EvolDir

May 1, 2012

Month in Review

Foreword

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

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

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

—— / ——

Conferences

Avignon France EvolBiol Aug28-31

Program now available here: https://colloque4.inra.fr/petit_pois_2012/Pre-programme
Never been to Avignon? Good news: the 34th “Petit Pois Deridé“ (Ha-pea meeting) will take place next August 28-31, 2012, in Avignon. This a yearly meeting of the French community of evolutionary biologists, population biologists and ecologists. Emphasis is on having students and postdocs present their work and exchange with more senior scientists. The event is organized by the INRA research groups in Avignon and Sophia-Antipolis, and the University of Avignon. Book these dates! (even if you've been to Avignon before)

Online registration is open at http://www.ppd2012.fr (you'll have to create a user account in order to submit abstracts)

Contact us: ppd2012@avignon.inra.fr

Hoping to see you soon, The organizers

vincent.calcagno@sophia.inra.fr

Brazil RECOMB CG Oct17-19

Tenth Annual RECOMB Satellite Workshop on Comparative Genomics

October 17-19, Niterói, Brazil

Website: www.uff.br/recombcg Contributions to the workshop are welcomed on any theoretical and/or empirical approach to genome-wide comparison. This includes genome evolution, algorithms for genome rearrangement, comparative tools for assembly, gene identification or annotation, comparison of functional networks, genomic variation in humans and model organisms, cancer genomics, duplication patterns of genes, segments and whole genomes, and comparative epigenetics. We encourage paper submissions that offer new biological findings or otherwise highlight their relevance to biology. Refereed papers will be published as open-access manuscripts in the journal BMC Bioinformatics.

KEY DATES

Paper submission deadline June 12, 2012

Acceptance notification July 03, 2012

Workshop October 17-19, 2012 - Niterói, Brazil

THEME AND SCOPE

The continuing advance of DNA sequencing technology has produced an avalanche of genome sequence and genome structural information across the evolutionary spectrum. Transforming that information into biological knowledge requires creative and innovative new computational and statistical methods for comparative genomics.

The RECOMB Satellite Workshop on Comparative Genomics aims to provide the premier forum for new computational developments applied to all aspects of comparative genomics. We solicit contributions on topics including comparison of genome structure and organization, genome function, and evolution. We particularly encourage contributions that use new computational methods to acquire new insight into biological processes. Advances in computational theory are welcome, though all submissions should include genome-scale analyses informed by comparative data.

All peer-reviewed and accepted RECOMB-CG manuscripts will be published in a supplement to BMC Bioinformatics as open-access, author-subsidized, articles.

Specific topics of interest include but are not limited to:

Gene and genome duplication Gene family evolution Genome structural variation Algorithms for comparative genomics Genome rearrangement Ancestral genome reconstruction Multiple genome alignment Genome sequence comparison Modeling genome evolution Comparative genomics for genome annotation Gene tree reconciliation Species and gene tree inference Comparative metagenomics Comparative genomics linked to proteomics, metabolomics, and other ˜omic data Comparative genomics and gene expression and regulation Applications of comparative genomic methods

CALL FOR PAPERS

Papers should be submitted via the EasyChair system: https://www.easychair.org/conferences/?conf=recombcg12. Submissions must be received in electronic form by 11:59pm (Samoa time), June 12th, 2012.

Papers submitted for review should represent original, previously unpublished work. At the time the paper is submitted to the conference, and for the entire review period, the paper should not be under review by any other conference or scientific journal.

At least one author per each successful submission is required to register and present the paper at the workshop. The paper will be included in the conference proceedings, which will be published in BMC Bioinformatics as open-access author-subsidized articles.

Authors are encouraged to use the BMC document templates when preparing manuscripts. Templates are available in Microsoft and LaTeX formats. [Otherwise, submissions should be typeset as double-spaced A4 pages with at least 1-inch margins all around in a minimum of 10 point font.] Submissions should be limited to 16 pages, everything included (title, authors, addresses, abstract, references, figures, tables). Exceptions to this limit may be granted by consultation with the Program Committee Chairs. Submissions must include the corresponding author's email address.

When preparing your submission please follow the instructions for authors of BMC supplements: http://www.uff.br/recombcg/docs/Instructions-for-authors-BMC-Appendix-B.pdf . Submitted manuscripts must be rendered to PDF format prior to upload into EasyChair at the review stage.

Address any questions to the program committee chairs: Mathieu Blanchette (blanchem at mcb.mcgill.ca), Marilia D. V. Braga (mdbraga at inmetro.gov.br) and Marie-France Sagot (Marie-France.Sagot at inria.fr).

PROGRAM COMMITTEE

Chairs: Mathieu Blanchette (McGill University, Montréal, Canada) Marilia D. V. Braga (Inmetro, Rio de Janeiro, Brazil) Marie-France Sagot (Université Claude Bernard, Lyon, France)

Other members: Robert Beiko (Canada) Anne Bergeron (Canada) Jeremy Buhler (USA) Cedric Chauve (Canada) Aaron Darling (USA) Zanoni Dias (Brazil) Nadia El-Mabrouk (Canada)

— / —

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

---

Dublin SMBE 2012 Jun23-26 UndergradTravel 2

SMBE UNDERGRADUATE TRAVEL AWARDS

2012 ANNUAL MEETING OF THE SOCIETY FOR MOLECULAR BIOLOGY AND EVOLUTION

June 23-26, Dublin, Ireland

CONFERENCE WEBSITE

www.smbe2012.org DEADLINE FOR RECEIPT OF NOMINATIONS/APPLICATIONS: April 25, 2012

PROGRAM OUTLINE

The Society for Molecular Biology and Evolution (SMBE) is pleased to make available 10 awards for undergraduate students to participate in a Mentoring and Diversity Program. Five of these positions will be reserved for undergraduates from traditionally underrepresented groups in our scientific discipline.

The goals of this program are: (1) to provide students with the opportunity to experience the excitement of attending and presenting at an international scientific conference, (2) to foster enthusiasm for molecular biology and evolution as well as a possible career in this field, and (3) to promote diversity at the SMBE annual meeting.

To achieve these goals, each recipient of an SMBE Undergraduate Mentoring and Diversity Program Award will be paired with one mentor (postdoctoral fellow or faculty member). Mentors will serve as contact points for the students, attend some sessions with the students, and, more generally, explain the 'goings-on' at a multi-day scientific conference in order to minimize the anxiety often felt by first-time conference attendees. The mentors will also facilitate connections to graduate students, postdoctoral fellows and faculty members.

ELIGIBILITY

Candidates must currently be enrolled as undergraduate students (i.e. pre-doctoral students, e.g. a Bachelor's level degree in USA) or have graduated within the last 6 months at the time of application. Some awards will be reserved for undergraduates from traditionally underrepresented groups in our scientific discipline.

CONFERENCE PARTICIPATION

Recipients of an SMBE Undergraduate Diversity Mentoring Program Award will be invited to present their research at a special reception/poster session attended by their mentors, supervisors and other interested conference participants.

AWARDS

Ten awards will be given. Award recipients residing in Europe will receive US $1,000 to be used to help cover the cost of airfare, accommodation, and meeting registration. All other recipients will receive US $1,500. Each participant will also receive an online student subscription to the journal Molecular Biology and Evolution for the year of 2013.

APPLICATION

1. Faculty members may nominate undergraduates by sending a brief letter of recommendation and the abstract of the work to be presented at the poster session. The single PDF file should be sent to Dr. Laurent Duret (Laurent.Duret@univ-lyon1.fr).

OR

2. Students may apply for the award themselves by providing information on their background, academic status, the email address of their supervisor, and an abstract of the work to be presented at the poster session. The single PDF file should be sent to Dr. Laurent Duret (Laurent.Duret@univ-lyon1.fr).

TRADITIONALLY UNDERREPRESENTED GROUPS

Applications for one of the awards reserved for undergraduates from traditionally underrepresented groups should contain a brief statement of eligibility for these awards.

DEADLINE

The deadline for receipt of nominations/applications is April 25, 2012.

Laurent Duret <Laurent.Duret@univ-lyon1.fr>

Dublin SMBE Jun23-26 UndergradTravel

SMBE UNDERGRADUATE TRAVEL AWARDS

2012 ANNUAL MEETING OF THE SOCIETY FOR MOLECULAR BIOLOGY AND EVOLUTION

June 23-26, Dublin, Ireland

CONFERENCE WEBSITE

www.smbe2012.org DEADLINE FOR RECEIPT OF NOMINATIONS/APPLICATIONS: April 25, 2012

PROGRAM OUTLINE

The Society for Molecular Biology and Evolution (SMBE) is pleased to make available 10 awards for undergraduate students to participate in a Mentoring and Diversity Program. Five of these positions will be reserved for undergraduates from traditionally underrepresented groups in our scientific discipline.

The goals of this program are: (1) to provide students with the opportunity to experience the excitement of attending and presenting at an international scientific conference, (2) to foster enthusiasm for molecular biology and evolution as well as a possible career in this field, and (3) to promote diversity at the SMBE annual meeting.

To achieve these goals, each recipient of an SMBE Undergraduate Mentoring and Diversity Program Award will be paired with one mentor (postdoctoral fellow or faculty member). Mentors will serve as contact points for the students, attend some sessions with the students, and, more generally, explain the 'goings-on' at a multi-day scientific conference in order to minimize the anxiety often felt by first-time conference attendees. The mentors will also facilitate connections to graduate students, postdoctoral fellows and faculty members.

ELIGIBILITY

Candidates must currently be enrolled as undergraduate students (i.e. pre-doctoral students, e.g. a Bachelor's level degree in USA) or have graduated within the last 6 months at the time of application. Some awards will be reserved for undergraduates from traditionally underrepresented groups in our scientific discipline.

CONFERENCE PARTICIPATION

Recipients of an SMBE Undergraduate Diversity Mentoring Program Award will be invited to present their research at a special reception/poster session attended by their mentors, supervisors and other interested conference participants.

AWARDS

Ten awards will be given. Award recipients residing in Europe will receive US $1,000 to be used to help cover the cost of airfare, accommodation, and meeting registration. All other recipients will receive US $1,500. Each participant will also receive an online student subscription to the journal Molecular Biology and Evolution for the year of 2013.

APPLICATION

1. Faculty members may nominate undergraduates by sending a brief letter of recommendation and the abstract of the work to be presented at the poster session. The single PDF file should be sent to Dr. Laurent Duret (Laurent.Duret@univ-lyon1.fr).

OR

2. Students may apply for the award themselves by providing information on their background, academic status, the email address of their supervisor, and an abstract of the work to be presented at the poster session. The single PDF file should be sent to Dr. Laurent Duret (Laurent.Duret@univ-lyon1.fr).

TRADITIONALLY UNDERREPRESENTED GROUPS

Applications for one of the awards reserved for undergraduates from traditionally underrepresented groups should contain a brief statement of eligibility for these awards.

DEADLINE

The deadline for receipt of nominations/applications is April 25, 2012.

DURET LAURENT <Laurent.Duret@univ-lyon1.fr>

Durham RecombinationEvolution Jul14-17

Reminder– early bird deadline (May 13) approaching, as well as deadline for student workshop to defray travel expenses (May 1)!

The 2012 annual meeting of the American Genetic Association will be held from 14-17 July at the Durham Convention Center in Durham, North Carolina, USA. The conference is entitled "Recombination: Molecular Mechanisms & Evolutionary Consequences".

We are also hosting an NSF- (and Duke University-) funded graduate student/ postdoc preconference workshop on 14 July, with a focus on communicating science to the public and mass-media. A subset of students & postdocs attending the workshop will receive funding that can be used to defray their conference expenses. Sign up before May 1 to avail yourself of this funding!

Registration and conference information are online (http://www.theaga.org/2012/), and we invite contributed talks & posters. Early bird registration rates end May 13, 2012. If you would like additional information about these exciting events, please email noor@duke.edu . Hope to see you there!

Brian Charlesworth- University of Edinburgh, UK Adam Auton- Albert Einstein College of Medicine Justin Blumenstiel- University of Kansas Francesca Cole- Sloan Kettering Greg Coperhaver- University of North Carolina Justin Fay- Washington University (St Louis) Bret Payseur- University of Wisconsin Tom Petes- Duke University Jeff Sekelsky- University of North Carolina Nadia Singh- North Carolina State University John Willis- Duke University

Mohamed A. F. Noor noor@duke.edu Earl D. McLean

Professor Tel: 919-613-8156 & Associate Chair 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

Edinburgh QuantGenetics Jun17-22 Program

4th Int. Conf. Quantitative Genetics, Edinburgh June 17-22 2012

Text:

The 4th International Conference on Quantitative Genetics, Edinburgh June 17-22 2012.

The exciting full programme for this conference is now available to view and registration information is also at http://www.icqg2012.org.uk/ There is still time to submit an abstract for poster presentation. Again these can be submitted at http://www.icqg2012.org.uk/ The final abstract submission deadline is Friday 6 April.

Among satellite events, please note the European Institute for Statistical Genetics, running short courses either side of the ICQG meeting itself. Information at: http://www.eisg2012.org.uk/ On behalf of the organising committee,

Josephine Pemberton

Prof. J.M. Pemberton Institute of Evolutionary Biology School of Biological Sciences University of Edinburgh West Mains Road EH9 3JT

tel 0131 650 5505 fax 0131 650 6564 http://wildevolution.biology.ed.ac.uk/ The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

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

Finland PhDStudents EvolBiol Sep25-30

Event: EMPSEB 18 (PhD Students in Evolutionary Biology) Date: 25-30 September, 2012 Location: Finland

REGISTRATION REMINDER (2 weeks left) for the 18th European Meeting of PhD Students in Evolutionary Biology (EMPSEB 18), which takes place from 25-30 September 2012 in Virrat, Finland. The event aims to bring together PhD students studying Evolutionary Biology to let them present their research, get feedback from top scientists in the field, and develop collaborations with their peers. There will also be a special symposium (speaker and discussion) about ethics in science.

Registration will close 30 April 2012. More information is available at www.empseb18.com. Students will be able to apply for travel grants.

Confirmed plenary speakers include:

Frank Ryan (University of Sheffield- United Kingdom) Martine Maan (University of Groningen- Netherlands) Mikael Fortelius (University of Helsinki- Finland) Hanna Kokko (Australia National University- Australia) Marc Johnson (University of Toronto at Mississauga- Canada) Thomas Flatt (University of Veterinary Medicine Vienna- Austria) Craig Primmer (University of Turku- Finland) Leena Lindström (University of Jyväskylä- Finland) Naomi Pierce (Harvard University- United States)

– Robert Hegna EMPSEB 18 University of Jyväskylä Dept. of Biology & Env. Science FINLAND www.empseb18.com "Robert Hegna, EMPSEB 18" <president@empseb18.com>

LundU EvolutionaryTheory May8

Dear All,

We proudly announce the first annual Golden PEG Award Symposium - awarding two distinguished theorists in ecology and evolutionary biology.

The aim is to acknowledge the importance of theoretical work in those fields and to recognize prominent and important contributors to the development of the discipline. The symposium is organized by the Theoretical Population Ecology and Evolution Group (ThePEG) and the awards fall into the categories "Lifetime Achievement" and "Rookie of the Year".

The sympoisum will take place in the Ecology Building, Lund, Sweden, on May 8. It is open to everyone and free of charge. No registration necessary. More info: www.teorekol.lu.se/thepeg/GoldenPEG.pdf www.teorekol.lu.se/thepeg/index.html Best regards, ThePEG (The Theoretical Population Ecology and

Evolution Group) Biology Dept., Lund Universtiy, Lund, Sweden

–

Jörgen Ripa Theoretical Population Ecology and Evolution Group Ecology Building, SE-223 62 Lund, Sweden phone: +46-46-222 3770, +46-70-999 3570 email:jorgen.ripa@biol.lu.se www:http://www.teorekol.lu.se/thepeg/staff/jripa/index.html jorgen.ripa@biol.lu.se

LundU PostISBE Aug18

Dear EvolDir members,

There will be six post-conference symposia (see details below) and they will take place the day after the regular ISBE-meeting on August 18 2012. It is now possible to register for each symposium online

http://tinyurl.com/bvfl8lf

Please note that the registration deadlines might vary for the symposia, so please check the details here

http://www.isbe2012lund.org/post-conference-symposia/ Note that the post-conference symposia are free of charge and are organized independently from the ISBE. There is thus no need to register at the ISBE conference to participate in these symposia.

Post Conference Symposia (invited speakers in brackets)

Behavioural Responses to a Changing World: Mechanisms and Consequences (Dan Blumstein, Bart Kempenaers, Andy Sih, Iain Barber)

Oxidative Stress as Evolutionary and Behavioral Constraints V Where Are We Now? (Geoffrey Hill, Pat Monaghan, Neil Metcalfe, Peeter Horak, Mats Olsson, more to be announced)

Recent Developments in Sexual Selection Research: History, Trends and New Horizons (to be announced)

The Behavioural Ecology of Animal Movement (Gesa Feenders, Andy Sih, Daniel Rubenstein, John B Phillips, Tim Guilford, Christine Merlin)

The Evolution of Mechanisms for Avoiding Predation (to be announced)

The Role of Behaviour in Non-Ecological and Non-Adaptive Speciation (Mark McPeek, John Wiens, Kerry Shaw)

We hope to see you in Lund!

Maren Wellenreuther

Marie Curie Postdoctoral Researcher Department of Biology Lund University SE-223 62 Lund SWEDEN

Phone: +46 46 222 9014 Mobile: +46 709 429930 Fax: +46 46 222 47 16

Homepages *http://marenwellenreuther.com/index.html http://www.lu.se/meel/people/postdocs/maren-wellenreuther < http://www.lu.se/o.o.i.s/26164 >

I support WINGS http://www.lu.se/wings/working-group/maren-wellenreuther-coordinator-Lund Postdoctoral Society *http://ced2.srv.lu.se/lupodnew/contact.aspx* Maren Wellenreuther <maren.wellenreuther@biol.lu.se>

Marseilles EvolutionaryBiol Sep18-21 2

Dear All,

The registration and abstract submission for the 16th Evolutionary Biology Meeting at Marseilles, September 18-21, 2012, are open. Please visit the web site of the meeting http://sites.univ-provence.fr/evol-cgr where you will find all relevant information. The dead line is the 30 of june

The following subjects will be discussed:

- Evolutionary biology concepts and modelisations - Biodiversity and Systematics; - Comparative genomics and post-genomics (at all taxonomic levels); - Functional phylogenomics; - Environment and biological evolution; - Origin of Life and exobiology; - Non-adaptative versus adaptative evolution; - The ≪ minor ≫ phyla: their usefulness in evolutionary biology knowledge; - Convergent evolution

Pierre

Pierre.Pontarotti@univ-provence.fr

Moscow MolecularPhylogenetics Jul31-Aug4

Dear colleagues,

We are pleased to announce the 3rd Moscow international conference on molecular phylogenetics, ≪Molecular Phylogenetics MolPhy-3≫, which will take place at the New School Building of Moscow State University, 31 July - 4 August 2012.

The conference mission is to provide a stimulating platform for the exchange of ideas and experiences in contemporary phylogenetics, molecular evolution and bioinformatics, and for developing methodology, algorithms, and applications for state-of-the-art analyses of molecular genetic data. The primary scope is in molecular phylogenetics and systematics, phyloinformatics, evolutionary genomics, reconstructing the Tree of Life, and applied phylogenetics.

Renowned scientists will give plenary lectures on hot topics. Participants can present findings in 15-minute talks, poster sessions, and software demonstrations. The conference aims to stimulate cross-disciplinary interactions, and establish long-term national and international collaborations. Young investigators are encouraged to participate.

The conference language is English.

Important dates:

May 15, 2012- registration deadline, abstracts submission deadline. May 21, 2012- abstract acceptance notification date. May 31, 2012- early registration fee payment deadline.

Additionally, the organizers announce that the international course ≪Computational Phyloinformatics 2012≫ will follow on from the MolPhy-3 conference, 06-17 August 2012. This course is a 12-day intensive summer workshop co-organized by Moscow State University, NESCent, Institute for Information Transmission Problems (Russian Academy of Sciences), and the Phyloinformatics Research Foundation, Inc. The workshop aims to give biologists practical knowledge and hands-on programming skills in support of high-throughput phylogenetics, functional genomics, and phyloinformatics, using scripting languages that include Perl, Ruby, and SQL. Instruction is in English and participants are encouraged to bring their own computers. Detailed information on the syllabus and admission can be found on the workshop website at http://academy.nescent.org/wiki/Moscow_2012 . Further information is available on the conference website at www.en.molphy.ru. You are welcome to reach the organizers by telephone +7-(495)-939-1440, +7 (495) 939-7185, fax +7-(495)-939-3181, or email molphy@molphy.ru with any inquiries.

Sincerely, Organizers of MolPhy-3

roussine@yandex.ru

NHM Frankfurt MammalDiversity Sep4-8

Dear colleagues,

I am pleased to send this SECOND circular of the annual conference of the German Society of Mammalogy. As you know, this year this international conference will be hosted at the Senckenberg Institute and Natural History Museum in Frankfurt (Main), Germany. PLEASE DO NOT FORGET TO REGISTER! Main organiser is the Conservation Genetics Group, and several other Senckenberg and BIK-F groups are involved as well. DEADLINE FOR ABSTRACTS: MAY 28 !!!

–> http://www.senckenberg.de/dgs2012 <–

The conference theme is "The Past, Present and Future of Mammalian Diversity", and hence all topics in Mammalian Biology are covered in a modern and multidisciplinary atmosphere. There will be three days of conference with talks and poster sessions, divided into the (non-exclusive) topics:

- past (palaeontology, ancient DNA, phylogeny, phylogeography, evolution ...) - present (population structure and distribution, behaviour, physiology, morphology, current policy, other open topics ...) - future (conservation, policy making, predictive modelling, climate change, evolution again ...)

We have invited three plenary speakers to cover and introduce cutting-edge research in each of these groups of topics:

- Michael Hofreiter (http://www.york.ac.uk/biology/research/ecology-evolution/michael-hofreiter/) - Phil Stephens (http://www.dur.ac.uk/philip.stephens/welcome.htm) - Herbert H.T. Prins (http://www.reg.wur.nl/UK/Staff/Prins/)

We are looking forward to a major event this late summer, and hope to welcome participants from a diverse range of topics and backgrounds.

With best regards, on behalf of the organising committee,

Robert

Dr. Robert H.S. Kraus Conservation Genetics Group

Senckenberg Research Institute Research Station Gelnhausen Clamecystrasse 12, D-63571 Gelnhausen, Germany tel. 0049-(0)-6051-61954-3130 fax. 0049-(0)-6051-61954-3118 robert.kraus@senckenberg.de www.senckenberg.de "Chance favours a prepared mind"

Senckenberg Gesellschaft für Naturforschung Rechtsfähiger Verein gemäß Â§22 BGB Senckenberganlage 25 60325 Frankfurt Direktorium: Prof. Dr. Dr. h.c. Volker Mosbrugger, Prof. Dr. Michael Türkay, Dr. Johannes Heilmann, Prof. Dr. Pedro Martinez Arbizu, Prof. Dr. Georg Zizka, Prof. Dr. Uwe Fritz Vorsitzender des Präsidiums: Dietmar Schmid Aufsichtsbehörde: Magistrat der Stadt Frankfurt am Main (Ordnungsamt)

Ottawa Evolution2012 Jul6-10

1st Joint Congress on Evolutionary Biology (i.e. Evolution2012 and more!) July 6-10, 2012 - Ottawa, Canada www.evolution2012.org REMINDER: EARLY REGISTRATION DEADLINE IS FAST APPROACHING (Apr. 30)

The 1st Joint Congress is a merging of the traditional 'Evolution' meeting (the annual meeting of the American Society of Naturalists, the Society for the Study of Evolution, and the Society of Systematic Biologists) with the annual meeting of the Canadian Society for Ecology and Evolution and the (normally biennial) meeting of the European Society for Evolutionary Biology. Along with a full range of topics in evolutionary biology, with the joint participation of the CSEE and the ASN, we look forward to increased representation of our ecologists.

IMPORTANT POINTS - Separate registration for several optional (and exciting) pre/post congress workshops is NOW OPEN (see http://www.confersense.ca/-Evolution2012/workshops.htm)

- Ottawa is a tourist city and accommodation is often in high demand. Booking hotel/residence NOW is STRONGLY RECOMMENDED. We have gone to substantial lengths to ensure that our conference hotel rates are the best possible; please book through our registration process and not via the hotels directly.

- Coming from outside CANADA? You WILL need a passport (INCLUDING IF YOU'RE DRIVING OR FLYING FROM THE USA).

- Most people will not require a visa; check here to find out for sure: http://www.cic.gc.ca/english/visit/-visas.asp#exemptions - Our new congress blog site is up and running and will soon feature all sorts of useful information (http://evolution2012ottawa.com/-wordpress/)

HIGHLIGHTS - The meeting will be held at the state-of-the-art, newly opened Ottawa Convention Centre, situated in the heart of downtown Ottawa.

- Optional pre/post congress tours now available for booking, including world-class whitewater rafting on the Ottawa River.

- Child care is available onsite at the congress venue (book now).

- Affordable residence accommodation at the University of Ottawa, only a short walk from the congress venue, along with an array of hotel options.

- A plenary address and two symposia sponsored by each society.

- Various optional pre/post-congress workshops/symposia, along with the iEvoBio satellite conference (July 10-11).

- Final congress dinner and farewell party (no speeches) at the spectacular Canadian Museum of Civilization (transportation included).

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

Conference organizers:

Howard Rundle (uOttawa) Andrew Simons (Carleton University)

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

---

Ottawa Evolution2012 Jul6-10 reminder

1st Joint Congress on Evolutionary Biology (i.e. 'Evolution2012' and more) July 6-10, 2012 - Ottawa, Canada www.evolution2012.org ***EARLY REGISTRATION DISCOUNT ENDS IN A FEW DAYS (i.e. MONDAY, APR. 30 @ midnight UTC/GMT -4 hrs)***

APPLICATIONS FOR STUDENT VOLUNTEER DISCOUNTS, TRAVEL GRANTS, AND TALK/POSTER AWARDS ALSO CLOSE APR. 30

The 1st Joint Congress is a merging of the traditional 'Evolution' meeting (the annual meeting of the American Society of Naturalists, the Society for the Study of Evolution, and the Society of Systematic Biologists) with the annual meeting of the Canadian Society for Ecology and Evolution and the (normally biennial) meeting of the European Society for Evolutionary Biology. Along with a full range of topics in evolutionary biology, with the joint participation of the CSEE and the ASN, we look forward to increased representation of our ecologists.

IMPORTANT POINTS

- Our new congress blog is up and running and will feature all sorts of useful information, including immediate conference updates (http://evolution2012ottawa.com/-wordpress/)

- Separate registration for several optional (and exciting) pre/post congress workshops is OPEN (see http:/-/www.confersense.ca/Evolution2012/workshops.htm)

- Ottawa is a tourist city and accommodation is filling - Please book now! We have gone to substantial lengths to ensure that our conference hotel rates are the best possible; please book through our registration process and not via the hotels directly.

- Coming from outside CANADA? You WILL need a passport (INCLUDING IF YOU'RE DRIVING OR FLYING FROM THE USA).

- Most people will not require a visa; check here to find out for sure: http://www.cic.gc.ca/english/visit/-visas.asp#exemptions - All posters will be accepted. Oral presentations (i.e. talks) will be accepted until capacity is reached. Abstracts are NEVER collected (except for student award applications).

- Travel discounts (airline and train) have been posted.

HIGHLIGHTS

- The meeting will be held at the state-of-the-art, newly opened Ottawa Convention Centre, situated in the heart of downtown Ottawa.

- Optional pre/post congress tours now available for booking, including world-class whitewater rafting on the Ottawa River.

- Child care is available onsite at the congress venue (book now).

- Affordable residence accommodation at the University of Ottawa, only a short walk from the congress venue, along with an array of hotel options.

- A plenary address and two symposia sponsored by each society.

- Various optional pre/post-congress workshops/symposia, along with the iEvoBio satellite conference (July 10-11).

- Final congress dinner and farewell party (no speeches) at the spectacular Canadian Museum of Civilization (transportation included).

- The full conference program will be available on a cross-platform customizable mobile app.

- Numerous free workshops (e.g., 'Survival of the Fittest: Tips on How to Get a Job in Academia'; 'How to get published'; NSF/NSERC/ERC funding agency information sessions)

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

Conference organizers:

Howard Rundle (uOttawa) Andrew Simons (Carleton University)

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

howard.rundle@uottawa.ca

Ottawa iEvoBio Informatics Jul10-11 CallForSoftware

The Call for Software Bazaar entries is now open for the 2012 conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio), at http:/-/ievobio.org/ocs2/index.php/ievobio/2012. See below for instructions.

The Software Bazaar features presenters demonstrating their software live on a laptop. At iEvoBio, this session takes the place of a poster session, and will be approximately 2.0 hours in duration. Conference attendees will be able to walk from one demonstration to the next and talk with the presenters. Please also see our FAQ (http://ievobio.org/faq.html).

Entries should be software aimed at advancing research in phylogenetics, evolution, and biodiversity, and can include interactive visualizations that have been precomputed (such as SVGs, or Google Earth-compatible KML files). Note that commercial marketing activities are not permitted - presenters wishing to promote commercial or proprietary services or products should contact the Evolution conference about exhibitor space (http://www.confersense.ca/Evolution2012).

Submissions consist of a title, which will typically be the name of the software (or visualization method) being presented, the URL of a website where more information can be obtained, and the license under which the source code is available. The website must contain a link to where the source code (and possibly binaries) can be downloaded. If it is not obvious from the website, the submission must describe what the software does. Reviewers will judge whether a submission is within scope of the conference (see above), and need to be able to verify whether the open-source requirement(*) is met.

Presenters are expected to bring their own laptops for presentation, and any auxiliary devices necessary (such as a mouse). Power will be available at the presentation tables (110V/60Hz, US-style plugs; international presenters need to bring a suitable adaptor). Please let the organizing committee know as much in advance as possible if you expect to have unusually high demands for wireless network bandwidth, a large display, or other hardware.

Review and acceptance of Software Bazaar submissions will be on a rolling basis. The deadline for submission is the morning of the first day of the conference (July 10), but, because space for Software Bazaar presentations is finite, we cannot guarantee the availability of slots for late submissions. We cannot accept submissions until the open-source requirements are met.

Software Bazaar demonstrations 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) Birds-of-a-Feather gatherings. The Calls for Challenge entries (http://ievobio.org/challenge.html) and Lightning Talks (same submission URL as above) remain open, and the Birds-of-a-Feather call is forthcoming.

More details about the conference and program are available at http://ievobio.org. You can also find continuous updates on the conference's Twitter feed at http://twitter.com/iEvoBio and Google+ page, or subscribe to the low-traffic iEvoBio announcements mailing list at http://groups.google.com/group/ievobio-announce . iEvoBio 2012 is sponsored by the US National Evolutionary Synthesis Center (NESCent) and by Biomatters Ltd., in partnership with the Society for the Study of Evolution (SSE) and the Systematic Biologists (SSB).

The iEvoBio 2012 Organizing Committee: Hilmar Lapp, US National Evolutionary Synthesis Center (chair) Robert Beiko, Dalhousie University Nico Cellinese, University of Florida and Florida Museum of Natural History Robert Guralnick, University of Colorado at Boulder Rebecca Kao, Denver Botanic Gardens Ellinor Michel, Natural History Museum, London Nadia Talent, Royal Ontario Museum Andrea Thomer, University of Illinois at Urbana-Champaign

(*) iEvoBio and its sponsors are dedicated to promoting the practice and philosophy of Open Source software development (see http://www.opensource.org/docs/definition.php) and reuse within the research community. For this reason, software to be demonstrated to conference attendees must be licensed with a recognized Open Source License (see http://www.opensource.org/licenses/), and be available for download, including source code, by a tar/zip file accessed through ftp/http or through a widely used version control system like cvs, Subversion, git, Bazaar, or Mercurial. Authors are advised that

— / —

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

---

Ottawa iEvoBio Jul10-11 DeadlineExtension

The deadline for submitting abstracts for full talks to the 2012 conference on Informatics for Phylogenetics, Evolution, and Biodiversity (iEvoBio) has been extended to Monday, April 9, 2012. We hope that this will give those interested in contributing sufficient time to do so.

Please see http://bit.ly/iEvoBio2012_CfA for the full Call for Abstracts and author instructions. We still expect to be able to notify accepted talks in time for the early registration deadline of iEvoBio (and Evolution).

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 (http://twitter.com/iEvoBio) or Google Plus page (http://bit.ly/iEvoBio-on-Gplus), and there is a Google group you can join at http://groups.google.com/group/ievobio-announce to receive announcements.

iEvoBio 2012 is sponsored by the US National Evolutionary Synthesis Center (NESCent) and by Biomatters Ltd., in partnership with the Society for the Study of Evolution (SSE) and the Society of Systematic Biologists (SSB).

The iEvoBio 2012 Organizing Committee: Hilmar Lapp, US National Evolutionary Synthesis Center (chair) Robert Beiko, Dalhousie University Nico Cellinese, University of Florida and Florida Museum of Natural History Robert Guralnick, University of Colorado at Boulder Rebecca Kao, Denver Botanic Gardens Ellinor Michel, Natural History Museum, London Nadia Talent, Royal Ontario Museum Andrea Thomer, University of Illinois at Urbana-Champaign

hlapp@nescent.org

Ottawa PhysiologicalEvolution Jul8

As part of the 1st Joint Congress on Evolutionary Biology the ESEB are supporting a symposium on:

"The physiological mechanisms that shape life histories" A symposium to help explain how, when, and why, we develop, reproduce, and die. Sunday July 8th 1.15 - 4.45 Organizers: Emma Barrett (University of East Anglia) Dan Nussey (University of Edinburgh) http://www.confersense.ca/Evolution2012/symposia.htm https://www.facebook.com/events/401567733202790/ Speakers: John Speakman Pat Monaghan Serge Morand Gro Amdam Thomas Flatt Kevin Matson

Information about symposium

Traditional life history theory attempts to describe the ultimate processes involved in the evolution of phenotypes and how traits are constrained by energetic trade-offs. This approach conventionally ignores the underlying proximate mechanisms, and yet the fundamental problems in life history evolution can only be fully resolved with an understanding of the underlying developmental, physiological, and genetic mechanisms. Our symposium highlights current research that uses novel molecular techniques and study systems to shed new light on traditional life-history questions.

Information on speakers

John Speakman (University of Aberdeen, UK) Developed double labelled water system to investigate energy expenditure and balance in animals. Known for work related to caloric restriction, obesity and ageing. http://www.abdn.ac.uk/energetics-research/ http://en.wikipedia.org/wiki/John_Speakman Pat Monaghan (University of Glasgow, UK) A pioneer of maternal effects on sex allocation and condition of offspring, she has since worked on the effects of early life environment on ageing phenotypes. http://www.gla.ac.uk/researchinstitutes/bahcm/staff/patmonaghan/ http://www.universitystory.gla.ac.uk/biography/?id=3DWH1650&type=3DP Serge Morand (Université Montpellier, France) Host-parasite interactions and how the immune system can shape life-histories http://www.eec.univ-montp2.fr/people/serge-morand/ Gro Amdam (University of Arizona State University, USA / Norwegian University of Life Sciences, Norway) Discovered a the vitellogenin mechanism of life-history trade-offs between eusocial honey bees http://sols.asu.edu/people/faculty/gamdam.php Thomas Flatt (University of Veterinary Medicine Vienna, Austria) Investigates how hormonal signalling pathways affect the phenotypic expression and evolution of life history trade-offs and aging http://i122server.vu-wien.ac.at/pop/Flatt_website/flatt_home.html Kevin Matson (University of Groningen, Netherlands) Studies how the physical landscape effects the selection on immunity phenotypes http://www.matsonk.fmns.rug.nl/ ***PLEASE NOTE THAT EARLY-BIRD REGISTRATION FOR THE 1ST CONGRESS ON EVOLUTIONARY BIOLOGY ENDS ON APRIL 30TH***

Dr. Emma Barrett Postdoctoral Research Associate, Room 6/01.24 School of Biological Sciences University of East Anglia Norwich Norfolk NR4 7TJ UK +44 (0) 1603 592947 +44 (0) 7961 863204

The physiological mechanisms that shape life histories ESEB sponsored conference at the 1st Joint Congress on Evolutionary Biology, Ottawa, Canada July 6-10, 2012 http://www.confersense.ca/Evolution2012/symposia.htm https://www.facebook.com/events/401567733202790/ Emma.Barrett@uea.ac.uk

---

Salzburg EvolutionofPhysiologicalTraits 29June

Dear Colleagues

We are pleased to announce that a two-day session on the Evolution of Physiological Traits will be held as part of the Society for Experimental Biology (SEB) Annual Meeting in Salzburg (29th June-2nd July 2012). We have a number of slots that are held open for contributed talks, and invite you to submit an abstract and / or register to attend the meeting. Submission of abstracts closes on 4th May, and the deadline for early bird registration is 11th May.

Full details on the conference, its venue, and instructions on how to submit your abstract can be found at: http://www.sebiology.org/meetings/-Salzburg2012/Salzburg.html SEB supports the attendance of students and other early career scientists via travel grants: http://www.sebiology.org/-meetings/Salzburg2012/grants.html Overview Recent advances in phylogenetics, genomics, physiology and paleobiology have brought major advances in our understanding of how physiological processes have evolved in autotrophic organisms (microbes and plants). This session will bring together leading figures in each of these fields, aiming to provide a stimulating, multidisciplinary view of physiological trait evolution and, tackling a number of key questions. What were the important evolutionary innovations in the history of autotrophic organisms? What do we know about the origins of these physiological processes? What are the key drivers of trait diversification? Does selection favour distinct combinations of physiological traits? What are the biophysical constraints on the adaptive landscape? How have the same physiological syndromes evolved independently in multiple lineages? How have past evolutionary events changed the Earth System, and how will ongoing global change drive physiological adaptations in wild and agricultural plant species? We welcome contributions in any of these areas.

Speakers * Bill Martin (Heinrich Heine University) - Cyanobacterial phylogenomics and the origins of plastids. * David Beerling (University of Sheffield) - The deep evolutionary origins of stomatal physiology. * Karl Niklas (Cornell University) - Biophysical constraints and opportunities in physiochemical evolution: a macroevolutionary perspective * Paul Falkowski (Rutgers University) - The microbial engines that drive Earth's biogeochemical cycles. * John Raven (University of Dundee) - Carbon dioxide fixation by autotrophs: alternatives to the Benson-Calvin cycle. * Howard Griffiths (University of Cambridge) - Photosynthesis in early land plant life forms and the origins of carbon concentrating mechanisms. * Lawren Sack (UCLA) - Adaptation of leaf venation in terrestrial plant radiations. * Erika Edwards (Brown University) - A phylogenetic perspective on the evolution of succulence. * Lisa Donovan (University of Georgia) - Evolution of the leaf economic spectrum and related traits. * Pascal-Antoine Christin (Brown University) - Drivers of the repeated origins of carbon concentrating mechanisms. * Jonathan Leake (University of Sheffield) - Co-evolution of trees and mycorrhizal fungi drives mineral weathering, carbon and phosphorus cycles.

