutants in Arabidopsis to answer fundamental questions about Arabidopsis genome structure and function across environments). There will be extensive opportunities for professional networking during interactions among partner institutions involved in the project (including Barnard College, Hampden-Sydney, and U. Georgia). In addition to Arabidopsis research opportunities, the UnPAK postdoc can be involved in collaborative efforts in building educational resources. This postdoc will also have opportunities to learn about educational research, as the UnPAK network will serve as a context for understanding the impacts on undergraduates of participating in a research network Initially, teaching would be within the College of Charleston course BIOL211, see http://catalogs.cofc.edu/pdf/-Undergraduate_Catalog_2011-2012.pdf, page 148. Inquiries about this position can be sent to Matt Rutter (rutterm@cofc.edu), Courtney Murren (murrenc@cofc.ed) or Allan Strand (stranda@cofc.edu). Applications should include a CV, a cover letter, and contact information for 3 references and can be sent as PDF files directly to Allan Strand (stranda@cofc.edu). Review of applications will begin immediately and will continue until the position is filled. The College of Charleston is an Equal Opportunity/Affirmative Action Employer and encourages applications from women and minorities.

A short overview of UnPAK The research community has generated a set of T-DNA insertion lines aimed at elucidating the functions of the ~27,000 genes in Arabidopsis thaliana. These lines are thought to represent "knockouts" of most A. thaliana genes, yet the vast majority display subtle if any morphological phenotypes. This "absence of phenotype" phenomenon has been observed in other model systems. In yeast, researchers have turned their focus to characterizing performance attributes of knockouts, such as population growth rate and fitness as well as the plasticity of these traits across environments. This strategy has succeeded in finding phenotypic differences where none had been previously observed. Given this proof of principle and its utility for answering questions about genetic redundancy and genomic evolution, we are applying a similar approach to the study of A. thaliana as a multicellular and autotrophic model. We are doing so through collaboration among primarily undergraduate institutions (PUIs), thus training future researchers in the process of building a body of published work in genomics and applied ecology and a network of collaborators.

– Allan Strand, Biology http://linum.cofc.edu College of Charleston Ph. (843) 953-9189 Charleston, SC 29424 Fax (843) 953-9199

stranda@gmail.com

CornellMedSchool ComputationalBiol

Postdoctoral Positions Available in Computational Biology

Postdoctoral positions in the areas of computational biology, systems biology, and bioinformatics are now available in the New York City laboratory of Jason Mezey (http://mezeylab.cb.bscb.cornell.edu/) located at Weill Cornell Medical College. We are looking for postdoctoral associates who are interested in developing and applying novel computational and statistical approaches to a wide variety of problems in population genomics and medical genomics. We are interested in individuals whose focus is algorithm development or who are interested in working with high-throughput (next-generation sequencing) data, and who enjoy the prospect of working in collaboration with experimental biologists and medical researchers.

Our group includes members trained in computational biology, statistics, and machine learning who interact in a dynamic environment that spans two campuses: Cornell University (Ithaca, NY) and Weill Cornell Medical College (New York, NY). We work on a number of problems in computational genomics, evolutionary genomics, and systems biology (please see our website for representative research directions and publications: http://mezeylab.cb.bscb.cornell.edu/). Our work includes the development of new algorithms and analysis of high-throughput data, where we work closely with researchers in a number of fields including evolutionary genomics, agricultural genetics, and medicine.

Ideal candidates will have a background in computational biology, bioinformatics, statistics, or machine learning. To apply for these positions, please send an email with a single collated PDF including (1) CV, (2) names and contact information of three references, (3) statement of research interests, to Jason Mezey <jgm45@cornell.edu>.

jgm45@cornell.edu

Drosophila Viruses Wolbachia

Applications are invited for three post-doctoral positions studying Wolbachia-induced protection to viruses in Drosophila. The aim of this Wellcome Trust funded project is to use an interdisciplinary approach to investigate, at the molecular level, how these bacterial symbionts interfere with insect viral infection.

One position will be based at the Department of Genetics at the University of Cambridge, working on the evolution and genomics of this interaction with Dr Frank Jiggins. The second position will be based at the MRC-University of Glasgow Centre for Virus Research, working on molecular virology with Dr Alain Kohl. The third position will be based at the Instituto Gulbenkian de Ciência in Portugal working on Drosophila genetics with Dr Luis Teixeira.

The closing dates for applications are 18 July 2011 (Cambridge and Portugal) and 8 July 2011 (Glasgow). Details of how to apply and the experience required for the different posts are available through these links:

Cambridge: http://www.jobs.ac.uk/job/ACT179/post-doctoral-research-associate Glasgow: http://www.jobs.ac.uk/job/ACT907/postdoctoral-scientist-career-development-f ellow/

Portugal: http://www.igc.gulbenkian.pt/node/view/9

fmj1001@cam.ac.uk

EMBL Cambridge MolecularPhylogenetics

SHORT-TERM POST-DOCTORAL FELLOWSHIPS IN MOLECULAR PHYLOGENETICS

Description: There is the possibility of one or more post-doctoral fellowships being awarded to permit researchers with established molecular phylogenetics projects to work with Nick Goldman's group at the EMBL-European Bioinformatics Institute for periods of approx. 2–6 months.

For further details of the work already undertaken in the group, see http://www.ebi.ac.uk/goldman. We are happy to consider applicants working on phylogenetic theory, or on applications with a strong theoretical component. We are particularly interested in ideas exploiting next generation sequencing data.

Anyone interested in this possibility is encouraged to contact Nick Goldman directly, at goldman@ebi.ac.uk or at the address below.

Nick Goldman tel: +44-(0)1223-492530 EMBL - European Bioinformatics Institute fax: +44-(0)1223-494468 Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK

goldman@ebi.ac.uk

EMBL Cambridge SchistosomaEvolution

THREE-YEAR POST-DOCTORAL FELLOWSHIP IN COMPARATIVE INSIGHTS INTO TRANSCRIPTION AND EXPRESSION IN SCHISTOSOMA, A NON-MODEL METAZOAN PARASITE

Applications are invited for a three-year post-doctoral fellowship held jointly at the Sanger Institute and EMBL-European Bioinformatics Institute under these institutes' "ESPOD" fellowship programme (http://www.ebi.ac.uk/training/postdoc/ESPOD).

The above webpage includes a link to an abstract of this project (and others in the programme). Full project details are available at http://tinyurl.com/3g27op9. The successful candidate will work in the Goldman Group at EMBL-European Bioinformatics Institute (http://www.ebi.ac.uk/goldman) and Matt Berriman's Parasite Genomics group at the Sanger Institute (http://www.sanger.ac.uk/research/projects/parasitegenomics).

Applications should be sumitted by e-mail to Tracey Andrew <tandrew@ebi.ac.uk> by 15 August 2011.

Nick Goldman tel: +44-(0)1223-492530 EMBL - European Bioinformatics Institute fax: +44-(0)1223-494468

Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SD, UK

goldman@ebi.ac.uk

EmoryU GeneticsDrosophila ParasiteInteractions 2

Drosophila Genetics Postdoctoral Position Emory University, Atlanta, GA USA Laboratory of Dr. Todd Schlenke

We are looking for a highly motivated postdoctoral researcher to work on the genetics of Drosophila resistance against parasitic wasps. Drosophila are a model system for study of innate immunity, and wasps are one of the most common pathogens of fruitflies in nature. It is the interaction between the innate immune response of the flies and the venom of the wasps that determines the outcome of any infection. We currently have funding to use a combination of candidate gene approaches, QTL mapping, and association mapping to identify fly loci that control resistance. The resistance genes we identify will be functionally characterized using a variety of cell and molecular biology techniques, and any history of adaptive evolution at such loci will be determined with population genetic and molecular evolution analyses. Applicants will preferably have a background in some combination of Drosophila biology, host-pathogen interactions, population genetics, genetics, and molecular biology.

The Schlenke lab (http://www.biology.emory.edu/research/schlenke/) is part of Emory's Biology Department (http://www.biology.emory.edu/) and is affiliated with the Genetics and Molecular Biology (GMB) and Population Biology, Ecology and Evolution (PBEE) graduate programs. These groups have a strong emphasis on host-pathogen interactions, Drosophila molecular genetics, and bioinformatics, and we regularly collaborate with multiple labs across campus. Atlanta is also a great place to live.

Interested candidates should send a CV, along with a brief statement of interests and experiences in the above-mentioned areas, to Todd Schlenke by June 25th, 2011. Candidates can start any time between now and January 2012.

Dr. Todd Schlenke Emory University Department of Biology tschlen@emory.edu

"Schlenke, Todd" <tschlen@emory.edu>

FHCRC Washington BayesianPhylogenetics

Dear EvolDir community–

We have an opening for a postdoc to come work on methods and applications in Bayesian phylogenetics. This is an opportunity for you to bring your independent research program to bear on novel data sets with real-world consequences.

So far we have been working on methods to detect superinfection in HIV with Julie Overbaugh's group, and evolutionary history of newly discovered heterochromatin genes in Drosophila with Harmit Malik's group. But there are a number of projects here that are currently waiting for a champion, such as:

* inference of "founder" sequences for SIV/HIV infection * high-throughput Bayesian phylogenomics methods for environmental sequence data * phylogeography of cancer-causing viruses

We will provide you with a solid salary, computational support, and a long list of interesting questions and data sets. In return, we just ask that you engage with the other researchers at the center and assist in the applied work (which may well lead to your next theoretical advance!)

The University of Washington is a short distance away, home of Joe Felsenstein and Vladimir Minin, so you won't be lacking in a wider community. Powerful computing resources and a helpful IT staff await you. This position will come with a very competitive postdoc-level salary with great benefits, for a one-year contract that can be renewed if things are going well.

Fred Hutchinson Cancer Research Center, home of about 190 faculty including three Nobel laureates, is an independent, nonprofit research institution dedicated to the development and advancement of biomedical research. The environment is lively yet casual, with a strong emphasis on collaborative work. The center is housed in a lovely campus next to Lake Union within walking distance from downtown.

You can find out more about our group by visiting:

* http://matsen.fhcrc.org/ * http://github.com/fhcrc * http://github.com/matsen Requirements:

* Ph.D. in biology, computer science, math, or another

relevant area * solid foundation in Bayesian phylogenetics * linux and computer programming proficiency * clear ability for independent research

To apply, send the following materials to Nerreda Chavez at nchavez@fhcrc.org:

* two representative publications * 2-3 paragraph statement of research interests * names and email addresses of three references * CV

Erick

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

HarvardU BostonU EvolutionaryTranscriptomics

Postdoctoral Position in Evolutionary Transcriptomics Harvard University and Boston University

A NSF-funded postdoctoral position is available in the laboratories of Hopi Hoekstra, Jonathan Losos (Harvard University) and Christopher Schneider (Boston University) to study convergent evolution of colorful pigmentation in Anolis lizards. Specifically, this project focuses on identifying genes involved in dewlap pigmentation using within- and between-species comparisons in a phylogenetic context. The work is integrative and combines phenotypic (spectrophotometry, histology, HPLC) and genomic (RNA-seq) approaches. The project may include fieldwork depending on the candidates interest and experience.

The candidate should have strong training in evolutionary biology and experience with RNA-seq data generation and analysis, with strong bioinformatic and analytical skills. The position will be awarded for one year with the possibility of renewal for an additional two years beginning September 1, 2011 (at the earliest), contingent upon final approval of funding. Salary and benefits are competitive.

Applicants should submit a single pdf file containing (1) a statement of intent, (2) a CV, and (3) names and contact information for three references by July 14th to Christopher Schneider at cschneid@bu.edu.

Christopher Schneider Biology Department Boston University 5 Cummington St. Boston, MA 02215

Ph: 617 353 5566 FAX: 617 353 6340

Christopher Schneider <cschneid@bu.edu>

IST Austria EvolutionaryTheory

A postdoctoral position is available, for research in evolutionary theory. Possible topics include quantitative genetics, evolution of recombination, speciation, spatial population structure, and evolutionary computation, but other areas can be considered.

The position will be available for three years; the salary scale starts at euro 44,982 p.a. Applicants should have a Ph.D. in a relevant area (including computer science, mathematics, statistical physics, and population genetics), with strong mathematical and computing skills, and an interest in fundamental research. For further details, please contact nick.barton@ist.ac.at. Applications should be sent by July 15th, and should include a CV, a statement of research interests, and names of referees.

The Institute of Science and Technology is a new multidisciplinary research institute, located in the Wienerwald, just outside Vienna (www.ist-austria.ac.at< http://www.ist-austria.ac.at/ >). The Institute encourages multidisciplinary research, and has strong groups at the interface between biology and physics, and in computer science. There are close links with other evolution groups in Vienna (www.univie.ac.at/evolvienna).

Nick.Barton@ist.ac.at

London Bioinformatics

Research Associate in Bioinformatics

Salary Range: £26,860 - £39,130 p.a.

Applications are invited for a Research Associate in Bioinformatics to join the Department of Infectious Disease Epidemiology based at the St Mary's Campus, Paddington. The Department is based within a five star research institute equipped with the latest technologies and facilities. The post holder will be a member of the MRC Centre for Outbreak Analysis and Modelling and will join a small, dynamic and well-funded research group led by Dr Francois Balloux and comprising Dr Thibaut Jombart, Dr Lucy Weinert and Dr Hanna Larner-Svensson. This team is running in-house projects and is involved in a number of exciting international collaborations including some they are heading themselves.

The post holder will be encouraged to take part in collaborations and to develop his/her own ideas. In addition, he/she will be expected to be involved in two ongoing projects. The first is part of a long-term effort aiming at understanding the relative role of past demography and natural selection in shaping the human genome. More specifically, he/she will be exploiting a dataset of about 2,000 - 3,000 de novo sequenced complete human mitochondrial genomes from individuals, which will also be typed at autosomal markers. This dataset will allow answering various questions including a quantification of the extent to which past climate has shaped worldwide human mitochondrial sequence variation.

The second main project will be to help with the assembly and exploitation of an exceptional dataset of 900 Methicilin Resistant Staphylococcus aureus (MRSA) samples from a single outbreak, for which detailed epidemiological information is available. Complete genome sequences will be generated for all these isolates and the post holder will be involved in the assembly, SNP-calling, annotation and downstream analyses such as the reconstruction of the host-to-host transmission dynamics using both the genomic and epidemiological information.

Applicants should have basic quantitative skills and a strong background in one or more of the following areas: bioinformatics, molecular genetics, genetic epidemiology or population genetics. Applicants should be motivated, well organised and able to work effectively as part of a team.

This is a full time post and is for a fixed-term until 31 January 2013 in the first instance.