Sponsorship This Plant Session is jointly sponsored by the Society for Experimental Biology (SEB) and the British Ecological Society (BES), through the Plant Environmental Physiology Group.

We look forward to seeing you in Salzburg!

Colin Osborne (c.p.osborne@sheffield.ac.uk)

Colin Osborne Dept. Animal and Plant Sciences University of Sheffield

tel: +44-114-222-0146 skype: cposborne lab pages: http://osbornelab.group.shef.ac.uk ecological informatics: www.grassportal.org c.p.osborne@sheffield.ac.uk

---

Shanghai SystemsModelling Aug30-Sep6

Dear all,

The Otto Warburg Summer School and Research Symposium 2012 is taking place in Shanghai from August 30th to September 6th and will discuss “Genes, Metabolism and Systems Modelling”. It is being organised by the Partner Institute for Computational Biology of the Chinese Academy of Sciences and the Max Planck Society. Confirmed speakers are:

Alexander Bockmayr (Freie Universität Berlin) Paul Jensen (University of Virginia) Mustafa Khammash (University of California, Santa Barbara) Edda Klipp (Humboldt University, Berlin) Ina Koch (Johann Wolfgang Goethe-University, Frankfurt) Satoru Miyano (University of Tokyo) Eytan Ruppin (Tel Aviv University) Denis Thieffry (Ecole Normale Superieure, Paris) Lorenz Wernisch (MRC Biostatistics Unit, Cambridge)

The scientific coordinators are Martin Vingron and Jun Yan. 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 genetic research and systems modelling 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 before the 15th of June. The registration fee is 4800 RMB (approx 580 Euro). Costs for meals, accommodation and social events will be covered. The programs (and video streams) of previous Summer Schools can also be found on the school's website.

Registration and further information at: http://www.picb.ac.cn/owiss/index.shtml

Regards, Kirsten

Kirsten Kelleher IMPRS-CBSC Coordinator 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 www.imprs-cbsc.mpg.de kelleher@molgen.mpg.de

UMissouri Metagenomics May7-8

The Organizing Committee would like to invite you to attend a *free* Symposium on "Frontiers in Metagenomics" to be held in the beautiful Monsanto Auditorium at the Christopher S. Bond Life Sciences Center on the University of Missouri campus in Columbia, Missouri from May 7-8, 2012.

The objective of the Frontiers in Metagenomics Symposium is to expose you to a dazzling range of current applications which will be presented by a stellar group of accomplished scientists. The symposium will span the Kingdoms of Life and will address both the generation and analysis of metagenomic data.

Due to the generous sponsorship of the Mizzou Advantage Program and the Stadler Genetics Symposium, there will be no charge to attend. However preregistration is required by April 23, 2012 due to space limitations and there will be a $40 charge to attend the spectacular symposium dinner that will be held at Les Bourgeois Vineyards and Winery situated on the bluffs overlooking the Missouri River in Rocheport, Missouri.

Symposium information and registration details can be found at the conference website:

www.muconf.missouri.edu/metagenomics/index.html If you require more information, please do not hesitate to contact me.

Best regards on behalf of the Frontiers in Metagenomics Symposium Organizing Committee: Michael Calcutt, Perry Gustafson, Mark McIntosh, Melanie Mormile, Daniel Oerther, Chris Pires, Jack Schultz, Gary Stacey and Judy Wall.

We hope to see you in Columbia!!!!

Jerry Taylor Curators' Professor and Wurdack Chair in Animal Genomics Division of Animal Sciences University of Missouri 920 East Campus Drive Columbia, MO 65211-5300 Voice: (573) 884-4946 E-mail: taylorjerr@missouri.edu

taylorjerr@missouri.edu

UOslo EvolutionaryProtistology Jul29-Aug3

On behalf of the International Society of Protistologists (ISOP) and the International Society of Evolutionary Protistology (ISEP), we invite you to attend their combined 2012 meeting, in Oslo, the capital of Norway. The meeting will be held 29 July - 3 August 2012, on the campus of University of Oslo. The scientific sessions themselves will begin on July 30th .

Register now! The registration for the conference closes at May 1.

The webpage for registration, submission of abstracts and information is http://www.protist2012.org . Watch this site in the coming months for registration and submission information, and for details on what we anticipate will be an excellent series of lectures and talks.

You may also follow us on twitter http://twitter.com/#!/Protist2012 and Facebook http://www.facebook.com/pages/Protist2012/217343201672896 Hope to see you all at Protist2012.

Anders K. KrabberÃd PhD student

Microbial Evolution Research Group (MERG) Department of Biology University of Oslo P.b. 1066 Blindern N-0316 Oslo Norway

"Anders K. KrabberÃd" <anders.krabberod@gmail.com>

UOslo ProtistEvolution Jul29-Aug3

On behalf of the International Society of Protistologists (ISOP) and the International Society of Evolutionary Protistology (ISEP), we invite you to attend their combined 2012 meeting, in Oslo, the capital of Norway. The meeting will be held 29 July - 3 August 2012, on the campus of University of Oslo. The scientific sessions themselves will begin on July 30th .

The webpage for registration, submission of abstracts, and information is http://www.protist2012.org . Watch this site in the coming months for registration and submission information, and for details on the general program.

You may also follow us on twitter http://twitter.com/#!/Protist2012 and Facebook http://www.facebook.com/pages/Protist2012/217343201672896 Hope to see you all at Protist2012. Feel free to forward this mail to anyone working on microbes and protists.

Anders K. KrabberÃd

PhD Student

Tlf: +47 91532079

Microbial Evolution Research Group (MERG) Department of Biology University of Oslo P.b. 1066 Blindern N-0316 Oslo Norway

“Anders K. KrabberÃd” <anders.krabberod@gmail.com>

Virrat Finland PhDStudentsEvolBiol Sep25-30 reminder

Event: EMPSEB 18 (PhD Students in Evolutionary Biology) Date: 25-30 September, 2012 Location: Finland

ONLY A FEW DAYS LEFT TO REGISTER for the 18th European Meeting of PhD Students in Evolutionary Biology (EMPSEB 18), held in Finland. The event aims to bring together PhD students studying Evolutionary Biology to let them present their research, get feedback from top scientists in the field, and develop collaborations with their peers.

There will also be a special Ethics of Science Symposium with speakers and a discussion session sponsored by the International Union of Biological Sciences (IUBS).

REGISTRATION WILL CLOSE 30 April 2012. Participation fee is 300euros, and only payable upon acceptance to the meeting (includes meals, lodging, and some transportation). After 30 April, any applicants will be placed on a waiting list. Students can apply for travel grants. More information is available at www.empseb18.com Confirmed plenary speakers include:

Frank Ryan (University of Sheffield- United Kingdom) Martine Maan (University of Groningen- Netherlands) Mikael Fortelius (University of Helsinki- Finland) Hanna Kokko (Australia National University- Australia) Marc Johnson (University of Toronto at Mississauga- Canada) Thomas Flatt (University of Veterinary Medicine Vienna- Austria) Craig Primmer (University of Turku- Finland) Leena Lindström (University of Jyväskylä- Finland) Naomi Pierce (Harvard University- United States)

SPONSORS for EMPSEB 18 include: ESEB, IUBS, Peerage of Science, Centre of Excellence in Biological Interactions, Allgenetics, Biomatters, Wiley Blackwell, University of Jyväskylä, University of Helsinki, LUOVA graduate school, New England Biolabs, University of Turku, Royal Society Publishing, & the International Paleontological Association.

Robert Hegna EMPSEB 18 Committee Finland

“Robert Hegna, EMPSEB 18” <president@empseb18.com>

GradStudentPositions

BournemouthU ParasiteDiversity

Fully funded PhD Opportunity at Bournemouth University, UK

Identifying drivers of parasite diversity hotspots and disease emergence in the UK. Emergence of disease is a major threat to biodiversity. Due to the intense sampling effort involved, factors driving disease emergence are studied at a microecological level. A holistic approach in managing biodiversity including data on parasite diversity patterns, climate and socioeconomic parameters will provide far more informative results. Here we propose the use of extensive datasets on parasite diversity and socioeconomic factors to determine parasite diversity hotspots in the UK. The project will combine multivariate statistical models and new data to identify the major drivers affecting disease emergence, resistance to parasite invasion and biodiversity homogenization. A predictive model to identify hotspots of future disease emergence will be developed.

Application deadline: 31st May, 2012 For more information:

On the project:

http://www.bournemouth.ac.uk/research/-studentships/docs/pdfs2012/as_andreou.pdf How to apply: http://www.bournemouth.ac.uk/research/-graduate_school/apply_phd_studentships.html or contact:

Dr Demetra Andreou (PhD) Lecturer in Environmental Science School of Applied Sciences Bournemouth University Christchurch House, Talbot Campus, Poole, Dorset BH12 5BB

E-mail: dandreou@bournemouth.ac.uk

http://onlineservices.bournemouth.ac.uk/-academicstaff/Profile.aspx?staff=dandreou Demetra Andreou <dandreou@bournemouth.ac.uk>

BrunelU EvolutionaryPsychology

MSc in EVOLUTIONARY PSYCHOLOGY

Department of Psychology, Brunel University

This programme provides an exciting opportunity for advanced study in Evolutionary Psychology, i.e. psychological science informed by explicit consideration of the fact that the human mind, like the human body, is a product of evolutionary processes. This course is particularly suited to students in the life sciences or social sciences who are interested in finding out how principles from evolutionary biology can provide a framework for the scientific study of human psychology and behaviour.

More information on the Evolution & Behaviour Group at Brunel... http://www.ebb-web.org.uk/ More information on the MSc Programme... http://www.brunel.ac.uk/courses/postgraduate/-C864PEVPSYC Dr Nicholas Pound Department of Psychology School of Social Sciences Brunel University Uxbridge UB8 3PH UK Phone: 01895 266311 (internal 66311) Fax: 01895 269724 Email: Nicholas.Pound@brunel.ac.uk

Nicholas Pound <Nicholas.Pound@brunel.ac.uk>

CzechRepublic AntEvolution

PHD POSITION IN ANT ECOLOGY

Laboratory of Ecology and Evolution of Social Insects Biology Center, Czech Academy of Sciences is looking for a PhD student for project:

MECHANISMS STRUCTURING ARBOREAL ANT COMMUNITIES IN TROPICAL FORESTS

We are looking for a motivated student to join our research team focused on ecology of tropical insects and plants (V. Novotn. Basset group). The PhD candidate will study ecology and diversity of ants of New Guinea. He/she will participate on processing of unique material and datasets from one of the last unknown frontiers rain forest canopies. She/he will combine traditional taxonomic methods with molecular tools (barcoding, species phylogeny) and analyse ecological community data. He/she will work on available material and have opportunity to conduct research at our field stations in Papua New Guinea.

We offer 4 years scholarship at PhD program at Faculty of Science, University of South Bohemia (http://-www.prf.jcu.cz/en/) and grant contract (50% position) at Biology Center, Czech Academy of Sciences (http://-www.entu.cas.cz/en/). All research costs are fully covered. The scholarship including salary (˜7000 annually) is highly sufficient to cover all living expenses in the Czech Republic.

Starting date for the position is flexible between April and September 2012.

Requirements:

Master degree (or equivalent) in biology & environmental sciences enthusiasm for the topic and motivation to learn new things analytical experience with R and/or other statistical packages fluent English and ability to communicate within an international team

We offer:

participation in cuttingedge tropical ecology research access to unique ecological and biological data and original research topics opportunity to learn novel methods combination of lab and field work

Candidates should send a statement of interest, a CV, and support letters from two referees to Dr. PETR KLIMEÅ: peta.klimes@gmail.com. Deadline for applications is 1st April.

For further information do not hesitate to contact:

Petr KlimeÅ, Biology Center, Czech Academy of Sciences Branisovska 31, 370 05, Ceske Budejovice, Czech Republic, Ph.N. + 420 387 775 332 Information sources: www.newguineants.org, www.entu.cas.cz/png/research.htm

– Tom Fayle

Laboratory of Tropical Ecology University of South Bohemia Branisovka 31 370 05 Ceske Budejovice Czech Republic

Forest Ecology and Conservation Group Imperial College London Silwood Park Campus Buckhurst Road, Ascot Berkshire SL5 7PY, UK

Tel: +44 (0)7816 092365 / +420 777083800 Email: t.fayle@imperial.ac.uk Web: www.tomfayle.com Recent publication: Optimising diversity assessment protocols for high canopy ants in tropical rain forest (2012). Biotropica 44: 73-81.

Key to the ant genera of Borneo in Malay and English: http://www.tomfayle.com/research%20link.htm Tom Fayle <tom_fayle@hotmail.com>

EawagETH Zurich PathogenResistance

A PhD-student position is available at Eawag (Swiss Federal Institute of Aquatic Research) and ETH Zurich (Swiss Federal Institute of Technology Zurich) in Switzerland

PHENOTYPIC SELECTION AND QUANTITATIVE EVOLUTIONARY RESPONSES IN IMMUNE DEFENCE TRAITS IN NATURE

Parasites present a serious and continuous threat for natural populations of most free-living species. Immune defence is generally considered as an important trait in determining organisms' fitness as it eliminates harmful parasites. Therefore, understanding the evolution of immune defence is one of the key topics in predicting dynamics of host-parasite interactions. However, knowledge on the type and strength of selection on quantitative immune defence traits and their evolutionary responses are generally lacking in most natural systems. In this project, phenotypic selection and its relation to quantitative genetic variation in host immune defence traits will be examined in natural populations of a freshwater snail Lymnaea stagnalis. The goals of the project are to assess (1) the type and strength of phenotypic selection on immune defence traits and their potential responses to selection across host populations depending on the risk of infection and host genetic polymorphism, (2) variation in selection imposed by different parasite types (specialist parasites, opportunistic microbes), and (3) what is the relative importance of immune defence traits in determining hosts' susceptibility to infections when considering factors that determine their exposure (i.e. contact with parasites)?

We invite highly motivated students with a good background in evolutionary ecology to apply for the position. A MSc or equivalent degree is required. Earlier experience with snails or immunological work is not required. The student will work in a research group led by Prof. Jukka Jokela (Eawag/ETH Zurich, Switzerland). The project is funded by Swiss National Science Foundation for 3 years.

Starting date: earliest 1st July 2012

If interested, please submit your CV, contact information for two references, and a brief summary of research experience and interests to Otto Seppälä (otto.seppaelae@eawag.ch). Application deadline is 30th April 2012. Top candidates will be interviewed.

Dr. Otto Seppälä Prof. Jukka Jokela

Otto.Seppaelae@eawag.ch

GroningenU MarineMammalGenomics

PhD position in Marine Mammal Evolutionary genomics (1.0 fte) (Reference number 212075)

Organisation

The PhD position is with the Marine Evolution and Conservation (MarECon) group at the Centre for Ecological and Evolutionary Studies (CEES) which is placed with the Faculty of Mathematics and Natural Sciences at the University of Groningen in the Netherlands. The research conducted by the members of MarECon is aimed at the evolution and conservation of pelagic marine organisms, in particular marine mammals. We are interested in those processes that partition genetic variation within those species that inhabit this comparatively open environment. Our primary research approach is population genetics and genomics. The research is conducted with a global network of collaborators who collect data and tissue samples in the field.

Job description

The pinnipeds and cetaceans represent some of the most derived mammal groups. The many convergent features in these two groups provide clear evidence of the strong natural selection the mammal “bauplan” is subjected to when transitioning to a marine existence. The combination of strong convergent evolution in different lineages of mammals constitutes an excellent opportunity to gain insights into the genomic underpinnings of the evolution and adaptation in pinnipeds and cetaceans and the subsequent radiations into different distinct marine habitats.

The objective of this PhD project is to utilize genome enabled methods to identify those traits under past and recent selection in pinnipeds and cetaceans. The research will mainly consist of genome wide-scans in select population samples and subsequent bioinformatics and population genomic analyses of those data. The newly fitted laboratory is situated in the new green building Linneausborg on the Zernike Campus with excellent facilities for this kind of work.

The PhD student will be supervised by Dr. Martine Bérubé and Prof. Per Palsbøll.

Qualifications

We are looking for a highly motivated person with a master's degree in biology or equivalent discipline, with a strong background in empirical and theoretical population genetics. The ideal candidate for this position has good quantitative skills and the ability to conduct bioinformatics analyses of the large amounts of short-read sequence data. Programming skills (or the interest and ability to acquire such) is a necessity. The candidate should be able to work and solve problems independently. Some knowledge of marine mammals is beneficial, but not a prerequisite. It should be noted that the opportunities for fieldwork will be few and brief. A good command of English is required. The candidate will be enrolled in Groningen Graduate School of Science, attend graduate courses within the Research School Ecology and Evolution and participate in our teaching program (10% of time).

Conditions of employment

The University of Groningen offers a salary of EUR 2,042 gross per month in the first year up to a maximum of EUR 2,612 gross per month in the final year.

The employment is initially in a temporary position of 1.5 years with possible extension with another 2.5 years provided satisfactory performance during the first year. The PhD candidate will be evaluated after the first year in order to determine the likelihood of the successful completion of the PhD thesis within the following three years. If a successful completion is deemed unlikely, the employment will not be extended. The main objective of the position is to publish research articles in peer-reviewed scientific journals. These publications will form the basis of the doctoral thesis and obtaining the PhD degree (Dr) at the University of Groningen.

Application A full complete application in English consists of a letter describing your personal motivation for applying for this position outlining which skills pertinent to the position you have, past experience as well as a brief explanation what you think the main research questions in evolution and conservation are today for marine mammals. Also make sure to add a complete curriculum vitae along with names and addresses, including telephone/fax and e-mail addresses for three referees.

We would like to receive applications until 15 May 2012, 24:00 CET by means of the application form.

Start date before 1 September 2012.

Information

For information you can contact: Dr. Per Palsboll, p.j.palsboll@rug.nl palsboll@gmail.com

CEES< http://www.rug.nl/fmns-research/cees/index >

Applications should be submitted on-line at http://www.rug.nl/corporate/vacatures/vacaturesRUG(the reference number for this position is 212075) before May 15^th 2012.//

– Per J. Palsboll, Professor

Marine Evolution and Conservation Centre for Ecological and Evolutionary Studies University of Groningen Nijenborgh 7 9747 AG Groningen

— / —

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

MississippiStateU PlantAnimalCoevol

Evolutionary Biologist Ph.D. graduate student positions available

The Klink lab in the Department of Biological Sciences at Mississippi State University currently is seeking Ph.D.-level graduate students to begin in fall, 2012. The Klink lab focuses in on understanding the processes of plant-animal coevolution through niche establishment, development and maintenance by a pathogen in its host. Central to the work is cell-type-specific gene expression profiling. The model for the work is the soybean-soybean cyst nematode pathosystem, which has allowed for the identification of genes that relate to niche development (Matsye et al. 2011). The genome of the allotetraploid soybean has been sequenced (Schmutz et al. 2010), allowing for a number of cellular and developmental questions concerning the evolution of polyploidy to be addressed at the molecular level (Matsye et al. in review). This work includes genotype-specific allele analyses and quantitative studies of gene expression in specific root cells undergoing infection. This knowledge allows for addressing the subfunctionalization and neofunctionalization of homeologs and adaptive evolution of the complex trait. The development of a genetic engineering pipeline has permitted the high throughput testing of genes, allowing for the determination of how the genes function in the process. The Klink lab is housed in the newly renovated Harned Hall that has all the necessary modern equipment to perform the research. For inquiries, please contact Dr. Vincent Klink, vklink@biology.msstate.edu. Applications from motivated students are being sought. Application information can be obtained at the Mississippi State University Graduate School website: http://www.grad.msstate.edu/ . Vincent Klink, Ph.D. Department of Biological Sciences Harned Hall; Rm 212 (office), 310 (lab) Mississippi State University Mississippi State, MS 39762

Phone: 662.325.4577 Fax: 662.325.7939

Vincent Paul Klink <VKlink@biology.msstate.edu>

MNHN Paris AdaptiveVariation

PhD proposal in Paris on the Origin and persistence of adaptive variation in heterogeneous environment.

We just obtained a grant from the LABEX BCDiv to finance a PhD at the National Museum of Natural History in Paris (France) on the topic ≪ Origin and persistence of adaptive variation in heterogeneous environment ≫. This PhD thesis will be supervised by Violaine Llaurens (junior CNRS researcher in the unit 7205 entitled Origin, Structure and Evolution of Biodiversity) and Marc Théry (senior CNRS researcher in the unit 7179 entitled Adaptive Mechanisms: from Organisms to Communities).

The starting date will be October 1st, 2012. The PhD consists in a 3- years fixed term contract with the CNRS with 21 000 per annum gross salary. The shortlisted candidates will be interviewed in May 2012.

We are looking for a dynamic and motivated student to perform this PhD. Fluency in French is not requested. If you wish to apply, please send us the following documents before April, 18th 2012 by email (llaurens@mnhn.fr and thery@mnhn.fr):

- A detailed CV, including your previous research experience and the marks or ranking obtained for your Master's degree (or equivalent diploma),

- A cover letter, stating in particular the match between your profile and the PhD project,

- Two reference letters to be sent directly to us by email.

Abstract of the PhD project:

Understanding the origin and persistence of diversity within and among species in a central question in evolutionary biology. Genetic dominance among variants in a population plays a key role in the invasion success of new adaptive traits.

This Phd project focuses on the distribution of morphological and genetic variation of mimic patterns in neotropical butterflies from the genus Heliconius. In these species, many species exhibit a mutual adaptive resemblance. This convergence so called mimicry constitutes an aposematic signal of their unpalatability, which can be learned by predators. Several mimicry rings coexist in a given habitat and some polymorphic species are involved in few distinct mimicry rings. These polymorphic species constitute an ideal model to understand how new adaptive traits can be established and can be favored by selection.

In this context, since the level of dominance is modifying the expression of different variants, it had an influence on their resemblance to the mimic patterns. Hence the origin and persistence of new variants depends both on dominance and discrimination capacities of predators. We thus aimed at jointly investigating how the variation is genetically controlled in the polymorphic species Heliconius numata and how predators can perceive this variation.

Few selected publications of the supervisors linked to this PhD project:

- Théry M., Gomez D. 2010 Insect colors and visual appearance in the eyes of their predators. Advances in Insect Physiology. 38: 267-353.

- Gomez D., Richardson C., Lengagne T., Plenet S., Joly P., Léna J.-P., Théry M. 2009 The role of nocturnal vision in mate choice: females prefer conspicuous males in the European tree frog (Hyla arborea). Proceedings of the Royal Society B, 276: 2351-2358.

- Llaurens V., Billiard S., Castric V., Vekemans X., 2009. Evolution of dominance in sporophytic self-incompatibility systems: I. Genetic load and coevolution of levels of dominance in pollen and pistil. Evolution, 63: 2427-2437.

- Llaurens V., Leducq J.-B., Billiard S., Castric V., Klein E.K., Vekemans X., 2008. Does frequency-dependent selection with complex dominance interactions accurately predict allelic frequencies at the self-incompatibility locus in Arabidopsis halleri? Evolution, 62: 2545-2557.

WEB pages :

http://www.mnhn.fr/oseb/Violaine-LLAURENS
http://www.mabiodiv.cnrs.fr/RubriquesEnAnglais/-IndividualFiles/Thery_File.html Violaine Llaurens (CR2 CNRS) Museum National d'Histoire Naturelle Laboratoire OSEB UMR7205 Batiment d'entomologie CP50 45, rue Buffon 75005 PARIS France

Phone : 00 33 (0)1 40 79 38 61 Fax : 00 33 (0)1 40 79 33 42

WebPage: http://www.mnhn.fr/oseb/Nouvelle-traduction-Violaine Violaine Llaurens <llaurens@mnhn.fr>

MonashU AvianEvolution

PhD Scholarships available at Monash Uni, Melbourne, Australia Deadline: 31 May 2012 http://www.mrgs.monash.edu.au/-futurestudents/researchapps/index.html http://-www.mrgs.monash.edu.au/futurestudents/eligibility/ Are you interested in pursuing a graduate career in avian behavioural and evolutionary ecology? I offer the following projects: Life-history trade-offs: the role of ecological immunology and oxidative stress Interactions between mating and breeding system in Australian fairy-wrens Avian colour signals: form and functions MHC immuno genetics and genetic diversity Heritability of behavioural and physiological traits Please contact me if you are interested in exploring research opportunities in any of these research areas. My research approaches include observational and experimental studies on mostly free-living but also captive birds. Potential techniques include behavioural observations, reflectance spectrometry, immune assays and manipulations, genetic/genomic analysis, oxidative damage analyses, hormone analysis and treatment by implants, animal models. I mainly use Australian fairy-wrens as model organisms. Field sites are in SE-Australia (superb fairy-wrens), and in the wild monsoonal tropics of NW-Australia (purple-crowned fairy-wrens; Kimberley). I have a population of colour-banded birds, existing samples (blood, plasma) and an detailed database available (purple-crowned fairy-wrens).

This round is under-subscribed, but contact me soon if you are interested (anne.peters@monash.edu).

Dr. Anne Peters Senior Lecturer / ARC Future Fellow School of Biological Sciences, Monash University Melbourne, VIC 3168 Australia Ph +61-(0)3-99056287

http://www.biolsci.monash.edu.au/staff/peters/index.html My Researcher-ID: http://www.researcherid.com/rid/A-1821-2010 http://scholar.google.com/citations?user=jpoOPNEAAAAJ anne.peters@monash.edu

---

NewZealand Insect Genomics

Genome evolution, speciation and molecular population genetics of stick insects

Supervisor: Associate Professor Thomas Buckley Co-supervisors: Associate Professor Richard Newcomb, Dr Howard Ross

Next generation DNA sequencing and analysis of whole genomes has opened new possibilities for testing fundamental questions in speciation and adaptation. The successful candidate for this PhD project will generate a draft genome sequence for a New Zealand stick insect (Clitarchus hookeri) and use this as a tool for exploring detailed questions on adaptation within a species and between closely related species. The common stick insect (Clitarchus hookeri) is widespread through much of New Zealand. This species is particularly interesting at it is a geographic parthenogen and has hybridized with closely related species. The successful candidate will perform Illumina sequencing and assemble and annotate a draft genome. This draft genome will be used as a scaffold for RAD-tag studies of SNP variation within C. hookeri and among closely related species. Transcriptome data will also be collected and mapped to the draft genome to obtain candidate genes underlying phenotypic traits for further studies on selection and adaptation. Variation at candidate genes will be measured and compared within and among populations of C. hookeri and among related species. The successful candidate should have experience in molecular evolution and genomics with an interest in developing skills in the assembly and analysis of Next Generation DNA sequence data. This project is funded by the Allan Wilson Centre for Molecular Ecology and Evolution and includes a $25,000 NZD per year scholarship, $5,000 for tuition fees, and funding for international travel.

For more information and host institutions and supervisors' research interests see the following links:

Associate Professor Thomas Buckley http://www.landcareresearch.co.nz/research/staff_page.asp?staff_num=1110 http://www.bioscienceresearch.co.nz/staff/thomas_buckley/ Associate Professor Richard Newcomb http://www.bioscienceresearch.co.nz/staff/richard-newcomb/ Dr Howard Ross http://www.bioscienceresearch.co.nz/staff/howard-ross/ To apply for this position please contact Thomas Buckley at the email address below. Potential candidates should submit a CV, two references, and a short statement of research interests to:

Thomas Buckley (buckleyt@landcareresearch.co.nz)

Thomas Buckley Research Group Leader, Landcare Research Associate Professor, University of Auckland Principal Investigator, Allan Wilson Centre for Molecular Ecology & Evolution

Tel: (+64 9) 574 4116 | Fax: (+64 9) 574 4101 | Email: buckleyt@landcareresearch.co.nz

Post: Private Bag 92170, Auckland, New Zealand | Web: http://www.landcareresearch.co.nz/research/staff_page.asp?staff_num=1110 BuckleyT@landcareresearch.co.nz

RiceU EvolutionaryBiol

The Department of Ecology and Evolutionary Biology at Rice University (Houston, TX) invites applications for admission into our graduate program (M.S. and Ph.D. degrees) for August 2012. While this is not our traditional admissions cycle, our department has recently acquired resources to support additional students beginning Fall 2012. Faculty research interests span population and community ecology, ecological genetics, and the evolution of genes and genomes (see http://eeb.rice.edu/faculty.html). Particular areas of emphasis include the eco/evolutionary dynamics of inter-specific interactions, the ecology and evolution of introgressive hybridization, and molecular and computational evolutionary genomics. Prospective students are encouraged to contact one or more faculty members with matching interests. Please include a CV, brief statement of purpose, and contact information for three references.

Diane Hatton Administrative Coordinator Dept of Ecology and Evolutionary Biology Rice University

Diane Hatton <rdh@rice.edu>

Roscoff SeaweedEvolution

The following PhD position is currently advertised at the Scottish Association for Marine Science (Oban, UK). The application form is available at: http://www.smi.ac.uk/education/postgraduate/-phd-research-at-sams Please note that eligibilty is essentially restricted to UK students (full details available at:http://www.nerc.ac.uk/funding/-application/studentships/studentbook2011.pdf). Don't hesitate to get in touch with Claire Gachon (claire.gachon@sams.ac.uk) for informal enquiries.

Title: Disease, immunity and pathogen recognition in marine seaweeds: a physiological and genomic investigation

Supervisors: Dr Claire Gachon Scottish Association for Marine Science, Scottish Marine Institute, Oban, Argyll PA37 1QA claire.gachon@sams.ac.uk Dr J.M. Cock and Dr Philippe Potin CNRS UMR Station Biologique de Rosocoff, 29682 Roscoff cedex, France.

Introduction Brown algae (Phaeophyta) are multicellular marine organisms that diverged from animals and land plants over a billion years ago. They are predominant primary producers in temperate and cold coastal seas, and of relevance to the rapidly-expanding aquaculture industry. Like any other species, brown algae are plagued by diseases, and their pathogens are increasingly recognised as pleiotropic environmental and evolutionary drivers [1]. The host laboratory has established the interaction between the genome model seaweed Ectocarpus siliculosus [2] and the oomycete pathogen Eurychasma dicksonii as a model to elucidate the defence reactions of brown algae. The overarching objective of this project is to understand how and why some brown algae are capable to resist pathogen infection, when others are not.

This project encompasses the following research objectives: 1) comparative description of cellular events characteristic of disease susceptibility and resistance. The hypersensitive response (HR) has been the cornerstone of plant pathology for over a century. Significantly, we found that across Phaeophyta, disease resistance is also mediated by HR. This is accompanied by the specific deposition of fluorescent secondary metabolites, cell wall reinforcement and expression of specific cell death markers. The student will undertake further in-depth characterisation of these responses using real-time PCR, immunostaining biochemical assays, and highly innovative spatially- resolved metabolite and protein imaging techniques. 2) detailed characterisation of recently identified Ectocarpus candidate pathogen receptors We recently discovered in the Ectocarpus genome two families of candidate pathogen receptors that display unusual, if not unique, structural and evolutionary features [3]. The project includes the bioinformatic and experimental characterisation of LRR- ROCO and NB-ARC-TPR genes in order to reconstruct the history of these two gene families at different time scales. SAMS is a vibrant multidisciplinary research organisation with world class facilities, and the student will work in close association with leading experts. He / she will acquire in-depth knowledge in the burgeoning field of algal host-parasite interactions, whilst developing transferrable skills in biochemistry, molecular biology, bioinformatics, science communication and project management.

Methodology Unique biological material, substantial proteomics, transcriptomics and genomic data, and all necessary molecular techniques are available at SAMS. The PI recently secured NERC funding to generate a comparative RNAseq analysis of disease susceptible and disease resistant Ectocarpus. The project will involve a few short research stays in the Roscoff Marine Station, where the student will be able to access unsurpassed MALDI imaging facilities. The student will be encouraged to exploit these opportunities to develop his/her own original lines of research.

Further reading 1. Gachon et al. (2010) Trends in Plant Science 15: 633-640. 2. Cock JM et al. (2010). Nature 465: 617V621. 3. Zambounis A et al. (2012) Molecular Biology and Evolution doi: 10.1093/molbev/msr296.

Dr Claire GACHON Principal Investigator in Molecular Phycology Scottish Association for Marine Science Scottish Marine Institute PA37 1QA Oban United Kingdom claire.gachon@sams.ac.uk Skype contact : claire.gachon Tel: 0044 16 31 559 318 Fax 0044 16 31 559 001 http://www.smi.ac.uk/claire-gachon Claire Gachon <Claire.Gachon@sams.ac.uk>

SUNY Binghamton EvolutionaryGenetics Yeast

SUNY_Binghamton.EvolutionaryGenetics.Yeast

We are seeking one or two PhD-seeking students to join an NIH-funded research program investigating mitochondrial-nuclear epistasis.

Natural genetic variation in mitochondrial and nuclear genomes impacts phenotypic variation at ecologically important traits, contributes to organismal adaptation and affects genome evolution. We are taking an evolutionary genetics approach to study mt-nuclear interactions using wild isolates of Saccharomyces yeasts. Specifically, we hope to reveal how mt-nuclear interactions contribute to phenotypic variation between strains, identify patterns of organelle coevolution, and map the genetic basis underlying these interactions.

Successful candidates should have a strong background in genetics, microbiology, or evolutionary biology. Experience with (or a strong desire to learn) statistics and bioinformatics is particularly beneficial. Students may choose either the EEB or BCMB graduate tracts within the Department of Biological Science at Binghamton University. (http://www2.binghamton.edu/biology/graduate/index.html)

Interested candidates should contact Dr. Heather L. Fiumera (hfiumera@binghamton.edu) (http://bingweb.binghamton.edu/ ˜ hfiumera/index_html/Welcome.html) with a statement of interests and a CV/resume. Applications are still welcome for Fall 2012, or Spring 2013.

Heather L. Fiumera Assistant Professor Department of Biological Sciences Science 3 G48 Binghamton University Binghamton, NY 13902 607-777-2379 hfiumera@binghamton.edu http://bingweb.binghamton.edu/˜hfiumera Heather Fiumera <hfiumera@binghamton.edu>

UGiessen MolluscEvolution

PhD student position - biogeography and evolution of freshwater molluscs in Wallacea

A three year PhD student position is available at the Department of Animal Ecology and Systematics, Justus Liebig University as part of an international research project studying biogeographical processes in freshwater molluscs of the Wallacea region. It is a joint project with the Natural History Museum Berlin, Leibnitz Institute for Evolutionary and Biodiversity Research at the Humboldt University Berlin (Dr. Thomas von Rintelen) in close cooperation with our Indonesian partners (mainly from Bogor University). Funding is provided by the Deutsche Forschungsgemeinschaft (DFG). The salary is (65% TVL-13) according to the German system.

We are seeking a student with a MSc or equivalent degree in biology. The successful candidate should have experience with molecular systematics (DNA sequencing and/or microsatellite analyses) and should have a strong interest in biogeography and evolutionary biology. Good communication skills, the ability to work independently and the willingness to conduct extended fieldwork in South and Southeast Asia are essential.

We offer an intellectually stimulating research environment in a young and dynamic group and a department with well-equipped state-of- the-art lab facilities. A tight cooperation with one of the world's leading natural history museums is given.

To apply, please send an e-mail application including CV, names and addresses of two referees and a brief letter explaining why you are interested in this PhD position by April 30 to Christian Albrecht: Christian.Albrecht@allzool.bio.uni-giessen.de.

Dr. Christian Albrecht

Department of Animal Ecology and Systematics Biodiversity and Systematics Group Justus Liebig University Giessen H.-Buff-Ring 26-32 D-35392 Giessen

Tel.: 0049-641-9935722 Fax.: 0049-641-9935709

E-mail: christian.albrecht@allzool.bio.uni-giessen.de

Internet: www.uni-giessen.de/wilke; www.wallacea.info

Christian Albrecht <Christian.Albrecht@allzool.bio.uni-giessen.de>

UGottingen CepeaVariation

The Courant Research Centre Geobiology at the University of Göttingen (Germany) is offering 1 of the following positions to work on the molecular genetics of a molluscan pigmentation system:

Post-doctoral position (100% TV-L 13: 39,8 hours/week) or PhD position (65% TV-L 13: 25,87 hours/week)

Either position is initially available for 6 months starting 15th June 2012, and will be extended for up to 3 years following satisfactory performance during this trial period.

Variation in shell pigmentation patterns of the common garden snail Cepaea nemoralis have long served as a model for population geneticists, however very little is known about the molecular mechanisms that generate this morphological diversity. Positions are available within the research group headed by Daniel Jackson to identify and characterise the molecular basis of these mechanisms.

These positions require individuals with strong molecular biology skills and familiarity with the analysis of large computational datasets such as RNA-Seq. Lab skills such as RACE-PCR, whole mount in situ hybridization, micro-injection and familiarity with some bioinformatic techniques are highly desirable.

Candidates for the post-doctoral position should hold a doctorate in evolution, cell biology, developmental biology, molecular biology, or a related field. Candidates for the doctoral position should hold an excellent first degree in one of the same fields. In addition to their academic qualifications, candidates should have excellent communication and team-working skills, be committed to the topic and to working in a dedicated, interdisciplinary research environment. The working language of the group is English, and applicants from abroad are encouraged to apply.

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

All applications should be made in English, and must include the following 3 items (incomplete applications will not be considered):

1. A full academic CV including any published or unpublished academic work. 2. A 1-2 page letter outlining the candidate's research interests and motivation for applying to this position. 3. Letters of reference and the contact details of 2-3 referees (ideally previous supervisors).

Submit your application or any informal enquiries directly to djackso"at"uni-goettingen.de

The application deadline is May 15, 2012.

For more information about the Jackson group see http://www.uni-goettingen.de/en/102705.html "Jackson, Daniel" <djackso@gwdg.de>

UIdaho GeneticPopMonitoring

PhD Graduate Project Opportunity

University of Idaho

We are currently recruiting a highly motivated PhD student to begin in the summer of 2012 in the Fish and Wildlife Department at the University of Idaho. The project is fully funded by the U.S. Department of Defense and will design and implement monitoring programs for Sonoran pronghorn and coyotes in southern Arizona based on combining non-invasive genetic sampling with capture-recapture modeling. The project will involve developing a spatio-temporal sampling design for collection of fecal DNA, field sampling, laboratory genetic analyses, and mark-recapture modeling. Beyond this, the project offers the opportunity to develop other research topics including, but not limited to, the study of predator prey dynamics, metapopulation dynamics, and population viability. The project is a collaborative effort with U.S. Department of Defense, USFWS, as well as state and university biologists. Graduate stipend is ~$20K/year and will also include payment of tuition and fees.

We are seeking applicants who have obtained a Master^{1}s degree in wildlife sciences, natural resources, conservation biology or a related field. Applicants should have the ability to develop independent research avenues, have strong quantitative skills and have a demonstrated ability to publish research findings. Because some fieldwork will occur on U.S. military installations, applicants must be U.S. citizens.

Interested applicants should send CV/resume, cover letter/statement of purpose, transcripts, GRE scores plus names and contact info for three references. Please note that we do not need official transcripts and GRE scores at this stage. If you are selected to join our research group, then we will ask you to send all official documents and 3 letters of recommendation to the University of Idaho graduate school applications office. Electronic (email) submission of applications is encouraged (jhorne@uidaho.edu) but mail is also fine. Review of applications will begin April 23, 2012 and continue until the position is filled. If you previously applied for a similar position in Dec2011/Jan 2012, your application has been retained and will still be considered.

For more information contact Drs. Lisette Waits (lwaits@uidaho.edu) or Jon Horne (jhorne@uidaho.edu)

Lisette Waits, PHD Professor Fish and Wildlife Resources Center for Research on Invasive Species and Small Populations Laboratory for Conservation and Ecological Genetics University of Idaho PO Box 441136 Moscow, ID 83844-1136 Phone: (208) 885 7823 Fax: (208) 885 9080 lwaits@uidaho.edu http://www.uidaho.edu/cnr/fishwild/lisettewaits http://www.cnr.uidaho.edu/crissp http://www.cnr.uidaho.edu/lecg/ http://www.cals.uidaho.edu/igert2/ Lisette Waits <lwaits@uidaho.edu>

ULyon GenomeEvolution

Proposition for a Ph-D subject - LBBE, University of Lyon 1, France

Title : Models of gene relationships

Laboratory: UMR CNRS 5558 “Biométrie et Biologie Evolutive” (LBBE), University of Lyon, Villeurbanne, France Scope: Computational Biology - Bioinformatics - Genomics - Molecular evolution

Supervisors: Eric TANNIER (INRIA) eric.tannier@inria.fr Laurent GUEGUEN (University of Lyon 1) laurent.gueguen@univ-lyon1.fr

Funding: Three-year grant from the “investissement d’avenir” programme, project ANCESTROME

The selected candidate will work in the LBBE lab, which offers a highly stimulating scientific environment. It is located in Lyon, which is a beautiful, history rich, lively city. The PhD student will interact with the molecular evolution team, and be part of the ancestrome project, involving also the ENS Paris, Institut Pasteur, and ISEM in Montpellier.

Ph-D subject:

This subject aims at studying genome evolution, where a genome is not only seen as a set of independent genes, but also a structure, a functionning, a complex set of interactions within an environment.

At many evolutionary scales (from recent evolution to the origin of life), and for many living group (mammals, plants, bacteria, as well as protists or yeasts), we propose to establish the methodological bases for reconstructing the genomes of extinct species, integrating a wide range of data from extant ones, such as proximity between genes, protein interactions, metabolic capacities, gene expression, regulations, or life history traits of organisms, like longevity for animals, optimal growth temperature for bacteria.

In the LBBE lab, we have developped methods to simultaneously reconstruct species and gene histories integrating sequence evolution, gene birth, duplication, transfer and loss. These methods give a first hint at the gene content of ancestral species, but they do not give information about the relationships between these genes. Moreover, they assume every gene evolves independently from each other, while in reality the set of genes is an evolving graph, because they are physically linked by they organization on chromosomes, or because they are linked inside a functional network.

The selected candidate will have to explore the mathematical and computational problems for detecting and explicitely modeling the evolution of these relationships. Then, the models will be added to the models of gene evolution in order to build gene and species histories, integrating information from the evolving graphs.

All methods will be integrated in the Bio++ library, which will help the integrative project and ensure longevity of the codes. For parallel implementations, it will be possible to use high perpormance computing ressources, owned by the lab or borrowed to national structures.

The models and algorithms will be applied to biological data from all kingdoms of the living.

Requirements :

The ideal candidate has a good knowledge of molecular evolution, and solid bases in algorithmics and probability. She/he is familiar with bioinformatics and phylogenetic concepts. Last she/he is autonomous in C++ programming.

Eric Tannier <Eric.Tannier@inria.fr>

UMelbourne AncientDNA

PhD position in Ancient DNA

The department of Anatomy at The University of Melbourne and the Australian Centre for Ancient DNA (ACAD) at the University of Adelaide invite applications for a PhD position in ancient DNA. The project will examine the genetic diversity of ancient human populations from the region of Samtavro and environs in the Republic of Georgia (3500 BC V 600 AD), as part of an ongoing research project on the archaeology of the Central Caucasus funded by the Australian Research Council (DP120103142). Classic and new generation DNA sequencing techniques and SNP genotyping will be used to study familial relationships, migration and admixture.

The PhD candidate will have a strong background in molecular biology and bioinformatics, with previous studies in biochemistry, skeletal biology, physical anthropology, archaeology, and palaeontology. The position will be based at Melbourne University with an extended research stint at ACAD. Funding for the position will be through a competitive PhD scholarship: Australian Postgraduate Award (APA) for local students, International Postgraduate Research Scholarship (IPRS) or Melbourne International Research Scholarship (MIRS) for international students (for details see http://cms.service.unimelb.edu.au/-scholarship/pgrad). To be competitive for the scholarship the student will have a strong academic record and evidence of research engagement through conference presentations and publications.

For expressions of interest please contact:

Dr. Varsha Pilbrow

Department of Anatomy and Neuroscience Medicine, Dentistry and Health Sciences Faculty University of Melbourne Parkville, VIC 3010, Australia

Telephone: +61 3 8344 5775 Fascimile: +61 3 9035 8837

Email: vpilbrow@unimelb.edu.au

and/or

Dr. Wolfgang Haak

Australian Centre for Ancient DNA School of Earth & Environmental Sciences Darling Building The University of Adelaide SA 5005, Australia

Telephone: +61 8 8303 3952 Facsimile: +61 8 8303 4364

Wolfgang Haak <wolfgang.haak@adelaide.edu.au>

UNeuchatel EvolutionaryEcology Sparrows

PhD Position in evolutionary ecology, University of NeuchÃtel, Switzerland

A fully-funded 3-year PhD position is available in Fabrice Helfenstein's lab at the University of NeuchÃtel, Switzerland, to work on the causes and consequences of oxidative stress in avian semen. The position and research project are funded by the Swiss National Science Foundation.

Oxidative stress is pervasive and represents a major selective pressure throughout the animal kingdom. In particular, vertebrate spermatozoa are very susceptible to oxidative stress, which may affect sperm performance and male fertility. Oxidative processes are thus hypothesised to have a profound impact on the development of male reproductive strategies and antioxidant allocation strategies in species where males face sperm competition, the circumstance where sperm of two or more males compete to fertilise the same batch of eggs. This project will test whether antioxidant allocation strategies underlie the development of male reproductive tactics in relation to social status as predicted by sperm competition models. This goal will be achieved using a combination of field observations, field experiments and aviary experiments on house sparrows Passer domesticus.

The ideal candidate is highly motivated and creative with a keen interest in evolutionary questions. He/she shows a capacity to work both independently and as a team member and has excellent writing and communication skills in English. She/he has a background in evolutionary biology, behavioural ecology and/or ecophysiology. Previous experience with bird handling, lab work, experimental design and/or statistics is not essential but desirable. A MSc (or equivalent) in Biology is required. The successful applicant will be based at the Institute of Biology, University of NeuchÃtel. This post offers opportunities to collaborate and interact with researchers working in related and complementary fields (http://www2.unine.ch/biol/page-7860_en.html). Our research groups are international and our working language is English. Knowledge of French is useful, but not essential. NeuchÃtel is an attractive city, situated by a beautiful lake at the foot of the Jura mountains and facing the Berner Oberland mountains. The city provides plenty of opportunities for cultural activities and sports and offers a high quality of life. Its excellent public transports make it easy to leave the city and head to the mountains for outdoor activities such as hiking, climbing or skiing.

Starting date: October 1, 2012.

Application requirements: Applications should include 1) a 1-2 page cover letter outlining motivations, research interests and relevant experience, 2) a CV with list of publications (if any), 3) copies of academic qualiï, 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-ïto fabrice.helfenstein@unine.ch Applications received before July 31, 2012, will be given full consideration. For more information, please do not hesitate to contact me!

Fabrice Helfenstein, Assistant Professor SNF Please note that Fabrice Helfenstein is currently based at the University of Berne, but, from september 1, 2012, will be based at the Institute of Biology, University of NeuchÃtel, Emile-Argand 11, CH-2000 NeuchÃtel, Switzerland. Phone: +41 (0)79 427 44 24. Email: fabrice.helfenstein@unine.ch Webpage: http://www.iee.unibe.ch/content/staff/helfenst/index_eng.html fabrice.helfenstein@free.fr

UNeuchatel Evolution Ecology Parasites

PhD Position in evolutionary ecology of parasites, University of Neuchâtel, Switzerland

A PhD position funded by the Swiss National Science Foundation (for three years) is available for research on the ecology and evolution of Lyme disease. This tick-borne disease is caused by several different bacterial species that belong to the Borrelia burgdorferi sensu lato complex. In Europe, certain Borrelia species appear to be specific for either bird or mammalian hosts. This host-specificity of the bacteria is at odds with the presumed generalist feeding habits of the tick vector, Ixodes ricinus. The proposed thesis topic is this potential tick-pathogen conflict over host choice.

Job requirements: The position requires an independent, highly motivated, enthusiastic, and scientifically curious individual with a background in ecology, evolutionary biology, immunology or related fields. Molecular techniques, field experience, and statistical data analysis skills are all highly useful. The applicant must have a Master's degree. The position requires some teaching of undergraduate biology labs.

Neuchatel is located in the French part of Switzerland and is an attractive city with a high quality of life. The city is located on the shore of Lake Neuchatel with the Jura Mountains to the North and a view of the Bernese Alps to the South. For outdoors enthusiasts, this is an excellent area for outdoor activities such as hiking, climbing or skiing.

Start data: The position is available as early as July 1, 2012. Starting dates are flexible.

Application requirements: Formal applications should include: a 1-2 page cover letter (in English) indicating research interests, your CV, and two letters of reference. Application deadline is May 31, 2012. Applications and informal enquiries can be submitted by email to: maarten.voordouw@unine.ch

Université de Neuchâtel UniMail Institut de Biologie Parasitologie Rue Emile-Argand 11 CH-2000 Neuchâtel

0041 32 718 3114 (outside Switzerland) 032 718 3114 (inside Switzerland)

mjvoordouw@gmail.com

UNeuchatel Protist diversity

PhD position in protistology

A PhD position is available at the Laboratory of Soil Biology, Institute of Biology, University of Neuchâtel, starting in September 2012 (or before, earliest possible date: June 1st).

The successful candidate should have a diploma or M.Sc degree in biology. We are looking for a highly motivated student with a strong background in natural history and classical protistology (i.e. cultures, microscopy) and interest for molecular methods.

The position involves teaching basic protistology and soil biology (protistology part) at the undergraduate and graduate levels. This is an institutionally funded teaching assistant position and it is not linked to a specific research project. Good communication skills in French and English constitute an advantage (teaching is in French and the student will be expected to master this language sufficiently well to teach by the 2nd year).

Interested candidates are requested to send by e-mail to edward.mitchell@unine.ch their cv, motivation letter, list of 2-3 reference persons, a description of own research experience and visions (2 pages) and a short personal research proposal (2 pages) on a topic they would be interested in developing, within the general topics protist diversity, ecology and evolution. Evaluation of applications will start on April 25th.

Potential applicants are encouraged to visit the lab website http://www2.unine.ch/biolsol/page-6096.html to learn about on-going projects and research interests of the lab and to contact Enrique Lara enrique.lara@unine.ch and Edward Mitchell for further information.

edward.mitchell@unine.ch

UOslo MicrobialDiversity

A 4-year PhD position in microbial biodiversity is available at the Department of Biology, University of Oslo, Norway. The fellowship is for a period of up to 4 years, with 25 % compulsory work. Starting date no later than 1 August, 2012.

Lakes are ideal systems for testing predictions and responses related to biodiversity since they are units with well-defined boundaries, as inverted islands isolated by land. The project will involve analyzing diversity of planktonic prokaryotes and protists in environmental DNA samples collected in a survey of lakes in southern Norway and Sweden. The selected PhD candidate will conduct high throughput DNA sequencing analyses of the samples to explore the diversity and community composition patterns of the planktonic prokaryotes and protists.

For more information about the position and application process see http://uio.easycruit.com/vacancy/-711935/64322?iso=no havard.kauserud@bio.uio.no

USheffield OptimalBehaviour

Dear colleagues,

please bring this fully-funded PhD opportunity for UK/EU students to the attention of potentially interested parties.

Best wishes, James Marshall

Optimal Foraging Theory for Root Proliferation in Heterogeneous Soils

This project will break new ground in developing and applying optimal foraging theory, developed to describe the behavior of animals, to the experimental study of plant root growth. The candidate will develop and test optimal foraging theories using a combination of mathematical models and laboratory experiments (using isotope labeling studies in pots and microcosms). The candidate will conduct non-destructive imaging experiments using X-ray or neutron imaging of roots; however no prior experience necessary of these is necessary. The ideal candidate will have a first degree in a mathematical discipline (mathematics, physics, computer science) with an interest in developing experimental skills, or an experimental life sciences background with an interest in acquiring mathematical modelling skills.

For more details, including how to apply, please visit: http://shine.sheffield.ac.uk/doctoral-training/-project2/ James A. R. Marshall Behavioural and Evolutionary Theory Lab Department of Computer Science and Kroto Research Institute University of Sheffield http://staffwww.dcs.shef.ac.uk/people/J.Marshall/ James Marshall <James.Marshall@sheffield.ac.uk>

UWesternSydney Biodiversity

HAWKESBURY INSTITUTE FOR THE ENVIRONMENT

University of Western Sydney

The Hawkesbury Institute for the Environment, UWS, is seeking excellent doctoral candidates to undertake research within the areas of: - ecology, biodiversity, and sustainability of terrestrial ecosystems, particularly forests, savannas and grasslands - soil science and molecular microbial ecology including plant- microbe interactions, soil biogeochemistry and ecological genomics - plant-animal and plant-insect interactions, including animal ecology, insect herbivores and their multi-trophic interactions - ecology, physiology, biochemistry and genetics underpinning adaptation of plants to a changing environment.

Approaches could include laboratory, controlled environment and field-based experiments, genomics, observational studies, and computer modelling and simulation. During the course of the project, students will work with internationally recognised scientists. There is a possibility of the successful candidate spending a period of time at collaborating research institutions overseas to further the scope of their research training.

CRITERIA The successful applicant should: demonstrate excellent academic performance related to the research areas listed above, hold qualifications and experience equal to an Australian First Class Bachelor Honours degree, be highly motivated to undertake further study at an advanced level. International applicants must also demonstrate a high level of proficiency in the English language. Please refer to the University^{1}s web site for information about English language requirements at www.uws.edu.au/international/admissions/-english_language_requirement

WHAT DOES THE SCHOLARSHIP PROVIDE? Tax-free stipend of AU$33,728 per annum and a funded place in the doctoral degree. International candidates will receive a fee waiver. Funding is also available for project costs.

NEED MORE INFORMATION? Applicants are asked to discuss their research aspirations and eligibility with potential supervisors in the Hawkesbury Institute www.uws.edu.au/hie/people

HOW TO APPLY Submit an application form, a research proposal developed with your proposed supervisor, and CV by the closing date.

Details of what to include in your research proposal can be found at www.uws.edu.au/research/-future_research_students/ apply The application form can be downloaded from the web: www.uws.edu.au/-research/scholarships

APPLICATIONS CLOSE: 25 MAY 2012

Dr Markus Riegler Hawkesbury Institute for the Environment University of Western Sydney m.riegler@uws.edu.au http://www.uws.edu.au/hie/-markusriegler

M.Riegler@uws.edu.au

Zurich EvolutionaryGenetics SnowVoles

3-Year PhD position in the group of Dr. Erik Postma at the University of Zurich, Switzerland

Individual-level causes and population-level consequences of variation in fitness in an alpine rodent

This PhD project, funded by the Swiss National Science Foundation, combines ideas and techniques from the fields of population and quantitative genetics, evolutionary biology and population ecology, and applies them to long-term individual-based data for an isolated snow vole population (Chionomys nivalis), located in the Swiss Alps. In particular, we are interested in which ecological and evolutionary processes are responsible for the generation and maintenance of variation in body size, reproductive success and lifespan, and how this variation shapes population dynamics.

We are seeking somebody who is independent, creative and highly motivated, with an interest in (quantitative and population) genetics and (evolutionary and population) ecology. Our ideal candidate has no fear of equations and statistics, but is not afraid to get his or her hands dirty in the lab and the field either. Although experience with programming in R is not essential, the willingness to learn this is crucial. Fieldwork takes place in rough terrain and is physically demanding. The views are superb, however. Previous experience handling small mammals is not required.

We are working together closely with the group of Prof. Lukas Keller, as well as several other groups within our institute (www.ieu.uzh.ch). This offers a stimulating and social working environment and excellent facilities (including a well-equipped molecular lab). The student will participate in the PhD program in evolutionary biology of the University of Zurich.

Although the preferred starting date is June 1 2012, the actual starting date is negotiable.

Zurich 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 its central location and excellent public transport system, it is extremely easy to get out of the city and head for the mountains.

Applicants should have an MSc (or equivalent) in a relevant field. Applications should include 1) a cover letter, including a brief description of what you have to offer to the project and our group, and what you hope to get back in return, 2) a detailed curriculum vitae, 3) the contact details of two references and 4) a 1-page summary of your MSc or undergraduate work. This should be sent as a single .pdf file to erik.postma@ieu.uzh.ch

Review of applications starts on 23 April 2012, but candidates are considered until the position is filled.

If you have got any questions, don't hesitate to contact Erik Postma (erik.postma@ieu.uzh.ch), or visit www.erikpostma.net . – Erik Postma

Institute of Evolutionary Biology and Environmental Studies University of Zürich-Irchel Winterthurerstrasse 190 CH-8057 Zürich Switzerland

Phone: +41 (0)44 635 49 73 Fax: +41 (0)44 635 68 18 Skype: erik_postma

website: www.erikpostma.net erik.postma@ieu.uzh.ch

Jobs

AarhusU FishBreeding

Academic Employee in the field of fish breeding

Center for Quantitative Genetics and Genomics (QGG), Aarhus University, seeks an academic employee to join the project "Breeding in Danish Aquaculture". The aim of the project is to strengthen the competitiveness of Danish Aquaculture via improved selection and breeding programs. The project, which is a cooperation between Aarhus University, Danish Aquaculture and Danish fish breeders, is funded by the Ministry of Food, Agriculture and Fisheries and the European commission. The project period is from April 2012 to December 2013.

The appointment will terminate in December 2013, although an extension may be possible.

An immediate start is desirable. The primary workplace will be Research Center Foulum.

The main work tasks will be:

- Establish schemes for collection and recording of data at the fish farms - Preparation and follow up on individual breeding plans in cooperation with the fish farms - Predict expected genetic gain - Manage the routinely breeding value estimation - Advice and communicate results within the group of participants

Some travelling will be required in connection with the visits and collection of data at the fish farms.

The candidate possesses the following qualifications and competences:

- A M.Sc. degree in Life Science (Aquaculture, Agriculture or Bioscience) - Documented knowledge in quantitative genetics and/or population genetics

* An interest in practical field work, as a large part of the work will be on the participating farms * Preferably practical experiences with one or more of the tasks * Good communication skills * The ability to work independent and structured

All applications must be made online and received by 6. May 2012. For more information on the position and how to apply, please visit http://www.au.dk/en/-about/job/nat/academicpositions/ .

Kind regards Louise Dybdahl Pedersen Co-ordinator

Dept. of Molecular Biology and Genetics Aarhus University Blichers Allé 20, Postboks 50 DK-8830 Tjele

Tel.: +45 8715 7779 Mobile: +45 5135 4543 Email: Louise.DybdahlPedersen@agrsci.dk

Tel.: +45 8715 6000 Web: www.agrsci.au.dk Louise.DybdahlPedersen@agrsci.dk

CharlesDarwinFoundation ProgramDirector

Dear Friends & Colleagues,

the Charles Darwin Foundation for the Galapagos Islands continues to build a team for transforming and revitalizing the organisation. I am looking for a Program Director to join me in my work.

The Program Director will be: - Primarily responsible for managing and developing the portfolio of scientific project of the Charles Darwin Research Station in the Galapagos Islands, and the teams of scientists that are behind these projects. - Work closely with the organization's Board and Program Committee to ensure the organization sticks to its medium and longer-term science priorities. - Work and interact with local public institutions (Galapagos National Park, Government Council, Ministries).

Applicants need to have a PhD and be fluent in Spanish. For more details, please see the attached terms of reference. These were written with very ambitious requirements, e.g. we even included know-how and involvement in managing the operations / administration of the research station. These ToR are in many ways a wish-list, and I have an open mind about applicants (being myself someone who does not fit the conventional profile for my position). One of the key tasks for the Program Director will be to help make this organization be relevant and impactful.

We are seeking applications by April 15th, although applications that come in a few days later will still be considered by the small committee that we have formed to select the final candidate (please check with me for exact dates). Salary and other details are negotiable. The position should be filled as soon as possible, although we do understand that international applicants need some extra lead time for relocating. It is important that the applicant comes with the idea in mind to stay in this position for three years or more, as we need continuity and stability.

Please do pass on this email to anyone who you think might be interest in this position. When advertising the position for my Executive PA I experienced the power of our Foundation's network, where forwarded emails lead to high calibre candidates from around the world applying for the job. I am also happy for anyone who would like to post this on Facebook and other networking sites.

The Charles Darwin Foundation for the Galapagos Islands was set up in 1959, following a scientific expedition of IUCN, UNESCO and the Government of Ecuador. In 1964, the Charles Darwin Research Station was inaugurated and it has since then seen several generations of scientists, scholarship students, volunteers and employees pass through its doors. Our mission is to provide science for the conservation of the Galapagos Islands, an archipelago that to this day remains the world's most pristine tropical archipelago with World Natural Heritage Site status. The Galapagos Islands have appr. 25,000 residents. Ecuador is a stunning country and it is itself undergoing a transformation. There could probably not be a more exciting time to join our efforts out here in the middle of the Pacific Ocean.

Do not hesitate to email me if you have any specific questions.

Best wishes Swen Lorenz CEO, Charles Darwin Foundation swen.lorenz@fcdarwin.org.ec

pwimberger@pugetsound.edu

ETH Zurich OMA ProjectLeader

OMA Project Leader

The group of Prof. Gaston Gonnet (Computer Science Department, ETH Zurich and Swiss Institute of Bioinformatics) has an open position for an experienced and motivated project leader for the OMA project. OMA is a leading resource to identify orthologs among >1000 complete genomes (see refs. below). The successful applicant will manage operational and tactical aspects of the project, and contribute its software development.

Job requirement:

- management (50% of time) -> a) coordinate with services within SIB and worldwide; b) seek additional funding; c) oversee operations, supervise students/interns/future collaborators; d) organise outreach activities with users, etc..

- software developer (50% of time) -> a) maintain and develop OMA pipeline (computations) b) maintain and develop interfaces (web, raw data, DAS, etc)

The position is ideally suited for a postdoc interested to steer his/her career towards project management and a career in either the industry or bioinformatics infrastructure.

Profile requirement:

- Several years of experience in computational biology (ideally PhD) - Strong writing skills - Technical proficiency (SQL database, programming, web technologies) - Leadership skills - Prior experience with bioinformatics databases and/or services - Good command of English

Salary and conditions:

CHF ~90,000 per annum (EUR ~75,000, GBP ~60,000). Contracts will be 12- month renewable, with a 3-month probatory period.

Job start date is 1st July 2012, and job location is ETH Zurich, Universitaetstr. 6, 8092 Zurich, Switzerland

How to apply:

Send a single PDF with cover letter, CV, and the contact details of 3 references tomadeleine.bernard@inf.ethz.ch. To ensure full consideration, apply by May 15th, 2012.

More info on OMA:

http://nar.oxfordjournals.org/content/39/suppl_1/D289.full http://www.omabrowser.org dessimoz@ebi.ac.uk

FloridaStateU UndergradSummer

Undergraduates interested in gaining research experience in evolutionary biology are invited to apply for a summer National Science Foundation Research Experience for Undergraduates (REU) position available this summer in the lab of Emily Moriarty Lemmon at Florida State University. The summer REU student will help analyze frog vocalization data to test whether Upland Chorus Frog (Pseudacris feriarum) calls change throughout the range due to differences in habitat characteristics. The REU student will learn to use sound analysis software and gain experience in the statistical analysis of vocalization data. The REU student will also be introduced to molecular genetic techniques for working with DNA molecules and bioinformatic techniques for analyzing sequence data. Candidates should have interest in frog vocalizations and a keen interest to learn methods for analyzing sound data. Compensation will be $400 per week (corresponding to $10.00/hr; for approximately 8 hours/day ; 5 days/week) for a total of 8 weeks and will include a $1,200 stipend for housing and $2,100 for subsistence during the 8 week period. For students planning on graduate school, this experience would look great on your resume.

To apply for this position, please contact Dr. John Malone at jmalone@bio.fsu.edu and include a CV along with contact information for three references.

jmalone@bio.fsu.edu

InstForestGenetics Germany Bioinformatics

Bioinformatician/Computational Biologist

The Institute of Forest Genetics at the Johann Heinrich von Thünen-Institute, Federal Research Institute for Rural Areas, Forestry and Fisheries has an opening for a research scientist to develop the institute's data infrastructure. This is a temporary position fixed for two years.

The Institute of Forest Genetics has comprehensive collections of data that developed over time. These represent an important resource for investigations into current questions of forest conservation and management. Research at the institute focuses on the conservation of biodiversity in forest ecosystems, e. g. implementing national and international wood tracking and tree species identification systems, the survival and adaptation of long-lived tree species in a rapidly changing environment, as well as, the selection and breeding of fast growing woody plant lineages.

The successful candidate is expected to develop the concept of an extensible data infrastructure for the institute in close cooperation with the scientists of the four research areas, to implement the system and to coordinate the process. She/He will be part of an active team of scientists and IT professionals from across the Thünen-Center working towards the institutions research focus of designing and building an institution-wide data infrastructure.

Job responsibilities * Development of the concept of a database system that consolidates data from research in evolutionary biology, genomics and tree breeding. * Administration of the central hard- and software under Linux. * Successive programming of the database system and transfer of existing databases and data into the new structure, standardizing of data. * Definition and implementation of data exchange formats, implementation of web-based user interfaces, development of workflows for biostatistical analyses. * Analyses of existing datasets and scientific publications in cooperation with scientists from the institute's research areas.

Required qualifications The successful candidate should have a Master degree in bioinformatics or informatics and an understanding of and interest in applications in biology, genomics or forestry; or a degree in the life- or forest sciences with a strong background in biostatistics and computer programming. Extensive experience in database design and programming (SQL) is required, as well as proficient scripting skills, in e.g. Perl, Python, PHP, R. Knowledge of current ontologies in the areas of interest and experience with the analysis of geo-referenced and genomic datasets are preferred. Knowledge of the German language would be advantageous, but is not a necessary requirement. The institute is multilingual (German, French, English).

The full-time position is available starting July 1, 2012. Salary and benefits are according to a German public service position at pay scale TVÖD E13.

The Thünen-Institute promotes the professional equality of women and men. Women are therefore strongly encouraged to apply. Equally qualified severely handicapped applicants will be given preference. A minimum of physical aptitude is required.

For more information about the position, please contact Dr. Jutta Buschbom (phone: +49 (0)4102 696-147, email: jutta.buschbom@vti.bund.de). If you would like to learn more about the Institute of Forest Genetics and the Thünen Institute, visit our website at http://www.vti.bund.de/en/startseite/-institutes/forest-genetics.html . To apply, please submit your application by mail or preferably email with the usual supporting documentation, as well as, the names and contact information of three references until May 27, 2012 to

Johann Heinrich von Thuenen-Institute Institute of Forest Genetics Dr. Jutta Buschbom Sieker Landstrasse 2, 22927 Grosshansdorf Germany

jutta.buschbom@vti.bund.de

Norway FishBreeding

Vacancy Scientists - Aquaculture Genetics and Breeding Nofima is an applied research institute working in research and development for the aquaculture, fisheries and food industry in Norway. Nofima was established on 1 January 2008, and has about 440 employees. The institute's total turnover in 2011 was about NOK 500 million. The main office is located in Tromsø in northern Norway, while the research divisions are located in six places: Ås, Stavanger, Bergen, Sunndalsøra, Averøy and Tromsø. Nofima's research within aquaculture genetics and breeding has been the basis for development of modern breeding programs for important aquaculture species like Atlantic salmon, rainbow trout, cod, tilapia, carps and warm water shrimps. Nofima's department for Aquaculture Genetics and Breeding, which has an overall goal to contribute with R&D to efficient and sustainable breeding programs for aquaculture species, has about 15 researchers with a very good track record of scientific publication and industrial implementation of research results (lately documented in international institute evaluations). We are now seeking scientists with strong skills in the following areas: Quantitative genetics and/or analyses of molecular genetic data (bioinformatics including next generation sequence data). Good skills in computer programming, including simulations and modelling is also preferred.

The position requires a PhD, preferably within animal science, and experience within aquaculture would be an advantage, but not necessary. Young talented PhD's as well as senior scientists with a good publication record are encouraged to apply. The successful candidates will participate in the whole research process including generating research ideas, writing research proposals, project work and management, publishing results in peer-reviewed journals and communicate the results to the industry. The positions will therefore require good communication and cooperation skills, high working capacity and a strong motivation to develop and explore new ideas and projects. Position type: Research scientist Extent: Full-time Work hours: Day Application deadline: April 26, 2012 Location: Ås (30 km south of Oslo)

Contact: Olai Einen Phone: +47 458 66 151

For more information: http://www.nofima.no/en/-stilling/724303 celeste.jacq@nofima.no

---

RanchoSantaAna SeedConservationManager

Seed Conservation Program Manager - Rancho Santa Ana Botanic Garden

http://www.rsabg.org/employment/726-seed-conservation-program-manager Position Title: Seed Conservation Program Manager Reports To: Director of Horticulture Hours: Full Time, 40 Hours Week, Exempt Position

Position Summary

The Seed Conservation Program Manager serves as curator of the seed collections in support of the organizations programs in horticulture, conservation, and research; is responsible for coordinating and directing Seed Conservation Program daily operations; prepares the program operating budget; manages the Garden's Index Seminum Program and is responsible for the distribution of seed as well as plant tissue samples from the Living Collection; develops, coordinates, and/or conducts seed-related activities and contractual agreements that enhance the organization's role and contribution in conservation, horticulture, and public education; and fosters mutually beneficial cooperative relationships with other botanic institutions, government regulatory and land management agencies, conservation and local community organizations, and private industry.

Duties and Responsibilities

* Direct, coordinate, and accomplish the cleaning, testing, packaging and storage of all seed collections in accordance with current best practices. Order necessary supplies and schedule necessary repairs and/or maintenance of Seed Bank equipment. In conjunction with supervisor, prepare and adhere to annual budget. * Maintain BG-BASE computer data records and files for all seed accessions. With the assistance of the Plant Records Manager and the Garden's Webmaster, produce annual institutional seed list and publish the Index Seminum on the RSABG webpage. * Process requests and distribute seed and tissue samples from the Garden's Seed Bank and Living Collection. * Advance a connection between the Seed Conservation Program and retail nursery operations, locating and obtaining wild collected local genotype seed for use in production of retail plants. * Train, direct, and oversee organizational volunteers, interns, and students in accomplishing Seed Conservation Program activities. * Initiate projects and activities that maintain and/or improve the quality and usefulness of the seed collection and that increase current understanding of seed processing, storage, and germination techniques. Provide advice and assistance on seed-related activities as required by RSABG staff and students. * Prepare written proposals and contracts for seed collection, storage, and consulting projects. Is responsible for scheduling, budgeting, monitoring and report writing as required for the implementation of contract agreements. * Participates in or leads seed collecting efforts for the living collection, in collaboration with the curator of the living collection and/or Director of Horticulture. * Obtain seed from the living collection for use in propagation for plant sales. * Present talks, classes, and tours of the Seed Bank facilities. * Work cooperatively with other RSABG program managers. * Participate in other appropriate RSABG activities as required.

Qualifications

* Bachelors degree in botany, biology, horticulture, or related science and/or related practical work experience. * Masters degree in seed biology, physiology or ecology preferred. * Working knowledge of the California flora, basic taxonomic principles, characteristics of major plant families, and field work experience desirable. * Ability to type and basic computer skills essential. * Good communication skills and willingness to work cooperatively and collaboratively with other department staff, volunteers, students and associates outside the institution. * Physical stamina and agility to conduct field work. * Ability to effectively train, su-

pervise, motivate, and coordinate the work of students, volunteers, and interns. * Must possess a California State Driver's License.

"Linda M. Prince" <linda.prince@cgu.edu>

RiceU EvolutionaryBiology

INSTRUCTOR IN ECOLOGY AND EVOLUTIONARY BIOLOGY. The Ecology and Evolutionary Biology Department of Rice University (http://eeb.rice.edu/) anticipates hiring an instructor for a non-tenure track faculty position to start in the fall semester 2012. The responsibilities of this position include teaching (lecture and lab courses), assisting with undergraduate advising, and coordinating additional educational activities. There are also opportunities for research particularly involving undergraduates. A PhD in ecology, evolution or a related field is required. An application (curriculum vitae and statement of teaching and research interests) and three letters of recommendation should be submitted via e-mail to Diane Hatton, rdh@rice.edu. Please write "EEB instructor position" in the subject line. Application review will begin May 10, 2012 and continue until the position is filled. A full description of the position can be found at http://eeb.rice.edu/jobs.html. For further questions and informal inquiries please contact Dr. Michael Kohn hmkohn@rice.edu or Dr. Scott Solomon scott.solomon@rice.edu. Rice University is an Equal Opportunity / Affirmative Action Employer

Diane Hatton

Administrative Coordinator

Dept of Ecology and Evolutionary Biology

Rice University

Diane Hatton <rdh@rice.edu>

Smithsonian ResTech Invert

Please excuse the cross posting but we are hoping to get the word out to all people interested in invertebrate morphology.

We are hiring a new research technician in the Department of Invertebrate Zoology so if you know anyone looking for a great long-term technician position please pass this along and encourage serious applicants to contact me for further information. We are looking for someone with experience in at least two of the following areas:

invertebrate morphology invertebrate specimen handling and archiving macro-photography microscopy (high-end light microscopy, SEM, confocal, TEM, or automated slide scanning) histology (tissue prep, sectioning, staining, and imaging) databasing (cataloguing, MS Excel, bibliographic, general computer skills, either Mac or PC) Adobe Creative Suite (primarily Photoshop and Illustrator)

The opening is only until May 8, so time is short. It is a US federal position so only US citizens can apply - sorry.

Thank you for spreading the word, Karen

Karen Osborn osbornk@si.edu<mailto:osbornk@si.edu> Research Zoologist/Curator Department of Invertebrate Zoology Smithsonian National Museum of Natural History, MRC-163 P.O. Box 37012 Washington, DC 20013-7012 USA

Job Title:Museum Technician (Zoology) Agency:Smithsonian Institution Job Announcement Number:12R-JC-297552-DEU-NMNH SALARY RANGE: $34,075.00 to $44,293.00 / Per Year OPEN PERIOD: Tuesday, April 24, 2012 to Tuesday, May 08, 2012 SERIES & GRADE: GS-1016-05 POSITION INFORMATION: Full-Time, Permanent - Federal PROMOTION POTENTIAL: 07 DUTY LOCATIONS: 1 vacancy(s) in the following locations: Washington DC Metro Area, DC, US

WHO MAY BE CONSIDERED: This position is open to all U.S. Citizens or U.S. Nationals. JOB SUMMARY:

This position is located in the Department of Invertebrate Zoology, National Museum of Natural History. The employee provides support by performing such tasks as assisting with a broad spectrum of research projects and helping to maintain the zoology collection and associated records.

The Smithsonian Institution values and seeks a diverse workforce. Join us in "Inspiring Generations through Knowledge and Discovery."

KEY REQUIREMENTS

* Pass Pre-employment Background Investigation * May need to complete a Probationary Period * Maintain a Bank Account for Direct Deposit/Electronic Transfer * Males born after 12/31/59 must be regis-

tered with Selective Service. * Requires working at the Museum Support Center, Suitland, MD.

DUTIES: Back to top< http://www.usajobs.gov/-GetJob/ViewDetails/315042700#TopofPage >

* Handles and processes incoming specimen collections. Sorts, prepares labels, and applies appropriate preservation techniques for intended research (e.g., freezing, fixation, transfer through alcohol series, subsampling specific tissues for DNA studies, etc.). * Develops and maintains databases to support curatorial research. * Photographs specimens and processes images in support of curatorial research. * Prepares and images histological thin sections to support curatorial research.

QUALIFICATIONS REQUIRED: Back to top< http://www.usajobs.gov/GetJob/ViewDetails/-315042700#TopofPage >

Experience: One year of full-time experience at the GS-4 level that is close or similar to the work of this job. The experience includes activities such as as handling and processing invertebrate specimen collections in a museum setting or through college-level courses, and working with computer software applications in order to maintain collections data.

The experience should be related to the operation or management of a museum or similar collection of valuable objects. Examples of qualifying specialized experience include collections management, registration, cataloging, research, preservation, restoration, or conservation of collections of museum material, or other experience related to the position to be filled. Most positions require a particular subject-matter specialization, e.g., zoology.

Part-time and/or unpaid experience related to this position will be considered to determine the total number of years and months of experience. Be sure to note the number of paid or unpaid hours worked each week.

Or Education: 4 years above high school leading to a bachelor's degree with major study or 24 semester hours of course work in a related field.

Or a Combination: Education and experience may be combined to meet the basic qualifications. For a full explanation of this option please see the Qualification Standards< http://www.opm.gov/qualifications/-policy/ApplicationOfStds-05.asp >.

— / —

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

---

StockholmU EvolutionaryEthology

The Department of Zoology at Stockholm University has just opened a search for a Senior Lecturer / Associate Professor in Ethology

The position involves research, teaching and supervision in the field of ethology, construed as a study of animal behavior that integrates explanations involving the mechanisms of behavior with those based on its adaptive function. At the Department of Zoology, research is being pursued in ecology, ethology, functional morphology, population genetics and systematics and evolution. The spirit of research is collaborative, both within the department and internationally. The department has 45-50 researchers and 45-50 PhD students.