For informal enquiries please contact Dr Francois Balloux via e-mail: f.balloux@imperial.ac.uk

Our preferred method of application is online via our website http://www3.imperial.ac.uk/employment Reference number: SM067-11.

Closing date: 29 June 2011.

Dr François Balloux MRC Centre for Outbreak Analysis and Modelling, Department of Infectious Disease Epidemiology, Faculty of Medicine, Imperial College, St Mary's Campus, Norfolk Place, London W2 1PG, United Kingdom Tel: 0044 (0)20 7594 3260 E-mail: fballoux@imperial.ac.uk Web: http://www1.imperial.ac.uk/medicine/people/-f.balloux/ f.balloux@imperial.ac.uk

London EvolutionBehaviour

Interested in doing postdoctoral work in London, on the evolution of sensory systems, behaviour, and cognition?

Applications currently invited for Marie-Curie postdoctoral fellowships (deadline: August 11).

Please email your CV asap to L Chittka at l.chittka@qmul.ac.uk to discuss possibilities.

Lars Chittka <l.chittka@qmul.ac.uk>

McMasterU P450 Evolution

Graduate and Post-doctoral Opportunities in P450 Function and Evolution

MSc (2 year), PhD (4 year) and post-doctoral positions are available in the laboratory of Dr. Joanna Wilson at McMaster University, Hamilton, Canada. We are looking for students interested in the function and evolution of the cytochrome P450 (CYP) 1 and 3 families in fish, with development of a label free assay for CYP activity. Our lab studies the evolution and function of CYPs in fish, environmental physiology, and aquatic toxicology. Lab members have diverse backgrounds and interests including environmental sciences, toxicology, biochemistry, chemistry, molecular biology, physiology, and molecular evolution. We study several species of fish and extensively use zebrafish as a model organism. A description of the laboratorys research can be found at http://www.biology.mcmaster.ca/-faculty/jwilson/jwilson.htm Cytochrome P450 (CYP) enzymes are critical component of the chemical defensome and are highly expressed in liver. We have heterologously expressed CYP1A, CYP1B1, CYP1C1, CYP1C2, CYP1D1 and CYP3A65 from zebrafish and begun to characterize their function (Scornaienchi et al 2010 Arch Biochem Biophys and Scornaienchi et al 2010 J Endocrinol). The expressed proteins will be examined in a high throughput screening laboratory to identify possible substrates in a small molecule library. Functional characterization of the CYP1 or CYP3 families will lead to an understanding of structure-activity relationships for these enzymes as well as evolution of function within protein families. This research intersects protein family evolution, molecular biology, biochemistry and toxicology.

The successful candidate(s) will have a strong background in at least one of the key areas (evolution, molecular biology, biochemistry and toxicology) and a strong interest in interdisciplinary research. The successful candidate should have strong research skills, experience in a molecular biology laboratory, be highly motivated, and can work independently.

To be considered, please send a Curriculum Vitae in PDF format, including publication list, a statement of research interest, transcripts, and a list of three academic referees. The positions are available for a Fall 2011 or January 2012 start date. Information on graduate studies in and application procedures for the Department of Biology at McMaster University can be found online at www.biology.mcmaster.ca/-bio_grad.htm . Dr. Joanna Wilson Assistant Professor Department of Biology McMaster University

1280 Main Street West Hamilton ON L8S 4K1

Tel: 905-525-9140 ext 20075 Fax: 905-522-6066 joanna.wilson@mcmaster.ca

Joanna Wilson <joanna.wilson@mcmaster.ca>

Melbourne RoyalBotanicGardens

Postdoctoral Fellow Royal Botanic Gardens Melbourne

An outstanding opportunity exists to fill the role of Postdoctoral Fellow within the Plant Sciences and Biodiversity Division of the Royal Botanic Gardens Melbourne, one of Victoria's premier scientific and cultural organisations.

The National Herbarium of Victoria is the major centre for taxonomic and systematic botanical studies in Victoria and the collection of approximately 1.2 million plant specimens is one of the largest and most important in Australia.

This exciting project, supported by Bush Blitz grant funding for 3 years, will investigate the taxonomy and systematics of the tussock grasses, tribe Poeae, using DNA barcoding techniques and morphological studies.

The successful candidate will have a PhD in Botany (or equivalent field) and a thorough understanding of current issues and techniques in DNA barcoding, taxonomy, and species delimitation. It is essential to have extensive research experience in generating and analysing DNA sequence data. Excellent written and oral communication skills are also essential in order to communicate effectively with colleagues, the public, international and national researchers, and successfully prepare results of research for publication.

Please send applications to recruit@rbg.vic.gov.au or mail to Royal Botanic Gardens, Private Bag 2000, Birdwood Avenue, South Yarra VIC 3141, Australia. For any enquires about this opportunity or to find out more about the role please contact Daniel Murphy, Molecular Systematist, Plant Sciences and Biodiversity, Royal Botanic Gardens Melbourne daniel.murphy@rbg.vic.gov.au (03) 9252 2377.

For a copy of the Position Description please visit: http://www.rbg.vic.gov.au/about-us/job-opportunities

Please note that applications close COB Wednesday, 06 July 2011.

Dr Daniel J. Murphy Royal Botanic Gardens Melbourne Private Bag 2000 Birdwood Avenue South Yarra 3141 Victoria AUSTRALIA

Ph: +61 3 9252 2377 Fax: +61 3 9252 2413 daniel.murphy@rbg.vic.gov.au

daniel.murphy@rbg.vic.gov.au

MichiganStateU GenomeEvolution

A postdoctoral position is available at Michigan State University (http://shiulab.plantbiology.msu.edu) to study (1) the evolutionary processes underlying duplicate gene retention and loss, and (2) the mechanisms and evolution of transcriptional response to environmental perturbation in plant and fungal model systems. Candidates should have a background in the one or both of the following areas: (1) molecular evolution or population genetics, (2) genomics, transcriptomics, or systems biology. Preference will be given to candidates with experience in computational biology or bioinformatics. Candidates with mainly an experimental background are also welcome but must have experience in basic programming (in any language) and large-scale data analysis (e.g. analysis of microarray or Illumina data).

The project is inherently interdisciplinary and the successful candidate can be involved in both computational and experimental work. The PI is a member of multiple inter-departmental programs and centers, and the successful candidate will interact with a large number of evolutionary biologists and computational biologists in BEACON, an NSF Center for the Study of Evolution in Action (http://beacon-center.org/). In addition to exciting research and collaborative opportunities, the postdoctoral fellow will be encouraged to attend workshops in career development and in college education to enhance their training experience.

Interested candidates please send an email with the title "Postdoctoral position" to Shin-Han Shiu (shius@msu.edu) with the following information attached as a single PDF:

1) Cover letter (1-2 pages): Provide information on your research interests and how your interests synergize with the advertised position. Please also provide information on your experience in computational biology, bioinformatics, programming, and/or data analysis. 2) CV: In your CV please provide academic/work experience, awards, publications, and names/emails for 3 references.

Applications will be reviewed as they are received. Please inquire should you have any question.

–

Shin-Han Shiu Dept. of Plant Biology Michigan State University East Lansing, MI 48824 http://-shiulab.plantbiology.msu.edu shius@msu.edu

NewYorkU PlantGenomics

Several postdoctoral scientist positions are open in the laboratory of Michael Purugganan at the NYU Center for Genomics and Systems Biology.

Applicants interested in plant evolutionary and ecological genomics, and systems biology are welcome. There are opportunities in our laboratories in New York or in NYU Abu Dhabi. Applicants with an interest in regulatory network evolution and experience in genome-wide gene expression studies are particularly welcome. Interested parties can email an inquiry and their CV to mp132@nyu.edu

– Michael Purugganan Dorothy Schiff Professor of Genomics

Department of Biology Center for Genomics and Systems Biology 12 Waverly Place New York University New York, NY 10003

Tel. (212) 992 9628 Web: http://biology.as.nyu.edu/-object/MichaelPurugganan.html Michael Purugganan <mp132@nyu.edu>

PennsylvaniaStateU HumanCranioEvolution

Post doctoral positions at The Pennsylvania State University

Department of Anthropology

Post-doctoral opportunities:

The complex genomic architecture of biological traits and their evolution, with application to craniofacial development and evolution

The Penn State Department of Anthropology involves a widely recognized research program in developmental and evolutionary genetics. We collaborate with local bioinformatics, computational biology, genomics, and neuroscience centers. We are searching for postdoctoral research scientists in three areas. The positions will integrate biological insight and analysis involving existing software and programming of new applications (Linux & MacOS):

1. Evolutionary simulation and analysis of complex genetic architecture. This project involves the use of a forward evolutionary simulation package (ForSim) that we have developed to simulate the genomic architecture and evolution of complex traits such as neurologic disease and the morphogenesis of craniometric traits. How well can this architecture be inferred by current methods such as whole-genome sequence or marker-based GWAS or family data? Are there better criteria than statistical significance for understanding complex genomic causation? Script writing is essential, C++ programming desirable.

2. Simulation of quantitative developmental morphogenesis. We are developing morphometric simulations of the intercellular signaling interaction interactions among tissues in craniofacial development and its evolution. The goal is to generate ‘movies' of simulated tissue interactions and their resulting overall shape, that can be compared to morphometric data from high-resolution MRI and CT imaging of normal

and transgenic mouse models generated in our laboratories. This position involves programming (current modeling is in C++).

3. Bioinformatics/Genomic data analysis and modeling. We are doing genomewide mapping on normal craniofacial variation in mouse and baboon models. This project involves the dissection of implicated genome regions by integrating results from different species and other sources of externally derived information such as regulatory networks and genomic sequence conservation. We relate these results to our other work in neurologic and craniofacial dysgenesis (Down syndrome, craniosynostosis). Ability to use genome database and other bioinformatics resources is required.

These integrated research projects have existing NSF and NIH funding. We will be filling 1-year appointments, that can be extended to 2 or more years. Salary will be NIH/NSF post-doctoral levels based on experience, and starting date can be any time. Penn State is committed to affirmative action, equal opportunity and the diversity of its workforce and our group is already an appealing and successful mixture of different but collaborative people of various genders and cultural backgrounds. Contact Ken Weiss (kenweiss@psu.edu) or Joan Richtsmeier (jta10@psu.edu) for information, or to apply submit CV and names of 3 potential persons we could contact as references.

Penn State is committed to affirmative action, equal opportunity and the diversity of its workforce.

Faye L. Maring Administrative Support Coordinatori Department of Anthropology College of the Liberal Arts The Pennsylvania State University 414 Carpenter Building University Park, PA16802814-867-0006 (phone)814-863-1474 (fax)www.anthro.psu.edu "Faye L. Maring" <fmaring@la.psu.edu>

QueenMaryU EvolutionaryBiol

Queen Mary University of London will support Evolutionary Biology posdocs wishing to write fellowship to work in the School of Biological and Chemical sciences.

We have experience of helping postdocs to draft successful applications for Marie Curie fellowships. There are opportunities for postdocs moving to London from outside Europe, or from another country in Europe.

Details of the schemes are here: http://-cordis.europa.eu/fp7/dc/index.cfm?fuseaction=-3DUserSite.FP7ActivityCallsPage&id_activity SBCS can provide opportunities in evolutionary approaches in Biological and experimental psychology: Ecology and behavioural biology: Evolutionary and organismal biology:

(Details and contacts here http://-www.sbcs.qmul.ac.uk/research/16201.html#6)

We are also happy to consider other topics proposed by applicants.

richard.alan.nichols@googlemail.com

Raleigh MicrobialBiodiversity

Chief Scientist for Micro-Genomics Laboratory Do you have a passion for cutting-edge science and educating the public about it?

The North Carolina Museum of Natural Sciences in Raleigh, NC will open an 80,000 square-foot innovative facility called the Nature Research Center (NRC) in early 2012 to serve as a public laboratory for both local and global scientific research (www.naturesearch.org). The NRC seeks a senior scientist in genomics/molecular biology/microbiology (including but not limited to genetic engineering; biodiversity; molecular systematics, genetic basis of disease in humans, wildlife, or agriculture; microbial genetics, diversity, and disease; molecular genetics (DNA/RNA research), and others) in a joint position with North Carolina Central University, part of the UNC university system. The scientist will be based in Raleigh and directing a laboratory at the NRC, but have opportunities to collaborate with faculty at NCCU, create innovative distance learning pathways, conduct research and host graduate students, interns, citizen scientists, and colleagues on both campuses. Must have a PhD in health, agriculture, biology, genetics, environmental sciences or related fields; a distinguished research career that translates successfully to public education outreach, extensive leadership credentials and be willing to dedicate part of their effort to communicating with the public. Preference given to research that can interface with the public and be safely conducted in a public facility. The chief scientist will hold two titles: chief scientist at the Museum, and research professor at NCCU; salary is split-funded between the two institutions, with a competitive benefits package. Each applicant must complete and submit a separate

North Carolina State Application for Employment form (PD-107), listing the position number (65012981) and job title for the position. Resumes will not be accepted in lieu of a PD-107 form, but may be submitted as supplemental materials. For a more detailed job description please visit our website at http://-osp.its.state.nc.us/positiondetail.asp?vacancykey=-4328-65012981&printit=no . Original applications, signed and dated must be emailed or faxed to: Laura Oakley by 5 PM on June23, 2011 (laura.oakley@ncdenr.gov; fax: 919-733-1573). A PD-107 application form may be found at the bottom of web page http://www.osp.state.nc.us/jobs/-gnrlinfo.htm#app

StockholmU RibonucleotideReductaseEvol

Post-doctor in Astrobiology “Evolutionary and environmental studies of the ribonucleotide reductase enzyme family” at the Department of Molecular Biology and Functional Genomics/Astrobiology Centre. Reference number SU 619-1676-11. Deadline for applications: August 1, 2011.

At the Astrobiology Centre participates research groups from the Departments of Geological Sciences, Molecular Biology and Functional Genomics, Astronomy, Physics, and Nordita at Stockholm University.

Project: Organisms store their genetic information in the form of DNA. Ribonucleotide reductase (RNR) catalyzes the sole de novo pathway that provides building blocks for the DNA biosynthesis. RNR is an essential enzyme in all free-living organisms and was a prerequisite for DNA-based life on Earth. Different classes of RNR have different oxygen requirements, and the repertoire of RNR classes in an organism is therefore likely to limit its ecological reach. The project involves studies on the types and occurrences of RNR genes in contemporary organisms and metagenomes to further our understanding of the evolution of the RNR genes, and the influence that environmental factors have on their current distributions, e.g. via horizontal gene transfer events.

Qualifications: PhD in molecular biologi with specific emphases on microbiology and enzymology, and bioinformatic experience.