Informal enquiries can be made to Prof. Olof Leimar (olof.leimar@zoologi.su.se). Note that applications should be submitted through the Stockholm University website, where further details also are available:

http://www.su.se/english/about/vacancies/lecturers-researchers/senior-lecturer-in-ethology-1.84190 Closing Date: Monday 21 May 2012

Olof Leimar, Professor Department of Zoology Stockholm University SE-106 91 Stockholm Sweden

olof.leimar@zoologi.su.se http://www.zoologi.su.se/-research/leimar/ olof.leimar@zoologi.su.se

---

SungkyunkwanU EvolutionaryBiol

Faculty Position at Sungkyunkwan University, Seoul Korea

As a part of a strategic development in the area of Ecology, Evolution and Environmental Biology, the Department of Biological Sciences at Sungkyunkwan University invites applications for multiple faculty positions to start as early as September 1, 2012. The Department wishes to attract candidates with interests in the areas of 1) ecology and environmental biology who applies experimental, field, computation, and/or theoretical approaches to ecological research at relevant scales, 2) quantitative, population or evolutionary genetics or genomics, bioinformatics, systematics, and 3) cross-disciplinary fields such as, evolutionary ecology, evolutionary developmental biology, conservation and biodiversity science, biogeography, etc.

The successful candidate will demonstrate innovation in addressing fundamental questions at the core of ecology and/or evolution. We are seeking individuals whose research interests will focus on whole organisms. Appointment will be made at either tenure-track (Assistant and Associate) or Full Professor rank (with tenure). We especially encourage highly productive, distinguished junior or senior scholars from diverse ethnic backgrounds (either Korean or non Korean citizenship) who will provide leadership in establishing a program of national/international repute in ecology and evolutionary biology research at Sunkgkyunkwan University.

Interested applicants must contact Professor Jeong Ha Kim (jhkbio@skku.eduor jhkimbio@yahoo.co.kr; +82-31-290-5915), a Chair of Search Committee, and submit a CV and statements of research and teaching interests. Review of applications will begin after June 1, 2012 and continue until the positions are filled.

Dr. Seung-Chul Kim *Associate Professor Department of Biological Sciences Sungkyunkwan University 300 Cheoncheon-Dong, Jangan-Gu Suwon, Korea 440-746*

e-mail: sonchus2009@gmail.com or sonchus96@skku.edu or sonchus96@yahoo.com

Office tel: +82-031-299-4499 Lab tel: +82-031-299-4508

Fax: +82-031-290-7015

Skype: sonchus96

Seung-Chul Kim <sonchus2009@gmail.com>

Sweden ConservationGenetics

NordGen - Nordic Genetic Resource Center - is an institution under the Nordic Council of Ministers, working with conservation and sustainable use of genetic resources of farm animals, forest trees and agricultural plants. Our main objectives are to secure genetic diversity and thus, the biological basis for renewable resources, and to be in forefront at the international level both as a service and knowledge centre for the management of genetic resources of farm animals, forest trees and plants. NordGen is responsible for the Nordic Gene Bank of seed and administrates the Svalbard Global Seed Vault. NordGen has 25 persons employed and has its main office at Alnarp, Sweden, close to Malmoe. NordGen also has a smaller division at Ås, Norway. For more information, see www.nordgen.org NordGen is seeking a senior advisor for NordGen Farm Animals

NordGen offers an interesting position with variable and challenging work in conservation and sustainable management of farm animal genetic resources in the Nordic and international arena. NordGen is seeking a person with a strong interest in farm animal genetic resources, with higher academic education (MSc or PhD) in population genetics, conservation genetics, quantitative genetics and/or animal breeding or related disciplines. Working experience obtained from research and development, animal breeding organizations, conservation organisations, international processes and networking and/or public administration is appreciated. Strong English communication skills are required as well as knowledge of one of the Scandinavian languages.

Main responsibilities:

* Knowledge and capacity building within sustainable use and conservation of farm animal genetic resources in collaboration with universities, international organizations, conservation and breeding organizations. * Project development and initiation * Project participation, management and communication. * Contribution to the development of networks with Nordic and international stakeholders and promotion of current networks through workshops, seminars and meetings. * Participation in the information and communication tasks (presentations, publications) and production of information materials for NordGen's website including the Nordic-Baltic Farm Animal Breed Registry. * Acting as coordinator and secretary of NordGen Farm Animals project and working groups. * Contribution to meetings, seminars and the daily team-based work of NordGen Farm Animals and at NordGen's headquarters. The position requires some travelling.

NordGen offers:

* An exciting position in a professional and international working environment.

Employment contract according to the regulations of the Nordic Council of Ministers. The employment contract will be signed first for 4 years with the possibility for an additional 4 years.

* Salary according to individual agreement, other working conditions are given by the regulation of the employment agreements of the State of Sweden. * Possibilities

to develop personal competence.

The post is located at the Norwegian Forest and Landscape Institute, Ås, Norway. The number of employees of NordGen-Farm Animals is three persons. The senior advisor will report directly to Head of NordGen Farm Animals.

Information about the position can be obtained from Director Árni Bragason, +46738171215 or +4640536644 or Head of NordGen Farm Animals, Dr. Peer Berg, +45 8715 7576 or +45 2229 1226

Applications, including CV and references should be sent no later than May 2. 2012 to Nordic Genetic Resource Center, Financial Manager Eva Jorup Engström eva.jorup-engstrom@nordgen.org or to the mailing address: Eva Jorup-Engström, NordGen, P.O. Box 41, SE-23053 Alnarp, Sweden.

Peer Berg <Peer.Berg@agrsci.dk>

Sweden USA Bioinformatics

POSITION AVAILABLE AS PROGRAMMER/BIOINFORMATICIAN (TO BE FILLED AS SOON AS POSSIBLE)

TASKS You will participate in a research collaboration between the University of Gothenburg and Gothenburg Botanical Garden in Sweden (Alexandre Antonelli's lab: www.antonelli-lab.net) and the University of Arizona in the USA (Mike Sanderson's lab: http://loco.biosci.arizona.edu), with funding from the Swedish Research Council. Your role will be to further develop and adapt the PhyLoTa browser (http://www.phylota.net/) for producing large-scale, time-calibrated phylogenetic trees, which will be used in ongoing research on Neotropical biogeography. You will participate in setting up a pipeline to download, handle, and merge data from online databases containing DNA sequences, geo-references, fossils, bioclimatic variables, etc.

QUALIFICATIONS We expect you to have previous experience in bioinformatics, phylogenetics or genomics, and intimate knowledge of the computational methods and software used in the field. Experience in Perl and the Unix environment is essential; experience in other languages (such as Python and R) is an advantage. Previous experience with similar tasks is also advantageous. Part of the project will be carried out at the University of Arizona, Tucson (USA). You must therefore be fluent in English and have excellent communication skills. We will attach great importance to personal characteristics and independence in working, creativity and documented productivity.

STARTING DATE AND PLACEMENT The position will be filled as soon as possible. It is funded for 6 months and will be formally based at Gothenburg Botanical Garden.

INFORMATION AND QUESTIONS about the position may be obtained from Dr. Alexandre Antonelli, Scientific Curator at Gothenburg Botanical Garden and Assistant Professor at University of Gothenburg, by e-mail alexandre.antonelli@bioenv.gu.se or phone +46 703 989570.

APPLICATION with personal letter (ca. 1/2 page) and CV should be sent to alexandre.antonelli@bioenv.gu.se.

UNION REPRESENTATIVE for this position is Mats Havström, phone +46 702 775190

Dr. Alexandre Antonelli Assistant professor, Scientific curator http://antonelli-lab.net Gothenburg Botanical Garden Carl Skottsbergs gata 22A, 413 19 Göteborg, Sweden & Department of Biological and Environmental Sciences University of Gothenburg Carl Skottsbergs gata 22B, 413 19 Göteborg, Sweden

Mobile: + 46 (0) 703 989570

alexandre.antonelli@bioenv.gu.se

UEastAnglia MolecularEvolution

Lecturer/ Senior Lecturer/ Reader in Molecular Ecology - Ref: ATR1050

This post will add to our research strengths at UEA in evolution and ecology, and the post holder will join our vibrant Organisms and Environment Theme (http://www.uea.ac.uk/bio/bioresearch/eeb), where we address both pure and applied questions at varying levels from the ecosystem to the gene. We particularly seek applicants who are employing modern and emerging molecular techniques to answer important fundamental questions in ecology and evolution, at any level from the individual to the ecosystem.

This post is available from 1 September 2012 or as soon as possible thereafter.

Full details of the post along with further information about the University of East Anglia, the Schools of Study and the Faculty of Science, along with contact details for informal discussions are available at: www.uea.ac.uk/hr/jobs/< http://www.uea.ac.uk/hr/jobs/ >

Closing date for this post: 12 noon on Friday 4 May 2012 Interviews will take place during June and July 2012.

David S Richardson Reader in Molecular Ecology Centre for Ecology, Evolution and Conservation School of Biological Sciences University of East Anglia ph: (44) 01603 591496 Norwich NR4 7TJ, England fax: (44) 01603 592250

e-mail: david.richardson@uea.ac.uk<mailto:david.richardson@uea.ac.uk> http://biobis.bio.uea.ac.uk/biosql/fac_show.aspx?ID=325 "David Richardson (BIO)" <David.Richardson@uea.ac.uk>

UKansas ResTech DrosophilaEvol

An NIH-funded Research Technician position is available in Stuart Macdonald's lab in the Department of Molecular Biosciences at the University of Kansas. The Macdonald lab explores the genetic basis of complex phenotypic variation within and between species using Drosophila as a model system. We seek an enthusiastic individual to supervise and carry out large-scale genetics/genomics projects, and to oversee various lab activities. The responsibilities of the technician will include helping to maintain and use a large panel of Drosophila strains (see King et al. 2012), and running a range of quantitative genetic experiments to uncover the genetic basis of stress- and drug-resistance, and the genetics of male sexual trait variation (see McNeil et al. 2011). The successful candidate should be motivated, organized, and careful, and should have excellent oral and written communication skills. Salary will be commensurate with experience and will include benefits.

Required qualifications are a Bachelors degree in biology or a related field, and lab experience with a (broadly-defined) "model" genetic system such as Drosophila, C. elegans, mouse, Arabidopsis, and so on. Preference will be given to candidates with significant experience in the laboratory (including troubleshooting and optimizing protocols, and managing projects), and individuals holding a Masters degree.

The position is open and review of applications will begin on April 23 and continue until the position is filled. Informal inquires are welcome and can be directed to Stuart Macdonald (sjmac@ku.edu). To apply, complete an online application at https://jobs.ku.edu (search for position number 00207966). Attach a cover letter (describing your interest in the position and any relevant expertise), a full CV, and complete contact information for 3 referees. EO/AA Employer.

McNeil et al. 2011 http://www.g3journal.org/content/1/5/343.full King et al. 2012 http://genome.cshlp.org/content/early/2012/04/10/gr.134031.111.abstract Dr. Stuart J. Macdonald Department of Molecular Biosciences 4043 Haworth Hall 1200 Sunnyside Avenue University of Kansas Lawrence KS 66045

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

ULeeds EvolutionaryBiol

Two lectureships in Animal Biology/Zoology and 2 academic fellowships are available within the School of Biology at the University of Leeds, UK.

Applications from strong candidates in any relevant research area will be considered.

For the fellowships, applications from candidates with a background in the following subjects are particularly encouraged:

Animal population or evolutionary genetics Animal ecology, behaviour and evolution Biodiversity conservation, landscape management and ecosystem function Vertebrate developmental biology at a cellular or organismal level Cellular and physiological plant sciences relating to growth and stress Application of genomics to crop development and improvement

For more details please see the University Of Leeds recruitment pages:

Lectureships: http://jobs.leeds.ac.uk/fe/tpl_universityofleeds01.asp?s=3DFoQnTYvIgXJoLlXgd&jobid=81227,4114238652&key=78908699&c=585634544835&pagestamp=sevxwbidzxctigqtjb

Closing date: 17 April

Fellowships: http://jobs.leeds.ac.uk/fe/tpl_universityofleeds01.asp?s=3DEXgIfLQnAyPBgDdPyv&jobid=81419,0298235983&key=78908699&c=585634544835&pagestamp=sejbrcrkcwkvtwugmn

Closing date: 23 April

Dr Simon Goodman School of Biology University of Leeds Miall Building, Clarendon Way Leeds, LS2 9JT, UK

S.J.Goodman@leeds.ac.uk

ULeicester Bioinformatics

Dear Colleagues,

The B/BASH (Bioinformatics and Biostatistics Analysis Support Hub) team at the University of Leicester, UK is looking to hire a full time Research Assistant on a one year fixed term contract.

The post would suit a recent graduate with a BSc / MSc in Bioinformatics / Biostatistics or a Biological Sciences degree with a strong computer programming or statistics component. The role is to develop, coordinate and extend the Training and Outreach functions of the Hub. You will also actively promote the use of the Hub services throughout the College / University and contribute to the analysis support function of the B/BASH team. More details about B/BASH can be found at: http://www2.le.ac.uk/colleges/medbiopsych/facilities-and-services/cbs/bbash The post is advertised on jobs.ac.uk (http://www.jobs.ac.uk/job/AEH391/research-assistant) and the full details further particulars are available at the University of Leicester job search site (http://www2.le.ac.uk/offices/jobs/opportunities/jobsearch) by searching for reference: MBP00583

Informal enquiries about the post are very welcome, contact details below

Many thanks

Richard

Dr Richard Badge, Lecturer rmb19@le.ac.uk Department of Genetics, University of Leicester, Leicester LE1 7RH Tel: 0116 2525042

rmb19@leicester.ac.uk

ULiverpool ResTech DiseaseEvolution

A full-time Research Technician position is available in the Institute of Integrative Biology, University of Liverpool, UK

A research technician post is available starting on June 1, 2012 to work on dynamics of within- and between-species parasite transmission in a natural small mammal community in the UK. This will be part of a NERC funded grant led by Andy Fenton (University of Liverpool), Amy Pedersen (University of Edinburgh) and Owen Petchey (University of Zurich) to quantify host species contributions to parasite transmission and persistence across a diverse, natural multi-host-multi-parasite community. This work will involve a combination of fieldwork (small mammal trapping), large-scale ecological manipulation experiments and laboratory assays.

The main role of the research technician post is to undertake and assist with the planning of small mammal trapping at our field sites on the Wirral, record data on each mouse caught and take blood and faecal samples. In addition the technician will be involved in the maintenance of sampling equipment, field-measuring equipment, sample storage and transportation etc. as well as analysing faecal and blood samples in the lab to identify the parasites within them. This will lead to the compilation of a unique and extensive database on the parasite communities of these wild rodents.

The technician will work closely with, and receive training from, a senior technician (Grade 6), and be involved with the supervision of a number of undergraduate volunteer workers throughout the summer months. In addition, the technican will be part of a wider team involving the PIs on the project and a Post-Doctoral researcher, all of whom will be part of the trapping and data collection team.

The post will be for up to 35 months and will be based within the lab of Andy Fenton at the Institute of Integrative Biology, at the University of Liverpool, and will be fully integrated within the wider research team from the Universities of Edinburgh and Zurich. For more information on the research groups please see the following websites: http://www.liv.ac.uk/integrative-biology/staff/andrew-fenton/ http://www.biology.ed.ac.uk/research/groups/apedersen/

Applications will be accepted until May 11, 2012.

For the Research Technician position (Ref. #: S-577616) application and specific job description, please go to: http://www.liv.ac.uk/working/job_vacancies/technical/S-577616.htm For specific information about the project, please email Andy Fenton (a.fenton@liverpool.ac.uk) or Amy Pedersen (amy.pedersen@ed.ac.uk).

Amy B. Pedersen, Advanced Fellow Centre for Immunity, Infection and Evolution

Institutes of Evolutionary Biology, Immunology & Infection Research School of Biological Sciences University of Edinburgh Kings Buildings Ashworth Labs, West Mains Road Edinburgh EH9 3JT, UK

amy.pedersen@ed.ac.uk +44(0) 131 650 8674

Ashworth 2 - 4.07 http://www.biology.ed.ac.uk/research/groups/apedersen/ Amy Pedersen <amy.pedersen@ed.ac.uk>

UMississippi FreshwaterEvolution

Professor and Doherty Chair in Freshwater Science Department of Biology and Center for Water and Wetland Resources The University of Mississippi

The University of Mississippi's Department of Biology and Center for Water and Wetland Resources (CWWR) seek an exceptional individual to expand their programs in freshwater science. The successful candidate will hold the title of Doherty Chair, with office and laboratory space at the CWWR located at the UM Field Station. We seek a model mentor, teacher and researcher with an established, extramurally funded research program who is qualified to hold the position of tenured professor in the Department of Biology. The Doherty Chair will be expected to 1) ensure excellence in scholarship, teaching and service; 2) increase the level and scope of extramural funding that supports academic and research initiatives in the Department of Biology and the CWWR; 3) provide leadership in developing a national reputation for the university's freshwater science programs; and 4) enhance outreach efforts in the community and the region. It is expected that the Chair's research will be conducted at least in part at the CWWR. Teaching will be commensurate with the Chair's research commitment and interests. Graduate assistantships are associated with the position.

The Department of Biology consists of 18 faculty and annually educates approximately 800 undergraduate biology majors and 35 graduate students (M.S. and Ph.D.). Departmental research spans all levels of organization from the cell to the ecosystem. More detailed information concerning the department is available at http://www.olemiss.edu/depts/biology. The Center for Water and Wetland Resources is a specialized research unit located at the 740-acre UM Field Station, approximately 12 miles from the main campus, which includes natural and constructed wetlands, more than 200 experimental ponds from 0.1 to 2 acres, and several springs and small streams. More information concerning the CWWR and field station is available at http://www.baysprings.olemiss.edu/ . Founded in 1848 as the state's first public university, the main campus of The University of Mississippi is located in Oxford, Mississippi, one of the top college towns in the U.S., and a community known for its many outstanding educational and cultural opportunities. More detailed information on Oxford is available at http://www.oxfordms.net/. The University is a growing, vibrant institution that offers nationally ranked academic and research programs, and has been cited by Forbes Magazine as one of the nation's 20 Best College Buys and by the Chronicle of Higher Education as one of the 10 top "Great Colleges to Work For". Within the last 12 years, the University has produced eight Goldwater Scholars, two Rhodes Scholars, six Truman Scholars, seven Fulbright Scholars, one Marshall Scholar, one Udall Scholar and one Gates Cambridge Scholar.

To apply, please visit our Online Employment Service at jobs.olemiss.edu. Applications should include: (1) cover letter outlining interest and suitability for the position, (2) curriculum vitae, (3) statement of research interests, (4) reprints of up to five recent publications, and (5) a list of three references. Letters of nomination should be addressed to Dr. Marjorie M. Holland, Chair, Search Committee for Doherty Chair in Freshwater Science, Department of Biology, University of Mississippi, University, MS 38677.

Consideration of applications will begin immediately and continue until the position is filled. The University of Mississippi is an EEO/AA/TITLE IX/SECTION 504/ADA/ADEA EMPLOYER.

Ryan Garrick rgarrick@olemiss.edu

Ryan Garrick Department of Biology 402 Shoemaker Hall University of Mississippi University, MS 38677-1848, USA

webpage: http://www.rcgarrick.org rgarrick@olemiss.edu

UNewSouthWales VertebrateEvolution

Lecturer / Senior Lecturer in Terrestrial Vertebrate Evolutionary Biology / Ecology

FACULTY OF SCIENCE SCHOOL OF BIOLOGICAL EARTH AND ENVIRONMENTAL SCIENCE

REF 8734

Salary range: Lecturer $86K V $102K per year, Senior Lecturer $105K V $120K per year depending on qualifications and experience. There is an additional 17% employer superannuation. Lecturer (level B) roughly equates to assistant professor and SeniorLecturer (level C) to associate professor in the North American system. The School of Biological Earth and Environmental Sciences (BEES) is seeking to appoint a biologist to undertake research, postgraduate supervision and teaching within one of Australias most dynamic research environments. The appointee will be expected to build a research program in areas of whole-organism biological sciences, specifically in the area of terrestrial vertebrates, and tosupervise Honours and postgraduate students with interests in the biological sciences. UNSW was one of only four universities within Australia to achieve an average research ranking over 4 in the 2010 Australian Research Councils national ERA research assessment. BEES was a majorcontributor to UNSW obtaining rankings of 5/5 for biological sciences (well above world research standards) and 4/5 for earth sciences (significantly above world standards). BEES is a large, multi-disciplinary,research intensive school in the Faculty of Science at the University of New South Wales, dedicated to pure and applied research in natural systems spanning the biological sciences to the earth sciences. The school incorporates a range of environmentally-relevant disciplines enabling it to undertake comprehensive education and research in the broad fields of Biology, Marine Science, Geography and Geology. Within the biological sciences, the school has research strengths in evolutionary ecology, wetlands and rivers ecology, marine biology and palaeobiology and is regrowing the general areas of mammalian biology and plant systems that have been traditional strengths. Over the last decade UNSW has oriented its whole-organism biology research towards a focus on integrative and conceptual biology V particularly at the interface of evolution and ecology. The School is home to the Evolution & Ecology Research Centre, the Australian Wetlands and Rivers Centre, the Australian Tsunami Research Centre and the Palaeontology & Palaeoecology research group, as well asbeing a partner in the Sydney Institute for Marine Sciences, the National Groundwater Centre for Research and Teaching, the Centre for Marine Bioinnovation and the Climate Change Research Centre. UNSW maintains field research stations in NSW at Fowlers Gap, Wellington (semi-arid) and Smiths Lakes (coastal). The UNSW Fowlers Gap Arid Zone Research Station covers 40,000ha in western NSW and has a range of research facilities. Preference may be given to applicants with potential to lead or contribute to research projects using this major field facility. The position is a continuing appointment pending satisfactory progress. Women and people from EEO groups are encouraged to apply.

Applicants should address the selection criteria found within the position description, in their online application. For further information about the position, please contact Associate Professor David Cohen on telephone (+61 2) 9385 8084 or email d.cohen@unsw.edu.au<mailto:d.cohen@unsw.edu.au>.

With many thanks,

Professor Rob Brooks Director, Evolution & Ecology Research Centre The University of New South Wales Www.eerc.edu.au

Www.robbrooks.net

Rob Brooks <rob.brooks@unsw.edu.au>

UParis TermiteEvolution

job : position of assistant professor (CNU : 69 section, neurosciences ; Composante : LSHS, Université Paris 13) in Ecology and ethology of social insects (termites)

Laboratory: BIOEMCO/LEEC Description : This position is a special MaÃtre de Conférences position called ≪ chaire mixte d'excellence ≫ based on cooperative research program , with several advantages for the successful candidate: 1) the teaching load is reduced to 1/3 of the normal teaching; 2) a scientific prize of about 10Kâper year in addition to the normal salary; 3) funding for research between 10K and 20 K per year.

Teaching: Psychophysiology in the Psycology curriculum for students in Licence and Ecology and Behaviour for students in Master 1 and 2 of Ethology. Lectures and practicals. Contact :Stéphane Chameron :

chameron@leec.univ-paris13.fr

Research: Eco-ethological study of termite species of economical and ecological importance Qualifications: Applicants should have a solid and significant expertise in relevant aspects of insect biology and high profile publishing in their field. A good knowledge of insect ecology and ethology (communication, reproductive strategies, intra- and inter-specific interactions), and experience with working in the tropics will be appreciated.

Research project: The successful candidate will develop a collaborative research project involving the LEEC (University of Paris 13) and the IBIOS (Team BIOEMCO IRD France Nord). The project concerns investigation of the social organisation (division of labour, caste partitioning, nestmate recognition, reproductive strategies, etc.) and the biological and molecular features of several species of termites with different food regimes. The aim of this comparative and integrated approach should be to determine the evolutionary, ecological and ethological conditions responsible of the spreading of species that are potentially pest of tropical cultivars, in order to develop novel strategies for insect control.

deadline to Galaxie application: 27/03/2012, 16h The two laboratories to contact: 1) IRD France-Nord : UMR BIOEMCO Ãquipe IBIOS Corinne ROULAND-LEFEVRE, Director of IRD station France-Nord corinne.rouland-lefevre@ird.fr ; tel : 01 48 02 56 34

2) Université Paris 13 : LEEC EA 4443 Dominique Fresneau, lab's director mail : Dominique.Fresneau@leec.univ-paris13.fr ; Tél: 01 49 40 32 18 Patrizia d'Ettorre mail : dettorre@leec.univ-paris13.fr ; Tél : 01 49 40 31 96

Agricultural sciences, Tropical agriculture, Soil science, Forest science Environmental science, Ecology

—

Chaire mixte IRD/Université Paris 13 Type : MaÃtre de Conférences(MC) CNU : 69 section, neurosciences Composante : LSHS, Université Paris 13 Laboratoire d'accueil : BIOEMCO/LEEC Profil court : Ecologie et éthologie des insectes sociaux

Description : Cette chaire mixte d'excellence IRD-Université Paris 13 est proposée en vue de développer un projet de recherche en collaboration entre le laboratoire IBIOS (Equipe BIOEMCO, IRD France Nord) et le LEEC (Université Paris 13) en éco-éthologie des termites. Ce poste présente plusieurs avantages : le lauréat devra assurer un service d'enseignement réduit à l'Université (1/3 d'un service normal) et bénéficiera d'une prime scientifique moyenne de 10Kâ¬*paranetsesrecherchesréaliséesÃl′IRDrecevrontunedotationa*

Enseignement : Filières de formation concernées : parcours de psychophysiologie en licence de psychologie (L1 ÃL3) et Master d'éthologie (M1et M2). - objectifs pédagogiques et besoin d'encadrement: Cours magistraux et Travaux Dirigés de Neurobiologie, Ethologie (L1 L3), Sciences du Comportement (Master 1 et 2). - Département : Département de Psychophysiologie Lieu(x) d'exercice : UFR Lettres et Sciences de l'Homme et des Sociétés Contact :Stéphane Chameron : chameron@leec.univ-paris13.fr

Recherche : Etude éco-éthologique d'espèces de termites ayant un impact économique et écologique Pré requis : Le candidat devra présenter une expérience avérée dans le domaine de la biologie des insectes et un très bon profil de publications. Une bonne connaissance de l'éthologie et l'écologie des insectes (communication, reproduction, relations intra- et inter- spécifiques) ainsi qu'une expérience de recherche en zones tropicales seront appréciées.

Recherche : Le candidat aura pour tÃche de développer un projet de recherche en collaboration entre le LEEC (Université Paris 13) et IBIOS (Equipe BIOEMCO, IRD France Nord) visant Ãcomparer l'organisation sociale (division du travail, régulation des castes, reconnaissance coloniale, reproduction), les caractéristiques biologiques et moléculaires chez

— / —

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

UPittsburgh ResTech EvolColorVision

Dear Colleagues,

I am looking for a research technician to join my lab group at the University of Pittsburgh. We study the evolution of coloration and color vision in invertebrates with a specific focus on the Lepidoptera. The major responsibility of the technician will be maintaining several large laboratory cultures of butterflies, both exotic and native. Strong organizational skills, personal initiative and attention to detail are essential attributes. Preference will be given to applicants who have prior research experience and are willing to commit to two years of employment.

This is a potentially long-term position in a growing lab group with opportunities for international fieldwork and authorship on publications.

The University of Pittsburgh is situated in the heart of one of the most culturally vibrant and livable cities in the US. I appreciate your help in bringing this job opportunity to the attention of qualified individuals you would recommend. More specific information about the position can be found below.

Sincerely,

Nathan Morehouse

Assistant Professor Department of Biological Sciences University of Pittsburgh 223 Clapp Hall 4249 Fifth Avenue Pittsburgh, PA 15260 Office: (412) 624-3378 Lab: (412) 624-3351 Fax: (412) 624-4759

nim@pitt.edu

http://www.biology.pitt.edu/person/nathan-morehouse JOB TITLE: Research Specialist - Color Evolution Research Group at the University of Pittsburgh

JOB DESCRIPTION: Research Specialist will work in a lab focused on the evolution of color ornaments and other sexual traits in invertebrates, including butterflies and spiders. Job duties will involve rearing and husbandry for maintenance of several laboratory-based populations of butterflies (native and exotic), including the preparation of artificial diets, growing of host plants and mating of adults in greenhouse areas. The research specialist will also play a key role in several planned selection experiments within these lab populations, as well as associated biochemical and spectrophotometric analyses. Other duties will include ordering of supplies, record keeping and the training of undergraduate assistants needed in some research areas. Strong organizational skills, personal initiative and attention to detail are essential attributes. Duties may include field work at nearby locations, the University's Pymatuning Laboratory of Ecology field station, and international locations in Africa and Asia.

QUALIFICATIONS: A bachelor's degree in a related subject is required. Prior research experience preferred. Preference will be given to applicants who are willing to commit to two years of employment.

STARTING DATE AND LOCATION: The position will be filled as soon as possible.

The Research Specialist will be based at the main Oakland campus of the University of Pittsburgh, in Pittsburgh, PA.

SALARY: Annual salary will start at $22,500 with full benefits.

INFORMATION AND QUESTIONS: For more about this job opportunity, contact Dr. Nathan Morehouse (nim@pitt.edu). More information on the research group can be found at the following website:

http://www.biology.pitt.edu/person/nathan-morehouse . TO APPLY: Further information about how to apply for this job can be found at the following website: https://www.pittsource.com/postings/57251 .

UppsalaU MolEvol

CORRECTED LINK TO APPLICATION FORM

Permanent faculty-funded position Group leader in Molecular Evolutionary Biology

Evolutionary Biology Centre, Department of Ecology and Genetics, Sub-Department of Evolutionary Biology.

Application no later than 2012-05-04.

This is a faculty-funded permanent position for an independent researcher with an own research profile at the level equivalent to Assistant or Associate Professor. For an overview of on-going research at the Sub-Department, please see http://www.ebc.uu.se/-Research/IEG/evbiol/research/ Work description: Independent research in either evolutionary genomics, molecular evolution or molecular ecology, or related areas. Teaching including supervision of own PhD students may be included.

Required qualifications: PhD in a relevant subject area and several years of post-doctoral research experience. The research profile of the successful candidate is expected to complement and reveal synergism with ongoing research at the Sub-Department.

The position comes with significant start up funds.

More information about the position can be obtained from Professor Hans Ellegren, tel. +46 18 471 6460, hans.ellegren@ebc.uu.se.

You are welcome to submit your application no later than May 4th, 2012.UFV-PA 2011/1345. Use the link below to access the application form.

http://www.uu.se/jobb/others/-annonsvisning?languageId=3D1&tarContentId=-3D176669 How to apply: The application should include a short description of the applicant and his/her research interests. It should also include a CV, list of publications and other relevant documents including e.g. letters of recommendation or names of reference persons.

The Evolutionary Biology Centre (EBC) of Uppsala University is a leading international arena for research in evolutionary biology, see http://www.ebc.uu.se/-Research/IEG/ and http://www.ebc.uu.se/Research/-IOB_eng/. It offers a most stimulating atmosphere characterized by a high proportion of international students (at Master as well as PhD level) and post-docs, frequent seminars, an active grad school program geared towards the integration of genomic approaches in evolutionary biology (http:/-/www.ebc.uu.se/education/postgrad/gradschool/) and unusual possibilities for cross-disciplinary work. EBC scientists have recently attracted five highly competitive European Research Council (ERC) Grants. EBC is connected to the Science for Life Laboratory initiative (http://www.scilifelab.se/) which is a competitive centre for high-throughput biosciences.

hans.ellegren@ebc.uu.se

Vienna MolecularBiodiversity

The University of Natural Resources and Life Sciences, Vienna, invites application for a tenured professorship in “Integrative Biodiversity Research with special emphasis on molecular methods”. This position is assigned to the Institute of Integrative Nature Conservation Research at the Department of Integrative Biology and Biodiversity Research. The professorship involves commitment to Biodiversity research alongside with the development and use of latest state-of-the-art laboratory techniques for the collection of data on population-genetics and biodiversity. Research should focus on molecular biodiversity and support applications to in-situ and ex-situ conservation, including, in particular, molecular analysis of the diversity of species, phenotypes and population biology. Expertise in this area is expected to enable and instigate research on the interaction of man, land use, organisms and populations.

A critical consideration will be the extent to which the candidate has a collaborative orientation and is able to contribute to interdisciplinary research in the scientific network of our university, particularly with the Institute of Botany. Teaching duties involve: - lectures and field courses for students of “Agricultural Sciences” and “Environmental and Bio-resource Management”, - teaching in vegetation science, plant systematics and ecology, and biodiversity research, - supervising bachelor and master theses, - supervising and mentoring doctoral dissertations, - organizing and mentoring seminar papers, as well as the active participation in the development of curricula is expected, notably in questions of adequate positioning of the research field.

An important further duty will consist in assuming responsibilities at various levels of the university administration and in the active participation in the work of academic committees. Prerequisites required for successful candidates are: - Venia docendi (Habilitation) or an equivalent scientific qualification, - above-average experience in the acquisition and management of competitive research projects, - publications in high-ranking international scientific journals, - teaching skills and proven teaching experience - including mentoring young scientists, - ability for cooperative teaching and research (also on an international level), as well as for interdisciplinary dialogues among natural sciences and related disciplines, - management competence and leadership qualities, communication and team skills, aptitude for the handling of public relations, - willingness to participate in all activities started to further the development of the department and the university, willingness to assume academic responsibilities, - willingness to act as a member of national and international scientific advisory boards and institutions.

Applications (six copies) should be sent to the Rector of the University of Natural Resources and Life Sciences Vienna, Peter-Jordan-Straße 70, 1190 Wien, Austria, no later than 20th May 2012 (date of postmark). The application should include: - a curriculum vitae with a detailed account of professional, teaching and research activities, - a list of publications (refereed and non-refereed), talks and projects, - copies of five recent publications considered particularly representative, - a broad concept for research and teaching describing the envisaged focus, - a brief analysis (max. 1 page) of why you think you are particularly qualified for this position.

By applying, you imply your consent to co-operation with a personnel consultancy within the framework of the selection procedure. The University of Natural Resources and Life Sciences, Vienna, strives to increase the proportion of women in its employment and particularly invites qualified women to apply. In the case of equal qualification and in the absence of any other outweighing factors, female candidates will be preferred. Regarding to the collective agreement for employees of universities the position is classified as A1. The minimum monthly gross salary of 4.571,20 Euro (14 times per annum) will be overpayed.

schlotc@gmail.com

Other

Bad interval Bottleneck

Dear List:

I am having a problem executing program BOTTLENECK (Cornuet and Luikart 1997). For one very rich microsatellite locus, the program is unable to get past calculation of He. For the calculation of Heq, it tries various values of theta for likelihood, which for this locus hasn't exceeded about 0.040. This apparently prompts it to try again, giving the following error message: "Maybe a bad interval. Be patient, I try again [sic] ..." It has tried thousands of times over about four days and always fails. The same locus in another population worked fine. I am using the TPM model, the variance set at 12, proportion of SMM in TPM is 90, and 1000 iterations. There are about 450 individuals in this population, about 250 in the population where this locus had no problems. Any suggestions? Is there a hard-coded minimum likelihood value that I could relax? Should I try more iterations? Based on Figure 2 in Luikart and Cornuet and the richness of this allele (ks) perhaps I need to have it exploring larger values of theta (it currently usually tries between 100 and 1000)?

Thank you for your time. Steve Kimble

Steve Kimble PhD candidate, Department of Forestry and Natural Resources Purdue University skimble@purdue.edu sjkimble@gmail.com 205.337.4843 http://web.ics.purdue.edu/~rodw/Steve%20Kimble.htm steve kimble <sjkimble@gmail.com>

Biogeographic barriers

Dear All,

Lessios et al published on gene flow across the “World’s most potent marine biogeographic barrier” (Eastern Pacific Barrier). What would be considered the world’s most potent ’freshwater biogeographic barrier’ for freshwater fishes? Wallace’s Line perhaps?

Thanks for any advice, Regards, Mark de Bruyn reply to: markus.debruyn@gmail.com

Dr Mark de Bruyn Molecular Ecology and Fisheries Genetics Lab Environment Centre Wales Biological Sciences Bangor University Bangor, LL57 2UW UK

bss808@bangor.ac.uk

BluefinTuna samples

Dear colleagues, I am a Marie Curie fellow working at the Hellenic Center for Marine research. We are planning to do transcriptome sequencing of bluefin tuna (Thunnus thynnus) and we are looking for samples suitable for RNA extraction. We are especially interested in samples from from Eastern Mediterranean, but samples of any origin are more than welcome. We have an extensive collection of bluefin tuna samples from the Mediterranean Sea, but we are lacking a few high quality samples needed for next gen sequencing. We are open to cooperation and any help will be gratefully acknowledged in publications and reports.

Thank you very much,

Gianpaolo

Dr. Gianpaolo Zampicinini Institute of Marine Biology and Genetics (IMBG) Hellenic Centre for Marine Research (HCMR) Gournes Pediados, P.O.Box 2214, 71003, Iraklio, Crete, Greece Tel.: +30 2810 337741 Fax: +30 2810 337870

gpaolo@her.hcmr.gr

CallCollaborators GarlicMustardAdaptation

Other:, Call for Collaborators V Garlic Mustard Project

Dear Colleagues,

The Global Garlic Mustard Field Survey is entering its fourth field season, now with demographic data and seed collections from over 300 populations across Europe and North America! This year we are looking for (i) new collaborators to collect data and seeds from poorly-sampled areas (see below), and (ii) returning collaborators to contribute to a temporal dimension by resampling populations from previous years.

In addition to collecting valuable field data on the demography, performance, abundance and distribution of Alliaria petiolata (Garlic Mustard) across its entire global distribution, we are developing genetic resources (e.g. immortal inbred lines and recombinant inbred lines) appropriate for studying a variety of evolutionary phenomena, including local adaptation to climate, the role of migration vs. de novo mutation in contemporary evolution, evolution of herbivore resistance chemistry, phylogeography, and the genetic basis of invasiveness.

Participation involves a very basic protocol that standardizes sampling across sites, and takes place in late spring/early summer. The estimated duration of sampling for a team of two people is 3-6 hours per population.