Terms of employment: The employment is fulltime ’post-doctoral researcher’ for one year and may be extended for one additional year. Salaries at Stockholm University are individually negotiated.

The Stockholm University is an equal opportunity employer.

Further information: For additional information, please visit the website of Stockholm University Astrobiology Centre, http://astrobiology.physto.se, and Prof. Britt-Marie Sjöberg’s research pages at the Department of Molecular Biology and Functional Genomics, http://www.molbio.su.se, or through e-mail to: britt-marie.sjoberg@molbio.su.se.

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

Applications: Your application should be marked with the reference number SU 619-1676-11 and should include a CV, full publication list, contact details of 2 referees, a brief (1 page) statement of interest, and arrive no later than August 1, 2011, to: Stockholm University Registrar/PÄ SE-106 91 STOCKHOLM SWEDEN

or by e-mail to: registrator@su.se.

Applications sent electronically should preferably be in Word or pdf format. Please note! Specify the reference number SU 619-1676-11 in the subject line. –

Britt-Marie Sjoberg Dept. of Molecular Biology & Functional Genomics Stockholm University Tel: 46-8-164150, Fax: 46-8-166488 S-10691 Stockholm E-mail: Britt-Marie.Sjoberg@molbio.su.se Sweden Homepage: http://www.molbio.su.se bitte@molbio.su.se

Tanzania MalariaEvolution

University of Glasgow College of Medical, Veterinary and Life Sciences School of Veterinary Medicine

Research and training post-doctoral position in malaria vector ecology, Ifakara Health Institute, Tanzania & University of Glasgow, UK Ref: M00269

We are seeking a highly motivated postdoctoral researcher who is committed to applying their expertise in cutting-edge ecology and quantitative analyses towards improving the prediction and control of malaria vectors within the African settings where they impose the greatest health burden.

This post has been generated through a new collaboration between the University of Glasgow, the Ifakara Health Institute, Tanzania and the University of California, Davis. This individual will join a dynamic team of mosquito vector biologists based at the Ifakara Health Institute (IHI) in Tanzania, an international leader in the field of malaria research. At the IHI, s/he will lead the National Institute of Health, USA funded project Ecological and genetic determinants of malaria transmitting behaviours in the African vector Anopheles arabiensis.

The primary objective of this 5-year initiative is to identify the contribution of environmental and mosquito genetic factors to variation in the mosquito feeding and resting behaviours that determine their transmission ability and susceptibility to control measures. A further objective is to assess the phenotypic and genetic response of vector populations to the up-scaling of control measures that target specific vector behaviours (e.g. Insecticide-Treated Nets, targeting mosquitoes that bite indoors at night) and evaluate evidence for mosquito behavioural shifts in response to their use.

These issues will be investigated by the establishment of longitudinal field studies of mosquito vector behavior, demography and transmission intensity within several populations of the Kilombero Valley of Tanzania, where the coverage of indoor-based mosquito control measures is anticipated to significantly rise throughout the duration of the study.

In concert with directing the research activities of this project, this individual will be responsible for leading the development of research capacity in disease ecology at the Ifakara Health Institute, through provision of onsite supervision and training to high quality Tanzanian postgraduate students pursuing research associated with this project. By facilitating the transition of these students to independent scientists through publication and presentation of their results, the candidate will have opportunity to make a substantial contribution towards improving research capacity in malaria vector management in Tanzania.

Apply online at www.glasgow.ac.uk/jobs Closing date: 8th July 2011

The University is committed to equality of opportunity in employment.

The University of Glasgow, charity number SC004401.

Lyndsey McLaughlin | Advertising Assistant College of MVLS/ College of Social Sciences University of Glasgow Human Resources Department Tel: 0141-330-3379 Email: Lyndsey.McLaughlin@glasgow.ac.uk The University of Glasgow, charity number SC004401

Lyndsey McLaughlin <Lyndsey.McLaughlin@glasgow.ac.uk>

TexasAMU 2 Bioinformatics Genomics

Two Post Doctoral positions available in the Department of Veterinary Integrative Bioscience at Texas A&M University. Please see the descriptions below.

POSITION #1 TITLE: Post-Doctoral Research Associate in Bioinformatics LOCATION: Texas A&M University, College Station, TX SALARY: Commensurate with experience CLOSING DATE: Open until filled DURATION: Two years with a possibility of extension depending on performance and funding

DESCRIPTION: The Chowdhary & Cai lab (http://vetmed.tamu.edu/labs/cytogenics-genomics & http://www.genomezoo.net) is seeking a joint appointment post-doc that will apply the latest bioinformatics tools towards understanding equine diseases (including laminitis, recurrent airway obstruction, and stallion subfertility), phenotypes, and evolution of equids. The Chowdhary lab is focusing on characterizing genetic factors involved in major equine diseases, sexual development, and reproductive disorders. The approaches applied include genetic association analysis using the equine SNP chip, microsatellites, copy number variation tiling array, re-sequencing of candidate genes, gene expression microarrays, next-generation sequencing, protein expression analysis, RT-PCR, RH mapping, karyotyping, and FISH. In addition, the lab is also working on describing the PAR and the MSY of the equine Y chromosome including gene loss, gain, function, and the roles Y genes play in stallion fertility. The Cai lab focuses on the interaction between the genotype and phenotype using computational genomics to identify the causal variants underlying genetic disorders and complex traits of different organisms. Projects will focus on applying next-generation sequencing to follow up associations found with more traditional methods. The work is funded by USDA-CREES, USDA-NIFA, American Quarter Horse Foundation, and Morris Animal Foundation.

We seek a motivated postdoc that is interested in applying the latest bioinformatics tools to understand the genomic factors that play a role in diseases and phenotypes of horses, and other important domestic, agricultural, and wild animals. The post-doc will be required to write manuscripts and proposals, and will have opportunities to develop additional projects in line with their areas of interest. The successful applicant will work as part of a multidisciplinary team and will develop skills in bioinformatics, genomics, and translational medicine.

REQUIREMENTS: Ph.D. in a relevant biological discipline with previous research experience using genomic bioinformatics tools. Knowledge of both genomics and computational analysis of genomic data is required, as is familiarity with Linux, Python, Matlab, and Perl, and the ability to write scripts. Excellent writing, communication skills, and the ability work as part of a team are also required. Previous work with large data sets, SNP analysis, and next-generation sequencing data is preferred. Knowledge and experience with horses, other domestic animals, or wildlife is also preferred.

TO APPLY: For inquiries or to apply, email Dr. Jan Janecka (jjanecka@cvm.tamu.edu) a (1) a 1-page cover letter with as summary of your primary research experience and interests, (2) your CV, (3) and contact information for three references.

Bhanu P. Chowdhary Associate Dean for Research and Professor Department of Veterinary Integrative Biosciences Texas A&M University College Station, TX 77843 - 4458 Tel. 979-845-5092

POSITION #2 TITLE: Post-Doctoral Research Associate in Genomics LOCATION: Texas A&M University, College Station, TX SALARY: Commensurate with experience CLOSING DATE: Open until filled DURATION: Two years with a possibility of extension depending on performance and funding

DESCRIPTION: The Chowdhary lab (http://vetmed.tamu.edu/labs/cytogenics-genomics) is seeking a post-doc that will use the latest genetic tools towards understanding equine diseases (including laminitis, recurrent airway obstruction, and stallion subfertility), phenotypes, and evolution of equids. The Chowdhary lab is focusing on characterizing genetic factors involved in major equine diseases, sexual development, and reproductive disorders. The approaches applied include genetic association analysis using the equine SNP chip, microsatellites, copy number variation tiling array, re-sequencing of candidate genes, gene expression microarrays, next-generation sequencing, protein expression analysis, RT-PCR, RH mapping, karyotyping, and FISH. In addition, the lab is also working on describing the PAR and the MSY of the equine Y chromosome including gene loss, gain, function, and the roles Y genes play in stallion fertility. Projects will integrate diverse methods, but focus on applying

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TexasCU BirdEvolution

Postdoctoral Position in Wind-Wildlife Interactions

A postdoctoral position in wind-wildlife interactions is available in the lab of Dr. Amanda Hale at Texas Christian University, Fort Worth, Texas. The initial appointment is for one year, with an additional year's funding conditional on satisfactory performance. In partnership with NextEra Energy Resources, we have been investigating the direct and indirect impacts of wind energy on birds and bats at Wolf Ridge Wind, LLC in north-central Texas since 2009. Over the past two years we have made significant progress toward understanding the indirect effects of wind turbines on grassland birds. We have also developed a robust methodology for estimating bird and bat fatality rates. A major research focus for 2011 and 2012 will be to experimentally test the effectiveness of two curtailment strategies at reducing wind turbine associated bat fatality rates. The postdoc will oversee all aspects of the post-construction fatality monitoring from July through October in 2011 and 2012. The postdoc will also be encouraged to develop his/her own independent research projects. Housing at the field site will be provided during the field season.

Required Qualifications:

* A PhD in ecology & evolutionary biology, wildlife biology, or a related field and prior experience with field work

* Demonstrated ability to work independently and collaboratively

* A strong background in data analysis

* Familiarity with GIS

* Strong communication skills and demonstrated ability to manage a large and diverse field crew

* A valid U.S. driver's license and a clean driving record

* Be willing to adhere to all personal safety requirements associated with working on a wind farm

* Rabies pre-exposure vaccination, recent titer check, or willingness to obtain vaccination

Preferred Qualifications:

* Research experience in bat behavioral ecology

* Experience mentoring undergraduate or graduate student research projects

To apply, please e-mail (a.hale AT tcu.edu) with the following information: a statement detailing your research interests and qualifications, a CV, and the names and contact information (e-mail address and phone number) for three references. In your statement, please describe what interests you about this research project and whether you have any additional wind-wildlife projects that you would like to pursue.

Review of applications will begin April 8 and will continue until the position is filled. For full consideration, please have your application submitted by April 22, 2011. The anticipated start date is June 1, 2011. For more information, please e-mail Dr. Amanda Hale (a.hale AT tcu.edu).

This position is funded by the TCU-Oxford Univeristy-NextEra Energy Resources Wind Research Initiative (www.wind.tcu.edu< http://www.wind.tcu.edu >), at $42,000 per year plus benefits. NextEra Energy Resources provides unrestricted access to company data; however, the researchers have complete independence in all aspects of the analysis, conclusions, and decisions to publish the research.

Amanda M. Hale Assistant Professor, Biology Department Texas Christian University 2800 S. University Drive Room 412 Winton Scott Hall Fort Worth, TX 76129 office phone: 817-257-6182

a.hale@tcu.edu a.hale@tcu.edu

TexasTechU PoplarAdaptation

Postdoctoral Associate Position Population Genetics/Forestry

A postdoctoral research associate position is anticipated to work on local adaptation across latitude in balsam poplar (Populus balsamifera) beginning in September 2011. The successful candidate will have strengths in population genetics and bioinformatics, interests in plant physiology, and an earned PhD. The project focuses on identification of genes underlying locally adapted traits in trees from populations spanning latitudes from southern Canada to northern Alaska. The position will require extensive analysis of whole genome sequence data and the successful applicant is expected to be familiar with the Unix environment and basic scripting in Perl or a related language. Resulting analyses will have implications for plant migration responses to climate change, effects of local adaptation on genome-wide and population-level polymorphism, and tree breeding. Further information regarding this and related projects can be found in publications Olson et al. 2010 New Phytol.186:526-536; Keller et al. 2010 Mol.Ecol. 19:1212-1226; Sollanayakanahally et al. 2010 PC&E 32:1821-1832. Salary will be commensurate with qualifications and experience. Interested applicants should send a letter of interest, CV, and names and email addresses of 3 references to Matt Olson, Department of Biological Sciences, Texas Tech University, P.O. Box 43131, Lubbock, TX USA 79409-3131, or email matt.olson@ttu.edu. Texas Tech is an Equal opportunity/affirmative action employer.

"Olson, Matt" <matt.olson@ttu.edu>

TrentU WalleyeEvolutionaryEcology

Postdoctoral Fellow: Genetics, Evolutionary Ecology, Conservation, and Management of Walleye in the Great Lakes

We are seeking a postdoctoral fellow with research experience in the areas of landscape genetics, population genetics, and evolutionary ecology. The postdoctoral fellow will be expected to analyze and publish existing spatial and temporal data from genetic studies of walleye (Sander vitreus) in the Great Lakes. This work will contribute towards building a genetic map of the number, range, diversity, and relatedness of walleye stocks throughout the Great Lakes, as well as assessing and informing management and rehabilitation efforts. The successful candidate will also be strongly encouraged to explore independent research questions using next generation sequencing technologies within the framework of this project.

Research will be conducted within the Natural Resources DNA Profiling and Forensic Centre (www.nrdpfc.ca) at Trent University that includes a collaborative team of research scientists from Trent University and the Ontario Ministry of Natural Resources (OMNR), including the OMNR Fish Genetic and Stock Assessment Unit (http://web.nrdpfc.ca/-fishlab.htm). This research centre houses an impressive array of molecular biology equipment including a

Roche 454 next generation sequencer, two ABI 3730 genetic analyzers, an ABI 7900 Real-Time PCR machine, and a suite of automated liquid handlers.

The first year of the fellowship will be funded by the Ontario Ministry of Natural Resources at a salary of $40,000/year plus benefits, including extended family health coverage, with potential for renewal for a second year with an expanded focus on bioinformatics using next-generation sequencing. There is also the optional potential for the successful candidate to pursue a light teaching load at Trent University to augment this salary and develop their teaching portfolio.

All candidates should submit a letter of application, curriculum vitae, and names and contact information for three referees (send to both Dr. Kyle and Wilson). Applications will be accepted until August 1, 2011 or as soon as a suitable candidate is found before that date. The position could start as early as September 1, 2011, but no later than Jan 1, 2012.

Dr Chris Wilson, Research Scientist, Aquatic Biodiversity and Conservation Unit

Ontario Ministry Of Natural Resources, Trent University, 2140 East Bank Dr.

Peterborough, Ontario, Canada K9J 7B8

Phone: (705) 755-2260; Fax: (705) 755-1559

chris.wilson@nrdpfc.ca ; chris.wilson@ontario.ca

http://web.nrdpfc.ca/cwilson.htm Dr. C. J. Kyle, Assistant Professor, Research Chair in Wildlife Genetics and Forensics

Natural Resources DNA Profiling and Forensics Centre

Forensic Science Department, DNA Building, Trent University

2140 East Bank Drive, Peterborough, ON, K9J 7B8

Tel. 705-748-1011 ext 7055 Fax. 705-748-1132

chris.kyle@nrdpfc.ca

http://web.nrdpfc.ca/bios/dr_chriskyle.html christopherkyle@trentu.ca

UArizona MicrobialEvolution

Postdoctoral Position in Microbial Evolution

The Baltrus Lab at the University of Arizona (http://www.cals.arizona.edu/research/baltruslab/Baltrus_lab/Home.html) is seeking to hire an independent and open minded postdoc to investigate the genomic basis of host range evolution in phytopathogens. Our lab is currently using a variety of approaches to understand functional and regulatory changes during adaptation of the plant pathogen Pseudomonas syringae to a broad range of hosts and environments. Ideally the candidate will have experience working with microbes, and an understanding of genomics and next generation sequencing or experimental evolution is a plus.