Participation is open to anyone and those who contribute will have the opportunity to participate in manuscripts resulting from the work and access to data and seed resources prior to their release to the general scientific community. Please use this website to sign-up for the 2012 field season: http://www.surveymonkey.com/s/signup2012 Collections are welcome from any area, but data and seed samples from the following regions are particularly needed: *Asia/Middle East*: China, India, Japan, Kazakhstan, Nepal, Pakistan, Russia *Australia* V recent invasion *Europe/Mediterranean*: Azerbaijan, Belarus, Britain, Bulgaria, Croatia, Estonia, Finland, France, Georgia, Greece, Hungary, Italy, Norway, Latvia, Lithuania, Morocco, Portugal, Romania, Serbia, Spain, Sweden, Turkey, Ukraine, *North America*: Canada (see map, below), Georgia, Illinois, Kansas, Kentucky, Missouri, North Carolina, North Dakota, South Carolina, Tennessee, West Virginia, Wisconsin *South America* V recent invasion

For previous sample sites and preliminary results, see the maps at http://www.GarlicMustard.org/-populations.html .

For herbarium records and known distribution of Garlic Mustard, see the map at http://data.gbif.org/species/-5376075/p .

Sampling protocol and additional information are available at our website: www.GarlicMustard.org . North-American Coordinator Dr. Robert Colautti Biology Department Duke University rob.colautti@duke.edu

Eurasian Coordinator Dr. Oliver Bossdorf Biology Department University of Bern bossdorf@ips.unibe.ch

Seed Collections Coordinator Dr. Steven Franks Biology Department Fordham University franks@fordham.edu

Rob Colautti <rob.colautti@duke.edu>

Comments for ARWallace website

Contribute to "The Alfred Russel Wallace Page" Website

Some years ago I solicited what I termed "commentaries" for a feature on my "Alfred Russel Wallace Page" website (http://people.wku.edu/charles.smith/-index1.htm), transcriptions of Wallace publications. Almost all of Wallace's 1000+ published works are now to be found there (http://people.wku.edu/-charles.smith/wallace/writings.htm), and I am hoping additional parties might be interested in contributing one or more such "commentaries" to this array. These typically have been 250 to 350 words in length, and would feature your slant on why a particular Wallace article remains of interest - historically and/or currently. A good example may be found at the end of: http://-people.wku.edu/charles.smith/wallace/S184.htm .

It is not important that you may not consider yourself a "Wallace expert," and in fact most of those who have contributed in the past are not. If you do not wish to wade through the entire list of Wallace's publications to choose a subject writing, I can suggest a handful of articles (many quite short) that might be of most interest to you.

2013 is the one hundredth anniversary of Wallace's death, and some dozen book projects and conferences are in preparation/planning accordingly. If you feel you might be interested in contributing to my site (and in turn to the anniversary celebration), please contact me for more details at: charles.smith@wku.edu<mailto:charles.smith@wku.edu> . Thanks very much for your time and attention!

–Charles H. Smith, Ph.D., FLS, Western Kentucky University

"Smith, Charles" <charles.smith@wku.edu>

Commercial antibody suggestions

I am considering having antibodies made for a protein that I've been working on, Malic enzyme, a metabolic enzyme. Does anyone have experiences, positive or negative, they can share about the various companies offering antibody production services? Specifically, I've been looking at Abmart, a company that offers to go from a text file of the amino acid sequence to a set of monoclonal antibodies.

Any comments, cautions, or suggestions will be appreciated.

Thomas

Thomas Merritt, PhD Associate Professor Tier 2 Canada Research Chair Department of Chemistry and Biochemistry Laurentian University 935 Ramsey Lake Road Sudbury, Ontario P3E 2C6 Canada e-mail: tmerritt@laurentian.ca phone:705-675-1151 ext. 2189

Thomas Merritt <tmerritt@laurentian.ca>

CORRECTION Phyloseminar RichardGoldstein Apr30

Hello Evoldir community–

I'm sorry to say that I got the date wrong in the last announcement. The correct date is Monday, April 30th.

Here is the correct announcement:

"Simulating evolution with in silico models of protein thermodynamics" Richard Goldstein (National Institute for Medical Research, London)

Many of the most basic issues of protein evolution are difficult to determine from the relationship between existent protein sequences. We would ideally like to analyse the complete evolutionary record: what mutations were attempted when in what lineage, which ones were deleterious or advantageous and by how much, which ones were accepted, and how these substitutions affected further mutations and the overall evolution of protein properties. In the absence of available biological data, we can create our own - simulate protein evolution in silico, such as in our work modelling how proteins would evolve given their need to be thermodynamically stable. These simulations allow us to explore a range of phenomena and develop a conceptual framework that tells us which questions may be interesting and important to consider in real proteins. Such simulations can also illuminate which conditions are necessary and/or sufficient to explain observed protein characteristics. We consider how evolution of protein thermostability explains why proteins are generally marginally stable, why eukaryotes may have more disordered proteins than prokaryotes, and what the consequences of this are for biochemical networks. We also consider how various locations in a protein can co-evolve, and how this can inform the next generation of substitution models.

West Coast USA: 10:00 (10:00 AM) on Monday, April 30 East Coast USA: 13:00 (01:00 PM) on Monday, April 30 UK: 18:00 (06:00 PM) on Monday, April 30 France: 19:00 (07:00 PM) on Monday, April 30 Japan: 02:00 (02:00 AM) on Tuesday, May 01 New Zealand: 05:00 (05:00 AM) on Tuesday, May 01

Thank you,

Erick

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

CultivatedSpecies GeneticVariation

Dear evoldir members,

We have characterized and isolated nuclear microsatellite loci from enriched libaries for Aloe vera, a widely cultivated species. We have tested polymorphism However, none of the 30 microsatellite tested showed polymorphism in samples from naturalized and cultivated populations from different islands and archipelagos from Macaronesian, and other localities. We have detected polymorphism in samples of other species of Aloe from the North of Africa. Have any body developed polimorphic microsatellites for this species?, Have any body found this absence of genetic diversity in a cultivated species?.

Thank in advance,

Miguel Angel

Miguel Angel González Pérez Investigador Doctor en Proyecto Departamento de Biología Universidad de Las Palmas de Gran Canaria 35017 Las Palmas Islas Canarias Spain mgonzalez@dbio.ulpgc.es t +34 928 454 543 p +34 928 452 922

canariensis750@hotmail.com

DeputyManagingEditor MolEcol

The Molecular Ecology Editorial Office is looking for a part-time Deputy Managing Editor to help run Molecular Ecology and ME Resources. The position chiefly involves monitoring the peer review process and interacting with subject editors, reviewers, and authors. There is also considerable scope to develop our online resources, particularly for someone with programming skills (MySQL, PHP and WikiMedia).

The ideal candidate would have postgraduate level expertise in the field of molecular ecology, a talent for critically evaluating scientific papers, and an excellent eye for detail. Strong writing and time management skills are also essential.

The position is available immediately and is based in Vancouver, Canada; telecommuting from elsewhere may be feasible. Salary is negotiable depending on experience, and will be based on working between 15 and 20 hrs per week.

If this is the right job for you, please email your resume and the names of two referees to managing.editor@molecol.com

Tim Vines

Tim Vines Managing Editor, Molecular Ecology & Molecular Ecology Resources Zoology Dept, UBC 6270 University Blvd. Vancouver BC, V6T 1Z4, Canada Tel: ++ 1 778 989 8755 Fax: ++ 1 604 822 8982

managing.editor@molecol.com managing.editor@molecol.com

DNA from museum specimens

Dear EvoLDir Members:

I am currently carrying out some aDNA analyses on bird toe pads from museum specimens aged between 50 and 150 years. Specifically, I am going to amplify 200 bp long fragments of the mitochondrial DNA Control Region. I would appreciate very much to get some indications and suggestions with reference to:

- the removal of potential inhibitors of the PCR such as gasoline, butane, formalin, arsenic powder: is it advisable to wash the samples with ethanol before extraction to get rid of them? - the advisability of grinding the samples into as much tiny as possible pieces in order to maximize the surface contact area and so the action of lysis solution and proteinase K: isn't it risky because of the possible spreading of residual inhibitors to the whole sample? - the feasibility of using betaine, BSA and Exonuclease III to improve PCR amplification: what about their amount provided a final reaction volume of 50 microliters?

Thanks

Giovanni Forcina PhD student University of Pisa Department of Biology Via A. Volta, 6 I - 56126 Pisa (PI) Italy

"cosrit@libero.it" <cosrit@libero.it>

Evolution 7 videos

Dear all,

Now that we have recently published the seventh and last movie of our project, I would like to tell you about the short movies about evolutionary research which Yannick Mahé and I have published on our website< http://www.evolution-of-life.com/ > and our youtube channel< http://www.youtube.com/user/evolutionoflife09/videos >.

The last one of the movies (about the evolution of lactase persistence, starring Joachim Burger and Sarah Tishkoff) was just uploaded a few days ago (Good Milk / Bad Milk < http://www.evolution-of-life.com/en/observe/video/fiche/good-milk-bad-milk.html >).

The topics of the other movies are: 1. antibiotics resistance (The bacteria resist< http://www.youtube.com/watch?v=zjR6L38yReE&feature=plcp&context=C477c39fVDvjVQa1PpcFMBYolJ7nmWN63RkumOJo_4qnRpmN1Sk >) 2. experimental evolution (Evolution before your eyes< http://www.youtube.com/watch?v=OjI5ZglXJLE&feature=plcp&context=C4b12959VDvjVQa1PpcFMBYolJ7nmWN_gxyOi20cooA4i-1NmwRbM= >) 3. fisheries-induced evolution (The case of the shrinking cod< http://www.youtube.com/watch?v=DEtKj88UPmM&feature=plcp&context=C4272a0eVDvjVQa1PpcFMBYolJ7nmWN-aMMmju9kVojyltH87O8Kk= >) 4. Darwin (Darwin on the evolution trail< http://www.youtube.com/watch?v=e7w0HkMeqWc&feature=plcp&context=C458c963VDvjVQa1PpcFMBYolJ7nmWNzFXKXz81kwbsb4IMEz4tJ >) 5. coevolution between ants and their parasites (An evolutionary arms race< http://www.youtube.com/watch?v=hKuCbLP8nCM&feature=plcp&context=C4e37c96VDvjVQa1PpcFMBYolJ7nmWN9YV17DeafJxlx5PBqOfrEU >) 6. the origin of life (O as origin< http://www.youtube.com/watch?v=bi3SaCX5LkU&feature=plcp&context=C45dc4a3VDvjVQa1PpcFMBYolJ7nmWN4IgAtkSEeV4NIyuC2xnEC >)

Each of the movies was made by a different team of people, and so they will look and sound quite different. "The bacteria resist", "Darwin on the evolution trail" and "O as origin" are completely animated, whereas the other movies are mostly documentaries. All of them are less than 10 minutes long.

All movies are available in English, French and German (mostly dubbed, the last movie currently has subtitles only). On our youtube channel, there are a few movies with Rumanian and Spanish subtitles as well, see http://www.youtube.com/user/evolutionoflife09/videos .

Our project is mainly funded by the Volkswagen Foundation in Germany as part of their evolutionary biology program. We won several awards with the project, most importantly the Medea award for European collaborations, see http://evolution-of-life.blogspot.com/2010/12/medea-european-collaboration-award-2010.html We hope that our movies will be useful for you if you are teaching evolution classes to high school students, undergrads, lay audiences etc. Feedback is welcome, of course!

Best wishes, Pleuni Pennings

Pleuni Pennings http://scholar.harvard.edu/

pennings/home "Pennings, Pleuni" <pennings@fas.harvard.edu>

Evolution teaching survey

I am interested in how professors across the world teach a course on evolutionary biology at the undergraduate level. In particular, I am interested in 1) who you are; 2) if I can contact you (by email) and ask you some questions about how you teach; 3) whether you use a textbook and if you do, which one you use; and 4) whether the course is required or not for a major in biology. Please respond to

Andrew Martin am@colorado.edu

Thanks.

Andrew Martin Professor University of Colorado "Any real teacher knows that the job of the teacher is to draw out the genius that resides in each student." Michael Meade

Andrew Martin <Andrew.Martin-1@colorado.edu>

Genbank submission instructions

I thought folks might find the following site useful. It has detailed instructions on submitting phylogenetic or phylogeographic datasets to GenBank, as well as brief details on Dryad and TreeBase. Essentially, for GenBank it describes a process for entering most of the information GenBank needs in the submission file rather than entering those detail in sequin.

http://peter.unmack.net/molecular/data.sub/data.deposition.instructions.html Cheers Peter Unmack National Evolutionary Synthesis Center Durham NC, USA

peter.mail2@unmack.net

Insect tissue storage

Other: storage of insect tissue for flow cytometry

Dear All,

I am planning to apply flow cytometry to tissue samples from several sexual and asexual insect (Microcoryphia, jumping bristletails) species. I understand that it is common to use fresh material for these measurements. However, as these insects are hard to keep in husbandry and fieldwork is often unpredictable, I would like to preserve samples both over the short (for better streamlining my workflow) and the long term (extra samples as backup).

Does anyone have experience with storage of insect tissue for use in flow cytometry? Ideally, the method should (1) be applicable in the field (potentially combined with later refrigeration), (2) allow for high-quality flow cytometry measurement even after one year or more, and (3) not degrade DNA.

I know my demands are quite high; I would be very grateful for any suggestion.

Kind regards,

Thomas Dejaco

Molecular Ecology Group Institute of Ecology University of Innsbruck, Austria http://www.uibk.ac.at/ecology/forschung/molecular_ecology.html

Introns exons videos

Introns and Exons

The discovery of introns in 1977 led to numerous hypotheses on their origin. As our knowledge increased many of these fell by the wayside. Given the now narrow field of contenders, a historical account of ideas leading up to modern perceptions would seem timely. Thus, extending the previous three series of videos on Evolutionary Principles, Natural Selection, and Blending Inheritance, a fourth series on Introns and Exons is now launched. As before, the new series follows the style of Salman Khan's highly successful "Khan Academy" (http://www.khanacademy.org/), and may be accessed either directly on You Tube (http://www.youtube.com/playlist?list=PL378EB17561C23228&feature=edit_ok), or by way of my webpages (http://post.queensu.ca/~forsdyke/videolectures.htm).

Donald Forsdyke, Department of Biomedical and Molecular Sciences, Queen's University, Canada forsdyke@queensu.ca

Journal Society Coevolution

Dear All,

A few colleagues and I have discussed for some time the possibility of establishing a Society of Coevolution and launching a Journal of Coevolution. We thought it appropriate to solicit feedback from EvolDir readers.

1) Society of Coevolution: I will create a web page for you to register your interest as a founding member of the society. Will announce the URL in a few days.

2) Attached below is a draft proposal for Journal of Coevolution. I should greatly appreciate your feedback.

Proposal for Journal of Coevolution

Title Journal of Coevolution

Background 1) There is no journal that explicitly cover the area of coevolution or molecular coevolution. 2) Research publications on coevolution is scattered over many journals. However, these publications all share a set of distinctive features that set them apart from other evolutionary studies. There is a strong need for coevolutionary research to have its own publication venue. 3) Recent availability of high-throughput data and their associated databases have created an unprecedented opportunities for coevolutionary studies, which include receptor-ligand coevolution, codon-anticodon coevolution, bacteriophage-bacterial host coevolution, etc. 4) Organismal coevolution such as host-parasite coevolution and predator- prey coevolution not only remain academically strong, but also invigorated by their molecular details. 5) Granting agencies are receiving more and more grant applications in the area of molecular coevolution

Aims and Scope The journal will cover all research topics elucidating the coevolution of two or more biological entities. It will include two sections:

1) Molecular coevolution section including, but not limited to, research fields such as receptor-ligand coevolution, codon-anticodon coevolution, bacteriophage-bacterial host coevolution, virus-host resistance coevolution. 2) Organismal coevolution section including, but not limited to, research fields such as host-parasite coevolution, predator-prey coevolution, culture-human coevolution.

There has been no journal that explicitly cover the area of coevolution or molecular coevolution. There has been no journal that has a section that explicitly cover the area of coevolution or molecular coevolution.

Editorial Structure 1) Two co-chief editors, one for the molecular coevolution section and the other for the organismal coevolution section. 2) A sets of six associate editors covering various aspects of coevolutionary studies. 3) An editorial board of about 20 members 4) A managing editor who will check the format and completeness of the submitted manuscript.

Content Research papers Reviews Letters (short/rapid communications

The Market Here is a compilation of publications that have used the word "coevolution" over the years.

————————————-

Period NumPaper

————————————-

2000-2001 5790 2001-2002 6550 2002-2003 7370 2003-2004 8500 2004-2005 9580 2005-2006 10600 2006-2007 11700 2007-2008 12200 2008-2009 13500 2009-2010 13100 2010-2011 14600 2011-2012 9940

————————————-

Best Xuhua

Xuhua Xia Professor Biology Department University of Ottawa Rm 278 Gendron 30 Marie Curie, Ottawa, Ontario Canada K1N 6N5 Tel: (613) 562-5800 ext 6886 http://dambe.bio.uottawa.ca http://www.biology.uottawa.ca/details.php?lang=-3Deng&id=3D31 xxia@uottawa.ca

Journal Society Coevolution clarification

Dear All,

I received many comments and suggestions on the draft proposal for Journal of Coevolution. Many are easily accommodated (e.g., adding plant-pollinator coevolution, sexual conflict and male-female coevolution, etc., etc.), but two issues may benefit from more feedback from the EvolDir community.

1. Should studies on co-speciation be included in a Journal of Coevolution?

Coevolution: evolutionary changes in Partner X leads to differential fitness among individuals of Partner Y. The latter then evolves in response to the selection force imposed by the former, and vice versa.

Co-speciation: evolutionary changes (e.g., measured by genetic divergence) in Partner X is induced by the evolutionary changes in Partner Y, with the consequent correlated changes leading to phylogenetic concordance between the two partners. It is better to illustrate this with an example of chewing lice-pocket gopher co-speciation. When gopher populations become fragmented and genetically diverged, the chewing lice carried on them become fragmented and genetically diverged as well, leading to phylogenetic concordance between the lice and the gopher. The population fragmentation of chewing lice is induced by the population fragmentation of the gophers, but not vice versa.

However, co-speciation could lead to coevolution. For example, if some gopher species become so clean that there is nothing in their hair for the lice to chew, then it would be beneficial the chronically hungry lice to evolve the ability to suck blood. If the gophers infested by the blood-sucking lice then evolved something in their blood that is toxic to the lice, then we have a bona fide case of coevolution.

For this reason, it would seem to make sense for a Journal of Coevolution to include studies on co-speciation because co-speciating partners are expected to have a high likelihood to coevolve.

One may consider the gopher-lice example as analogous to the fragmentation of land masses and the associated fragmentation of biota carried on them. Should such biogeographic patterns induced by continental movement be included in a Journal of Coevolution?

The answer is no, because the continent and the biota are not expected to have a high likelihood to coevolve.

2. Why should culture-human coevolution be included in a biological journal?

1) Culture-human interactions urgently need more studies from a biological perspective. Dramatically different cultures, religions, and social systems have evolved in different regions, and one naturally asks why there are so much differences. From a social biogeographic point of view, there are two possible explanations for why Culture A found in Area A is not found in Area B where you find Culture B instead. First, Culture A might just be "bad" for people in Area B. Second, Culture A is "fitter" than Culture B but has never got a chance to be practised by people in Area B.

Western politicians never consider the first possibility, and always insist that a single Culture A be brought to all regions to be practised. Similarly, advocates of some religions insist that their religions should be practised everywhere by all people in the world. They might well be right, but it would seem reasonable to examine the first possibility.

2) Culture-human do coevolve. A change in culture intuitively would lead to differential fitness among us (e.g., the increased cultural sympathy for the sick has substantially increased the fitness of carriers of certain genetic diseases), and changing genetic composition of human societies will have differential impact on different cultures.

I should appreciate your opinion, either to me or to EvolDir.

Best Xuhua

Xuhua Xia Professor Biology Department University of Ottawa Rm 278 Gendron 30 Marie Curie, Ottawa, Ontario Canada K1N 6N5 Tel: (613) 562-5800 ext 6886 http://dambe.bio.uottawa.ca http://www.biology.uottawa.ca/details.php?lang=eng&id1

MissouriBotanicalGarden SummerResearch REU

Undergraduate Research Opportunity, REU Missouri Botanical Garden Summer 2012

The Missouri Botanical Garden is recruiting candidates for a new Research Experience for Undergraduates (REU) program. This NSF-funded program provides full support for 10 students to work on mentored independent research projects for 10 weeks during the summer, from May 20 to July 29.

Students must be sophomores or juniors, or if seniors they must be returning to school after the REU summer.

The MBG program focuses on the areas of plant systematics, conservation biology, and ethnobotany. Potential projects include taxonomic description of new species and revisionary studies in Brassicaceae, Araceae, and Melastomataceae, DNA sequencing and phylogenetic analysis, DNA barcoding, pollen analysis, pollination biology of rare species, seed morphology and anatomy of Lythraceae and Passifloraceae, conservation biology of threatened species, ecology of invasive species, herbarium study of historically important collections, Native American ethnobotany, and revisionary studies of economically important plants. REU students have access to a herbarium of 6.2 million specimens, an excellent botanical library, rich garden collections, a 2,400 acre natural area, and a laboratory with facilities for plant anatomy, microscopy, digital imaging, SEM, and DNA analysis. Students are expected to work full-time on research and participate in twice-weekly lunch-time seminars and workshops, including subjects on botany, conservation, career development, ethics in research, writing and communication skills, and preparation for graduate school.

Students receive lodging near the Garden, a food allowance, research and travel expenses, plus a stipend of $500/week.

The deadline for application is April 15, 2012.

For more information and application procedures please see the program website at http://www.mobot.org/-mobot/research/reu/reu.shtml or contact the REU Coordinator at reu@mobot.org ,the PI David Bogler (david.bogler@mobot.org), or Co-PI Sandra Arango-Caro (sacpriv@yahoo.com)

David J. Bogler, PhD | Missouri Botanical Garden | P.O. Box 299, St. Louis, MO 63166-0299 Office: 314-577-0831 | fax: 314-577-0830 | david.bogler@mobot.org | http://www.davidbogler.com

David Bogler <david.bogler@mobot.org>

Phyloseminar RichardGoldstein Apr20

Next phyloseminar talk: "Simulating evolution with in silico models of protein thermodynamics" Richard Goldstein (National Institute for Medical Research, London)

Many of the most basic issues of protein evolution are difficult to determine from the relationship between existent protein sequences. We would ideally like to analyse the complete evolutionary record: what mutations were attempted when in what lineage, which ones were deleterious or advantageous and by how much, which ones were accepted, and how these substitutions affected further mutations and the overall evolution of protein properties. In the absence of available biological data, we can create our own - simulate protein evolution in silico, such as in our work modelling how proteins would evolve given their need to be thermodynamically stable. These simulations allow us to explore a range of phenomena and develop a conceptual framework that tells us which questions may be interesting and important to consider in real proteins. Such simulations can also illuminate which conditions are necessary and/or sufficient to explain observed protein characteristics. We consider how evolution of protein thermostability explains why proteins are generally marginally stable, why eukaryotes may have more disordered proteins than prokaryotes, and what the consequences of this are for biochemical networks. We also consider how various locations in a protein can co-evolve, and how this can inform the next generation of substitution models.

West Coast USA: 10:00 (10:00 AM) on Friday, April 20
East Coast USA: 13:00 (01:00 PM) on Friday, April 20
England: 18:00 (06:00 PM) on Friday, April 20 France: 19:00 (07:00 PM) on Friday, April 20 Japan: 02:00 (02:00 AM) on Saturday, April 21 New Zealand: 05:00 (05:00 AM) on Saturday, April 21

Frederick "Erick" Matsen, Assistant Member Fred Hutchinson Cancer Research Center http://-matsen.fhcrc.org/ Erick Matsen <matsen@fhcrc.org>

Physicians with EvolutionPhD

Evoldir:

As part of a NESCent-funded working group 'Infusing Evolutionary Thinking into Medical Education', we are looking for people with a PhD in evolutionary biology/biological anthropologywho are now practicing physicians/medical doctors or in training.

If you know of any such folk, please ask them to email one of us (a.read@psu.edu OR g.r.bentley@durham.ac.uk). If you have lost contact, please email their name and any contact details as you have (which medical school, roughly when they started), and we'll try to track them down. We are interested in all ages, all countries, and any area of evolutionary studies.

At this point we just want to discuss our working group topic with medical trainees and professionals who also have advanced evolutionary research training. But we might also try to grow this into an ongoing network to further broader professional interests.

Many thanks,

Andrew & Gillian

Andrew F Read PhD Director, Center for Infectious Disease Dynamics, Alumni Professor in the Biological Sciences, and Professor of Entomology, Penn State, University Park PA16802, USA www.thereadgroup.net

Gillian R Bentley PhD, Professor of Anthropology, and Professor of Health and Human Sciences, Centre for Integrated Health Care Research Centre for the Coevolution of Biology and Culture, Durham University, UK http://www.dur.ac.uk/research/directory/-staff/?mode=staff&id=4377

a.read@psu.edu

Randomly resolve polytomies

Hi, i would appreciate it if someone could tell me if there is a python module available that can be used to randomly resolve polytomies on phylogenetic trees.

Thanks in advance

Wasiu

Wasiu Akanni <waakanni13@gmail.com>

Robert Sokal has passed away

We are sad to report that Distinguished Professor Emeritus Robert R. Sokal passed away in Stony Brook on Monday, April 9, 2012 at the age of 86. Prof. Sokal was a founding member of the Department of Ecology and Evolution at Stony Brook University, co-founder of the methodological school of Numerical Taxonomy, and the principle investigator for major research programs in the spatial variation of insects and humans and the evolutionary response to selection in insects. He supervised the training of numerous Ph.D. students and taught biometry to a much larger number. He was a member of the National Academy of Sciences of the USA and received many other honors during his remarkable career. We in the Department of Ecology and Evolution at Stony Brook will miss his insights, support, and friendship.

Prof. Sokal was born into a middle class Jewish family on January 13, 1926 in Vienna, Austria, the only child of Klara and Siegfried Sokal. He fled the looming Nazi menace with his family in 1938 to Shanghai, China, which became the refuge for tens of thousands of European Jews during World War II. Robert attended secondary school and college in Shanghai, earning his B.S. degree in Biology from St. John's University in 1947. There he also met a young Chinese student, Julie Chenchu Yang, who became his wife and lifelong love. A book entitled Letzte Zuflucht Schanghai (Final Refuge Shanghai) by Stefan Schomann (2008) in German and translated into Chinese chronicled Robert's flight from Vienna, his family's refuge in Shanghai, and the start of his life with Julie, before he came to the United States for his graduate education.

Prof. Sokal received his graduate training at the University of Chicago, where he earned his Ph.D. in Zoology in 1952 under the direction of entomologist Alfred E. Emerson and was strongly influenced by Sewall Wright. He joined the Entomology Department at the University of Kansas in 1951 as an instructor, and rose rapidly through the academic ranks to Professor of Statistical Biology in 1961. He was recruited by Lawrence B. Slobodkin to the fledgling Department of Ecology and Evolution at the State University of New York at Stony Brook in 1968, where he spent the remainder of his career.

Prof. Sokal's scientific publications span a broad range of subjects and seven decades. He published major papers in ecology, evolution, anthropology, geography, statistics, and of course systematics. His papers appeared in Science, Nature, PNAS USA, and many of the best specialty journals in ecology, evolution, systematics, anthropology, and statistics. He is probably best known to evolutionary biologists and ecologists for his Biometry textbook with F. James Rohlf, the fourth edition of which he completed less than a year before his death. A recent search of Google Scholar indicated that the third edition of Biometry had been cited 19,851 times. Prof. Sokal is also well known as the co-founder of Numerical Taxonomy with Peter H. A. Sneath in 1963. This work promoted digital methods for classification and was controversial both because it advocated abandonment of traditional evolutionary systematics and led to the debate between the advocates of phenetic and cladistic methods. Regardless, it is undeniable that Prof. Sokal pioneered the use of rigorous, objective statistical methods and the employment of computers in systematics. Prof. Sokal started his career with dissertation research on patterns of geographical variation in Pemphigus aphids. Later, he initiated research on the evolutionary response to selection in laboratory populations of Tribolium beetles and house flies. His last major empirical project, which he pursued for more than two decades, focused on analysis of patterns of spatial variation in human populations for a variety of traits and the development of new methods for these analyses. Prof. Sokal published 12 books (5 translated) and 206 articles, and his publications have been cited tens of thousands of times.

Prof. Sokal came to Stony Brook University as a Professor in 1968. He was named Leading Professor in 1972 and Distinguished Professor in 1991. He retired in 1995 and became a very active Distinguished Professor Emeritus. He served as the Chair and Graduate Program Director of the Department of Ecology and Evolution at Stony Brook University from 1980 to 1983 and as Vice Provost for Research and Graduate Studies from 1981 to 82. He remained very active in scientific research, the Department of Ecology and Evolution, university affairs, and the National Academy of Sciences, even attending departmental colloquia until the last year of his life, when his declining health precluded it.

Prof. Sokal also served in many other prestigious capacities, including President of the Society for the Study of Evolution, the American Society of Naturalists, the Classification Society, and the International Federation of Classification Societies, the last of which he helped found.

— / —

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

RogueTaxa Bootstraps

Dear EvolDir members,

the consensus tree of a set of bootstrap trees can frequently exhibit poor resolution or sub-optimal branch support because of unstable taxa (also referred to as rogue taxa). Analogously, rogue taxa may also affect branch support values for maximum likelihood trees.

Recently, we made available a web-service, that allows to identify rogue taxa in a set of bootstrap trees. Optionally, if also a single best-known tree (under ML/MP) is provided, our algorithm can identify rogue taxa with respect to the branch support values drawn onto this tree (for both cases the set of rogue taxa is often similar, but not necessarily identical).

In other words, for consensus trees we can say that our algorithm produces a result that is a compromise between a potentially poorly resolved/supported consensus tree and a maximum agreement sub-tree (that often only comprises few taxa).

The URL to our server is http://exelixis-lab.org/roguenarok.html Using the web-interface, you can compare the results of various rogue taxon searches (including stability measures such as the taxonomic instability index and the leaf stability index). Finally, the websites integrates a tree viewer that can be used to visualize your consensus tree/best-known tree before and after removing various sets of rogue taxa.

Feedback and comments are most welcome, preferably via the RAxML google group.

Best regards, Andre J. Aberer

M.Sc. (Bioinformatics) Scientific Computing Group

Heidelberg Institute for Theoretical Studies (HITS gGmbH) Schloss-Wolfsbrunnenweg 35 D-69118 Heidelberg

Tel.: +49 6221 533 264 Fax: +49 6221 533 298 Email: andre.aberer@h-its.org WWW: http://www.exelixis-lab.org http://www.h-its.org/english/research/sco/index.php Amtgericht Mannheim / HRB 337446 Managing Directors: Dr. h.c. Dr.-Ing. E.h. Klaus Tschira, Prof. Dr.-Ing. Andreas Reuter

“Andre J. Aberer” <andre.aberer@googlemail.com>

Snake primers

Dear Evoldir members,

I would like to amplify a DNA mitochondrial fraction (maybe COI, 16S rDNA or 12S rDNA) from snakes. The samples that I have are museum specimens contaminated with human DNA and therefore I require primers that will only amplify reptile DNA to avoid contamination.

Thanks and best regards Michael Jowers

michaeljowers@hotmail.com

TravelGrants ConservationGenomics

TravelGrants - ConservationGenomics

Dear colleagues,

The European Research Networking Programme "ConGenOmics", supported by the European Science Foundation, invites applications for travel grants intended to foster collaborations between European researchers working on topics related to the programme.

We will support the exchange of researchers, ideally targeting at early career researchers such as PhD students and postdocs. We invite applications for short visits (1-2 weeks) as well as longer exchange visits (up to 4 months) to foster scientific interactions between institutions from different countries. The planned visits should be directly relevant to the scope of the ConGenOmics network, which include topics such as:

- Development and transfer of genomic knowledge and approaches in a conservation context

- Experimental study of the (genomic) mechanisms behind important biological processes of relevance for conservation

- Application and development of data handling and processing strategies in conservation genomics

- Application of community and metagenomics in conservation biological context

After assessment of scientific merit and relevance to the ConGenOmics network, priority will be given to applications in the following order:

- knowledge exchange between countries contributing (*) to this network

- knowledge exchange between a contributing country and a non-contributing ESF member country or the associated USA Ecogenomics network

- knowledge exchange between a contributing country and a non-ESF member country in Europe

- knowledge exchange between a contributing country and any country not covered by 1-3

* contributing member countries are: Belgium, Denmark, Finland, Germany, Greece, Italy, Luxembourg, Netherlands, Norway, Portugal, Spain, Sweden, Switzerland

Further information and instructions on how to apply are available at

http://www.ru.nl/congenomics/grants-application/-travel-grants/

Deadline for submission: 15 April 2012

p.vergeer@science.ru.nl

UMelbourne VolFieldAssist AvianPopulations

Volunteer field assistants: We are looking for field assistants to help monitor a colour-banded population of superb fairy-wrens near Melbourne, Australia for a study on animal personalities. Start date: September or October 2012. Time period: approx 4 months. Duties include regular censusing of colour-banded birds, searching for and monitoring nests, mist-netting, behavioural observations, video analysis, and data proofing. Working days are long, with early starts six days a week. Enthusiasm and a strong work ethic are a must. The study is based at Serendip Sanctuary, a small reserve on the outskirts of Melbourne. Qualifications: experience monitoring colour-banded birds, nest-searching, and mist-netting. Must also be early riser, physically fit, able to work in extreme weather conditions, and enjoy basic shared living conditions. Onsite accommodation in a house with shared dorm-style room is provided, but assistants cover travel to the site and their own food costs. The project will reimburse up to AUD$500/mo towards receipted food and travel expenses. For more information contact: Michelle Hall (hall.m@unimelb.edu.au) and Raoul Mulder (r.mulder@unimelb.edu.au). To apply, please email a letter outlining previous field research experience, and a resume including names and contact information for 3 referees.

Dr Michelle L Hall Research Fellow Department of Zoology, University of Melbourne Melbourne, VIC, 3010, Australia email: hall.m@unimelb.edu.au phone: + 61 3 83446232

hall.m@unimelb.edu.au

Wildfowl demography

Hello,

My name is Beth Roberts and I am doing research on wildfowl demography. Many species outside of Europe and North America have limited information. I am keen to source any demographic information on any wildfowl species. If anyone knows of any good information sources then please contact me by email b.roberts@mmu.ac.uk or via twitter bethroberts@duckgirl72.

Thanks, Beth

Beth Roberts Academic Support Tutor E418/ PhD Student "Macro-demography and the conservation of the World's wildfowl" Details of research- http://www.sste.mmu.ac.uk/users/smarsden/Research/BethRoberts.html School of Science & the Environment Manchester Metropolitan University 0161 2471529

Beth Roberts <B.Roberts@mmu.ac.uk>

Workshops Courses in Genomics

Colleagues,

An increasing number of labs I work with are moving towards 454, Illumina, or similar next generation genome or transcriptome sequencing projects. I am frequently asked about North American or UK workshops or courses for molecular biologists that wish to learn about generation and analysis of these data, particularly genome assembly. Most of these are Ph.D. level investigators but often without sophisticated computational skills. Could you please suggest appropriate courses for these investigators (Sanger, Woods Hole, Cold Spring Harbor?). Please reply to me directly and I will post a summary to EvolDir.

Much thanks, Andrew McArthur

Andrew G. McArthur, Ph.D. Bioinformatics Consulting Services Email: amcarthur@mac.com, Web: http://mcarthurbioinformatics.ca/ Phone: 905.296.3252, Mobile: 905.745.2794, Fax: 647.439.0829 Skype: agmcarthur

Based in Gothenburg, Sweden July 2012 through August 2013. Gothenburg is 6 hours ahead of the Eastern Time Zone (e.g. Toronto/Boston) and 9 hours ahead of the Pacific Time Zone (e.g. Los Angeles).

amcarthur@mac.com

Workshops Courses in Genomics answers

With thanks to those who replied, here is the information I gathered on possible Workshops/Courses in Genomics:

Programming for Evolutionary Biology March 17th - April 1st 2012 Leipzig, Germany http://evop.bioinf.uni-leipzig.de/ The Gulbenkian Training Programme in Bioinformatics (Portugal) http://gtpb.igc.gulbenkian.pt/bicourses/ Workshop on Genomics / Workshop on Molecular Evolution Czech Republic http://evomics.org/ On 2012-03-31, at 1:18 AM, evoldir@evol.biology.mcmaster.ca wrote:

Colleagues,

An increasing number of labs I work with are moving towards 454, Illumina, or similar next generation genome or transcriptome sequencing projects. I am frequently asked about North American or UK workshops or courses for molecular biologists that wish to learn about generation and analysis of these data, particularly genome assembly. Most of these are Ph.D. level investigators but often without sophisticated computational skills. Could you please suggest appropriate courses for these investigators (Sanger, Woods Hole, Cold Spring Harbor?). Please reply to me directly and I will post a summary to EvolDir.

Much thanks, Andrew McArthur

Andrew G. McArthur, Ph.D. Bioinformatics Consulting Services Email: amcarthur@mac.com, Web: http://mcarthurbioinformatics.ca/ Phone: 905.296.3252, Mobile: 905.745.2794, Fax: 647.439.0829 Skype: agmcarthur

Based in Gothenburg, Sweden July 2012 through August 2013. Gothenburg is 6 hours ahead of the Eastern Time Zone (e.g. Toronto/Boston) and 9 hours ahead of the Pacific Time Zone (e.g. Los Angeles).

Andrew McArthur <amcarthur@mac.com>

PostDocs

AarhusU FishPopulationGenomics

Postdoc position in fish population genomics

A two year postdoctoral position will be available at the Department of Bioscience, Aarhus University, Denmark, in the research group of Prof. Michael M. Hansen, starting 1 September 2012 or as soon as possible.

The appointed postdoc will work primarily but not exclusively on a project concerning contemporary evolution and adaptive divergence in three-spine sticklebacks using methods including RAD sequencing and RNAseq. Involvement in another project on speciation and footprints of selection in Atlantic Anguillid eels is also anticipated, along with other ongoing research activities. Some participation in teaching and supervision activities is also expected.

Applicants should have a Ph.D. in evolutionary biology and/or population genetics/genomics and must document good skills in statistical analysis of molecular markers/population genetic data and in writing scientific papers. Applicants who have experience with bioinformatics analysis will receive particularly serious consideration. Finally, applicants should be ambitious, show strong capabilities for team-work, and should also be able to take initiatives and responsibility.

Applications should be submitted online (see http://www.au.dk/en/about/job/nat/academicpositions/) and should include a CV, publication list, a 1-2 pages description of research experience and research interests, and the names and contact details of two-three persons who can be contacted for recommendations.

The Department of Bioscience offers an ambitious, scientifically strong but also socially pleasant working environment.

For more information about the Department of Bioscience, see www.bios.au.dk For further details on the position, please contact Michael M. Hansen (mmh@biology.au.dk)Deadline for applications is 3 June 2012.