Interested applicants please send an email with the title Postdoctoral Position describing your research interests and background to David Baltrus (baltrus@email.arizona.edu) along with an attached C.V.

Ultimately, applicants are required to submit a formal application through UA jobs (www.uacareertrack.com/hr) job #47815

Applications will be reviewed as they are received. Feel free to email with any inquiries concerning this job.

David Baltrus baltrus@email.arizona.edu

UBritishColumbia TeachingEvolutionBiol

Science Education - Postdoctoral Researcher -

Carl Wieman Science Education Initiative in Life Sciences - 2011

The Council of Life Sciences, which is coordinating curriculum reform for the Departments of Botany, Microbiology & Immunology, and Zoology at the University of British Columbia invites applications for Postdoctoral researchers for the Life Sciences Carl Wieman Science Education Initiative (LS-CWSEI), a five-year program for study of and innovation in science education (http://www.vpacademic.ubc.ca/CarlWieman/).

We are currently seeking three individuals to work with faculty to develop courses in physiology, genetics, and evolution as part of restructuring of the Biology curriculum. The work will involve assisting in the development of course and program level learning objectives, assessments, and pedagogy; development of material for class including interactive activities and pretests; administration and evaluation of assessments of student learning and of student attitudes toward science. Publication of research related to the impact of these interventions is also encouraged. For additional information about the Science Teaching and Learning Fellows positions see http://www.cwsei.ubc.ca/departments/-index.html Candidates should have: completed their Ph.D. in a biological science within the last three years with emphasis in physiology, genetics, or evolution; excellent organizational, interpersonal, and communication skills, and a strong personal commitment to science education. English fluency is also required. Experience in educational materials or curriculum development, on-line teaching, project management, and familiarity with current pedagogical research at the post-secondary level will be considered assets. Candidates with a Ph.D. in Education and a M.Sc. in Biology will also be considered.

The appointments will be for one year initially, and may be renewable for up to 3 years at the postdoctoral level.

Applicants should submit a resume, statement of teaching interests, and the names and complete contact information (including phone, fax and e-mail) of three references to: Shona Ellis, Associate Head of Biology, electronically to shona@mail.ubc.ca.

Review of applications will begin July 12, 2011, with appointments anticipated to begin on September 1, 2011.

UBC hires on the basis of merit and is committed to employment equity. We encourage all qualified persons to apply; however, Canadians and Permanent Residents of Canada will be given priority. The positions are subject to final budgetary approval. Salary and title will be commensurate with qualifications and experience.

Edythe Grant Office Manager/Assistant to the Head Department of Zoology University of British Columbia 6270 University Blvd. Vancouver, BC V6T 1Z4 604-822-6973

Edythe Grant <omgr@zoology.ubc.ca>

UCalifornia Davis EvolutionaryGenetics

TITLE: Postdoctoral researcher in evolutionary genetics and sociogenomics LOCATION: U.C. Davis Department of Entomology SALARY: Commensurate with experience; range begins at $40,000/year plus medical insurance CLOSING DATE: Open until filled DURATION: Three years with a possibility of extension depending on funding

DESCRIPTION: The Johnson lab in the department of Entomology at the University of California, Davis is seeking a postdoctoral researcher with an interest in the behavior, evolution, and genetics of honey bees. Opportunities will also exist for work on CCD and the honey bee immune system. RNA-sequencing, in particular, will be a major tool used by the lab to explore the genetic basis and evolution of social traits. The selected researcher will have some flexibility in choosing the aspect of honey bee biology on which to focus, but the position will be primarily molecular in nature.

REQUIREMENTS: Ph.D. in a relevant biological discipline. Knowledge and experience in the study of the genetics and or physiology of honey bees is desirable, but not necessary. Experience in functional genomics and the computational analysis of such data is a plus.

TO APPLY: Send via email a CV, cover letter briefly outlining research interests, and contact information for three references to:

Brian R. Johnson Assistant Professor University of California, Davis Department of Entomology 1 Shields Ave Davis, CA 95616 Tel. 858-397-3579 e-mail: brnjohnson@ucdavis.edu

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

Brian Johnson <brnjohnson@ucdavis.edu>

UCincinnati EnvironGenomics

Post-doctoral position in environmental genomics

A post-doctoral research associate position is available in the Baucom lab in the Dept of Biological Sciences at the University of Cincinnati to work on projects that can be best described as falling into the broad field of Environmental Genomics. One project will involve the examination of the bacterial community found in association with plants using next-generation sequencing. Other projects may include, but are not limited to, investigating the genetic basis and evolution of plant defense traits in both herbicide resistant and weedy plant species. Metagenomic and transcriptome sequencing and analysis of such sequence data will be integral components of the projects.

A PhD in Genetics, Genomics, Ecology and Evolutionary Biology or a closely related field of Biology is required, as is a strong background in molecular biology/bioinformatics and command-line capabilities. Relevant past training may include metagenomics, the development of genomic libraries, and programming in perl or python. The candidate will also be required to design, implement and analyze data from large field experiments at the UC field station, which is approximately 30 miles north of the main campus.

This position is contingent upon approval from UC human resources, and is available for a year with the possibility, upon significant progress, of another year of funding.

To apply, please send a CV, 3 relevant publications and the names and contact information for at least 3 references to Regina Baucom via email either zipped or as a single pdf: regina.baucom@uc.edu. Letters will be requested at a later date. Please feel free to email regina.baucom@uc.eduwith questions. Start date is somewhat flexible.

The Dept of Biological Sciences at the University of Cincinnati has an excellent group of evolutionary and organismal biologists with many possibilities for intellectual engagement.

http://homepages.uc.edu/ ˜ baucomra/Baucom_Lab/-Home.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

Regina Baucom <gina.baucom@gmail.com>

UConnecticut MicrobialComparativeGenomics

Job Posting Title: University Postdoctoral Fellow in Molecular Evolution and Comparative Genomics

Job Summary: The Department of Molecular and Cell Biology at the University of Connecticut is seeking a University Postdoctoral Fellow position in molecular evolution and comparative genomics of microorganisms.

This position is available immediately and is funded through the NSF Assembling the Tree of Life project on “Horizontal gene transfer and among phyla relationships”. The research will broadly aim to answer the question: How can horizontal transfer of genetic material be used to better understand the evolutionary history of organisms and the origin and evolution of metabolic pathways?

The successful candidate will be part of a team of experts in computational biology, microbiology, and evolutionary biology including the research groups of Drs. J. Peter Gogarten, Kenneth M. Noll, and R. Thane Papke at the University of Connecticut, Dr. Jinling Huang at the Eastern Carolina University and Dr. Ying Xu at University of Georgia, Athens.

The University of Connecticut, rated first among public universities in New England, is located in northeastern Connecticut with easy access to Boston and New York City. The web page of the Department of Molecular and Cell Biology is http://mcb.uconn.edu, information on recent research in the Gogarten-lab is available at http://gogarten.uconn.edu . Qualifications:

Minimum Qualifications: Applicants must have a Ph.D. in bioinformatics, statistics, microbiology, biology or a related field, with strong interest in molecular evolution or environmental microbiology; evidence of successful teamwork abilities; and excellent oral and written communication skills.

Preferred Qualifications: Experience in phylogenetic reconstruction, the Unix/Linux/Darwin operating system, and computer scripting (Perl, R, Python or similar).

Appointment Terms: The initial appointment is for one year with the possibility of renewal for up to two additional years contingent upon performance and funding. Salary will be offered commensurate with experience and skills. A competitive benefits package is included.

To Apply: Interested applicants should apply online using Husky Hire to send a single PDF file containing a cover letter, CV, one-page statement of research interests and contact information for three references. Correspondence can be addressed to Peter Gogarten at gogarten@uconn.edu. Review of applications will begin immediately and continue until the position is filled.

The University of Connecticut is an EEO/AA employer.

J. Peter Gogarten Board of Trustees Distinguished Professor Department of Molecular and Cell Biology University of Connecticut Unit 3125, BPB 404 91 North Eagleville Road Storrs CT 06269-3125 USA

Phone: 860 486 4061 (office) 860 486 1887 (lab) FAX: 860 486 4331 Email: gogarten@uconn.edu www: http://gogarten.uconn.edu/ jpgogarten@gmail.com

UExeter ExperimentalEvolution

Postdoctoral position: Experimental/Theoretical Evolution

Are you an experimentalist interested in contributing to the development and validation of new theories of microbial evolution? Or, are you a theoretician interested in gaining new skills by undertaking evolutionary experiments? Are you interested in being a part of a unique environments where experimentalists and theoreticians share common research goals?

We are looking for an Associate Research Fellow to join our interdisciplinary team in the group of Dr Ivana Gudelj based at the University of Exeter. Our focus is microbial evolution V from the adaptation to novel environments, diversification, through to the evolution of drug resistance. Our tools are lab based evolutionary systems and mathematical models V combining them gives us a powerful instrument for studying microbial evolution.

Applicants will possess a relevant PhD and be able to demonstrate sufficient knowledge in the discipline and of research methods and techniques to work within established research programmes. Experience in microbial experimental evolution and/or the genetics of microorganisms is desirable. The ability to communicate effectively with individuals from a wide range of disciplines is essential.

More information about possible projects and how to apply can be found at: http://people.exeter.ac.uk/-ig232/Positions.html Closing date is 18th July 2011

"Gudelj, Ivana" <I.Gudelj@exeter.ac.uk>

UFlorida HumanEvolutionaryGenetics

Postdoctoral position in Human Molecular Genetics

A postdoctoral position (two years at least) is available in Connie Mulligan's lab at the University of Florida.

Two NSF/NIH/UF-funded projects are currently ongoing and the successful candidate can work on one or both: 1) Examination of DNA methylation patterns in mothers and newborns from the Democratic Republic of Congo (DRC) to test whether epigenetic alterations mediate the effects of maternal exposure to stressors on fetal development and neonatal health. Specifically, we are testing if epigenetic modifications may mediate changes in gene expression in infants that result from maternal trauma and material deprivation associated with the war in the DRC. More broadly, we are interested in the idea that behavior and complex phenotypes may be shaped by early life experiences that alter gene expression through epigenetic alterations. 2) Investigation of the genetic and cultural underpinnings of complex diseases that exhibit racial inequalities, using hypertension in African-Americans as a model phenotype. We are combining the analysis of genome-wide SNPs, genetic ancestry estimates, and epigenetic variation with sociocultural data including experience of discrimination and social network analysis. By combining genetic and socio-cultural data, our goal is a more comprehensive investigation of complex disease and racial disparities than is possible with only one type of data. See related study - http://www.plosone.org/article/-info%3Adoi%2F10.1371%2Fjournal.pone.0006821 Qualifications: A PhD and a strong background in generation of genetic data (DNA sequencing, SNP detection, microarray analysis, etc.) and data analysis (gene association analysis, regression analysis, genetic ancestry estimation, etc) are essential. Experience generating methylation data or additional computational experience (e.g. computer programming, simulation analysis, etc) is a plus. In addition to the projects listed above, there are excellent opportunities for the successful candidate to develop new lines of research as well as productive collaborations outside the lab.

The University of Florida is a leading research institution with a university-wide commitment to genetics research. The Department of Anthropology (www.anthro.ufl.edu) has 30 full-time faculty with diverse interests and a very strong biological subfield, with emphases on molecular, paleo, and forensic anthropology. The department is one of the top rated programs in the country (6th among public institutions, 11th overall). The University of Florida Genetics Institute (www.ufgi.ufl.edu) is an inter-college entity with a new research building to enhance opportunities for collaboration. Gainesville is located in north central Florida (away from the hurricanes!), with average temperatures ranging from 45F to 90F. Beaches on the gulf and Atlantic coast are ˜ 2 hours away.

To apply: via email, send a CV, a statement of research interests, and the names and contact information (including email and phone) for three references. Applications and inquiries should be addressed to Connie Mulligan at cmulligan@ufl.edu.

Review of materials will begin June 1 and will continue until the position is filled. Start date is flexible and can start as early as Summer, 2011. Salary is commensurate with experience. Position may be extended for a total of three years. Informal inquiries prior to submitting a formal application are welcome. AA/EOE.

Connie J. Mulligan, PhD Professor, Department of Anthropology Associate Director, UF Genetics Institute 2033 Mowry Rd, PO Box 103610 University of Florida Gainesville, FL 32610-3610 Office: 409 Genetics Institute Telephone: 352-273-8092 Fax: 352-273-8284 Email: cmulligan@ufl.edu Website: http://www.clas.ufl.edu/users/mulligan/Webpage/index.html

"Connie J. Mulligan" <cmulligan@ufl.edu>

UHawaii EvolutionGenetics HawaiianDrosophila

Postdoctoral position: Evolutionary genetics, adaptation and speciation in Hawaiian Drosophila.

A two-year postdoc position is available focusing on genome level technology, (genome sequences, transcriptome, QTLs, etc.) to study speciation and adaptation in the planitibia group of Hawaiian Drosophila, particularly the D. heteroneura D. silvestris ethological species pair. Starting time is flexible, between August 2011 to February 2012.

Tropical Hawai'i is an unparalleled setting for the study of terrestrial evolution. A perfect example of this is the drosophilid species radiation. At least a third of the 2,000+ species in the world occur in Hawai'i, originating from a single introduction, the vast majority are endemic to parts of the archipelago and contain some of the most morphologically diverse Drosophila in the world. The Hawaiian Drosophila are used as a prime example in Dobzhansky's famous essay "Nothing in Biology Makes Sense Except in the Light of Evolution."

I am looking for someone with a Ph.D. or equivalent degree, with a high degree of familiarity in standard molecular genetics laboratory experience (DNA extraction, quantification, PCR, RT-PCR, cloning, transformation, sequencing). Experience in working with Drosophila is not essential and I would encourage applications from interested people in any relevant molecular biology field. Familiarity with population/evolutionary genetics is a plus. Programming, simulation, analysis experience with PERL, C, R and/or Mathematica is a plus. Database experience, e.g. MySQL, is a plus. This will be a first position in a new group being established by Floyd Reed, who is beginning in August 2011 (and to eventually move to a shared space that is currently under renovation) in The Dept. of Zoology (to merge and become The Dept. of Biology). I am looking for someone that I and others can learn from (e.g. microbiology techniques) as much as training in population genetics. There will also be opportunity to contribute to other planned projects, part of which will be focused on genetically modifying wild populations, with collaborative pilot experiments being planned in Culex mosquitoes and avian malaria, other possible pilot projects include DNA barcoding of Hawaiian diversity, and the detection and analysis of demographic history and forms of positive selection in various species using ABC approaches.

I do not discourage anyone from applying based on age, sex, race, political views, nationality, etc. Applicants will be selected based on scientific merit, e.g. a record of publication, experience, etc.

The University of Hawai'i, Manoa is the main campus of the Hawaiian state university system in the capital city of Honolulu, population 375,00 (900,000 in the metro area), on the 600 square mile island of Oahu.

Interested candidates should send an email message with a statement of interest and experience, an attached CV in PDF format and the names, affiliation and email addresses of three potential references to reed@evolbio.mpg.de with "Hawaiian Drosophila genomics application" in the subject line.

Floyd A. Reed, Ph.D.

The University of Hawai'i is an Equal Opportunity / Affirmative Action institution.

reed@evolbio.mpg.de

UKansas Phylogenetics

A POSTDOCTORAL POSITION is available in the laboratory of Dr. Mark Holder in the Department of Ecology and Evolutionary Biology at the University of Kansas (Lawrence, KS). The position is available for two years. The focus of the research will be the estimation of phylogenetic trees from unaligned sequences (simultaneous alignment and tree inference). Extending and developing software for this problem will constitute a significant component of the work. Candidates will be expected to have completed a PhD in Biology, Statistics, Computer Science or a related field. Preferably the candidate will exhibit competence in C or C++. Experience with the Python programming language would also be helpful for this position.

The ideal candidate will be enthusiastic, motivated, have a strong background in phylogenetics, and have experience implementing statistical inference techniques in software. The ideal candidate will have a strong background in bioinformatics as demonstrated by materials submitted through the application process, work experience, and letters of reference, and/or previous publications. Apply to: https://jobs.ku.edu and search for position number 00206565. Review of applications begin 8-03-2011. For more information, see the Holder web page at: http://www2.ku.edu/~eeb/faculty/holder.shtml EO/AA employer.

Sincerely, Mark Holder

mtholder@ku.edu http://phylo.bio.ku.edu/mark-holder Department of Ecology and Evolutionary Biology University of Kansas 6031 Haworth Hall 1200 Sunnyside Avenue Lawrence, Kansas 66045

lab phone: 785.864.5789

fax (shared): 785.864.5860

mtholder@ku.edu

ULondon BeeNematodes

Applications are invited for the post of Postdoctoral Research Assistant in Transcriptomics of Behaviour in a Host-Parasite system on a project funded through by the Leverhulme Trust. The project is a collaboration between Royal Holloway, University of London and the Institute of Zoology, Zoological Society of London, to investigate Are bumblebees the Extended Phenotype of nematodes? A transcriptomics approach. The aim of the project is to determine how a parasitic worm manipulates the behaviour of its bumblebee host for its own selfish benefit.

You will need to help to design and conduct the research. Duties include: bioinformatics analyses of next-generation sequencing data, preparation of RNA and cDNA libraries for Solexa analyses, behavioural experiments, infection experiments, rearing and maintenance of bumble bee colonies, data management and analysis, and manuscript writing. Training will be provided as necessary. You will work within the groups of Dr Mark Brown (RHUL) and Dr Seirian Sumner (IoZ).

This is a fixed term full-time post available from 1st October 2011 until 30th September 2013. You will need to hold a PhD in bioinformatics of next-generation sequencing or have equivalent experience, with an interest in the impacts of parasites on hosts. Prior experience conducting bioinformatics analyses of next-generation sequencing data, with evidence of successful publication, is required.

For informal enquiries please contact Dr Mark Brown mark.brown@rhul.ac.uk or Dr Seirian Sumner (Seirian.Sumner@ioz.ac.uk).

Further details and an application form are available to download at http://www.rhul.ac.uk/jobs/home.aspx or by contacting the Recruitment Team by email: recruitment@rhul.ac.uk or tel: 01784 414241

Please quote the reference: X0611/6406

Closing date: 12 noon 18th July 2011

Interviews are expected to take place on the 28th July 2011.

The College is committed to equality and diversity, and encourages applications from all sections of the community.

Mark Brown <Mark.Brown@rhul.ac.uk>

UManitoba MicrobialBioinformatics

PDF or Research Associate in Bioinformatics Microbial Genomics for Biofuels and Co-products from Biorefinaries Department of Plant Science, University of Manitoba Start date: 11 July, 2011 Closing date for applications: 20 June 2011, or until position is filled

Project Description: One position is available to conduct cutting-edge research employing the tools of bioinformatics in a multidisciplinary team including microbiologists, molecular biologists and biosystems engineers. This is an outstanding opportunity to contribute to research whose aim is to develop a sustainable energy source from cellulosic wastes. This collaborative project seeks to characterize both known and newly discovered cellulose-degrading microbes and their genomes, leading to metabolic engineering, and to the development of designer microbial consortia, to enhance synthesis of fuels and bioproducts. A range of organisms, approaches and biofuels will be investigated. A project summary can be viewed at http://www.microbialrefinery.com. This project is co-funded by Genome Canada and the Manitoba Ministry of Science, Technology Energy and Mines (STEM).

The successful applicant will join a team of bioinformaticists and information technologists who are mining and managing data from this project. This team carries out work in the following areas: de-novo annotation of newly-sequenced microbial genomes; development of high-throughput analytical pipelines; database design; software design; comparative genomics of cellulose degrading microorganisms; analysis and mining of microarray data; data mining and in-silico metabolic engineering. This project affords many opportunities for original contributions in both basic and applied reasearch in bioinformatics, as they relate to the project.

Qualifications: Qualified applicants must: possess a Ph.D. in Microbiology or Bioinformatics from a recognized University; have knowledge of microbiology and biochemistry with strengths in data mining and programming; have extensive experience in object-oriented programming in Java or Python on a Unix platform; have a demonstrated record of independent as well as collaborative research and scholarly publications; and excellent oral and written communication skills.

The University and Community: The University of Manitoba is located in Winnipeg, the largest city in the province of Manitoba. The city has a rich cultural environment including symphony, opera, dance, theatre, sports, and ethnic festivals. The region provides ample opportunities for outdoor recreation in all seasons. Learn more about Winnipeg at http://www.winnipeg.ca.

Applications: Applications are invited at the level of Post Doctoral researcher or Research Associate. Funding for the project is available through September 30, 2013. The University of Manitoba exercises a Canadian-first policy; however, all those qualified are encouraged to apply. The review of applications will continue until the position is filled. Application materials, including letters of reference, will be handled in accordance with the protection of privacy provisions of ?The Freedom of Information and Protection of Privacy? (Manitoba). Please note that your curriculum vitae will be provided to participating members of the search process. Applications, including curriculum vitae, short statement of research interests and the names and addresses (including phone, fax and e-mail addresses) of three referees should be sent to:

Dr. Brian Fristensky Associate Professor Department of Plant Science University of Manitoba Winnipeg, MB CANADA R3T 2N2 Phone: 204-474-6085 FAX: 204-474-7528 Email:frist@cc.umanitoba.ca http://home.cc.umanitoba.ca/~frist Brian Fristensky <frist@cc.umanitoba.ca>

UMontreal HumanPopulationGenomics

Postdoc: Human Genomics and Population Genomics, University of Montreal A postdoctoral position is available in the population and evolutionary genomics laboratory at the University of Montreal of Philip Awadalla (http://www.philip-awadallalab.org/). Researchers will be involved in the development of methods and collection/analysis of data generated in our ongoing studies of human genomics and disease. The successful candidate will be trained in population or statistical genetics, or have strong computational or statistical skills. Postdoctoral research scientists can work on interesting projects of their choosing related to the labs' general research interests or our current projects.

Possible/related projects include: 1) Next-generation tools and development of model and non-model based methods to study the role of common and rare genetic variants responsible for a number of human traits or disorders, mostly related to child health (cancer, immunodeficiencies, etc.). 2) Next-generation genomics applications for studying the critical co- regulatory factors associated with humans and malaria, sampled from populations globally. A “population biology” approach to identifying key genes and gene networks associated with infection and resistance in both humans and pathogens. 3) Molecular and statistical genomics projects examining the severity of sickle-cell disease in Africa and the North and South America. 4) Genetic and genomic epidemiology of endophenotypes from a deeply phenotyped Quebec cohort of 20,000 participants ages 40-69 - CARTaGENE (www.cartagene.qc.ca). CARTaGENE is an infrastructure for population genomics research. This resource will contribute to the development of better diagnosis, treatment and disease prevention programs.

Interested individuals with a Phd should please write to Philip Awadalla (philip.awadalla@umontreal.ca).

philip.awadalla@umontreal.ca

UMontreal PlantBioinformatics

Postdocs>UMontreal.PlantTranscriptomics

A postdoctoral position is available to study plant transcriptomics via deep RNA sequencing in a phytoremediation context. The objective of the project is to find candidate genes potentially involved in the degradation or accumulation of organic and inorganic pollutants. Our model plants are willows (Salix sp.) that have high phytoremediation potential because of their rapid growth, their high biomass production, and their ability to grow in highly contaminated soils. Experiments will take place in the greenhouse as well as in the field.

This position is part of a large genomic project that aims at increasing our understanding of phytoremediation. It is a highly multidiciplinary project that studies simultaneously soil chemistry, soil microorganisms, fungi, and plants.Â The work will be performed at the University of Montreal Biodiversity Centre (www.biodiversite.umontreal.ca/), which is part of the Plant Research Institute (www.irbv.umontreal.ca).

The successful candidate will be involved in the collection and processing of RNA samples. He will also be responsible for managing important amounts of deep RNA sequencing data, developing analytical tools and pipelines, and analyzing and interpreting the results. The successful candidate will also be involved in the redaction of research reports and scientific papers.

MINIMUM QUALIFICATIONS âÂÂÂ Ph.D. in transcriptomics, bioinformatics, or other relevant field. âÂÂÂ Proven research experience and a strong publication record. âÂÂÂ Solid analytical, computing, and statistical skills. âÂÂÂ Candidates should be comfortable working in a UNIX environment, have a strong programming background, and be proficient in working with large datasets.

PREFERRED QUALIFICATIONS âÂÂÂ Strong abilities for team work âÂÂÂ Experience with biological experimental designs such as randomized block designs âÂÂÂ Candidates with a background in interdisciplinary research, spanning both biological sciences and applied mathematics/computer science, are especially encouraged to apply. âÂÂÂ Candidates will ideally be conversant in a compiled programming language (e.g., C or C++), a scripting language (e.g., Perl), and a statistical environment (e.g., R).

APPLICATION DEADLINE: 1st August 2011

Funding is available for three years. The position will remain open until filled. To apply formally, submit the following documents in PDF format: 1.ÂÂÂ A brief statement of research interests, qualifications and experience and why you feel you are a good candidate for this position. 2.ÂÂÂ Curriculum vitae, including a list of scientific publications. 3.ÂÂÂ The names and contact details of at least two references willing to provide a confidential letter of recommendation upon request.

CONTACT Enquiries may be sent to: Simon Joly, Ph.D. Email: simon.joly@umontreal.ca

Simon Joly <simon.joly@umontreal.ca>

UNebraska StressAdaptation

A postdoctoral position is available for up to two years, starting on or after July 1 2011 at the University of Nebraska-Lincoln (UNL) to study adaptations to biotic and abiotic stressors in aphids. The position holder will join an interdisciplinary collaboration between members of the Department of Entomology (Nick Miller, Tiffany Heng-Moss, Blair Siegfried), the School of Biological Sciences (Jenn Brisson, Ryan Bickel, Tony Zera) and the Department of Biochemistry (Renu Nandakumar) at UNL. The project will study the transcriptomic, proteomic, and physiological changes that occur when soybean aphids (Aphis glycines) are challenged with selected stressors. Through this approach, we seek to identify mechanisms that are part of a general stress response and also those that are stressor-specific.

Because of the interdisciplinary nature of this project, candidates with a PhD and a background in molecular biology, evolutionary/population genetics, genomics, bioinformatics, insect physiology, enzymology or related disciplines are welcome to apply. A desire to develop new skills will be essential.

To apply, please send a CV, a brief statement of research interests, and the names and contact information of three references.

For more information or to apply, please contact:

Nick Miller Department of Entomology, Entomology Hall, University of Nebraska-Lincoln, Lincoln, NE 68583, USA, +1 402-472-6200, nmiller4@unl.edu

or

Jenn Brisson School of Biological Sciences, University of Nebraska-Lincoln, Lincoln, NE 68588, USA, +1 402-613-4135, jbrisson2@unl.edu

nmiller4@unl.edu

USouthDakota LotusEvolution

POSTDOCTORAL FELLOW TO WORK ON EVOLUTION OF LOTUS ON CALIFORNIA'S CHANNEL ISLANDS AND ON CONSERVATION GENETICS OF ISLAND ENDEMIC PLANTS A post-doctoral position is available in the laboratory of Kaius Helenurm in the Department of Biology at The University of South Dakota. This position would involve working on (a) the dispersal and differentiation of endemic Lotus on California's Channel Islands, and (b) the conservation genetics of endemic plants of San Clemente Island, CA. I am looking for a colleague that would like to express their independent, creative energies to plant evolution on islands and to the future development of the system.

The ideal candidate would be a recent Ph.D. with a strong background in population genetics and molecular techniques. The position is available for one year (funded by NSF and the U.S. Navy), with the possibility of renewal for a second year. The start date is flexible, but the position is available immediately. Applications will be considered until the position is filled.

Please apply via e-mail to Kaius Helenurm (helenurm@usd.edu), and include: (1) a brief cover letter describing your research interests and qualifications, (2) a full CV, (3) your preferred start date, (4) contact information (email, phone number) of three refereerences, and (5) pdf's of up to three representative publications. Please include "postdoctoral application" in the subject line of the e-mail. Informal inquiries are welcome.

Kaius Helenurm Professor and Chair of Biology Department of Biology The University of South Dakota

Email: helenurm@usd.edu Website: http://people.usd.edu/˜helenurm/Home.html Kaius.Helenurm@usd.edu

UStAndrews EvolutionaryBiol

Fixed-term Academic Research Fellow, University of St Andrews, Scotland.

The School of Biology at the University of St Andrews is one of the leading departments of Biology in the UK. We offer several different degree programmes, including Biochemistry, Cell Biology, Ecology & Conservation and Marine Biology as well as general Biology, and additional joint degree options.