Michael M. Hansen

Michael Møller Hansen <michael.m.hansen@biology.au.dk>

AustralianNatlU EvolutionBiodiversity

POSTDOCTORAL RESEARCH IN MACROEVOLUTION AND MACROECOLOGY.

A postdoctoral research position is available in the Centre for Macroevolution and Macroecology in the Evolution, Ecology and Genetics Division of the Research School of Biological Sciences at the Australian National University in Canberra. ANU is the top research institution in Australia, and ranks in the top 30 universities in the world. It provides an excellent research environment and career opportunities for researchers.

DIVERSIFICATION OF A HOTSPOT FLORA

The origins of biodiversity hotspots are still incompletely understood, particularly those located in Mediterranean-climate regions. This includes Australia's southwest, where there are over 7000 plant species, half of which are endemic. We are using phylogenetic, geographic and ecological data to investigate the spectacular diversity of southwest Australia, focusing on the massive radiation of the Proteaceae family as a case study. We are testing general explanations of diversity including models based on clade age, diversification rates, and ecological carrying capacity, as well as hypotheses more specific to the southwest. The postdoctoral researcher will be responsible for constructing large species-level molecular phylogenies, assembling databases of species geographic distributions and ecological traits, then using these to analyse patterns and test models of diversity.There is plenty of scope for development of novel and innovative analytical approaches. See http://jobs.anu.edu.au/PositionDetail.aspx?p=2692 for more details.

Position is for two to three years.A flexible appointment can be considered (e.g. part time or flexible hours). More information on the research project, employment conditions and application procedure are available from marcel.cardillo@anu.edu.au.

marcel.cardillo@anu.edu.au

AustralianNatlU Macroevolution

POSTDOCTORAL RESEARCH IN MACROEVOLUTION AND MACROECOLOGY.

A postdoctoral research position is available in the Centre for Macroevolution and Macroecology in the Evolution, Ecology and Genetics Division of the Research School of Biological Sciences at the Australian National University in Canberra. ANU is the top research institution in Australia, and ranks in the top 30 universities in the world. It provides an excellent research environment and career opportunities for researchers.

PHYLOGENETIC ANALYSIS OF PATTERNS OF EVOLVABILITY

Does the tempo and mode of evolution increase in particular times, places or lineages? Why are some lineages more or less successful over evolutionary time? Does evolution result in traits that increase the generation of variation or the efficiency of selection? The emphasis of this research program is to frame questions such as these in a way that allows them to be tested and applied to important case studies. The postdoc will develop and extend a broad-scale comparative approach to these questions, in particular making use of the analysis of large molecular phylogenies and patterns of molecular evolution. There is considerable scope for the postdoc to develop innovative and independent research within this program. See http://jobs.anu.edu.au/PositionDetail.aspx?p=2691 for more details.

Position is for two to three years.A flexible appointment can be considered (e.g. part time or flexible hours). More information on the research project, employment conditions and application procedure are available from lindell.bromham@anu.edu.au

marcel.cardillo@anu.edu.au

CityUNewYork Bioinformatics

I'm looking for a postdoc with bioinformatic experience and interested in using RNA-Seq or Illumina high seq applications to identify marine snail proteins. Postdoctoral candidates must be citizens or non-citizen nationals of the United States, or have been lawfully admitted to the United States for permanent residence.

Need not be in malacology to apply, but have to be knowledgable with cDNA/EST library construction and analysis.

The person would start this summer 2012. The appointment is for 2 years with a salary of $42K/year.

All interested candidates should send a CV and two letters of recommendations by April 16, 2012 to mholford@hunter.cuny.edu.

Please let me know if you need more info.

Thank you for your consideration,

Mands

Mandë Holford <mholford@york.cuny.edu>

CSIRO Biodiversity

CSIRO research is helping to underpin a national effort to halt biodiversity decline. This Post-doctoral research position will join the challenge by exploring and quantifying the importance of connectivity for the ecological function and persistence of plant species in patchy habitats.

In this PDF position you will use your experience developing multi-population computer simulation models to incorporate realistic genetic and demographic dynamics, at both the within- and between-population scales. You will be supported to identify, develop and/or pursuing novel research approaches calumniating in publication in high end journals and presentations to national and international conferences, as well as to biodiversity managers and policy makers.

Part of this role includes international travel to collaborate with leading scientists in this filed. Furthermore, CSIRO offers all Post- doctoral fellows a development plan, tailored to your experience and interests, to further your career in science. Part of the plan includes formal and on the job training with mentoring also an option. You will have access to CSIRO's extensive research facilities as well as the opportunity to collaborate with post-doctoral and research scientists in other CSIRO Divisions.

Specifically you will:

*Develop multi-population computer simulation models that include genetic and demographic processes

*Use models to explore the importance of connectivity for persistence of plant populations and the implications for landscape management

*Participate in field trips to collect data and international travel to attend conferences and work with collaborators

*Participate in the identification of further opportunities arising from research and initiate new lines of investigation

Location: Black Mountain, Canberra, Australia

Salary: AU$75K - $82K per annum plus up to 15.4% superannuation

Ref no: ACT12/00975

Tenure: 3 year term appointment

Do you have:

*PhD in population ecology or genetics with less than 3 years postdoctoral experience in a relevant field

*Experience in the development and application of simulation models to address population or evolutionary problems

*Experience in identifying, developing and/or pursuing novel research approaches

*Evidence publishing results of research in scientific journals and presentations at national or international meetings

*Demonstrated ability to achieve results

About CSIRO: Australia is founding its future on science and innovation. Its national science agency, CSIRO is a powerhouse of ideas, technologies and skills for building prosperity, growth, health and sustainability. It serves governments, industries, business and communities across the nation. Find out more! www.csiro.au< http://www.csiro.au >.

Find out more! For further information and instructions on how to lodge your application, please visit our website at CSIRO Careers http://csiro.nga.net.au/cp/-index.cfm, choose "Job Search" and insert Reference Number ACT12/00975 where indicated.

Kind Regards, Katie Wise

Recruitment Consultant CSIRO Human Resources Phone: +61 2 62464045

Katie.wise@csiro.au | Recruitmentteam-ACT@CSIRO.au | www.csiro.au RecruitmentTeam-ACT@csiro.au

---

DukeU nonmodelGenomics

One (possibly two) postdoctoral positions are available in the laboratory of Anne Yoder in the Department of Biology at Duke University. Lab interests are focused on the vertebrates of Madagascar, especially the iconic lemurs. Current projects in the lab include speciation dynamics in mouse lemurs, phylogeography and conservation genetics of Madagascars terrestrial vertebrates, the metagenomics of the gut micorflora in lemurs, and study of hibernation behaviors in mouse and dwarf lemurs. The successful applicant(s) will have opportunities to collaborate on these projects and/or to develop independent and complimentary projects.

This postdoctoral search is particularly focused on adding genomic and bioinformatics expertise to our current emphasis on PCR and Sanger sequencing techniques. With the advent of new sequencing technologies, opportunities exist for exploring genotype/phenotype connections in non-model organisms that were unthinkable, only a few years ago. As a successful candidate, you will have expertise in some or all of the following: RNA-seq methods, short-read sequencing techniques, and/or bioinformatic approaches to large data sets. The lab has an explicit evolutionary focus, so candidates should have familiarity with or proficiency in phylogenetic and/or population genetic methods.

The successful candidate(s) will be highly organized, mature, enthusiastic, and motivated. And dont forget to bring your esprit de corps and joie de vivre!

Conditions:

Current funding is for two years, with the possibility of a third year, depending upon successful performance evaluations and opportunities for additional funding. Salary is competitive, and the position(s) will carry full Duke benefits. Review of applications will begin on May 15, 2012. A start date of September 1, 2012 is ideal.

To Apply:

Via email, send current CV, publications, and contact information for three to four references to:

Anne D. Yoder, Professor Departments of Biology & Ev. Anth. Duke University, Box 90338 BioSci 130 Science Drive Durham, NC 27708 ph: 919-660-7275 fax: 919-660-7293 anne.yoder@duke.edu http://www.biology.duke.edu/yoderlab/ Director, Duke Lemur Center 919-489-3364, ex. 223 http://lemur.duke.edu/ Anne Yoder <anne.yoder@duke.edu>

EdinburghU PopulationGenomics

Post-doctoral Research Fellow in population genomics

Edinburgh University School of Biological Sciences / Institute of Evolutionary Biology

Vacancy Ref. No: 3015647

Closing date: 29 May 2012

Job description

Funding body: NERC Hours: Full time Start date: 09/2012 Duration: 3 years Supervisor: Prof Graham Stone Informal enquiries: Prof Graham Stone (graham.stone@ed.ac.uk) and Dr Konrad Lohse (Konrad.lohse@ed.ac.uk).

Job Profile

The post is funded as part of a NERC-funded project (NE/J010499) titled “Genomic approaches to inference of population history and multispecies community assembly”, with PI’s Graham Stone and Konrad Lohse (Edinburgh University) and James Cook (Reading University). The project combines development of new theory (PRDA) with generation and processing of genomic data for appropriate target species (project-dedicated Bioinformatician and NERC Genepool) to test alternative models for the history of assembly of biological communities. By design, all of the target species are wasps, which have haploid males - significantly simplifying data processing and analysis.

You will develop coalescent theory for non-equilibrium models of population structure. The main goal of the project is to devise analytical tools (both numerical likelihood and Approximate Bayesian Computation) for the analysis of genomic data. A particular focus is to find ways to jointly utilize information contained in the distribution of genealogies (multilocus-type methods, see Lohse et al. 2011) with information contained in patterns of linkage disequilibrium. A second aim is to develop hierarchical models that allow the analysis of multispecies data under complex historical scenarios (see Stone et al. 2012 and Wen et al. 2011). You will benefit from the expertise of project partners Prof Nick Barton (Institute of Science and Technology Austria) and Prof Mike Hickerson (Queens College - City University of New York) in these areas.

The new inference methods will be tested on both simulated data and de novo genome assemblies from insect host and parasitoid species (multiple individuals and populations sampled from a total of 20 target species) in two natural communities (Oak gallwasps and their natural enemies in Europe; figwasps and their natural enemies in eastern Australia). Comparisons of population histories across species and trophic levels will in turn be used to evaluate alternative models of community assembly (see Stone et al. 2012).

The hi-throughput sequence data will be assembled and prepared for population genetic analysis by a project-dedicated bioinformatician. The post includes some provision for training in genomic informatics with the NERC Genepool.

References

Wen H et al (2011). MTML-msBayes: Approximate Bayesian comparative phylogeographic inference from multiple taxa and multiple loci with rate heterogeneity. BMC Bioinformatics 12: Article Number 1, DOI: 10.1186/1471-2105-12-1.

Lohse K, Harrison R. J. and Barton N. H. (2011) A General Method for Calculating Likelihoods Under the Coalescent Process. Genetics 189(3): 977-U398

Stone GN et al. (2012) Reconstructing community assembly in time and space reveals enemy escape in a western Palearctic insect community. Current Biology 22: 1-6.

Person specification

We are looking for a highly motivated individual excited by the potential of high throughput sequencing data for exploring issues in population genetics and community ecology, and with the ability to explore novel inference methods.

Essential Desirable A PhD in biology (or a related quantitative discipline) and a strong research background in population genetics or statistics - ideally coalescent theory - are essential. This includes a track record of publishing high impact papers in these areas and a proven ability to work independently. A strong interest in the analysis of population and community level genomic data. Bioinformatics, programming experience and wet lab skills would be desirable. However, applicants from quantitative disciplines outside biology (such as applied mathematics) will be considered. Salary

The role is grade UE07 and attracts an annual salary of £30,122 to £35,938 for full-time hours. Salary is paid monthly by direct transfer to your Bank or Building Society account, normally on the 28th of each month. Salaries for part-time staff are calculated on the full-time scales, pro-rata to the Standard Working Week.

We anticipate interviews will be held in one/two weeks after the closing date. If you have not been invited for interview by this date, you have not been successful.

UKBA Certificate of Sponsorship

Should you require a visa to undertake paid employment in the UK you will be required to fulfil the minimum points criteria to be granted a Certificate of Sponsorship and Tier 2 visa. As appropriate, at the time an offer of appointment is made to you, you will be asked to demonstrate

— / —

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

---

FloridaStateU MarineEvolution

Postdoctoral Position in marine evolutionary ecology

I have a position in my lab for a postdoctoral researcher interested in the ecology and evolution of sperm and egg interactions in marine invertebrates. Our on-going research examines the evolution of gamete recognition proteins in sea urchins.We us field and laboratory experiments to examine the fitness consequences of variation in these proteins as well as other reproductive traits.There are a number of projects planned, but there is flexibility in the research direction for this position. Experience with molecular techniques and analysis of molecular evolution would be a plus, but not a prerequisite.

If you are interested, please send me an email with a statement of your research interests and CV to Don Levitan (levitan@bio.fsu.edu).The position is annually renewable for at least two years.Start date is flexible.

Don R. Levitan

Professor Department of Biological Science Florida State University Tallahassee, FL 32306 Phone (850) 644-2524 http://bio.fsu.edu/~levitan/

levitan@bio.fsu.edu

Don Levitan <levitan@bio.fsu.edu>

GeorgiaTech MarineMicrobialGenomics

Postdoc in Marine Microbial Genomics

The Stewart lab in the School of Biology at Georgia Tech is looking for a postdoctoral fellow in microbial metagenomics and metatranscriptomics. The position is part of a 5-year NSF-funded project to study the genomic diversity, physiology, and evolution of sulfur-metabolizing bacteria in marine oxygen minimum zones (OMZs). The project will involve research cruises to both the Gulf of Mexico and the Eastern Tropical North Pacific Ocean, beginning in summer 2012. Research tasks will involve the design of field and lab experiments, microcosm analysis of community gene expression, molecular analysis of bacterial nucleic acids and proteins, and comparative bioinformatic analysis of large sequence datasets. The postdoc will be encouraged to develop independent lines of research within the broader goals of the project and the lab, and will work collaboratively with Dr. Stewart and other lab members to perform research and synthesize results for publication.

The ideal candidate will be enthusiastic, motivated by experimental and analytical challenges, and proficient in a range of molecular and bioinformatics techniques. Candidates should have a Ph.D. in genomics, microbiology or a related discipline, with demonstrated expertise in comparative genomics, metagenomics, or transcriptomics. Knowledge of the physiology of anaerobic microorganisms, microbial evolution, and marine microbiology is desirable.

The School of Biology at Georgia Tech is a dynamic research environment with a particularly strong core of researchers interested in marine systems, microbiology, and genomics. The Institute as a whole offers exceptional resources for bioinformatics and high-performance computing, and exciting opportunities for cross-departmental collaboration with computational scientists and earth and atmospheric scientists. Georgia Tech was recently voted one of the best places to work, and Atlanta is consistently ranked among the top ten places to live for young professionals.

The start date for this position is flexible, but would ideally be June or July 2012. Funding is available for at least two years, but is contingent upon satisfactory progress in year one; applicants should express their ability to commit to the project for the initial two years. Informal inquiries about the position can be sent to Frank Stewart at frank.stewart@biology.gatech.edu. Application materials should be emailed to the same address and should include a cover letter (describing your interest in the position, work experience, and availability), CV, and contact information (name, email, phone number) for at least three references. Please include the word “Postdoc” in the subject line. Salary will be competitive and commensurate with experience and will include fringe benefits.

Georgia Tech is a unit of the University System of Georgia and an Affirmative Action/Equal Opportunity Employer and requires compliance with the Immigration Control Reform Act of 1986.

– Frank J. Stewart, Ph.D. Assistant Professor School of Biology Georgia Institute of Technology ES&T building, office #1242 311 Ferst Drive Atlanta, GA 30332-0230 office: 404-894-5819 www.fjstewart.org

Guelph PathogenGenomics

POST DOCTORAL POSITION IN PATHOGEN GENOMICS AT THE PUBLIC HEALTH AGENCY OF CANADA (PHAC)

Applications are invited for a post doctoral fellowship position available April 2012 in a Genomics Research and Development Initiative (GRDI) project at the PHACs Laboratory for Foodborne Zoonoses, Guelph, Ontario, Canada. Fellowships are awarded initially for one year with the possibility of renewal for a second year.

The project is focused on development of high resolution molecular subtyping of the highly clonal enteric pathogen, Salmonella Enteritidis. The approach is to use whole genome sequencing to identify variably present or absent loci or SNPs that will provide highly discriminatory identification of related and unrelated strains.

With open whole genome sequences of numerous selected strains now available, the candidate will undertake genome assembly, annotation and analysis to identify panels of loci and/or SNPs that potentially will provide the required discriminatory power. These panels will then be evaluated on a broad range of strains.

The successful candidate should have PhD/post doctoral experience in molecular biology, bioinformatics and computational genomics of microbes. Previous experience with genomics of pathogens will be an advantage.

The lead scientists on the project are Roger Johnson and Kim Ziebell, supported by PHAC collaborators including Vic Gannon, Matthew Gilmour, Andrew Kropinski, Chad Laing and John Nash.

For more information: Roger.Johnson@phac-aspc.gc.ca

Starting date: Spring/Summer 2012, Year 1: to March 31 2013. Year 2: April 1 2013- March 31 2014.

Application deadline: April 15 2012

Stipend: approx: CDN$47,200 per year, under the Visiting Fellowships in Canadian Government Laboratories program of the National and Scientific and Engineering Research Council of Canada. http://www.nserc-crsng.gc.ca/Students-Etudiants/PD-NP/Laboratories-Laboratoires/index_eng.asp How to apply: Email your application to Roger.Johnson@phac-aspc.gc.ca as a single pdf file containing your CV with publications, contact details of two referees, and a letter (maximum 1 page) with a description of your research interests and why you would be a suitable candidate for the position.

Roger Johnson MVSc, PhD, Research Scientist & Director of Reference Laboratories, Public Health Agency of Canada, Laboratory for Foodborne Zoonoses 110 Stone Road West, Guelph, ON, N1G 3W4 Tel: 519 826 2644; Fax: 519 822 2280; email: Roger.Johnson@phac-aspc.gc.ca

Roger Johnson <Roger.Johnson@phac-aspc.gc.ca>

Gulbenkian Lisbon CytoskeletonEvolution

Cytoskeleton Organization In Development, Disease And Evolution

Position: We have two postdoctoral/doctoral positions available, funded by the European Research Council, an EMBO installation grant and EMBO YIP. Fellowships may be taken for up to 3.5 years. Positions are available from August 2012 for highly motivated scientists.

Research projects: Our research focuses on the cytoskeleton in normal development, disease and evolution, with a focus on the centrosome, cilia and flagella. These structures are often altered in a variety of human diseases such as cancer and infertility. Our laboratory uses an integrated approach that combines cell biology, genetic and biochemistry studies in model organisms and in human cells, with bioinformatics, mathematical modelling and patient samples. One Fellowship will focus on studying the mechanisms of regulation of centrosome number, while the other focuses on the mechanisms controlling centriole structure, two properties that are often altered in human disease.

Publications: Brito et al, COCB, 2012; Carvalho-Santos et al, JCB, 2011; Carvalho-Santos et al, JCS, 2010; Cunha-Ferreira et al, Curr Biol, 2009; Rodrigues-Martins et al, Science 2007; Rodrigues-Martins et al, Curr Biol, 2007.

Location: The Gulbenkian Institute (IGC) is an international institute located in a sea-side town close to Lisbon, Portugal, and integrated in a multidisciplinary campus. It is a world-leading biology research center, providing modern facilities and an exciting research environment. The IGC Postdoctoral Research Program focuses on developing the postdoc research, independence and leadership skills.

Application: We are seeking extremely motivated scientists. Experience using human tissue cultured cells or genetically tractable organisms (yeast, Drosophila, C. elegans) is a plus, but we will consider all backgrounds, including biology, chemistry, biochemistry, physics and medicine. To apply, please submit your CV, letter of intent of research and names of two referees to Mónica Bettencourt-Dias by the 12th of May 2012. Email: mdias@igc.gulbenkian.pt

Lab Website: http://sites.igc.gulbenkian.pt/ccr/ Mónica Bettencourt-Dias, PhD Cell Cycle Regulation Lab Instituto Gulbenkian de Ciência Rua da Quinta Grande, 6 P-2780-156 Oeiras, Portugal e-mail: mdias@igc.gulbenkian.pt Telephone: +351 214407925 (lab); +351 214407945 (office) Fax: +351 214407970 http://sites.igc.gulbenkian.pt/ccr/ Mónica Bettencourt Dias <mdias@igc.gulbenkian.pt>

Hannover EvolutionaryAdaptation

Postdoctoral and PhD position available immediately in the Schierwater lab at TiHo Hannover (Germany) for a motivated young investigator to undertake molecular studies on Trichoplax and other placozoans. Interest in fundamental questions of evolutionary adaptation, development, comparative genomics and systematics is essential. Experience with molecular systematics and genetics or bioinformatics is desirable. The successful candidate will have ample opportunity to pursue additional projects within the broad molecular ecology/evolutionary genetics scope of the institute. Our setting and facilities for marine biological research on placozoans are outstanding.

Please email CV, brief statement of research interests and experience, and a list of 3 references to Bernd Schierwater (bernd.schierwater@trichoplax.com; bernd.schierwater@ecolevol.de).

Bernd Schierwater ITZ Ecology & Evolution TiHo Hannover Buenteweg 17d D-30559 Hannover Germany www.ecolevol.de . Regards

Tina Herzog Scientific Secretary to Prof. Bernd Schierwater

University of Veterinary Medicine Hannover, Foundation Institute of Ecology and Evolution Buenteweg 17d D-30559 Hannover Germany Contact: +49 511 953 8882 Fax: +49 511 953 8584 tina.herzog@ecolevol.de

Tina Herzog <tina.herzog@ecolevol.de>

Leipzig MPI ComputBiol

- Postdoctoral position in computational/evolutionary biology -

There is an opening for a post-doctoral researcher with a strong academic background to pursue a research project in our group at the Max Planck Institute for Evolutionary Anthropology (Department of Evolutionary Genetics). One main aim in the laboratory is the characterization of genes whose protein functions require the trace element selenium. These genes incorporate selenium in the form of selenocysteine, the 21st amino acid in the genetic code, and are known as selenoprotein genes.

The researcher will develop computational methods to annotate selenoprotein genes and their regulatory regions in selected species. The goal is to develop comparative annotation tools that incorporate the uncertainty of (divergent) alignments into the annotation process. The researcher will also integrate variation data from large resequencing studies in the lab to these annotations. We will incorporate these results into SelenoDB (www.selenodb.org) to allow comprehensive evolutionary analysis of selenium-dependent genes within and between species. In addition, ample opportunities for the analysis of primate genomes in collaboration with other groups in the Department will exist.

We are seeking a motivated, well-organized and creative person. Knowledge of Hidden Markov Models, C and Perl programming languages and SQL would be advantageous.

The researcher will receive a payment according to Max Planck Institute rates. The working environment of the institute is English-speaking, and the members constitute a highly international group. The institute is in Leipzig, a pleasant city of 500,000 inhabitants situated two hours from Berlin and three hours from Prague. Applicants should send their CV, transcripts and name and address of two references (in PDF format) to Dr. Sergi Castellano (sergi.castellano@eva.mpg.de).

Sergi Castellano

Department of Evolutionary Genetics Max Planck Institute for Evolutionary Anthropology Deutscher Platz 6 04103 Leipzig Germany

Tel: +49 (0) 341 3550 806 Fax: +49 (0) 341 3550 555 www.eva.mpg.de/genetics Sergi Castellano <sergi.castellano@eva.mpg.de>

MemorialSloanKettering EvolutionCancer

Postdoctoral fellowship available: Evolutionary biology approaches to cancer using zebrafish

A postdoctoral position is available in the laboratory of Dr. Richard White at the Memorial Sloan Kettering Cancer Center and Weill Cornell Medical College. The laboratory has a broad interest in the mechanisms underlying genomic evolution during cancer progression and metastasis. We utilize genetic and small molecule screening approaches in the zebrafish, a model organism which allows for characterization of tumor and host cells during each phase of tumor evolution.

The ideal applicant is interesting in utilizing techniques commonly applied to evolutionary biology in the setting of cancer. The relevance of this approach can be appreciated when considering the thousands of mutations found in a typical tumor, and we are interested in understanding the mechanistic basis of variant generation and selection pressures in the rapidly changing tumor microenvironment. We are particularly interested in understanding how the host genetic background interacts with DNA/RNA variants in the tumor cell itself. Our techniques include high throughput whole genome, RNA-seq and ChIP-seq, along with chemical biology techniques.

The position will offer the opportunity for extensive scientific collaborations across diverse disciplines in a highly stimulating, creative environment. No background in cancer biology is necessary or expected, as the goal is to approach questions in cancer biology from a novel perspective.

Please send a CV, cover letter and the names of 3 references to whiter@mskcc.org. Informal enquiries are encouraged.

whiter@mskcc.org

RoyalBotanicGardens Melbourne GrassPopGenetics

"Postdoctoral Fellow (Grassland Genetics). Fixed term 2 Â½ year contract anticipated to start in June 2012, Melbourne, Australia.

This postdoctoral position based at the National Herbarium of Victoria, Australia provides an outstanding opportunity to join the Royal Botanic Gardens, one of Victoria's premier scientific and cultural organisations, as a Postdoctoral Fellow for the Plant Sciences Branch of the Plant Sciences and Biodiversity Division. In this important role you will undertake genetics research using molecular techniques to advance our understanding of the evolution and population genetics of four Victorian grassland species.

The National Herbarium of Victoria located at the Royal Botanic Gardens in Melbourne, is a major centre for botanical studies in Victoria and the collection of approximately 1.2 million plant specimens available for scientific study, is one of the largest and most important collections in Australia.

The ideal candidate will have a PhD in evolutionary/conservation genetics, or similar with extensive research experience in plant population genetics using molecular techniques and analysis of molecular 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.

For a position description please visit www.rbg.vic.gov.au. Please send applications to elizabeth.james@rbg.vic.gov.au by close of business Wednesday 9 May 2012. For further enquiries please call (61 3) 9252 2378. All applications must address the key selection criteria as stated in the position description."

Elizabeth James Conservation Geneticist Royal Botanic Gardens Melbourne Private Bag 2000 Birdwood Avenue South Yarra VIC. 3141

www.rbg.vic.gov.au tel: 9252-2378/2300

Elizabeth James <Elizabeth.James@rbg.vic.gov.au>

RoyalOntarioMuseum Toronto CichlidFishPhylogenetics

The Royal Ontario Museum (ROM) is Canada's preeminent international museum - a superlative showcase of the world's culture and natural history - a place of discovery, learning, inspiration and imagination, for visitors and staff alike.

Rebanks Postdoctoral Research Fellowship

Department on Natural History

The Royal Ontario Museum in Toronto invites applications for a Rebanks Postdoctoral Research Fellowship in the Department of Natural History. The successful candidate will work full time in the López-Fernández lab developing a phylogenomic framework for the study of Neotropical cichlid evolution. Results from this project will add to ongoing studies of phylogenetics, diversification patterns, evolutionary ecology, and molecular evolution of Neotropical cichlid fishes. The candidate will be able to interact with various collaborating labs and will be part of the active and diverse community of evolutionary biologists at the ROM and the University of Toronto.

We seek applicants with excellent skills in generation and analysis of DNA sequences for phylogenetic analysis. Specifically, extensive experience in primer design, PCR optimization, high-throughput sequencing, sequence editing and alignment. Demonstrable familiarity with theoretical phylogenetics, including current developments in gene-tree methods, and experience with phylogenetic analysis software including MrBayes, BEAST and RAxML is a requirement for the position.

Experience with next generation sequencing protocols and data management is a bonus.

The Fellowship is tenable for two years with an annual salary of $50,000. Candidates should submit a letter of application detailing their research experience and interest in the position, curriculum vitae, and the names and contact details of three references electronically to: Dr. Hernán López-Fernández (hernanl@rom.on.ca), Associate Curator of Freshwater Fishes, Department of Natural History, Royal Ontario Museum, 100 Queen's Park, Toronto, Ontario, M5S 2C6, Canada. Application materials must be received by April 30, 2012 for consideration. Only Canadian citizens or Canadian landed immigrants who have received their Ph.D. in the last five years are eligible for the position. We especially encourage applications from women and members of minority groups.

Hernán López-Fernández, Ph.D. Associate Curator of Freshwater Fishes Royal Ontario Museum 100 Queen's Park, Toronto Ontario M5S 2C6, Canada

And

Assistant Professor Department of Ecology and Evolutionary Biology University of Toronto

Email: hernanl@rom.on.ca, hlopez_fernandez@yahoo.com

Web: http://www.rom.on.ca/collections/curators/-lopezfernandez.php http://www.eeb.utoronto.ca/-people/faculty/lopez-fernandez

Hernan Lopez-Fernandez <hernanl@rom.on.ca>

SmithCollege CiliateGenomics

Smith College invites applications for a full-time postdoctoral research position focusing on genome evolution in the ciliate Chilodonella uncinata. The initial appointment is for one year, with the possibility of extending for additional years. The position will be housed in Professor Laura Katz's laboratory in the Department of Biological Sciences (http://www.science.smith.edu/-departments/Biology/lkatz/Research.htm); questions should be directed to lkatz@smith.edu.

An ideal candidate will: 1) be a productive researcher with interests in genome evolution in microorganisms; 2) have experience in both molecular biology and bioinformatics, 3) have excellent communication and interpersonal skills; and 4) be interested in collaborating with graduate and undergraduate students in the laboratory.

The goals of the project are to characterize the distinctions between germline and somatic genomes within C. uncinata, and to interpret the resulting data in an evolutionary and phylogenetic context. Ciliates are defined by the presence of two distinct genomes - the -germline' micronuclear and -somatic' macronuclear - within each cell. Chilodonella uncinata provides an ideal model for this study as its macronuclear genome is highly processed yielding a streamlined genome with millions of gene-sized chromosomes (i.e. most non-protein-coding sequences are eliminated). Specific hypotheses focus on the role of alternative processing of micronuclear loci in generating macronuclear protein family diversity, the relationship between macronuclear copy number and expression level, and the varying patterns of molecular evolution between germline and somatic genomes.

To apply, submit application at http://jobs.smith.edu with letter of application, C.V., a statement of research interests, representative publications, and the names and contact information of three references. Review of applications will begin April 30th, 2012.

Smith College is a member of the Five College Consortium with Amherst, Hampshire, and Mount Holyoke Colleges and the University of Massachusetts Amherst. Smith College is an equal opportunity employer encouraging excellence through diversity.

lkatz@smith.edu

StellenboschU FishGeneticDiversity

Postdoctoral position available in the Department of Genetics, Stellenbosch University (2 April 2012)

A postdoctoral position is available in the Aquaculture Division, Department of Genetics, Stellenbosch University with the focus on Genetic Diversity and Population Structure of farmed kob, Argyrosomus japonicus and Argyrosomus inodorus, and the potential genetic impacts of farmed fish on associated wild fish populations. This project is a collaborative effort with Marine and Coastal Management (Dr Brett Macey, Dr Sven Kervath) and the University of Pretoria (Prof Paulette Bloomer).

Exciting new industry initiatives are presently underway that are exploring the culture potential of indigenous marine finfish in South Africa. Two such species currently under investigation are the dusky kob Argyrosomus japonicus and silver kob A. inodorus. The proposed cage farming operations along the South African coastline have, however, raised concerns from both the public and conservation management authorities about the potential genetic impacts of farmed fish on wild populations. The current project is therefore aimed at the identification of populations or stocks along the southern African coast followed by the establishment of a broodstock management programme that can assist in the appropriate placement of farms and hatcheries as well as and minimize the potential negative genetic impact of farmed animals on wild fish populations.

The successful candidate will primarily be responsible for: 1) The identification of populations/stocks of A. japonicus and A. inodorus along the southern African coast based on species-specific microsatellites. 2) Assisting with the formulation of recommendations for kob farming along the South African coast.

Minimum requirements: PhD with specialization in Population and/or Evolutionary Genetics or any closely related discipline. Candidates should have proficiency in the relevant population analysis software packages and experience with microsatellite data will be an added advantage. The ideal candidate should also have proven project management experience and ability to set deadlines and meet milestones.

This position is available for 2 years and commencement of duties is set for July 2012.

Interested researchers are requested to send their CV including details of at least 2 references to Dr. Rouvay Roodt-Wilding at roodt@sun.ac.za

Closing date: 30 April 2012

roodt@sun.ac.za

TexasAMU MolecularPopGenetics

Postdoctoral Research Scientist - Molecular Population Genetics/Ecology

Department of Wildlife and Fisheries Sciences Texas A&M University College Station, Texas 77843-2258

Responsibilities: Position responsibilities involve development and assay of nuclear-encoded microsatellites and mitochondrial DNA sequences for projects involving population genetics and molecular ecology of marine fishes. Primary responsibilities include data acquisition and analysis, and preparation of reports and publications. Additional responsibilities will be participation in studies involving next-generation DNA sequencing.

Qualifications: Dissertation or postdoctoral work in molecular population genetics and/or molecular ecology is required, as is documented experience with microsatellite and mtDNA data acquisition and analysis. Documented experience with major software programs (e.g., Arlequin, Genepop, Migrate, LdNe, etc.) also is required. Individuals with experience in analysis of next-generation-sequencing data will be given high priority. Applicants should be ambitious, able to work collaboratively with other lab members, and capable of to taking initiative and assuming .

Salary: Salary range is from $35,000 - $40,000/year and will depend on experience. Benefits include health care and retirement. Position is for 12-24 months.

Closing date: Position will remain open until filled.

Contact: Send curriculum vitae, description of research experience/interests, and names, addresses, phone numbers, and e-mail address of three references to: Dr. John R. Gold, Department of Wildlife and Fisheries Sciences, Texas A&M University, College Station, Texas 77843-2258. Electronic submissions are preferred: goldfish@tamu.edu<mailto:goldfish@tamu.edu>. International applicants will be considered if they hold the correct visa(s). Texas A&M University is an Equal Opportunity/Affirmative Action/Equal Access Employer.

John Gold <goldfish@tamu.edu>

UAlberta PopGenetics

Post-doctoral opportunity in "Mathematical Modeling of Insect Invasion Dynamics, as informed by Pathosystem Genomics Data"

Context

Insect invasions are characterized by systematic changes in population numbers over time and space as insects reproduce and disperse into new host territory. The mountain pine beetle in North America is a system where an indigenous species has recently increased its range to threaten novel host species. Although the population dynamics of the natural system within its previous host range (British Columbia, W. of the Rocky Mountains) is relatively well-researched, there is tremendous uncertainty within the new host range (Alberta, E. of the Rocky Mountains) on key parameters, including beetle dispersal rates, host suitability, host vigor, and fungal pathogenicity.

Opportunity

An interdisciplinary project is continuing to examine the population genetics and functional genomics of the beetle-fungus-tree interaction, in order to characterize the uncertainty surrounding key population processes affecting outbreak wave propagation eastward. We are seeking a qualified applied mathematician or quantitative biologist to work with its team of scientists to develop a mathematical and statistical model of mountain pine beetle invasion biology that will use genomics-based data to inform the spread model. These include population genomic (large, spatially co-referenced microsatellite and SNP datasets for the beetle, fungus, and tree) and functional genomic data (gene expression analyses, physiological and biochemical characterization of experimental samples) that relate to the beetle-fungus-host symbiotic interactions. Relationships with various geographic and climatic factors will also be explored.

The incumbent will have a PhD in mathematical sciences and/or biological sciences with demonstrated experience in the development of analytical mathematical models of epidemiological processes, and a familiarity with simulation modeling approaches. A strong interest in the use of population genetics and functional genomics data is essential. Familiarity and interest in the problems of error propagation, uncertainty analysis, stochasticity, and non-stationarity in complex (i.e. nonlinear, multi-causal) systems is desirable.

The incumbent will be expected to work within a team framework with other modellers, population geneticists and physiologists. While the modeling endeavour will incorporate genomic information, there is substantial freedom to define the methods according to the experiences, talents, and interests of the incumbent.

The incumbent will split their residence between the University of Alberta and the Northern Forestry Centre, both in Edmonton, Alberta. The position will be co-supervised by Dr. Barry Cooke (Canadian Forest Service), Dr. Mark Lewis (Canada Research Chair in Mathematical Biology, U. Alberta) and Dr. David Coltman (Biological Sciences, U. Alberta).

Particulars

This is a multiyear position. The initial appointment is until August 31, 2013 with a possibility of extension based on successful performance. Interested individuals should submit an application package (cover letter and curriculum vitae) and arrange to have three sealed letters of reference forwarded to the address below. Electronic applications are preferred. Salary is commensurate with experience. Application deadline is May 1, 2012 or until filled.

Matt Bryman

Project Manager - The Tria Project. Mountain Pine Beetle System Genomics

CW 420 Biological Sciences Building

University of Alberta

Edmonton, AB, Canada

T6G 2E9

mbryman@ualberta.ca

Informal enquiries are encouraged and should be addressed to Dr. Cooke (bcooke@NRCan.gc.ca), Dr. Lewis (mlewis@math.ualberta.ca) or Dr. Coltman (dcoltman@ualberta.ca).

Matt Bryman

Project Manager

THE TRIA PROJECT: Mountain Pine Beetle System Genomics

www.thetriaproject.ca Phone: 780-492-1990

Matt Bryman <mbryman@ualberta.ca>

UCalifornia Berkeley SpeciesAdaptation

The Berkeley Initiative in Global Change Biology (BiGCB) at the University of California, Berkeley, is seeking applications for a Project Coordinator and Postdoc for the W.M. Keck Foundation Funded Project entitled *Informatics Engine for Understanding Biotic Response to Global Change*< http://ib.berkeley.edu/-labs/globalchange/keck.html > .

Postdoc: http://academicemployment.chance.berkeley.edu/-DetailsJobSearch.cfm?recordID=1238
*Project Coordinator: * http://-academicemployment.chance.berkeley.edu/-DetailsJobSearch.cfm?recordID=1232 *Job Title: * Postdoctoral Scholar - Employee *Job Type:* Full-time, Temporary position *Location: * University of California at Berkeley *Closing date: * May 14, 2012 *Position length:* 1 year (renewable for 1 year) *Start

date: * Start date is flexible, but no later than July 2012

*For official posting please see: * http://academicemployment.chance.berkeley.edu/DetailsJobSearch.cfm?recordID=1238 *Job number: * 12-9P

The Berkeley Initiative in Global Change Biology (BiGCB) at the University of California, Berkeley, is seeking applications for a Postdoctoral Scholar for the W.M. Keck Foundation Funded Project entitled* Informatics Engine for Understanding Biotic Response to Global Change.*

The next generation of predictive models of the biotic response to environmental change must meet the challenge of incorporating the effects of complex interactions among organisms, climate, and their physical and biotic environments. A great variety of data types are required to meet this challenge, including current and past species' distributions, data on their genotypes and phenotypes and how these have changed in space and time, as well as empirical and modeled data on environmental and climate change. The goal of the project is to develop the informatics infrastructure needed to access, visualize, and analyze these rich data, thus providing the foundation for building the next generation of models of the biotic response to global change. Initially, the data to be integrated will be largely drawn from Berkeley's Natural History Museums, Field Stations, and faculty labs. Please see * http://ib.berkeley.edu/labs/globalchange/funding.html* for more information.