We are seeking to appoint an enthusiastic research fellow to join the School of Biology. You will work alongside leading academics with the potential to contribute to collaborative research projects. You will have a degree in the life sciences and will hold a relevant PhD. Ideally you will conduct research complementary to some of the School's research expertise established within the Centre of Evolution, Genes and Genomics and the Institute for Behavioural and Neural Sciences. The School is also developing a Centre for the study of Biological Diversity and has broad interests in molecular, cellular and ecological biology.

We are looking to appoint an early career stage researcher who can will prove successful in attracting funding for their research and publishing innovative research, complementary to our current expertise.

This is a 48-month appointment with an anticipated start date of 01 November 2011 or as soon as possible.

Informal enquiries to Prof Mike Ritchie, email: mgr@st-andrews.ac.uk

Formal applications MUST be made through the University's Human Resources application procedures. Look for application reference CD7082 at https://www.vacancies.st-andrews.ac.uk/welcome.aspx Mike Ritchie Acting Head School of Biology Dyers Brae House University of St Andrews St Andrews, Fife Scotland KY16 9TH

Phone: 0 (44 outside UK) 1334 463495 Fax: 0 (44 outside UK) 1334 463366

Websites: http://biology.st-andrews.ac.uk/ritchielab/ http://biology.st-and.ac.uk/supplemental/ritchie/papers.aspx Michael Ritchie <mgr@st-andrews.ac.uk>

UTexas PlantAdaptation

Postdoctoral opportunity in plant adaptation, evolutionary ecology and landscape genomics

The Texas Switchgrass Collaborative seeks a postdoctoral collaborator to join as an integral member of our 4-year NSF-funded project to study the ecological and evolutionary basis of biomass production in switchgrass, a biofuel candidate species. The project combines experimental, genomic and modeling approaches with the goal of understanding the basis of phenotypic expression in variable environments, including future climate scenarios. The successful candidate will establish an independent research focus within the general aims of the project. We are especially interested in candidates whose research interests would draw on two or more of our core approaches (experimental, genomic, modeling). We will consider candidates from a wide range of backgrounds and training. Three years of funding are available. The appointment will be made on an annual basis with renewal dependent on satisfactory performance. Salary is competitive with full benefits.

Interested candidates should email to tkeitt@keittlab.org a single PDF file containing: 1) a cover letter indicating interest in the project, 2) a current CV, and 3) the names, email addresses and telephone numbers of three professional references. The position is open until a suitable candidate is found.

For more information on participating labs see:

http://www.keittlab.org/ http://www.biosci.utexas.edu/ib/faculty/hawkes/lab/Default.htm http://w3.biosci.utexas.edu/juenger_lab/ http://www.ars.usda.gov/spa/gswrl/pfay http://www.ars.usda.gov/spa/gswrl/jkiniry The Texas Switchgrass Collaborative is described here: http://openwetware.org/wiki/Texas_Switchgrass_Collaborative tjuenger@austin.utexas.edu

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UTKnoxville EvolutionaryBioinformatics

Outstanding, motivated candidates are being sought for a post-doctoral position in the laboratory of Dr. Michael A. Gilchrist in the Department of Ecology & Evolutionary Biology at the University of Tennessee, Knoxville. Pending final approval of funding, the successful candidate will be supported by a three year NSF grant whose goal is to develop, integrate and test mathematical models of protein translation and sequence evolution using available genomic sequence and expression level datasets.

Publications directly related to this work include:

Gilchrist, M.A. 2007, Molec. Bio. & Evol. http://mbe.oxfordjournals.org/cgi/content/abstract/24/11/2362 and Shah, P. and M.A. Gilchrist 2011, PNAS http://www.pnas.org/content/early/2011/06/02/1016719108.abstract?sid=508b5987-4d01-444e-b850-1ee5f5028cac The emphasis of the laboratory is focused on using deterministic and stochastic models to analyze complex, heterogeneous datasets to answer biologically motivated questions. The research associated with this position draws upon a wide range of scientific disciplines including: cellular biology, evolutionary theory, differential equations, and probability/likelihood. Consequently, the ideal candidate would have a Ph.D. in biology, mathematics, or statistics with a solid background in at least one of the other areas. The researcher is expected to collaborate closely with the PIs (Drs. Michael Gilchrist and Russell Zaretzki) on this project but will also have time to collaborate on other research projects such as host-parasite evolution, life-history theory, protein folding, and phylogenetics. In addition, the researcher will have opportunties to interact with other faculty members in the Division of Biology as well as researchers at the National Institute for Mathematical and Biological Synthesis (www.nimbios.org)

Review of applications begins immediately and will continue until the position is filled. The start date is flexible with the earliest date being August 1st, 2011. To apply, please submit curriculum vitae, brief statement of research interests, up to 3 relevant manuscripts and 3 professional references via email to mikeg <at> utk <dot> edu.

Michael A. Gilchrist, Ph.D. Associate Professor Department of Ecology & Evolutionary Biology 569 Dabney Hall University of Tennessee Knoxville, TN 37996-1610

phone:(865) 974-6453 fax: (865) 974-6042

web: http://eeb.bio.utk.edu/gilchrist.asp mikeg@utk.edu

UWisconsin Madison EvolutionaryGenetics

Postdoctoral Position in Evolutionary Genetics/Genomics

A postdoctoral position is available in the Laboratory of Professor Carol Lee in the Center of Rapid Evolution (CORE) at the University of Wisconsin, Madison to work on a project in collaboration with Joana Silva at the Institute for Genome Sciences (IGS).

The research focuses on the evolutionary genetics and genomics of invasive populations. We are exploring the systematic and functional composition of microbial communities associated with an invading host, the copepod Eurytemora affinis, and how microbial-host interactions shift following habitat invasions. The project will make extensive use of microbiome and metagenome methodologies to study the microbiota, and of transcriptome sequencing and analyses to characterize metabolic shifts within the copepod host.

Requirements for this position include a Ph.D., a strong background in molecular biology/genomics and strong analytical and quantitative skills. Relevant training and experience might include research in metagenomics, culturing of bacteria from environmental samples, transcriptomics, and genomic data analysis.

Applicants should email a CV and up to three representative publications to: carollee@wisc.edu. Any questions regarding this position are welcome.

The University of Wisconsin, Madison provides an intellectually vibrant research environment, with ~37 biology departments and ~800 biology faculty, including a strong community of evolutionary biologists and geneticists. The University of Wisconsin is an Equal Opportunity/Affirmative Action Employer.

Carol Eunmi Lee, Ph.D. Professor Center of Rapid Evolution (CORE) 430 Lincoln Drive, Birge Hall University of Wisconsin Madison, WI 53706 carollee@wisc.edu

https://mywebspace.wisc.edu/carollee/web/Lee/-Lee.html carollee@wisc.edu

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UZurich EvolutionaryBiology

Postdoctoral position in experimental evolution

A postdoctoral fellowship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. We are looking for a researcher to study innovation in biological systems that range from molecules to large genetic networks. Ongoing projects involve laboratory evolution of yeast, E. coli and fruitflies, as well as in vitro evolution of ribozymes (e.g., Hayden et al., Nature 474, 92-95, Dhar et al., J. Evol. Biol 5 92-95). A sample of the laboratoryâs research can be found at http://www.ieu.uzh.ch/wagner/. Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and lifeâs fundamental organizational principles.

We are looking for an individual who has received his or her PhD within the last five years, who is highly self-motivated and can work independently on a project that he or she will develop. The labâs work is concept-driven instead of organism-driven, and projects are not restricted to the model systems mentioned above. A successful candidate will have substantial research experience with molecular biological techniques, acquired in research with an evolutionary orientation. The ideal candidate will also have experience with computational analysis of high-throughput data. State of the art experimental technology is available through the Functional Genomics Center Zurich, which provides platforms for ultra-high throughput sequencing, transcriptomics, proteomics, and metabolomics. Applications with a demonstrated interest and research history in evolutionary biology will be given strong preference. The position offers a highly competitive salary of up to three years on annually renewable contracts.

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

To be considered, please send a single (!) PDF file merged from the following parts to jobs_aw@bioc.uzh.ch: CV including publication list, a statement of research interests not exceeding three pages, and three academic references. A brief sketch of a proposed research project is also desirable. Please include the word âEXPPOST11â in the subject line. The application deadline is August 15, 2011. The position is available in late fall of 2011.

Many thanks and kind regards,

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

annette.schmid@ieu.uzh.ch

UZurich PlantNGS SNPs

Open Position at the University of Zurich

Position description: Applications are open for one 6-yr. position (3 yrs., renewable for a second 3 yr. term) at the level of advanced post- doc (Oberassistant, in the German-speaking countries) in the research team of Professor Elena Conti (http://www.systbot.uzh.ch/-Personen/ProfessorenundDozenten/ElenaConti.html). The ideal candidate will have a strong interest and expertise in ONE of the two following areas: 1) Applications of Next Generation Sequencing methodology in plant evolutionary biology; areas of special interest include (but are not limited to): phylogenetic analysis of multi-gene data sets; population genetics using SNPs; coalescent analysis of genetic data; molecular genetic control of plant reproduction (for example, in primroses); speciation genetics; bioinformatic analysis of NGS data; 2) Integration of Ecological Niche Modeling methodology with genetic data (both at the population and phylogenetic levels); areas of interest include: changes of ecological preferences and species ranges over time (present, past, and future projections) and transitions between mainland and different island systems.

The successful candidate will participate in joint and independent proposal writing and have access to intramural and extra-mural research funding. Additionally, s/he will contribute to Master and Ph.D. student advising in Contis group and teach one course of his/ her choice. The position can lead to the Habilitation. Salary will be commensurate with previous experience.

Requirements: Applicants must hold a Ph.D. degree. A proven record of academic achievement (including publications in peer-reviewed journals and evidence of successful application to competitive research funds) and previous post-doctoral experience are desirable.

Facilities: The University of Zurich is one of the leading European Universities in Biology. We offer a modern research environment with up-to-date molecular and computational infrastructure, excellent opportunities for collaboration among evolutionary biologists, molecular geneticists, niche modelers, and access to competitive funding sources both at the national and European level. For further information on facilities, research and teaching activities at the Institute of Systematic Botany, see http://www.systbot.uzh.ch/ index.html. The University of Zurich is associated with the Functional Genomics Center Zurich (http://www.fgcz.ch/).

How to apply: Send the following documents by email AS A SINGLE PDF FILE to Prof. Elena Conti, ContiElena@access.uzh.ch: I) a two- to three- page summary of your research goals and how your research will complement current projects in Prof. Contis group, leading to productive collaboration; II) a one- to two-page summary of courses that you would like to teach, explaining how they would complement current offerings at our Institute; III) your detailed curriculum vitae, including a list of scientific publications and grants obtained from competitive funding sources; IV) a copy of your Ph.D. degree certificate (if possible, also include a copy of graduate academic records); V) the names and full addresses of three or more referees; please, ask them to send their confidential assessment of your scientific achievements and academic potential directly to my email address.

Deadline for application: The position will remain open until a suitable candidate is found. Applications will be screened as they arrive, thus earlier applications might have an advantage.

Starting date: Negotiable, but candidates who can start sooner might be preferred, all other qualifications being similar.

Position description updated June 8, 2011

Prof. Elena Conti, Director

Institute of Systematic Botany and Botanic Garden University of Zurich

Zollikerstrasse 107, 8008 Zuerich, SWITZERLAND Ph: 0041 44 634 8424 Fax: 0041 44 634 84 03 email: elena.conti@systbot.uzh.ch

http://www.systbot.uzh.ch/Personen/-ProfessorenundDozenten/ElenaConti.html Elena Conti <ContiElena@access.uzh.ch>

VrijeU Amsterdam PlantMutualism

Postdoctoral position with Dr. Toby Kiers, VU University, Amsteram

Cooperation and Antagonism in resource rich environments

A postdoctoral position is available at the Department of Ecological Science, Faculty of Earth and Life Sciences, Vrije Universiteit Amsterdam.

The mutualism between plants and their arbsuscular mycorrhizal fungi is one of the most ancient and important ecological relationships on earth. However global nutrient enrichment has increased resource availability for plants, potentially driving a shift from mutualism to parasitism in the relationship. The postdoctoral researcher will investigate how antagonism can evolve from cooperation when resource availability changes.

Tasks: Daily tasks will involve work in greenhouses, laboratories and with fungal culturing. Researcher must have an excellent knowledge of spoken/written English. No prior knowledge of Dutch is required. Our group is a multidisciplinary, international team of ecologists, evolutionary biologists and plant physiologists.

Requirements: Candidates should have a PhD in Biology, Ecology & Evolution, Microbiology, or related fields, and a strong publication record. Experience in molecular biology, evolutionary game theory, isotope labelling, rhizosphere studies and/or plant physiology is a plus.

Salary: The salary will be in accordance with university regulations for academic personnel, and amounts 2.977,- gross per month in the first year up to 3.755,- in the fourth year (salary scale 10.5) based on a full-time employment. The appointment will be initially for 1 year. After satisfactory evaluation of the initial appointment, it can be extended for a total duration of 3 years.

Information: For additional information please contact: prof. dr. Toby Kiers Phone number +31 (0)20 5987085. E-mail: toby.kiers@falw.vu.nl.

Application: Applicants are requested to write a letter in which they describe their abilities and motivation, accompanied by a curriculum vitae and one or two names and contact info for references. Written applications should be sent before August 31th, 2011 to toby.kiers@falw.vu.nl and ccd to falw-vacatures@falw.vu.nl. Please mention the vacancy number in the e-mail header

“Kiers, E.T.” <toby.kiers@vu.nl>

Yale VirusEvolution

A two-year postdoctoral position is available on or after Dec 1, 2011 under the supervision of Dr. Paul Turner in the Department of Ecology and Evolutionary Biology at Yale University. The project bridges experimental evolution of RNA viruses, and computational models of intracellular virus growth. Experiments will test how genetic architecture (gene order) of virus genotypes impacts their sensitivity to innate cellular immunity, and adaptation to cancer-derived cells. The overall goal of the project is to advance the development of data-driven predictive models of virus growth. The project is funded through NIH and is in collaboration with Dr. John Yin at U Wisconsin. Experience with experimental evolution of viruses in tissue culture is preferred, but all strong candidates will be considered. Please direct inquiries to paul.turner@yale.edu

paul.turner@yale.edu

WorkshopsCourses

Barcelona StatGenetics Aug22-26

STATISTICAL GENETICS SHORT COURSE 22-26 August 2011

Barcelona, Spain Hosted by Centre Nacional d'Anàlisi Genòmica (CNAG)

http://www.genetics.ucla.edu/courses/statgene email: statgene@mednet.ucla.edu

We are offering a five full-day intensive workshop on state-of-the-art statistical methods for detection of genetic loci for complex traits.

Each day will include hands-on computer exercises using statistical genetics computer programs, especially the Mendel software package, with its new graphical front-end.

We will cover the general theory behind the methods as well as emphasize the practical aspects needed to give the best chances of success. The Course is designed to assist people who will be performing statistical analyses to discover the genetic basis of complex traits. The methods covered are appropriate to both human and non-human populations. Topics will include:

* Statistical Reviews * Genetic Study Design * Quality Control and other data issues * Haplotyping * Analysis of Qualitative and Quantitative Traits including: - Parametric and Non-Parametric Linkage (NPL) analysis - Methods for Large Pedigrees - Genome-Wide Association Studies (GWAS), or smaller scale, including: + Case/Control or Random Sample + Family-based Designs + Complex Pedigrees derived from Inbred Strains * Ethnic Admixture Analysis * Gene Co-Expression Network Analysis * Rare Variant Analysis Methods Applicable to SNP or Genome Sequence Data

Participants in the Course need no prior experience with these methods or programs. Participants will be required to bring a laptop computer to run the analysis exercises.

The Course features instructors from the Statistical Genetics Group of the UCLA Department of Human Genetics and other leading genetic researchers:

- Kenneth Lange - Simon Heath - Steve Horvath - Jeanette Papp - Janet Sinsheimer - Eric Sobel - Hua Zhou

The cost of the course, which includes lunch and snacks every day and a group dinner on Thursday, is:

900 EUR for students from non-profit institutions 1200 EUR for postdocs, staff, and faculty from non-profit institutions 1600 EUR for individuals from for-profit institutions

Transportation and lodging are not included.

The course will be held 22-26 August 2011 in Barcelona, Spain.

For more information, including the simple application process, please visit http://www.genetics.ucla.edu/courses/statgene Please email statgene@mednet.ucla.edu for more information or to submit the simple application material.

JanetS@mednet.ucla.edu

Berlin Evolutionary Genomics Sep14-22

The application deadline for the Otto Warburg International Summer School and Research Symposium (OWS) on Evolutionary Genomics has been extended until June 19th.

The OWS is being held in Berlin from September 14th to 22nd, 2011.

http://ows.molgen.mpg.de/ Some topics covered will include: The evolution of genome complexity The origin of complex adaptations Evolution of the mutation rate Selection and the evolution of genetics systems Noise and gene order evolution Selection at synonymous sites Evolution of gene expression levels Evolution of alternative splicing Transcriptional control in mammals Whole genome duplication in eukaryotes Compensatory evolution Biased gene conversion Short-term effects of gene duplication

The following speakers have confirmed their attendance at the school: Hans Ellegren (Uppsala) Nicolas Galtier (Montpellier) Laurence Hurst (Bath) Henrik Kaessmann (Lausanne) Fyodor Kondrashov (Barcelona) Michael Lynch (Bloomington) Duncan Odom (Cambridge) H. Allen Orr (Rochester) Dmitri Petrov (Stanford) Stephan Schuster (Philadelphia) Kenneth Wolfe (Dublin)

The scientific coordinators of the OWS are Martin Vingron, Peter Arndt and Brian Cusack at the Max Planck Institute for Molecular Genetics. The aim of this program is to bring together researchers and PhD students from different backgrounds (including molecular biology, bioinformatics, biological physics, mathematics) to discuss recent advances in evolutionary genomics in an interactive environment. The program focuses on high-level teaching and topical research seminars. Participants are expected to give poster presentations or contribute talks.

We invite applications from PhD students and a limited number of PostDocs. Please apply for attendance before June 19, 2011 via our website http://ows.molgen.mpg.de/ .

The registration fee is 950 Euros. Costs for meals, accommodation and social events will be covered. Some travel subsidies are available. The programs (and video streams) of previous Summer Schools can also be found on the school's website.

For questions please contact Kirsten Kelleher (kelleher@molgen.mpg.de)

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Kirsten Kelleher Max Planck Institute for Molecular Genetics Ihnestrasse 73 14195 Berlin

Tel: +49 30 8413-1154 Fax: +49 30 8413-1152 Email: kelleher@molgen.mpg.de http://ows.molgen.mpg.de

Calicut India Biocomputing Sep12-13 CallForParticipation

Dear Sir / Madam

National Institute of Technology Calicut (NITC), India and Indiana University Purdue University Indiana (IUPUI), USA are jointly organizing a two day Indo-US Workshop on Biocomputing (ISB 2011) on 12th and 13th of September 2011 at Hotel Taj Gateway, Calicut, India. This important event is sponsored by *I*ndo *US* *S*cience and *T*echnology *F*orum (IUSSTF), *N*ational *S*cience *F*oundation (NSF), USA and *D*epartment of *B*io*t*echnology (DBT), Government of India. The workshop includes expert lectures from established researchers both from India and the USA. This workshop is intended to bring together domain experts from India and the US and to create a bilateral forum which would act as a focal point for engineers, scientists and academicians, to exchange views, develop curricula and improve the quality of research in the area of bioinformatics for the benefit of both countries.

We are enclosing the Call for Participation for the workshop. Apart from the current list of speakers, which includes six from the US and five from India, three more experts from the US will be added to the list of speakers as soon as their confirmation is obtained. Participants who are presenting posters will be granted travelling allowance. Participants will be selected by the organizing committee based on merit. Only limited seats are available.

Please refer to the workshop website (http://www.isb2011.in) for more details.

The flyer of the workshop will also be mailed shortly to you.

Please apply online through the Applications link in the ISB website (http://www.isb2011.in/applications). Please give wide publicity for the same amidst interested researchers in the field.

Regards

Mathew Palakal, S.D Madhu Kumar and G.K Rajani Kant

Organizing Chairs

ISB 2011

Contact ISB2011 <contact@isb2011.in>

LaRochelle FishGenomics Oct5

Genomic approaches for aquatic species How can new technologies help to improve breeding and sustainability of farm aquatic resources? October 5, 2011 La Rochelle

Context: Biotechnology evolves quickly offering new tools to researchers and producers to advance in the knowledge of fish and molluscs' genomics with application in both ecology and production. AQUAGENET is a cooperation project funded by INTERREG IVB SUDOE program. Its main objective is to promote the interaction between scientists and aquaculture sector in the SUDOE area to apply the new biotechnologies to the sector. This synergistic cooperation implies an unique opportunity to join efforts to improve the competitiveness and development of aquaculture in this area.

Topic of the workshop: Due to the recent domestication history of aquatic species, the availability of applicable genomic tools is still scarce, especially for some species cultivated in the SUDOE area. Second generation sequencing technologies provide the means to rapidly increase the availability of such tools. This workshop will form a unique opportunity to gather researchers from various fields and stakeholders around the common theme of applied next generation sequencing in order to improve breeding and sustainability of farmed aquatic species.

Provisional program: One day workshop divided in four sessions, one dedicated to NGS technologies followed by three sessions dedicated to their use in fish, molluscs and their pathogens. Language of the workshop will be English.

Registration will be free of charge; first come first serve basis up to 100 participants. By e-mail only: aquagenet.workshop@ifremer.fr , providing name and affiliation, and whether you wish to propose a communication. More information about AQUAGENET project and workshop can be obtained at the following address: www.aquagenet.eu Marie-Laure BEGOUT <Marie.Laure.Begout@ifremer.fr>

Luebeck Germany SystemsBiology Sep5-9

Dear colleagues, researchers, and friends,

registration is now open for the

Workshop on Systems Biology together with the 2nd Baltic Autumn School

to take place in Luebeck during 5.-9.September 2011.

Invited speakers:

Tibor Antal (Edinburgh) Albert-Laszlo Barabasi (Notre Dame) Ofer Biham (Jerusalem) Angelika Börsch-Haubold (Plön) Stefan Bornholdt (Bremen) Theo Geisel (Göttingen) Bernhard Haubold (Plön) Marc-Thorsten Hütt (Bremen) Kunihiko Kaneko (Tokyo) Edda Klipp (Berlin) Jürgen Kurths (Potsdam) John Postlethwait (Eugene) Mamen Romano (Aberdeen) Kim Sneppen (Copenhagen) Peter Stadler (Leipzig) Marco Thiel (Aberdeen) Fred Turek (Evanston) Olaf Wolkenhauer (Rostock)

Early registration and poster submission: 15. July 2011. A few number of contributions may be selected for oral presentation.

See the workshop webpage for details and registration: http://www.inb.uni-luebeck.de/~as11/ We are looking forward to meet you in Luebeck!

Yours sincerely,

Jens Christian Claussen Amir Madany Mamlouk Katja Dau (GS-CMLS Events)

– PD Dr. Jens Christian Claussenclaussen@inb.uni-luebeck.de Institut f. Neuro- und Bioinformatik Univ. Luebeck +49-451-5005412 http://www.inb.uni-luebeck.de/ ~ claussen/ Jens Christian Claussen <claussen@inb.uni-luebeck.de>

Netherlands LifeHistoryTheory Sep25-30

Dear all,

it is my pleasure to announce to you that the following RSEE course is now open for registration for all who are interested:

Life History Theory (25 - 30 September 2011, Schiermonnikoog, NL)

Organizers: Prof. Joost Tinbergen (RUG), Prof. Jacques van Alphen (Emeritus RUL) Aim of the course Life History Theory deals with species-specific adaptive schemes of the distribution of the reproductive effort over the life of an organism. The general theoretical problem is to predict which combination of traits will evolve under specific conditions. The concepts used are also relevant to study within species variation in life history traits. The one week course aims at giving an overview of the field and will discuss methodology and recent developments.

Contents & Structure The subject will be worked out on the basis of lectures, case histories, discussion and literature. Attention will be paid to various groups of organisms such as birds, fishes, insects and plants. The contact with current research projects is guaranteed as concrete examples will be treated by scientists working in the field. In poster sessions work and/or plans of the participating students will be discussed with the whole group and we will use computer practicals to illustrate some of the concepts.

For more information on the course program and to register, please check the course website: http://www.rug.nl/biologie/onderzoek/onderzoekscholen/rsee/phdCourses/lifeHistoryTheory For a general overview of RSEE courses check http://www.rug.nl/biologie/onderzoek/onderzoekScholen/RSEE/phdCourses/courseCalendar Do not hesitate to contact me if you have any further questions regarding this, or other RSEE courses and activities.

Looking forward to welcoming you to one or more of our courses,

Kind regards,

Corine Eising

Dr. Corine M. Eising CEES beleidsmedewerker / PhD coordinator Centre for Ecological and Evolutionary Studies University of Groningen tel: ++.31-50-363-9140 fax: ++.31-50-363-2295 Email: c.m.eising@rug.nl

Visiting address: Centre for Life Sciences Nijenborgh 7, 9747 AG Groningen Office 08.76 (mon-wedn)

Postal address: P.O. Box 11103 9700 CC Groningen

C.M.Eising@rug.nl

NIMBioS UTennessee SocialComplexity Feb6-8

The National Institute for Mathematical and Biological Synthesis (NIMBioS) is now accepting applications for its Investigative Workshop, “Modeling Social Complexity,”* *to be held February 6-8, 2012, at NIMBioS. The workshop is co-sponsored by the National Evolutionary Synthesis Center.

Objectives:* * The great majority of humans today live in complex societies, which can exist only on a basis of extensive cooperation among large numbers of individuals. Ultrasociality, the ability of humans to cooperate in large groups of genetically unrelated individuals, presents a puzzle to both evolutionary and social theory. The workshop aims to bring together a diverse group of modelers with anthropologists, archaeologists and other social scientists to synthesize the state of knowledge in formal models of the evolution of social complexity, to identify unresolved issues, and to set an agenda for future collaborative work. The workshop will be organized around the following general themes: What theories and data are available? What are the empirical patterns that cannot be explained by the existing theories and data? How can we adapt existing models to make full use of the available data? What kinds of data are needed to better inform the models? What new modeling techniques and methods need to be developed? In so doing, we aim to achieve a true dialogue between modelers and empiricists.

Location:* *NIMBioS at the University of Tennessee, Knoxville

Co-Organizers:* * Peter Turchin (Ecology and Evolutionary Biology, Univ. of Connecticut, Storrs); Laura Fortunato (Santa Fe Institute, Santa Fe, NM); and Sergey Gavrilets (Ecology and Evolutionary Biology, Mathematics, Univ. of Tennessee, Knoxville) * *For more information about the workshop and a link to the online application form, go to http://www.nimbios.org/workshops/WS_social_complexity If needed, applicants may request travel and lodging support. Participation is limited, and those selected to attend will be notified within two weeks of the application deadline. Application deadline: September 30, 2011*

*The National Institute for Mathematical and Biological Synthesis (NIMBioS) (http:www.nimbios.org) brings together researchers from around the world to collaborate across disciplinary boundaries to investigate solutions to basic and applied problems in the life sciences. NIMBioS is sponsored by the National Science Foundation, the U.S. Department of Homeland Security, and the U.S. Department of Agriculture with additional support from The University of Tennessee, Knoxville.

Sergey Gavrilets Department of Ecology and Evolutionary Biology Department of Mathematics National Institute for Mathematical and Biological Synthesis (NIMBioS) University of Tennessee Knoxville, TN 37996

phone: (865) 974-8136 fax: (865) 974-3067 e-mail: gavrila@tiem.utk.edu web: www.tiem.utk.edu/~gavrila NIMBioS: www.nimbios.org Sergey Gavrilets <gavrila@tiem.utk.edu>

Portugal BioinformaticsTraining when

At Instituto Gulbenkian de Ciência, in Oeiras, PT

Three Bioinformatics Training courses (new themes) in the GTPB Programme still open for applications,

Hunting for Genes and Promoters with Alexander Kel and Enrique Blanco http://gtpb.igc.gulbenkian.pt/bicourses/HGP11 *Building Biinformatics Web Applications* with David Leader and Richard Cooper http://gtpb.igc.gulbenkian.pt/bicourses/BBWA11 *Knowledge Discovery and Management in Chemoinformatics* with Vladimir Poroikov and Alexey Lagunin http://gtpb.igc.gulbenkian.pt/bicourses/KDMC11 Pedro Fernandes

– Pedro Fernandes Instituto Gulbenkian de Ciência Apartado 14 2781-901 OEIRAS Tel +351 21 4407912 http://gtpb.igc.gulbenkian.pt Pedro Fernandes <pfern@igc.gulbenkian.pt>

Trento Italy ConsPopulationGenetics Sep20-22 2

Workshop: POPULATION GENETICS FOR ANIMAL CONSERVATION III 20-22 September 2011, Trento, Italy.