The successful candidate, who will be an integral part of the project, will help drive the intellectual exploration of the kinds of questions one might ask of these data, and help identify the data needed to conduct global change research. S/he will conduct cutting-edge, multidisciplinary research that will demonstrate the scientific power of this engine.

Qualifications:

- PhD and up to 3 years of postdoctoral research experience in a relevant discipline, such as: ecology, evolutionary biology, or computer science. - Demonstrated record of writing and/or publishing of manuscripts and reports. - Demonstrated experience collaborating with other researchers. - Experience and knowledge of biodiversity, ecology, conservation and/or bioinformatics and a keen interest in natural history data and collections.

*Salary: * Salary commensurate with experience.

To apply: Applicants should send a cover letter, CV, and contact information for three references to Sandra Richmond, HR Manager, Research Enterprise Service, 3101A Valley Life Sciences Building, Berkeley, California 94720-3160. The cover letter should address interest in and vision for natural history collections and/or field data within the context of global change biology. Letters of reference are not requested at this time. Electronic submissions are acceptable, but all materials must be uploaded into Adobe PDF and sent to sandyjbr@berkeley.edu, with the subject: BIGCB KECK Postdoc - [Applicant Name].

The University of California is an Equal Opportunity/Affirmative Action Employer and encourages qualified women and minority candidates to apply.

*Project Coordinator (Payroll title: Assistant/Associate Specialist, Job # 12-100) Berkeley Initiative in Global Change Biology (http://ib.berkeley.edu/labs/globalchange/) University of California, Berkeley

**Deadline for applications is May 3, 2012.*

The Berkeley Initiative in Global Change Biology (BiGCB) at the University of California, Berkeley, is seeking applications for a Project Coordinator for the W.M. Keck Foundation Funded Project entitled *Informatics Engine for Understanding Biotic Response to Global Change*. A one-year position is

— / —

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

UCIrvine MosquitoChromosomeEvolution

UCIrvine.MosquitoChromosomeEvolution

Applications are invited for a postdoctoral scholar position in the laboratory of Dr. José M. Ranz at University of California Irvine. The major goal of the project is to study the functional genomics of chromosomal rearrangements in the malaria vector Anopheles arabiensis. The position is available starting in June 2012 for two years. The successful applicant will be based the first 9 months at the Institut de Recherche en Sciences de la Santé (IRSS), Bobo-Dioulasso, Burkina Faso. The project involves the molecular analysis of breakpoints of chromosomal inversions involved in the adaptation of Anopheles arabiensis and the characterization of genome-wide patterns of expression divergence between alternative chromosomal arrangements. A strong background in mosquito genetics is required and some experience in cytogenetics, molecular biology, and bioinformatics is desired. Particularly encouraged are applicants with prior experience in field malaria research. Salary commensurate with experience. Applications should include a covering letter describing previous experience and fit to the position, full CV with a list of publications, and the name and address of two references. The deadline for applications is May 4th 2012. Applications should be sent to the email addresses below:

Dr. José M. Ranz jranz@uci.edu

Dr. Diego Ayala diego.ayala@nd.edu

Dr. Roch Dabiré dabire_roch@hotmail.com

The University of California, Irvine is an equal opportunity employer committed to excellence through diversity, has an active career partner program and a National Science Foundation Advance Gender Equity Program.

Jose Ranz <jranz@uci.edu>

UColorado Boulder SpeciationGenomics

Postdoctoral Fellowship on the Genomics of Speciation: The Safran lab in the Department of Ecology and Evolutionary Biology at the University of Colorado is looking for a postdoctoral fellow to work on a five-year NSF-funded project on the genomics of population divergence in barn swallows (genus Hirundo). This project will entail extensive sample collection in 35 countries across the northern hemisphere during the spring and summer months and assembly and analysis of large genomic data sets during most of the academic term. We are interested in someone who is able to travel flexibly and competently for sampling transects through the Middle East, and across all of Eurasia and North America, including some very remote and logistically difficult locations. The ideal candidate will be energetic and enthusiastic, have a track record in international field research, have expertise in speciation biology with knowledge of populationgenetics and an interest in learning cutting-edge population genomics tools, previous fieldwork experience on wild birds, and be able to work well within our growing lab group. The applicant must be able to commit to working on the project for at least 2 years and indicate interest in developing related yet independent lines of research. Please contact Dr. Rebecca Safran (Rebecca.Safran@colorado.edu) for additional information. To apply, please send 1) a letter of introduction which details your suitability for this position, and 2) a copy of your resume along with information on three references who might be contacted for additional information about your expertise. The anticipated start date of the position is November 2012. Application materials will be reviewed by 30 June 2012.

Dr. Rebecca J. Safran, Assistant Professor Department of Ecology and Evolutionary Biology N395 Ramaley Hall University of Colorado, Boulder UCB 334 Boulder, Colorado 80309

Phone: 303-735-1495 E-mail: rebecca.safran@colorado.edu http://www.colorado.edu/eeb/facultysites/safran/Home.html Rebecca J Safran <rebecca.safran@colorado.edu>

UEdinburgh EvolutionaryBiol

2 x Evolutionary Genetics Postdocs in Edinburgh

Two three-year postdoc positions are available at the Institute of Evolutionary Biology, School of Biological Sciences, University of Edinburgh, on a ERC Advanced Grant 'Wild Evolutionary Genomics' awarded to Prof. J.M. Pemberton.

Position 1

The appointee will investigate individual variation in recombination rate in a free-living mammal and its potential causes and consequences. The project is based on the long-term study of Soay sheep on St Kilda, Scotland, and will make use of pedigree information and genotypes for ~6,000 individuals genotyped on the International Sheep Genomics Consortium's 50K SNP chip. A PhD in a relevant field and previous experience of bioinformatic and statistical analysis is required. Further information and application via http://www.jobs.ed.ac.uk/ where the job reference no is 3015615 with application deadline 21st May 2012.

Position 2

The appointee will investigate the evolutionary genetics of fitness, especially the genetic architecture of inbreeding depression and additive genetic variation, in a wild mammal. The project is based on the long-term study of a wild population of red deer on the Isle of Rum, Scotland. A ~50K SNP chip for red deer is in preparation. Initially, the postdoc will prepare and submit DNA samples to a subcontractor for genotyping on the chip. Subsequently, the postdoc will QC data received and analyse it in relation to project objectives. Technical support will be available for the initial lab work. A PhD in a relevant field and previous experience of molecular laboratory work and statistical analysis, preferably in the area of quantitative genetics, are required. Further information and application via http://www.jobs.ed.ac.uk/ where the job reference no is 3015617 with application deadline 21st May 2012.

Informal enquiries for both positions can be made to j.pemberton@ed.ac.uk. Interviews for both positions will take place in late June/early July and appointees need to start by 1st Sept.

Prof. J.M. Pemberton Institute of Evolutionary Biology University of Edinburgh West Mains Road EH9 2LD

Tel: 0131 650 5505 Fax: 0131 650 6564 Web: http://-wildevolution.biology.ed.ac.uk/

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

Josephine Pemberton <j.pemberton@ed.ac.uk>

UFlorida AvianPhylogenetics

Post-doctoral position in the phylogenetics of the avian order Galliformes.

A post-doc position is available at the University of Florida (Gainesville, Florida) to work with Rebecca Kimball (http://people.biology.ufl.edu/rkimball) and Edward Braun (http://people.biology.ufl.edu/ebraun) on the phylogeny and evolution of the Galliformes. The order Galliformes includes the two most economically important birds (the chicken and turkey; both with complete genomes), some of the most spectacular and recognizable birds (such as peafowl and pheasants), and some of the most important avian model systems (e.g., the chicken and Japanese quail). Despite intensive research on galliforms in many areas, their evolutionary relationships remain poorly resolved, limiting the ability to put the extensive information about galliform species into a comparative framework. This project will use multiple genes to produce a well-resolved evolutionary tree for the avian order Galliformes by collecting sequences for many loci for a subset of taxa, and a smaller set of loci for a large number of taxa. One problem is this group arises from several rapid radiations at different evolutionary depths, and the collection of data from large numbers of loci will allow us to explore factors affecting resolution of these difficult phylogenetic problems. The data matrix will also allow examination of patterns of avian molecular evolution, complementing existing information available from mammals, while the resulting phylogeny should benefit comparative studies.

Candidates should have completed a PhD (or will very soon) and have a knowledge of phylogenetics. Ideal candidates will also have a background in computational phylogenetics, experience in managing large datasets, and/or strong molecular biology skills. Knowledge of birds (particularly galliforms) is not required. The position is for one year but is renewable.

Questions and applications should be addressed to Rebecca Kimball (rkimball@ufl.edu). Applications should include: 1) a cover letter outlining your research experiences, interests and career goals; 2) a c.v. including the names and contact information for at least 3 references; and 3) copies of up to 3 publications or manuscripts in review. Review of applications will begin on May 21, 2012 and continue until position is filled.

Rebecca Kimball Assoc Professor and Graduate Coordinator Dept. of Biology University of Florida

rkimball@ufl.edu

UGottingen CepeaVariation

The Courant Research Centre Geobiology at the University of Göttingen (Germany) is offering 1 of the following positions to work on the molecular genetics of a molluscan pigmentation system:

Post-doctoral position (100% TV-L 13: 39,8 hours/week) or PhD position (65% TV-L 13: 25,87 hours/week)

Either position is initially available for 6 months starting 15th June 2012, and will be extended for up to 3 years following satisfactory performance during this trial period.

Variation in shell pigmentation patterns of the common garden snail Cepaea nemoralis have long served as a model for population geneticists, however very little is known about the molecular mechanisms that generate this morphological diversity. Positions are available within the research group headed by Daniel Jackson to identify and characterise the molecular basis of these mechanisms.

These positions require individuals with strong molecular biology skills and familiarity with the analysis of large computational datasets such as RNA-Seq. Lab skills such as RACE-PCR, whole mount in situ hybridization, micro-injection and familiarity with some bioinformatic techniques are highly desirable.

Candidates for the post-doctoral position should hold a doctorate in evolution, cell biology, developmental biology, molecular biology, or a related field. Candidates for the doctoral position should hold an excellent first degree in one of the same fields. In addition to their academic qualifications, candidates should have excellent communication and team-working skills, be committed to the topic and to working in a dedicated, interdisciplinary research environment. The working language of the group is English, and applicants from abroad are encouraged to apply.

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

All applications should be made in English, and must include the following 3 items (incomplete applications will not be considered):

1. A full academic CV including any published or unpublished academic work. 2. A 1-2 page letter outlining the candidate's research interests and motivation for applying to this position. 3. Letters of reference and the contact details of 2-3 referees (ideally previous supervisors).

Submit your application or any informal enquiries directly to djackso"at"uni-goettingen.de

The application deadline is May 15, 2012.

For more information about the Jackson group see http://www.uni-goettingen.de/en/102705.html "Jackson, Daniel" <djackso@gwdg.de>

UHongKong AnnonaceaePhylogenetics

Postdoctoral Position in Plant Molecular Phylogenetics

Place: University of Hong Kong Job: Postdoctoral Fellow Reference: 201200219 – see http://jobs.hku.hk/ under "Academic-related Staff" Closing Date: 21/04/2012

I am looking for a postdoctoral researcher to join my lab at the University of Hong Kong. There will be considerable latitude for the appointee to influence research direction, although the main thrust will be molecular phylogenetics of the Annonaceae and its applications in character evolution, biogeography, etc. I am particularly keen to develop my lab's capacity to handle next-generation sequencing data.

The post is for 3 years, with a competitive salary. Applicants must submit a completed University application form, which should clearly state which position they are applying for and in which academic discipline, and the reference number, to the respective e-mail address specified below. They should also provide further information such as details of their research experience, publications, research proposals, etc. Application forms (341/1111) can be obtained at http://www.hku.hk/apptunit/form-ext.doc .Further particulars can be obtained at http://jobs.hku.hk/ or directly from me (saunders@hkucc.hku.hk).

Prof. Richard M. K. Saunders School of Biological Sciences The University of Hong Kong Pokfulam Road Hong Kong E-mail: saunders@hkucc.hku.hk Fax: (852) 2517 6082 Tel.: (852) 2299 0608 URL: http://web.hku.hk/~saunders/rmks.htm dthomas@hku.hk

ULibreBruxelles MicrobialEvolution

Post-doc position available at the Universit Libre de Bruxelles in the Bacterial Genetics and Physiology group, Institute of Molecular Biology and Medicine.

A position is available for enthusiastic and highly motivated post-doctoral associate expert in bioinformatics, microbial evolution, microbial genome analysis and microbial functional genomics. The main project will be the analysis of origin and diversity of toxin-antitoxin systems in bacteria.

This position is a temporary post-doctoral fellowship from the FNRS and is associated to an international mobility program. Therefore, the candidate must be of non Belgian nationality and should not have resided or studied/worked in Belgium for more than 2 years. The candidate must hold a PhD thesis for maximum 6 years. The position will start July 1st, 2012.

To apply send a CV, including the names and contact details of 2 academic referees, to Dr. Laurence Van Melderen by email: lvmelder@ulb.ac.be

A brief description of the groups research activities is available at http://www.ulb.ac.be/ibmm/homeuk_11.html Laurence Van Melderen <lvmelder@ulb.ac.be>

UmeaU WhitefishSpeciationGenomics

Post-doc position (2 years) - the genomics of ecological speciation in whitefish

Announced by the Department of Ecology and Environmental Science (EMG), Umeå University, within the project “Speciation in action”.

Project description Scandinavian populations of whitefish form distinct ecomorphs with separate spawning sites within 50-100 years. This finding provides a unique opportunity to study sympatric speciation “as it happens”. In this project we study the degree of differentiation in genetic and morphological traits by comparing diverging whitefish populations of different age (50-10 000 years). The objective is to produce a time line showing in which order different phenotypic and molecular traits change, and, ultimately, to provide a mechanistic understanding of the ecological and genetic mechanisms that leads to ecological speciation. We are now looking for a candidate with strong competence in molecular population genetics and genomics.

Requirements To qualify for the position you should have a PhD degree in evolutionary biology or equivalent. Knowledge of population genetics, molecular genetic methods (e.g. RNAseq, qRT-PCR, and genotyping) and bioinformatics/statistics is highly desirable. From the successful candidate, we expect a documented capability of autonomous scientific research work and skills in writing scientific publications in English. International applicants are encouraged to apply.

Application The application should include a short description of your research interests and why you are interested in the position, a CV, a publication list, copy of PhD certificate and publications, and contact information to 3 reference persons. The application should be written in Swedish or English and can be submitted either electronically (MS Word or PDF format) or in hard-copy (2 copies) form. For more information, contact Professor Göran Englund, phone: +46-(0)90-786 9728, e-mail: goran.englund@emg.umu.se, or Xiao-Ru Wang, phone: +46-(0)90-786 9955, e-mail: Xiao-Ru.Wang@emg.umu.se.

Your complete application should be sent to goran.englund@emg.umu.se to arrive May 15, 2012 at the latest.

We look forward to receiving your application!

Göran Englund <goran.englund@emg.umu.se>

UMichigan ComputationalPhylogenetics

Post-doctoral Position in Computational Phylogenetics

A Post-Doctoral position in computational phylogenetics is available in the lab of Stephen A. Smith at the University of Michigan, Ann Arbor (http://blackrim.org). The Post-doc will participate in a large collaborative endeavor supported by the NSF AVATOL Program that is aimed at synthesizing a comprehensive tree of life from published analyses, and developing novel tools for community-driven annotation of the tree. Specific responsibilities will include (1) development of methods and software for tree processing, integration, and synthesis; (2) coordination with a multi-laboratory team including software developers and systematists in the development and testing of these methods; (3) research in phylogenetic dataset assembly and large phylogenetic tree reconstruction and analysis.

Candidates are expected to be proficient in python and a language such as C, C++, or Java (C++ preferred). The ideal candidate will be a productive researcher with interests in methods development and the construction and interpretation of large-scale phylogenetic trees, will have excellent communication and interpersonal skills, and will seek a career involving both research and education.

It is anticipated that the position will be available beginning May 1, 2012. Up to three years of support is possible, depending on progress. Funding is contingent on final NSF approval.

To apply, e-mail a curriculum vitae, statement of research interests and career goals, evidence of programming experience (code repositories or products), PDFs of major publications, and names and e-mail addresses for three references. Applications from women and members of underrepresented groups in science are encouraged.

University of Michigan is an EEO/AA Employer.

Stephen A. Smith Ecology and Evolutionary Biology Department University of Michigan, Ann Arbor Ann Arbor, MI 48197 (734) 764-7923

eebsmith@umich.edu

UMontpellier HostPathogenCoevol

Postdoctoral Scientist in Host-Pathogen Coevolution

A two-year Postdoctoral Scientist position is available on or after October 1st, 2012 at the University of Montpellier II, France. The work will be performed in the research group headed by Dr. Michael Hochberg, and in association with Dr. Peter Thrall (CSIRO Canberra, Australia) and Prof. Jennifer Dunne (Santa Fe Institute, USA). The project is fully funded by a grant from the McDonnell Foundation.

Context: The proposed project will probe how environments influence the structure of antagonistic coevolutionary interactions. In nature individual organisms are confronted with diverse arrays of abiotic and biotic stresses and mortality factors. This generates higher order complexity because of the multi-scale nature of these interactions, and because both exogenous environments and organisms shift and change in ways which may be difficult to predict. Our goal is to explain patterns in the diversity of interactive traits between host and pathogen, by manipulating this complexity at different scales and teasing apart the contributions of its components to coevolutionary dynamics and population structure. We are interested in both fundamental approaches and their applications to the control of microbial pathogens and pests.

Requirements: PhD and demonstrated experience in microbial ecology and evolution. Candidates with experience in microbial molecular biology and having a solid training in evolutionary biology are also encouraged to apply. Excellent command of scientific English.

Interested candidates should apply by 1 June 2012 by sending (1) a letter of motivation, (2) a CV with publication list, and (3) the names, institutions and email addresses of three references to Dr. Michael Hochberg at mhochber@univ-montp2.fr

Recent group publications: Poisot T., Lepennetier G., Martinez E., Ramsayer J. & Hochberg M.E. 2010. Resource availability affects the structure of a natural bacteria/bacteriophage community. Biology Letters doi:10.1098/rsbl.2010.0774 Ramsayer J., Fellous S., Cohen J.E. & Hochberg M.E. 2011. Taylor's Law holds in experimental bacterial populations but competition does not influence the slope. Biology Letters DOI:10.1098/rsbl.2011.0895 Poisot T., Canard E., Mouquet N. & Hochberg M.E. 2012. A comparative study of ecological specialization estimators. Methods in Ecology and Evolution DOI: 10.1111/j.2041-210X.2011.00174.x Escobar-Paramo P., Gougat-Barbera C. & Hochberg M.E. 2012. Evolutionary dynamics of separate and combined exposure of Pseudomonas fluorescens SBW25 to antibiotics and bacteriophage. Evolutionary Applications. DOI: 10.1111/j.1752-4571.2012.00248.x Poisot T., Canard E., Mouquet N. & Hochberg M.E. 2012. A comparative study of ecological specialization estimators. Methods in Ecology and Evolution. DOI: 10.1111/j.2041-210X.2011.00174.x Kaltz O., Escobar-Paramo P., Hochberg M.E. & Cohen J.E. (In press). Bacterial microcosms obey Taylor's law: Effects of abiotic and biotic stress and genetics on mean and variance of population density. Ecological Processes Escobar-Paramo P., Coulouma G., Roger F., Gougat-Barbera C. & Hochberg M.E. (Submitted). pH affects the mode of bacterial evolution: a case study of rifampicin resistance in natural Pseudomonas fluorescens populations.

Dr. Michael Hochberg, CNRS Institut des Sciences de l'Evolution Université Montpellier II, France http://www.eec.univ-montp2.fr/people/mike-hochberg/ Michael Hochberg <mhochber@univ-montp2.fr>

UNebraska Lincoln Bioinformatics

Post-Doctoral Research Associate in Bioinformatics Programming

The University of Nebraska - Lincoln is seeking candidates for a post-doctoral research associate in bioinformatics programming to join a multi-disciplinary bioinformatics team. The successful programmer will develop databases and pipelines for microbiome and metagenome analyses. The individual will work within a highly collaborative environment focused on understanding host-microbe interactions and microbe-microbe interactions within complex ecosystems. Approaches involve high-throughput analysis of microbiome and metagenome composition using Next Generation DNA sequencing. Oversight for the position will be provided by Dr. Andrew Benson (Food Science & Technology), Dr. Stephen Kachman (Statistics) and Dr. Etsuko Moriyama (School of Biological Sciences). The original appointment is set at two years and is grant funded, however appointment beyond that time frame is possible. Position offers a competitive salary, flexible work hours, and excellent health benefits. Requires a PhD in Computer Science, Bioinformatics, or a related field and experience programming with Python, Perl, C, and SQL, and experience in processing Next Generation DNA sequence data. A background in biology or the life sciences is highly preferred. For further details and to apply for this position visit http://employment.unl.edu, requisition number 120309. Complete the Faculty/Administrative form and attach a Letter of Application, Curriculum Vitae and a list of professional references. Application review will begin on May 21, 2012 and continue until the position is filled. The University of Nebraska has an active National Science Foundation ADVANCE gender equity program, and is committed to a pluralistic campus community through affirmative action, equal opportunity, work-life balance, and dual careers.

Dr. Andrew Benson 402-472-5637 abenson1@unl.edu

emoriyama2@unl.edu

UOklahoma ancientDNA metagenomics

The University of Oklahomas Molecular Anthropology Laboratory is seeking evolutionary biology or anthropology applicants for a post-doctoral position in ancient DNA and/or metagenomics. Position includes a very competitive salary and is available for two years with the possibility of renewal/extension. Strong writing and analytical skills required. Previous publication record in ancient DNA, population genetics, microbiomes, and/or metagenomics preferred. Responsibilities include generation and analysis of genetic data and publication.

Earliest start date: July 1st, 2012.

Inquiries and applications (CV and three references) directed to

Dr. Cecil M. Lewis (cmlewis@ou.edu).

“Lewis, Cecil M. Jr.” <cmlewis@ou.edu>

UOxford PlantEvolutionaryGenet

Place: Department of Plant Sciences, University of Oxford, United Kingdom Job: Postdoctoral Research Assistant Reference: 102620 Closing Date: 27 April 2012 URL: www.plants.ox.ac.uk Project Title: Plant Evolutionary Genetics

I am looking for a postdoctoral researcher to join my group at the University of Oxford, United Kingdom. Funding is available for 12-month (in the first instance), with an immediate start date. The successful applicant will be involved in data analysis and manuscript preparation for a project focused on evolutionary genetics of adaptation process. Involvement in other projects (e.g. on sex chromosome evolution) is also possible and will be encouraged. Extensive genomic resources, including whole genome and transcriptome sequences from individuals adapted to different environments have already been generated during the previous work and the aim of this new research position is to speed up the analysis and make the most of the data available. The successful candidate will be encouraged to develop their own direction of analysis but guidance and training will be provided if necessary.

Dmitry A. Filatov, PhD University Lecturer in Evolutionary Genetics Department of Plant Sciences, University of Oxford, South Parks Road, Oxford OX1 3RB United Kingdom

Dmitry Filatov <dmitry.filatov@plants.ox.ac.uk>

URochester Drosophila Speciation Genomics

URochester.Drosophila_Speciation_Genomics

Postdoctoral position in Drosophila speciation and genomics

A 4-year NIH funded postdoctoral position is available in the laboratory of Dan Garrigan at the Department of Biology at the University of Rochester. The project focuses on speciation and evolutionary genomics of the three species of the Drosophila simulans clade. The work includes reconstructing evolutionary histories, both within and between species, from whole-genome next-generation resequencing data. Analyses will focus on models that include recombination, divergence, gene flow, and natural selection. Ultimately, the project aims to integrate genomic maps of evolutionary history with maps of hybrid male sterility factors.

Qualified candidates must have training in both bioinformatics and evolutionary genetics. The project is a collaborative effort with the laboratory of Dr. Daven Presgraves. The Department of Biology at the University of Rochester offers a rich intellectual environment, with a strong focus on research in speciation and adaptation.

Applicants should email a brief cover letter, a pdf of their current CV, and the names and contact information for two references to Dan Garrigan at dgarriga@bio.rochester.edu. Review of applications will begin immediately and continue until the position is filled. For more information, please visit the Garrigan lab website (http://kimura.biology.rochester.edu), or contact Dan Garrigan at the above email address.

The University of Rochester is an Equal Opportunity Employer.

Dan Garrigan, Ph.D. Assistant Professor Department of Biology University of Rochester Rochester, NY 14627 dgarriga@bio.rochester.edu http://kimura.biology.rochester.edu

daniel.garrigan@rochester.edu

UWesternOntario BehaviouralEvolution

Postdoctoral Position in Molecular and Behavioural Ecology

In the lab of Prof. Bryan D. Neff, Department of Biology, Western University, 1151 Richmond Street, London, ON N6A 5B7; Email: bneff@uwo.ca; web: http://publish.uwo.ca/~bneff Project: Gene expression and androgen-mediated parental care behaviour

Proximate mechanisms mediating parental care behaviour have interested biologists for decades. In vertebrates, androgen hormones such as testosterone appear to mediate aspects of parental care, particularly those behaviours involving defence of the young. High androgen levels, however, also appear to inhibit nurturing behaviours, which can lead to a trade-off between protecting young and caring for young. In the current study, nesting male bluegill sunfish (Lepomis macrochirus) were implanted with 11-ketotestosterone, a prominent androgen in fish, flutamide, an androgen-receptor blocker, or a placebo. Both aggressive behaviours displayed towards a brood predator and nurturing behaviours of the young were subsequently recorded, and at the termination of the experiment, brains were extracted from the nesting males for mRNA analysis. Androgen-implanted males displayed more aggression and less nurturing, whereas flutamide-implanted males displayed the opposite pattern relative to the placebo males. The current project will use the mRNA and microarray and qRT-PCR approaches to examine variation in gene expression with the goal of identifying candidate genes that are involved in mediating aggressive and nurturing behaviours during parental care.

Qualifications: A PhD with a record of research excellence as demonstrated by publications and conference presentations. Experience with microarrays and associated software analysis packages is essential, as is a background in evolutionary and behavioural ecology.

Pay: CDN $40,000 per year for one year with a possible second year extension.

Start: September 1, 2012

To Apply: Please send a cover letter detailing your qualifications and interest in the position, a CV, and names and contact information for two references via email to bneff@uwo.ca. Review of applications will begin on June 1, 2012.

Trevor Pitcher <tpitcher@uwindsor.ca>

UWitwatersrand AdaptationEvolution

Evolutionary Consequences of Physiological Adaptation:

Comparing the Allostasis and Reactive Scope Model in African Striped Mice (Rhabdomys pumilio)

A two-year postdoc position in eco-physiology is available at the School of Animal, Plant and Environmental Sciences at the University of the Witwatersrand. Field work will be done at the Succulent Karoo Research Station. The postdoc will be mentored by Dr. Neville Pillay and Dr. Carsten Schradin (currently University of Zurich and expected to be at the CNRS in Strasbourg, France, from October 2012 onwards).

Project: Evolution of physiological adaptation: how can animals survive and reproduce in an environment characterized by variable droughts?

The concepts of allostasis and reactive scope have been very successful in explaining physiological adaptation and stress in free ranging birds, but have been applied to only a limited number of species. We want to test predictions from both models for the first time in a mammalian species living in an extreme environment, the African striped mouse from the Succulent Karoo semi-desert of South Africa. We will test the predicted strong relationship between glucocorticoids and energy expenditure (allostasis model) and aim to measure homeostatic overload in free ranging animals, especially gluconeogenesis via muscle catabolism, i.e. muscle breakdown, a response to pathologically high glucocorticoid levels, as would be indicated by high uric acid blood levels (reactive scope model). We are especially interested in fitness consequences of ecologically mediated physiological adaptation.

Methods to be applied: The postdoc is expected to spend the majority of the time in the field. Methods include trapping, marking, measuring and observing striped mice. In the field, food availability will be measured via plant surveys. Blood samples will be collected for physiological measurements. An ABAXIS blood analyzer is available at the research station and the postdoc is expected to run this equipment. Blood glucose and blood ketone levels can be measured directly in the field. Experiments using hormone implants (increase of corticosterone levels during the dry season) will be possible. Blood samples will be sent to Dr. Schradin's laboratory for hormone measurements.

A respirometry laboratory has been set up at the research station. In collaboration with other projects currently running at the research station, it is possible to measure resting metabolic rate (RMR). We also plan to measure daily energy expenditure (DEE) using doubly labeled water in collaboration with Dr. S. Blanc from the CNRS in Strasbourg, France.

What we offer: Access to a unique long-term field study and a well-equipped field station. South Africa is country with many highlights, especially for ecologists and evolutionary biologists. The University of the Witwatersrand is in the centre of South Africa and offers good scientific infrastructure. It is internationally ranking similar to many European universities. The project offers opportunities for international collaborations.

The project is funded for two years by the South African National Research Foundation (NRF). This includes research expenses (e.g. ABAXIS analyzer) and costs of travel for the project.

The stipend from the NRF is 80 000 Rand / year and we anticipate to increase this to Rand135 000 / year via funding from the University of the Witwatersrand. This grant is sufficient for the living costs in South Africa (approx. 6000 Rand / month, including accommodation).

Requirements of the candidate: The postdoc we are looking for must be independent, creative and highly motivated. Applicants should have solid knowledge in at least two of these research areas: eco-physiology, behavioral endocrinology, evolutionary biology, ecology, physiology, animal behavior. Good statistical skills are a pre-requisite. Experience in field work and working with small mammals are of advantage. We expect the applicant to have good writing skills and a good publication record, since a minimum of two publications per year are expected from the successful candidate.

Application procedure and deadline: The position is available from June 2012 onwards. There is no deadline and applications will be reviewed in the order of applications. Applicants should make themselves available for skype interviews at the end of May. The application should be emailed to neville.pillay@wits.ac.za and cc to carsten.schradin@ieu.uzh.ch as a single pdf containing CV, list of publications, a statement of research interests, and the names of two to three references with contact details.

For additional information contact Neville Pillay at neville.pillay@wits.ac.za

Internet links:

School of Animal, Plant and Environmental Sciences at the University of the Witwatersrand: http://www.wits.ac.za/academic/science/apes/6725/home.html

— / —

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

UYork AphidEvolution

We are seeking a highly motivated postdoctoral research scientist to work on a project on bacterial symbionts in aphids led by Dr Julia Ferrari, based at the University of York (UK). We will investigate the ecological effects of coexisting symbionts on their hosts. The post is funded by the BBSRC.

You will be responsible for the project on a day-to-day basis, performing a range of entomological and molecular experiments assisted by a technician. You should hold a PhD in evolutionary ecology or a related discipline. Experience of working with insects and using molecular methods is highly desirable.

This post is available immediately for a period of up to three years.

Further details can be found here: https://jobs.york.ac.uk/wd/plsql/wd_portal.show_job?p_web_site_id=3D3885&p_web_page_id=147651 Informal enquiries are welcome and can be made directly to Dr Julia Ferrari (email: julia.ferrari@york.ac.uk).

julia.ferrari@york.ac.uk

Vienna EvolutionaryDynamics

We are searching for two postdocs to work on the analysis of next generation sequencing data. One position is available for the analysis of RNA-Seq data and another position for re-sequencing of genomic DNA. Both positions are associated with an ERC funded project using experimental evolution to understand the evolutionary dynamics of populations adapting to a novel environment. We are using Drosophila as a model system, since it is a sexual species with a short generation time that can be maintained at large population sizes in the laboratory. Both positions will be provided with access to proprietary data and the opportunity to further develop the project based on initial data analyses.

We are searching for applicants with a solid knowledge in at least two of these research areas: statistics, population genetics and bioinformatics. Previous experience with NGS data analysis is a bonus.

The position will be based at the Institute of Population Genetics at the Vetmeduni Vienna (Austria).). The research focus of the Institute is on understanding the genetics of adaptation. This central question in evolutionary biology is being tackled using up-to-date methods and a variety of approaches, including experimental evolution, quantitative genetics, examination of life history traits, Evo-Devo, empirical population genetics, bioinformatics and statistics.

In recent years, Vienna has developed into one of the leading centers in evolutionary biology (http://www.evolvienna.at). In addition to a stimulating scientific environment, Vienna also offers an extraordinarily high quality of life. Affordable housing, excellent public transport, great restaurants, a range of international schools, two operas, two music centers, many theaters and museums in combination with a pleasant climate make Vienna one of the most attractive cities in Europe.

The positions are available from July 2012. The minimum salary will be 47334euro /year. The application should be emailed to christian.schloetterer@vetmeduni.ac.at as a single pdf containing CV, list of publications, a statement of research interests, and the names of three references with contact details. While the search will continue until the position is filled, applications should be received by April 30, 2012 to ensure full consideration.

Christian Schlötterer Institut für Populationsgenetik Vetmeduni Vienna Veterinärplatz 1 1210 Wien Austria/Europe

phone: +43-1-25077-4300 fax: +43-1-25077-4390 http://i122server.vu-wien.ac.at/pop Vienna Graduate School of Population Genetics http://www.popgen-vienna.at schlotc@gmail.com

WayneStateU GenomicsBioinformatics

Job Title: Postdoctoral fellow

Location: Center for Molecular Medicine and Genetics (CMMG), Wayne State University School of Medicine. The CMMG is a unique interdisciplinary unit within Wayne State University's School of Medicine. The center is built around modern molecular genetics, and comprises basic researchers, physician-scientists, computational scientists, and genetic counselors. For more information please see http://cmmg.biosci.wayne.edu/ .

Description: Full-time position. We are seeking a postdoctoral fellow or research analyst who can take the lead on analyzing genomic data from multiple interrelated projects with the potential to yield multiple high-impact papers. Position would be jointly funded by two PIs with an extensive history of collaboration (Derek Wildman and Monica Uddin); successful applicants would work closely with both PIs.

Job Functions:

- Develop and implement statistically robust, systems biology approaches to analyzing gene expression and DNA methylation microarray data.

- Develop and implement statistical analyses of genomic data integrated across multiple levels (i.e. miRNA expression, gene expression, DNA methylation and DNA sequence variation).

- Analyze next generation sequencing data and compile the results from multiple species for evolutionary analysis.

- Draft manuscripts in part (i.e. methods, results) or whole, as the project requires.

- Provide oral and written progress updates to PIs and other lab members.

Qualifications: PhD in biostatistics or genomics required. Familiarity with analyzing genomic data (including gene expression and methylation microarray, next generation and exome sequencing) as well as expertise in evolutionary genetic and genomic analysis preferred. Experience with and facility using R, Bioconductor required; knowledge of SAS a bonus. Strong written and oral communication skills a must. Salary commensurate with experience. **Due to the funding source for this position, applicants must be a U.S. citizen or permanent resident and must not have been previously employed by, or studied at, Wayne State University.** Applicants meeting this requirement should make this explicit in their cover letter.

Contact: Please send CV and cover letter, including the contact information for three references, to Rich Soliven: rsoliven@wayne.edu

Monica Uddin, PhD Assistant Professor Center for Molecular Medicine and Genetics Department of Psychiatry & Behavioral Neurosciences Wayne State University School of Medicine 540 E. Canfield Ave. Detroit, MI 48201 USA Ph 313-577-3265

Derek Wildman, PhD Associate Professor Wayne State University School of Medicine 540 E. Canfield Ave. Detroit, MI 48201 USA 313-577-1253: voice dwildman@wayne.edu

http://homopan.wayne.edu

WorkshopsCourses

AWI Germany MarineEvolution Sep17-21

Sylt, Germany - Evolutionary potential in marine populations 17-21 Sept.

Workshop: 17-21 September 2012 Evolutionary potential in marine populations

Organisers: Lisa Shama & Mathias Wegner. Helmholtz-Zentrum für Ozeanforschung Kiel (GEOMAR) & Alfred Wegener Institut für Polar und Meeresforschung (AWI)

Venue: AWI Wadden Sea Station, List auf Sylt, Germany

http://www.awi.de/en/research/research_divisions/biosciences/coastal_ecology/events_courses/ http://en.sylt.de/ Workshop content: Our climate is changing at an unprecedented rate, and there is ample evidence that these changes have ecological consequences. The key question now being asked is whether species will be able to adapt fast enough to keep pace with changing environments. Some species will be evolutionary winners (e.g. invasive species), whereas others may not fare as well (e.g. ephemeral populations). This especially applies to marine ecosystems, where climate change has multi-facetted consequences (e.g. ocean warming and acidification, high rates of biological invasions and emerging diseases). Despite the growing awareness of this, very few studies to date have quantified the evolutionary potential of marine populations or the underlying mechanisms of adaptation. Moreover, with the increasing importance of epigenetic inheritance, the balance between genetic adaptation (selection on standing genetic variation) and epigenetic effects (e.g. transgenerational phenotypic plasticity) in response to fast-changing selective agents in the marine environment needs to be reset. In this workshop we will bring together researchers with a primary focus on the evolutionary potential of marine populations to adapt to rapidly changing environments. The workshop will be arranged into three broad topics that include:

1. Molecular and quantitative genetic approaches (e.g. neutral and adaptive genetic variation, standing genetic variation, candidate genes) to investigate adaptation in marine populations

2. Abiotic and biotic selective agents (e.g. climate variability, parasites) that lead to changes in genetic variation in marine populations

3. Epigenetic inheritance (e.g. transgenerational plasticity) as a mechanism to cope with rapid environmental change

Talks and posters will be presented in a relatively informal setting with the aim of promoting discussions, developing new ideas, and providing opportunities for collaborations and networking.

Confirmed plenary speakers:

Philip Munday, ARC Centre of Excellence for Coral Reef Studies andâSchool of Marine and Tropical Biology, âJames Cook University, Australia.

Jennifer Sunday, Earth to Oceans Research Group, Department of Biological Sciences, Simon Fraser University, Burnaby, Canada.

Juha Merilä, Ecological Genetics Research Unit, University of Helsinki, Finland.

Sinéad Collins, Royal Society University Research Fellow, University of Edinburgh, Scotland.

Hans-Otto Pörtner, Marine Biology/Ecological and Evolutionary Physiology, Alfred Wegener Institute, Bremerhaven, Germany

Abstract submission: please apply by 29 April 2012 by submitting an abstract (max. 300 words) to Lisa Shama (lisa.shama@awi.de). Please indicate in which of the three broad topics you prefer to present. Note: the workshop is limited to approx. 50 participants, and we will aim to have a wide variety of presentations within each of the three main topics.