REGISTRATION AND ABSTRACT SUBMISSION WILL CLOSE JUNE 30th

All relevant information, including registration and abstract forms, can be found at: http://pgac3.fem-environment.eu/ Brief description The Third edition of the workshop will be focussed on a well-recognized, yet unsolved issue in conservation genetics: how to bridge the gap between scientists and end-users, i.e. non-scientists such as policymakers, administrators, or park rangers that are directly involved in animal conservation and would like to design, implement and/or apply management and conservation plans using the most modern strategies and tools

Therefore, this workshop intends addressing this gap by focussing on five main themes identified as top priorities during a recent survey conducted by the European consortium ConGRESS of 100 end-users from across Europe:

1) Identifying units for conservation 2) Population connectivity and isolation 3) Reconstructing past population dynamics 4) Detecting and planning translocations and reintroductions 5) Genetic diversity and adaptation Each theme will be tackled in one 2-hour session (with lectures from invited speakers and contributions from attendees) with final-day round tables discussions where scientists and end-user will have the opportunity to examine, vis-a-vis, unresolved issues and possible solutions.

PGAC III hopes to bring together researchers from different fields (e.g. population genetics, ecology, conservation biology and related) and end-users with basic scientific knowledge and a strong desire to know more about applying population genetics tools to their particular conservation problem. The major aim will be to promote an effective interaction, using a common language, to fully exploit the potential of population genetics as applied to animal conservation.

Invited speakers: Giorgio Bertorelle (University of Ferrara, Italy) Josef Bryja (Academy of Sciences, Czech Republic) Mike Bruford (University of Cardiff, UK) Oscar Gaggiotti (Université J Fourier, Grenoble, France) Rus Hoelzel (University of Durham, UK) Jacob Hoglund (University of Uppsala, Sweden) Craig Moritz (University of California, Berkeley, USA) Richard Nichols (Queen Mary's College, UK) Craig Primmer (Univeristy of Turku, Finland) Gernot Segelbacher (University of Freiburg, Germany) Hans Siegismund (University of Copenhagen, Denmark) Per Sjogren-Gulve (Swedish Environmental Protection Agency) Carles Vilà (CSIC, Spain) Raj Whitlock (University of Liverpool, UK)

The Scientific Committee: Giorgio Bertorelle, University of Ferrara, Italy Mike Bruford, University of Cardiff, UK Heidi Hauffe, Fondazione Edmund Mach, S. Michele all'Adige, Trento, Italy Cristiano Vernesi, Fondazione Edmund Mach, Viote del Monte Bondone, Trento, Italy

Cristiano Vernesi Department of Biodiversity and Molecular Ecology Research and Innovation Centre - Fondazione Edmund Mach address: Centro di Ecologia Alpina, Viote del Monte Bondone - 38040 Trento - Italy tel +390461939523 - fax +390461948190 - skypename: cvernesi

vernesi@cealp.it

Trento Italy ConsPopulationGenetics Sep20-22 DeadlineExt

Workshop: POPULATION GENETICS FOR ANI-

MAL CONSERVATION III 20-22 September 2011, Trento, Italy.

DEADLINE FOR REGISTRATION AND ABSTRACT SUBMISSION HAS BEEN POSTPONED TO JULY 15th

All relevant information, including registration and abstract forms, can be found at: http://pgac3.fem-environment.eu/ Brief description The Third edition of the workshop will be focussed on a well-recognized, yet unsolved issue in conservation genetics: how to bridge the gap between scientists and end-users, i.e. non-scientists such as policymakers, administrators, or park rangers that are directly involved in animal conservation and would like to design, implement and/or apply management and conservation plans using the most modern strategies and tools

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Cristiano Vernesi Department of Biodiversity and Molecular Ecology Research and Innovation Centre - Fondazione Edmund Mach address: Centro di Ecologia Alpina, Viote del Monte Bondone - 38040 Trento - Italy tel +390461939523 - fax +390461948190 - skypename: cvernesi

Please, consider your environmental responsibility before printing this email

Cristiano Vernesi <vernesi@cealp.it>

UHelsinki ClimateAdaptation Sep11-14 reminder

Workshop: ADAPTATION TO CLIMATE FROM A SPATIAL PERSPECTIVE'- registration will close soon

Workshop: ADAPTATION TO CLIMATE FROM A SPATIAL PERSPECTIVE' 11-14 September 2011 at Lammi Biological Station, University of Helsinki, Finland

REGISTRATION WILL CLOSE NEXT WEEK (JUNE 30TH)

Short description: Advancing our understanding how organisms adapt to environmental variation lies at the core of ecology and evolutionary biology, and has become especially relevant in the light of current human-induced environmental change as a major threat to global biodiversity. When predicting species' responses to climate change, including range shifts and adaptation, it is crucial to take into account spatial patterns of local adaptation and population dynamics at the regional and geographical scale.

We organize a conference (~60 participants) with a primary focus on adaptation to environmental variation, in particular climatic and thermal adaptation, from a spatial perspective at the regional and geographic level. We intend to bring together current high-quality research at multiple levels of investigation, including ecology, evolutionary genetics, physiology, theory and conservation. We aim to combine studies including a broad range of organisms, including plants, vertebrates and aquatic organisms, but with a main focus on ectotherms.

The conference will be organised around three main sessions: - Latitudinal and altitudinal clinal variation - Landscape/metapopulation approaches to ecological and evolutionary dynamics - Ecological and evolutionary dynamics at the range margins

Keynote speakers: - Dr. Jon Bridle (University of Bristol, UK) - Prof. Klaus Fischer (Greifswald University, Germany) - Prof. Ilkka Hanski (University of Helsinki, Finland) - Prof. Pär Ingvarsson (UmeÃ University, Sweden) - Prof. Volker Loeschcke (Aarhus University, Denmark) - Prof. Juha Merilä (University of Helsinki, Finland) - Prof. Patricia Schulte (University of British Columbia, Canada) - Prof. Chris Thomas (University of York, UK)

Organizers: Maaike de Jong & Marjo Saastamoinen Metapopulation Research Group, Department of Biosciences, University of Helsinki

For more information and online registration (registration deadline is June 30th 2011): http://www.helsinki.fi/science/metapop/workshop/ "Saastamoinen, Marjo" <marjo.saastamoinen@helsinki.fi>

Vairao Portugal TeachingEvolution Sep27-30

workshop:

REMINDER: The deadline for applications to the following workshop is approaching

Invitation to Apply: FIRST IV at CIBIO/UP - Teaching Workshops in Biology

Dates of the event: 27 - 30 September 2011

Location: Vairao, Porto, Portugal

Senior PhD students, postdoctoral researchers and faculty in any field of biology are invited to participate in Faculty Institutes for Reforming Science Teaching (FIRST IV) for Faculty and Postdoctoral Scholars. FIRST IV focuses on reform of undergraduate biology education through professional development of postdocs and faculty. Participants will design an inquiry-based, student-centered undergraduate biology course. Key elements of FIRST IV include active learning, assessment and diversity in teaching. Participants will attend one workshop and a follow-up webinar during consecutive summers: a four-day workshop in 2011 followed by a webinar in 2012. During the academic year between the two workshops, participants will teach all or part of an introductory biology course (e.g., cell biology, genetics, ecology, organisms, populations, evolution) at their home institution using the course framework they designed during the workshop.

Who should apply? ?Senior PhD students, postdoctoral researchers and faculty who have an interest in and commitment to teaching. We encourage individuals or teams of two participants from one institution to apply.

Cost? 360 euros. The course fee includes lunch, morning and afternoon coffee-breaks, room and instructional materials.

Application due: June 26, 2011 Notification of acceptance: July 4, 2011?

Questions? Contact Rita Campos or Rui Faria, PopGen Research Group, CIBIO/UP, ritacampos@mail.icav.up.pt or rui.faria@upf.edu

Application is on the FIRST IV-like at CIBIO web site: http://popgencibio.org/web/

Please name your completed application file:**LastnameFirstname_

FIRSTIVCIBIOapp.pdf

Send all application materials as one PDF document to: ritacampos@mail.icav.up.pt

Rui Faria <rui.faria@upf.edu>

WageningenNL Call ESF PlantMicrobeInsect Aug18-20

ESF Exploratory Workshop Plant-microbe-insect interactions: from molecular mechanisms to ecological and evolutionary implications

Open call We are looking for ca. five enthousiastic participants working in the field of three-way interactions between plants, microbes and insects. Please send an application (abstract of proposed contribution) to a.biere@nioo.knaw.nl before June 15, 2011. Priority will be given to participants from EU countries not yet covered by the participant list (see below).

Venue The workshop will be held from August 18-20, 2011 in Congress Centre “De Wageningse Berg”, Wageningen, The Netherlands www.hoteldewageningscheberg.nl It will start on Thursday morning, right after the 14th Symposium on Insect-Plant Interactions (SIP, Wageningen, 13-18 August 2011) ends. The workshop will end on Saturday afternoon. All costs (travel, accomodation, meals) will be covered by ESF.

Organizers Arjen Biere, Dept. Terrestrial Ecology, NIOO-KNAW, Wageningen NL. a.biere@nioo.knaw.nl Sue E. Hartley, Dept. Biology, U. York, UK. sue.hartley@york.ac.uk Thure P. Hauser, Dept. Agriculture and Ecology, U. Copenhagen, DK. tpha@life.ku.dk Tamara van Mölken, Dept. Agriculture and Ecology, U. Copenhagen, DK. marm@life.ku.dk

Background and aims Plants are intimately associated with both microbes and insects. This gives rise to three-way interactions that have far-reaching consequences for the functioning and evolution of the organisms involved. After the initial disparate development of the fields of plant pathology and entomology, the past decades have brought fascinating insights as researchers started to address questions like: how do microbial symbionts/antagonists affect interactions between plants and herbivorous insects and vice versa ? To what extent are the patterns of activation of defense signalling pathways shared between different guilds of microorganisms and insects ? Are there predictable patterns in synergistic and antagonistic interactions between these players ? What are the consequences of alterations of herbivorous insect behaviour by their endosymbionts/pathogens ? We think the current challenge is to understand the ecological relevance of these interactions and their role in the functioning of plants in their multitrophic environment.

The aim is to bring together molecular and ecological researchers from this emerging field to give impetus to research on ecological and evolutionary implications of such three-way interactions and stimulate cross-talk between experts from the different subdisciplines of mycorrhiza, rhizobia, endophyte, viral/ fungal/ bacterial pathogen effects on insects and vice versa.

The workshop will be a first step towards starting up a European research network, and facilitate participants to explore new research areas and future collaborations, develop research plans to be submitted to the EU and other funding agencies, and explore potential topics for joint review papers.

Participants We aim at a group of circa 20-25 workshop participants. Eighteen invited participants originate from NL, DK, UK, GER, SP, CH, FIN. This call is for the remaining ca. 5 seats. We encourage application by participants from EU countries not yet covered above, working in the fields of plant-endophyte, -rhizobium, -pathogen, -mycorrhiza, and -insect interactions, and across the research disciplines of ecology, (co)-evolution, molecular biology and phytochemistry.

A.Biere@nioo.knaw.nl

WestVirginia MalariaEvolution Aug1-4

SECOND ANNOUNCEMENT

International Workshop on Malaria and Related Haemosporidian Parasites of Wildlife

Monday August 1st V Thursday August 4th, 2011

National Conservation Training Center, Shepherdstown, West Virginia

Sponsored by the NSF Research Coordination Network for Haemosporida of Terrestrial Vertebrates1

**The workshop is likely to be of interest to evolutionary biologists as it will center around the systematics of a very successful and diverse group of parasites of natural vertebrate populations and include laboratory exercises involving phylogenetic analysis of parasite lineages and readings and discussions on the evolutionary history of the parasites including cospeciation of hosts and parasites as well as the evolution of virulence.

Dear Colleagues,

The NSF-sponsored Research Coordination Network for Haemosporida of Terrestrial Vertebrates (MalariaRCN) is pleased to announce our first annual workshop on the malaria parasites and closely related haemosporidians of natural populations of vertebrates. The four day workshop will include both field and laboratory exercises as well as lectures and discussions led by RCN members2.

Topics to be covered through the workshops exercises include vertebrate and invertebrate field capture techniques, blood sampling and preparation of blood smears, vector identification and salivary gland preparation, sample vouchering and cryopreservation, light microscopy for parasite species identification and parasite and cell counts, DNA extraction and PCR screening of parasites, sequence data analysis including phylogenetics, and databasing. Discussion topics will include, but are not limited to, the basic biology, phylogenetics and systematics of Haemosporida, community ecology of parasites, coevolution ofparasites and hosts, the evolution of virulence, and conservation and disease.

The workshop will commence on Monday morning, August 1st, and continue through until the afternoon of Thursday, August 4th. The workshop will be followed by a three day meeting on the malaria and related haemosporidian parasites of wildlife, organized by the same RCN group.

All food, lodging and workshop events will take place at the US Fish & Wildlife Services National Conservation Training Center in Shepherdstown, West Virginia, a site easily accessible through Washington, D.C., area airports.

The workshop is geared towards graduate students, postdoctoral researchers, and other investigators new to the field of wildlife haemosporidians. We are currently accepting applications and encourage individuals from outside the United States, particularly from developing countries. Funding is available to cover the workshop cost, accommodation at the Shepherdstown facility, transportation from the Washington Dulles International airport (IAD), and meals for all participants. Additional funds may be available to help with travel costs. Application forms can be requested from the workshop organizers (email: MalariaRCNWorkshop@gmail.com). Additional information on the workshop including an overview of the four days of events will soon be made available on the official workshop website (http://malariarcn.org/). Decisions on participation will begin on Monday May 30th and continue until the workshop is filled. If interested, you are encouraged to apply for the workshop as soon as possible.

1 The Research Coordination Network for Haemosporida of Terrestrial Vertebrates (RCN), sponsored by the U. S. National Science Foundation and funded through 2015 at the University of Missouri-St. Louis, was established to promote communication among researchers working on the ecology and evolution of haemosporidian parasites of vertebrate wildlife populations.

2 Workshop organizers include Ellen Martinsen (Smithsonian Institution), Staffan Bensch (Lund University), Ravinder Sehgal (San Francisco State University), Carter Atkinson (USGS), and Gediminas Valkiunas (Nature Research Center, Vilnius). Other members of this RCN include Robert Ricklefs and Patricia Parker (University of Missouri V St. Louis), Robert Fleischer (Smithsonian Institution), Susan Perkins (American Museum of Natural History), Tom Smith(University of California, Los Angeles), and Robert Adlard (Queensland Museum).

"Fleischer, Robert" <FleischerR@si.edu>

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.