Cost: Depending on the final budget and sources of funding, we expect the registration cost to be approx. 100âper person. Registration includes accommodation in the AWI Guesthouse and meals during the workshop. Participants must cover the costs of travel to Sylt themselves.

Programme: Travel should be planned with arrival during the afternoon/evening on Monday, 17 Sept. The workshop begins with a welcome BBQ on Monday evening. The main body of the workshop takes place over 3 days, with departure on Friday morning 21 Sept.

Download a flyer and find details for travel to Sylt (announcement) at:

http://www.awi.de/en/research/research_divisions/-biosciences/coastal_ecology/events_courses/ For more information contact Lisa Shama (lisa.shama@awi.de).

Lisa Shama <Lisa.Shama@awi.de>

AWI Germany MarineEvolution Sep17-21 Reminder

Reminder: Workshop on Sylt, Germany - Evolutionary potential in marine populations 17-21 Sept.

Workshop: 17-21 September 2012 Evolutionary potential in marine populations

Organisers: Lisa Shama & Mathias Wegner. Helmholtz-Zentrum für Ozeanforschung Kiel (GEOMAR) & Alfred Wegener Institut für Polar und Meeresforschung (AWI)

Venue: AWI Wadden Sea Station, List auf Sylt, Germany

http://www.awi.de/en/research/research_divisions/-biosciences/coastal_ecology/events_courses/ http://-en.sylt.de/ Workshop content: Our climate is changing at an unprecedented rate, and there is ample evidence that these changes have ecological consequences. The key question now being asked is whether species will be able to adapt fast enough to keep pace with changing environments. Some species will be evolutionary winners (e.g. invasive species), whereas others may not fare as well (e.g. ephemeral populations). This especially applies to marine ecosystems, where climate change has multi-facetted consequences (e.g. ocean warming and acidification, high rates of biological invasions and emerging diseases). Despite the growing awareness of this, very few studies to date have quantified the evolutionary potential of marine populations or the underlying mechanisms of adaptation. Moreover, with the increasing importance of epigenetic inheritance, the balance between genetic adaptation (selection on standing genetic variation) and epigenetic effects (e.g. transgenerational phenotypic plasticity) in response to fast-changing selective agents in the marine environment needs to be reset. In this workshop we will bring together researchers with a primary focus on the evolutionary potential of marine populations to adapt to rapidly changing environments. The workshop will be arranged into three broad topics that include:

1. Molecular and quantitative genetic approaches (e.g. neutral and adaptive genetic variation, standing genetic variation, candidate genes) to investigate adaptation in marine populations

2. Abiotic and biotic selective agents (e.g. climate variability, parasites) that lead to changes in genetic variation in marine populations

3. Epigenetic inheritance (e.g. transgenerational plasticity) as a mechanism to cope with rapid environmental change

Talks and posters will be presented in a relatively informal setting with the aim of promoting discussions, developing new ideas, and providing opportunities for collaborations and networking.

Confirmed plenary speakers:

Philip Munday, ARC Centre of Excellence for Coral Reef Studies andâSchool of Marine and Tropical Biology, âJames Cook University, Australia.

Jennifer Sunday, Earth to Oceans Research Group, Department of Biological Sciences, Simon Fraser University, Burnaby, Canada.

Juha Merilä, Ecological Genetics Research Unit, University of Helsinki, Finland.

Sinéad Collins, Royal Society University Research Fellow, University of Edinburgh, Scotland.

Hans-Otto Pörtner, Marine Biology/Ecological and Evolutionary Physiology, Alfred Wegener Institute, Bremerhaven, Germany

Abstract submission: please apply by 29 April 2012 by submitting an abstract (max. 300 words) to Lisa Shama (lisa.shama@awi.de). Please indicate in which of the three broad topics you prefer to present. Note: the workshop is limited to approx. 50 participants, and we will aim to have a wide variety of presentations within each of the three main topics.

Cost: Depending on the final budget and sources of funding, we expect the registration cost to be approx. 100â¬*perperson.RegistrationincludesaccommodationintheAWIGue*

Programme: Travel should be planned with arrival during the afternoon/evening on Monday, 17 Sept. The workshop begins with a welcome BBQ on Monday evening. The main body of the workshop takes place over 3 days, with departure on Friday morning 21 Sept.

Download a flyer and find details for travel to Sylt (announcement) at:

http://www.awi.de/en/research/research_divisions/-biosciences/coastal_ecology/events_courses/ For more information contact Lisa Shama (lisa.shama@awi.de).

Dr. Lisa N.S. Shama

Alfred Wegener Institute for Polar and Marine Research Wadden Sea Station Sylt D - 25992 List

phone: +49 (0)4651 956 4204 fax: +49 (0)4651 956 200 email: lisa.shama@awi.de http://www.awi.de/People/show?lshama Lisa Shama <Lisa.Shama@awi.de>

BarHarbor Maine EvolutionMedicine Aug6-10

*Evolutionary Foundations for Medicine and Public Health: Focus on Infection and Cancer< http://www.mdibl.org/courses/Evolution_and_Medicine/398/ >

August 6-10 at the Mount Desert Island Biological Laboratory, Bar Harbor, Maine

Registration now open. < http://www.mdibl.org/courses/Evolution_and_Medicine/398/ > * CME credit available

This course will be limited to 40 participants. It will be appropriate for those with a background in biology and/or medicine at diverse levels. Special expertise in evolutionary biology is not required, however those who have already studied evolutionary biology will have specialized opportunities. In order to maximize benefits to this developing field, admission preference will be offered to physicians and professors who teach or anticipate teaching courses on the subject, and to members of minority groups who may be eligible for support from the National Evolutionary Synthesis Center. Researchers and students from advanced undergraduate to postdocs will be warmly welcomed. For more information on evolution and medicine, see The Evolution and Medicine Review

Faculty

Randolph Nesse - University of Michigan (Course director) Douglas Brash Yale University Carlo Maley - University of California San Francisco Athena Aktipis – University of California San Francisco and Arizona State University Andrew Read - Pennsylvania State University Mark SchwartzNew York University Stephen Stearns - Yale University Robert Woods – University of Michigan

Description

This intensive one-week course will introduce strategies for applying core principles of evolutionary biology to problems in medicine and public health, with a special focus on infection and cancer. The course will not attempt to cover all possible applications, it will focus on a few examples. Some especially relevant principles include life history theory, host pathogen co-evolution, the regulation of defenses, developmental plasticity, and trade-offs shaping reproductive strategies. These principles will be applied to clinically relevant topics including aging, antibiotic resistance, clinical management of fever, endothelial disease, prenatal experience and metabolic syndrome, and reproductive cancers. This year's course will have extensive special expertise available on topics related to cancer and infectious disease. Mornings will be devoted to lectures and structured discussions. After lunch, participants will gather in small groups for faculty led discussions on a number of specialized topics such as strategies to prevent antibiotic resistance, the role of infection in mental disorders, how social evolution theory might advance new chemotherapy strategies, how viral sequences get incorporated into genomes, the role of imprinting in controlling gene expression. Participants will be in small workgroups with faculty and others who share specialized interests. Most workgroups will investigate a specific topic, for instance, malignant melanoma, cervical cancer, breast cancer, sexually transmitted diseases, antibiotic resistance, or vaccine design. Other groups will address other topics such as strategies for educating physicians, creating curriculum materials, or current debates about levels of selection. Each group will develop a possible research or teaching project, for presentation on Friday. Individuals are also free to create their own projects. Late afternoons are not prescheduled, so participants can organize their own additional discussions and projects or pursue individual interests, including recreation in Acadia National Park. Several optional preplanned expeditions are available, including whale watching, and guided hikes in the park. More information about evolutionary medicine is at The Evolution and Medicine Review< http://evmedreview.com/ >

nesse@umich.edu

Basel MicrobiotaEvolution Sep12-14

THE APPLICATION IS NOW OPEN!!!

The Organizing Committee would like to invite you to attend a 3-day international workshop on the “Evolution and Ecology of Host-Associated Microbiota” to be held at the Zoological Institute, University of Basel, Switzerland on September 12- 14, 2012. The major aim of this workshop is to provide a synthesis of the emerging evolutionary and ecological patterns governing the complex interactions of host-microbiota across different biological systems. We have invited leaders in the field of host-associated microbiota and microbial ecology to share their insights on the evolutionary and ecological principles that shape bacterial community structure and host-microbiota interactions.

This workshop is intended for undergraduate students, graduate students, postdoctoral researchers and early career investigators (100 slots available) who wanted to be exposed to the evolutionary and ecological concepts and bioinformatics tools being applied on the study of host-associated microbiota systems and microbial ecology. Together with the lecture, a hands-on tutorial (bioinformatic tools and approaches encompassing microbial ecology, comparative genomics, molecular evolution) will be provided on the analysis of complex sequence data sets derived from next-generation sequencing.

Thanks to the generous funding from ProDoc of the Swiss National Science Foundation and the University of Basel, we are only charging a minimal fee of CHF 150 for registration (includes 3 lunches, 1 social dinner, 2 social mixers and snacks during the entire workshop) or CHF 250 (+ tutorial on the analysis of next-generation sequences; 50 slots available). We also have arranged for a number of rooms around Basel ranging from youth hostel dormitories (CHF 32-79/ day) to 3-star hotels (CHF 160- 250/ day). Application deadline for the tutorial is May 30 and for the lecture series is June 30, 2012.

Confirmed Speakers: Bioinformatics and Computational Tools

1. KNIGHT, Rob (University of Colorado Boulder, USA) - computational tools for understanding the evolution of microbiota through time and space

2. CAPORASO Greg (Northern Arizona University, USA) - QIIME (Quantitative Insights Into Microbial Ecology) and microbiota dynamics

3. HUSON, Daniel (University of Tubingen, DE) - MEGAN (MetaGenome ANalyzer) and phylogenetic networks

4. QI Weihong (ETH Zürich, CH) - Trends and applications of next- generation sequencing technologies

Microbial Diversity and Symbiosis

5. DUBILIER Nicole (Max Plank Institute, Bremen, DE) - Symbioses of bacteria and hydrothermal vent organisms

6. BRUNE, Andreas (Max Plank Institute, Marburg, DE) - Insect gut microbiology and symbiosis

7. EBERT Dieter (University of Basel, CH) - Daphnia parasites and microbiota

Microbiota Dynamics and Evolution

8. GILBERT Jack (University of Chicago, USA) - Microbial community dynamics and function

9. JANSSON, Janet (LNL, DOE-JGI, USA)- bacterial diversity in the environment

10. LEE Carol Eunmi (University of Wisconsin-Madison, USA) - Copepod microbiota and invasion success

11. Van der MEER Jan (University of Lausanne, CH) - Genetic adaptation and evolution of bacteria in the environment

Genomics of Health- and Nutrition-Associated Microorganisms

12. SVANBORG Catharina (University of Lund, SE) - Host imprints on human-associated bacterial genomes

13. VORHOLT Julia (ETH Zürich, CH) - Physiology of plant-associated microbes (metaproteomics)

Bacteria- host interactions and evolution

14. ROSENBERG Eugene and ZILBER-ROSENBERG, Ilana (University of Tel Aviv, IL) - Coral microbial communities and the hologenome theory

15. POULSEN, Michael (University of Copenhagen) - Multiple interactions between symbionts and host

16. HENTSCHEL, Ute (University of Würzburg, DE) - Mechanisms of interactions between sponges and their microbial communities

More information can be found at this website: http://evolution.unibas.ch/ebert/microbiota/index.htm Please direct any questions to the organizing committee: Marilou Sison- Mangus (m.sison@unibas.ch), Samuel Pichon (samuel.pichon@unibas.ch) and Dieter Ebert (dieter.ebert@unibas.ch)

Marilou P. Sison-Mangus, PhD Postdoctoral Researcher Evolutionary Biology, Zoology Institute University of Basel Vesalgasse 1, 4051 Basel Switzerland

Tel no: 061 267 03 72

m.sison@unibas.ch

Berlin AdaptiveCognition Jul3-10

ANNOUNCEMENT

Summer Institute on Bounded Rationality

Foundations for an Interdisciplinary Decision Theory

3 - 10 July, 2012

Directed by Gerd Gigerenzer Center for Adaptive Behavior and Cognition Max Planck Institute for Human Development, Berlin, Germany

It is our pleasure to announce the upcoming Summer Institute on Bounded Rationality 2012 - Foundations of an Interdisciplinary Decision Theory, which will take place from July 3 - 10, 2012 at the Max Planck Institute for Human Development in Berlin.

The Summer Institute will provide a platform for genuinely interdisciplinary research, bringing together young scholars from psychology, biology, philosophy, economics, and other social sciences. Its focus will be on “decision making in the wild” - how cognition adapts to real-world decision-making environments. One of its aims is to provide participants a deeper understanding of the way humans come to grips with a fundamentally uncertain world, with an emphasis on applied contexts such as social interactions, medicine, justice, business, and politics.

Talented graduate students and postdoctoral fellows from around the world are invited to apply by April 15, 2012. We will provide all participants with accommodation and stipends to cover part of their travel expenses. Details on the Summer Institute and the application process are available at http://www.mpib-berlin.mpg.de/en/research/adaptive-behavior-and-cognition/summer-institute-2012 Please pass on this information to potential candidates from your own department or institute.

Sincerely, G. Gigerenzer

Max Planck Institute for Human Development
Lentzeallee 94 14195 Berlin Germany

summerinstitute2012@mpib-berlin.mpg.de

Copenhagen HumanPopGeneticAnalyses

PhD Course in Human Population Genetic Analyses (5 ECTS)

July 2-6, 2012, Dept. of Biology, University of Copenhagen

Instructors: Andrew G. Clark, Yun S. Song, Anders Albrechtsen, Rasmus Nielsen, Line Skotte, and Ida Moltke.

This course provides a one week comprehensive introduction to a number of topics and common research tools used in analyses of human population genetic data. Topics include: genetic drift, coalescence theory, natural selection, population structure, human disease and evolution, linkage disequilibrium, association mapping, genomic control, haplotype structure, IBD mapping, admixture mapping, genotyping data, next-generation sequencing data, phasing and imputation, HapMap data, 1000 genomes project, online resources.

The fee for the course is 1800 dkr (approx. US $350) for participants who are not enrolled in a recognized PhD or Master’s program. It is free for PhD and Master’s students. The fee does not include food and accommodation.

For sign up and questions, please email: cphsummercourse@gmail.com

rasmus_nielsen@berkeley.edu

CostaRica Systematics May21-Jul9

“The Organization for Tropical Studies offers two to eight week courses that strengthen research skills and competencies on ecological, population genetics and evolutionary biology. For more information, please visit http://www.ots.ac.cr/index.php?option=com_content&task=section&id=6&Itemid317 .Next courses are:

-Tropical Lichens, (2 weeks, May 21-June 1, 2012)

- Systematics of Tropical Coleptera (2 weeks, June 6-19, 2012)

- Tropical Plant Systematics (5 weeks, June 6-July 9, 2012)

Thank you very much.

Pia Paaby, Ph.D.

Director of Education Organization for Tropical Studies, Costa Rica

pia.paaby@ots.ac.cr

Germany ProteinEvol Jul22-27

Dear colleagues,

this is just a brief information that the application deadline for our summerschool on protein evolution - May 1 - is approaching. There are still some slots available and we are looking forward to meeting you. Please find some more information below.

With kind regards,

Sonja Grath

Summerschool on Protein Evolution We are organizing a summer school for late Master/early PhD students. The summerschool will once again - for the 6th time - be held at the Abtei Frauenwörth (Lake Chiemsee, close to Munich and the Bavarian alps) from July 22nd till July 27th, 2012. Several international senior scientists will give general lectures and hands-on sessions on their topics within the field of protein evolution. Around 20 students (Master and early PhD level) will have the opportunity to join the summerschool and present their work in short oral presentations. In addition, there will be plenty of time for discussion with senior scientists about the students' projects and other questions. Deadline for application is May 1st, 2012. More information on the summerschool can be found on our website:http://www.eeslmu.de/eeswiki/Summer_school_2012 Dr. Sonja Grath Westfalian Wilhelms University Evolutionary Bioinformatics Institute for Evolution and Biodiversity Hufferstrasse 1, D-48149 Muenster, Germany http://ieb.uni-muenster.de/bioinf/people/Sonja-Grath.html s.grath@uni-muenster.de

---

Lisbon Python May28-Jun1

Title: Python 101: By biologists for biologists

Instructors: Bruno Vieira, Diogo N Silva, Francisco Pina-Martins

Date: May 28 - June 1, 2012

Location: Faculdade de Ciências da Universidade de Lisboa

Application deadline: May 21, 2012

Website: http://cobig2.fc.ul.pt/python101 Abstract: In the current scientific environment, acquiring a solid skill set in bioinformatics is something that any researcher in biological sciences is likely to need at some point. With the advent of Next-Generation sequencing and the evolution of high-throughput technologies, this need will continue to grow as the processing and analysis of large amounts of data requires automated tools to make sense of the results. Python is an opensource, interactive and powerful programming language that will answer to most of these needs by empowering users with the ability to develop tools that are tailored for their needs, from simple and quick scripts to large pipelines and applications. These features coupled with python's smooth learning curve make it one of the most popular programming languages in the field of bioinformatics. Whatever you require, python will provide a solution that significantly reduces workload and may enable the accomplishment of previously unreachable objectives or deadlines. This course aims to provide an introduction to the basics of python programming and lay a solid foundation for further and independent learning.

Attendees can expect an intensive hands-on training experience that will allow:

* The identification of some of the best ways in which python programming can improve their research/work;

* A basic understanding of how pre-existent python scripts work their “magic”;

* The development of their own simple scripts.

It is widely known that learning Python can dramatically reduce the workload of biological researchers while improving their results. Come and find out why and how!

Questions? Email: octavio.paulo@fc.ul.pt sgseabra@fc.ul.pt

Moscow Phyloinformatics Aug6-17

COMPUTATIONAL PHYLOINFORMATICS: Perl, Ruby, and SQL

August 6 2011 - August 17 2012

New School Building of Moscow State University, Moscow, Russian Federation Application Deadline: May 15, 2012

http://academy.nescent.org/wiki/Moscow_2012 Computational Phyloinformatics is a 12-day international course (August 6-17, 2012) co-organized by Moscow State University, the National Evolutionary Synthesis Center (NESCent), the Institute for Information Transmission Problems (Russian Academy of Sciences), and the Phyloinformatics Research Foundation, Inc. This course, which will take place at Moscow State University directly following the 3rd Moscow International Conference on Molecular Phylogenetics ("MolPhy-3" July 31 - August 4, 2012, www.en.molphy.ru), aims to give participants practical knowledge and hands-on skills in phyloinformatics.

SYNOPSIS Biologists are faced with ever-larger datasets, more complex evolutionary models, and increasingly elaborate analytical methods. Seldom is it sufficient to run a dataset with an off-the-shelf program on a desktop PC; increasingly, biologists need to write scripts to interface with internet services and databases, build analytical pipelines, customize analyses, and distribute computation over multiple processors. This course is designed for graduate students, postdocs, faculty, and researchers in phylogenetics interested in receiving practical, hands-on training in the use of Perl and SQL for workflows and applications in phyloinformatics.

The course is divided into six parts:

- Part I: A tutorial review of the UNIX shell environment - Part II: A tutorial review of Perl, including object oriented programming and building packages - Part III: Introduction and practical use of BioPerl and Bio::Phylo, (e.g. scripting for large tree inference engines, automating model testing, genomic-scale data mining and acquisition, supertree assembly, rate smoothing and branch calibration, tree traversal, etc). - Part IV: Introduction and practical use of BioRuby for molecular evolution and functional genomics (e.g. scripting multiple sequence alignment, gene duplication inference, tree inference, etc.) - Part V: Introduction to SQL and database design; computing and querying both large trees (e.g. NCBI) and large collections of trees (e.g. TreeBASE). - Part VI: A Mini Hackathon where participants, working in small teams, use the knowledge that they have acquired to solve elements of a common challenge

Participants will learn how to write basic phylogenetic or comparative analysis scripts, parse NEXUS files, traverse and compute over trees, and make practical use of phylogenetic software libraries. These skills will be learned in a biological context, touching on a diverse array of topics such as analysis of large datasets, automation of supertree assembly, querying for topological patterns in large collections of trees, etc. Participants will leave the course with a full set of installations and libraries on their computer ready to build phyloinformatic workflows for their own research projects, as well as continued access to a 200+ page wiki "textbook" containing step-by-step instructions, problem sets, and examples.

INSTRUCTORS AND COURSE ORGANIZERS Andrei Alexeevski, Christian Zmasek, Dmitry Sherbakov, Karen Cranston, Leonid Rusin, Rutger A. Vos, William H. Piel

APPLICATION DEADLINE May 15, 2012

TUITION RUB 12,000 (~US$ 400)

Participants are responsible for their own travel costs, including transportation and accommodation. University rooms are available for budget travelers upon request to the organizers. International participants will benefit by combining attendance with the 2012 MolPhy-3 meeting. A limited number of travel scholarships from NESCent are available for US-based students. Tuition subsidies are provided to all Russian students by the Russian Foundation for Basic Research and the Ministry for Education and Science of Russia. Preference will be given to students from underrepresented minorities.

PREREQUISITES

- Biology: A good understanding of phylogenetics - for example, having already taken the Workshop on Molecular Evolution (http://www.molecularevolution.org/) or equivalent coursework or experience.

- Computing: Prior experience with Perl or careful study of the suggested reading materials in advance of the class (see web site). Participants should have some experience with basic Unix shell commands.

- Equipment: Participants are expected to bring their own Mac OSX computer or a LINUX computer, else they will be provided with a computer with an additional rental charge. Participants who cannot bring their own computer and will be using a supplied machine, should consider bringing their own portable USB drive so that they can also

— / —

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

NESCent Durham PhenotypeOntologies Jul30-Aug3

Summer Course (1 week) on phenotype ontologies in evolutionary biology and genetics at the National Evolutionary Synthesis Center (NESCent), Durham, NC USA (July 30-Aug 3, 2012)

Primary instructors: Melissa Haendel, Matt Yoder Guest instructors: Jim Balhoff, Chris Mungall, Carlo Torniai, Erik Segerdell Dates: July 30 - August 3, 2012 Application deadline: April 6, 2012 Website: academy.nescent.org

Evolutionary research has been revolutionized by the explosion ofgenetic information available, and anatomy ontologies must play a central crucial in relating this knowledge to diversity. Anatomy ontologies and vocabularies are widely used to index data and are critical for relating gene expression and phenotype data across taxa. Within a single species, anatomy ontologies provide scaffolding that interconnects many kinds of observations; across species, they provide evolutionary, developmental, and mechanistic insights. In order for anatomy ontologies to successfully serve all of these purposes, they must be constructed consistently so that they can be utilized and understood by both researcher and software alike. This course aims to teach proper ontology design principles and practices such that anatomical interoperability across evolutionarily disparate taxa is achieved. It further seeks to promote community growth and adoption of ontology-based methods and tools. The subsequent benefit is in the form of shared access to the unique data store of each community (e.g. genetic, genomic, developmental, and evolutionary data).

The course covers a basic introduction to ontology design principles and usage, specific ontology considerations for anatomy, application of anatomy ontologies in the context of evolutionary phenotype comparison, and use of anatomy ontologies for image annotation in different taxa. There will be strong emphasis on hands-on exercises that will develop ontology skills and provide exposure to different software applications that are useful in variety of areas of evolutionary biology.

This course is co-sponsored by the Phenotype Ontology Research Coordination Network (http://www.phenotypercn.org/)

Questions? Email academy@nescent.org or one of the contacts below.

–

Karen Cranston, PhD Training Coordinator and Informatics Project Manager nescent.org Karen Cranston <karen.cranston@nescent.org>

or

Paula Mabee

PI, Phenotype Research Coordination Network (phenotypercn.org)

“Mabee, Paula” <Paula.Mabee@usd.edu>

NMNH Paris HumanEvolution Sep3-5

International Workshop

Revisiting the ’Negrito’ Hypothesis, An Inter-Disciplinary Synthesis of the Prehistory of Southeast Asia

More information on the website: www.mnhn.fr/mnhn/ecoanthropologie/paris2012negrito/negrito_index.html What: Anthropology When: September 3-5, 2012 Where: The National Museum of Natural History, Paris, France Who: Phillip Endicott, PhD, convener

Why: The ’negrito’ hypothesis was one of the first evolutionary paradigms to emerge from the nascent academic discipline of Anthropology in the late 19th Century. It posits that various indigenous groups throughout island and mainland Southeast Asia have a shared phenotype - defined by short but gracile stature, dark complexion, and tightly curled hair - due to common descent from a putative ancestral population, representing a pre-agricultural substrate of humanity in the region. The International Workshop to be held in Paris 3-5th September 2012 is designed to revisit the 'negrito' hypothesis within an inter-disciplinary framework involving contributions from Archaeology, Biological Anthropology, Cultural Anthropology, Physical Anthropology, Social Anthropology, Linguistics, and Population Genetics. Methodological approaches will be both synchronic and diachronic, and a comparative approach is actively encouraged. The workshop will present the latest research available and explore where there is a common framework between the different disciplines.

The workshop will be open for attendance by other interested scholars working in the fields of Anthropology (Social, Cultural and Biological), Archaeology, History, Linguistics, and Population Genetics of Southeast Asia.

More information on the website: www.mnhn.fr/mnhn/ecoanthropologie/paris2012negrito/negrito_index.html Dr. Franz Manni UMR 7206 National Museum of Natural History - Musée de l'Homme

Maître de conferences / Lecturer Executive Editor of "Human Biology", (Wayne State University Press, Detroit (MI), USA http://digitalcommons.wayne.edu/humbiol/ 1. Physical address: 61, Rue Buffon, 75005 Paris - France 2. Postal address: CP 139, 57 rue Cuvier, 75231 Paris Cedex 05 - France

Tel. 0033 1 44 05 72 84 / 0033 1 44 05 81 60 Fax. 0033 1 40 79 32 31 Email manni@mnhn.fr

Franz Manni <manni@mnhn.fr>

NMNH WashingtonDC Phylogenetics May20

Frontiers in Phylogenetics Spring Symposium

"Sequence Alignment and Tree Estimation"

Baird Auditorium National Museum of Natural History Washington, DC Sunday May 20, 2012, 9 AM to 5 PM

TOPICS and SPEAKERS

"Introduction and Welcome to the Smithsonian" Jonathan Coddington, Associate Director of Research and Collections, NMNH

"An Overview of Multiple Sequence Alignment Methods" Kazutaka Katoh, IFReC, Osaka University, Japan; CBRC, AIST, Japan.

"Phylogenomics Across the Green Plant Tree of Life" Jim Leebens-Mack, University of Georgia

"Bayesian Co-estimation of Alignment and Phylogeny" Ben Redelings, National Evolutionary Synthesis Center (NESCENT)

"Phylogeny-aware Progressive Sequence Alignment" Ari Löytynoja, Institute of Biotechnology, University of Helsinki, Finland

" SATe: Simultaneous Alignment and Tree Estimation for Large Datasets" Tandy Warnow, University of Texas at Austin

"Fast and Accurate Multiple Sequence/Structure Alignment Using MAFFTash" Daron Standley, Systems Immunology Lab, Immunology Frontier Research Center (IFReC), Osaka University

"A Simple Insertion-'Deletion Mixture Model for Phylogenetic Inference" Derrick Zwickl, University of Arizona

"Impact of DNA Sequence Alignment on Estimates of the Avian Tree of Life" Michael Braun, National Museum of Natural History

Registration is free but required. Please send name, affiliation, e-mail and phone number to Sarah Kingston (kingstons 'at' si.edu).

Okinawa QuantEvolGenomics Aug3-18

For the third summer, the Okinawa Institute of Science and Technology is hosting a workshop on Quantitative Evolutionary and Comparative Genomics (QECG) from August 3rd until August 18th of this year. This year's theme is to explore genomic responses to selection. QECG's aim is to provide opportunities for young researchers with quantitative interests, skills, or backgrounds to learn how they can contribute to the splitting edge of genome science. QECG combines lectures by leading scientists with tutorials and student projects. We will invite around 30 graduate students and post-graduate researchers. OIST will provide lodging and meals during the course and support travel expenses. Applications are due on May 1st. You can find additional information and the application at www.oist.jp/qecg2012 . The current list of lecturers is not yet complete, but includes

Patrick Abbot (Vanderbilt University) David Hillis

(University of Texas) Lacey Knowles (University of Michigan) Michael Lynch (Indiana University) Sergei Nuzhdin (University of Southern California) Sara Sawyer (University of Texas) Jay Storz (University of Nebraska) Jack Werren (University of Rochester)

We are also looking for tutors, post-doc level scientists who will stay the entire time, teaching a unique skill, and assisting with student project. Please contact me directly, if you are interested.

I hope to see you in Okinawa!

Yours,

Sasha

Alexander (Sasha) Mikheyev Assistant Professor (åææ) Okinawa Institute of Science and Technology 1919-1 Tancha Onna-son, Kunigami-gun 904-0495 Japan

mikheyev@gmail.com

Ottawa EvolutionEducation Jul6

Evolutionary biologists in the Ottawa area: please share this announcement with others who might be interested. This workshop is for all science teachers, from lower elementary through college and is held in conjunction with the Evolution 2012 conference.

Evo101: a teacher workshop

July 6, 2012

Ottawa, Canada

Science educators in the Ottawa area are invited to EVO 101: a one day workshop on evolution and using evolutionary data in the classroom. Come learn about exciting research in the field of evolution and attend sessions featuring hands-on activities designed to facilitate the integration of ecological and evolutionary data into your curriculum.

More information about the workshop is available here: http://www.nescent.org/courses/2012/Evo101_2012.php Register for the workshop here: https://www.signup4.net/Public/ap.aspx?EID=EVOL12E Contact Kristin Jenkins (kjenkins@nescent.org) or Louise Mead (lsmead@msu.edu) for additional information.

Kristin Jenkins, PhD Education and Outreach Program National Evolutionary Synthesis Center 2024 W. Main Street, Suite A200 Durham, NC www.nescent.org Cell 608.622.9394

Kristin Jenkins <kjenkins@nescent.org>

Portugal 3 SystemsBiology

http://gtpb.igc.gulbenkian.pt/bicourses/MPA12/ Deadline for applications: May 11th 2012 Notification of acceptance dates: EARLY: May 4th 2012 (on special request, see Application) NORMAL: May 12th 2012 Course date: May 21st - May 23rd 2012

Course description:

Within the growing field of Systems Biology, the mathematical modelling of metabolic networks plays a very important role. This has manifold medical and biotechnological applications, including the analysis and prediction of the effect of enzyme deficiencies, the detection of disease markers, the improvement of biosyntheses and bioproduction processes etc. In this course, we outline the basics and essential tools of Metabolic Pathway Analysis. After a short introduction into enzyme kinetics, we present the concepts of stoichiometry matrix, null-space, elementary modes and conservation relations. Moreover, the basic ideas of Flux Balance Analysis will be explained. In hands-on tutorials, software such as METATOOL, YANASquare, and GEPASI will be used.

Upcoming GTPB Courses BIG12, RNA12, MPA12, ADNMO, BFG12, BPB12 Paper: "Training Experimental Biologists in Bioinformatics" < http://downloads.hindawi.com/journals/abi/2012/672749.pdf > (open access)

Pedro Fernandes Instituto Gulbenkian de Ciência Apartado 14 2781-901 OEIRAS Tel +351 21 4407912 http://gtpb.igc.gulbenkian.pt http://gtpb.igc.gulbenkian.pt/bicourses/RNA12/ Deadline for applications: May 7th 2012 Notification of acceptance dates: EARLY: April 28th 2012 (on special request, see Application) NORMAL: May 8th 2012 Course date: May 15th - May 17th 2012

Description This course will give an overview of RNA and the informatic challenges associated with studying RNA. This course will be run as a mixture of lectures and hands-on problem solving sessions.

The course is practical in nature. After participating attendees will be aware of the difficulties in dealing with RNA. Current methods for addressing these challenges and the limitations of each approach. They should be able to predict RNA secondary structures, be able to use state of the art RNA homology search tools, predict RNA:RNA interactions, and use comparative methods for studying RNA structure. This course also offers training in small RNA analysis

Upcoming GTPB Courses BIG12, RNA12, MPA12, ADNMO, BFG12, BPB12 Paper: "Training Experimental Biologists in Bioinformatics" < http://downloads.hindawi.com/journals/abi/2012/672749.pdf > (open access)

Pedro Fernandes Instituto Gulbenkian de Ciência Apartado 14 2781-901 OEIRAS Tel +351 21 4407912 http://gtpb.igc.gulbenkian.pt ANDNMO12 Analysis of NGS Data from Non-Model Organisms

http://gtpb.igc.gulbenkian.pt/bicourses/ANDNMO12/ IMPORTANT DATES for ANDNMO12 Deadline for applications: May 18th 2012 Notification of acceptance dates: EARLY: May 5th 2012 (on special request, see Application) NORMAL: May 21st 2012 Course date: June 4th - 6th 2012

with Ludovic Orlando, Ed Green, Nicolas Galties and João Lourenço

Course description: The genomic revolution started in late 90's with the first genomes being sequenced. At the time, sequencing was costly and only major lab-organisms and humans were sequenced. The other "non-model" organisms studied in evolution and ecology were left behind. With the next generation sequencing (NGS) technologies, costs have greatly decreased and the genomic revolution now extends to these "non-model" organisms. A burst of full genome or transcriptome sequencing projects has followed but handling NGS data from "non-model" organisms is very challenging. This course addresses NGS data production, processing and analysis. The objective is to see how these data can be bioinformatically tracked and how to plan NGS sequencing to ease up processing, assembly and analysis.

Target Audience:

Course Pre-requisites: Basic experience in Genomics/Transcriptomics/Bioinformatics

Upcoming GTPB Courses BIG12, RNA12, MPA12, ADNMO, BFG12, BPB12 Paper: "Training Experimental Biologists in Bioinformatics" < http://downloads.hindawi.com/journals/abi/2012/672749.pdf > (open access)

Pedro Fernandes Instituto Gulbenkian de Ciência Apartado 14 2781-901 OEIRAS Tel +351 21 4407912 http://gtpb.igc.gulbenkian.pt

— / —

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

---

Portugal NGS Bioinformatics Jun4-6

ANNOUNCEMENT

Advanced Bioinformatics Training Course The Gulbenkian Training Programme in Bioinformatics

Analysis of NGS data from non-model organisms June 4-6, 2012. Instituto Gulbenkian de Ciência Oeiras (near Lisboa), Portugal

Course description: The genomic revolution started in late 90's with the first genomes being sequenced. At the time, sequencing was costly and only major lab-organisms and humans were sequenced. The other "non-model" organisms studied in evolution and ecology were left behind. With the Next Generation Sequencing (NGS) technologies, costs have greatly decreased and the genomic revolution now extends to these "non-model" organisms. A burst of full genome or transcriptome sequencing projects has followed but handling NGS data from "non-model" organisms is very challenging. This course addresses NGS data production, processing and analysis. The objective is to see how these data can be bioinformatically tracked and how to plan NGS sequencing to ease up processing, assembly and analysis.

NGS data requires special handling, different fom Sanger type sequencing data. NGS data consists of a large number of reads, all of them short and with even shorter overhang. Computationally, the assembly of many short reads with small overhang and varying quality is much more challenging. In practical terms, researchers need to deal with NGS data in a different way, many times requiring unique computational skills.

Participants in this course can expect to gain practical insights on how to use NGS data in their projects by a series of techniques that they will learn how to combine. These techniques help the user to address a variety of problems that are very common in research projects. Participants will start by learning how to to go from raw data to a usable dataset. And will end-up knowing how to look at genome assemblies and mapping to release the potential of large scale sequencing. They will also learn how to do NGS based comparative and population genomics analysis.

The instructors are:

- Ludovic Orlando, Associate Professor, Centre for GeoGenetics, Copenhagen, Denmark - Ed Green, Assistant Professor, UCSC, USA - Nicolas Galtier, CNRS Professor, Université Montpellier 2, France (assisted by João Lourenço)

Target Audience: Mainly biologists working on non-model organisms. Students, postdocs, experienced researchers are all welcome to apply.

Course Pre-requisites: Basic experience in Genomics/Transcriptomics/Bioinformatics

Registration fees: 240 Euro

Deadline for applications: May 18th

More information on the GTPB website: http://gtpb.igc.gulbenkian.pt/bicourses/ANDNMO12/ The organisers, Gabriel Marais, Raquel Tavares and Pedro Fernandes

Pedro Fernandes <pfern@igc.gulbenkian.pt>

Portugal Phython

http://gtpb.igc.gulbenkian.pt/bicourses/BPB12/ Open for Applications 5 days, 35 hours, Course fee Euro 400,00

Instructors: Allegra Via (Roma) and Kristian Rother (Berlin)

Course description

Python is an object-oriented programming language that is ideal for biological data analysis. The course will start with very basic language concepts and instructions and will cover all the main language aspects, including variables, types, modules, functions, exceptions, control of flux, input, output, and classes. All the examples and practical sessions will focus on solving particular biological problems. In particular, examples and practical sessions will cover: - working with DNA and protein sequences - data retrieval from files and their manipulation - running applications, such as BLAST, locally and from a script - finding motifs in sequences - parsing Swiss-Prot files, PDB files, ENSEMBL records, blast output files, etc. Biopython will be also introduced and applied to some of the mentioned examples. The course is meant to be highly interactive and the students will continuously put theory into practice while learning. By the end of the course, the students will have a good understanding of Python basics and will have acquired the skills to manage any type of bioinformatics record and to run applications from scripts. Unix/linux basic skills will be provided at the beginning of the course. Target Audience

End-users of bioinformatics databases and tools that aim at developing hands-on capabilities for biological data analysis, ie writing their own or adapting somebody else's Python scripts in an autonomous way. Course Pre-requisites

Basic familiarity with bioinformatics data resources such as Uniprot/Swiss-Prot, Blast, ENSEMBL, PDB, etc. The course is directed to biologists with little or no programming experience and aims at making them capable to use Python to autonomously manage and analyse biological data.

Upcoming GTPB Courses BIG12, RNA12, MPA12, ADNMO12, BFG12, BPB12 Paper: "Training Experimental Biologists in Bioinformatics" < http://downloads.hindawi.com/journals/abi/2012/672749.pdf > (open access)

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>

Roscoff MarineEvolGenomics Jun4-15

SUMMER COURSE ON MARINE GENOMICS AT THE MARINE BIOLOGICAL STATION OF ROSCOFF (F) >From June 4th - 15th, 2012 the 8th Summer Course on Marine Evolutionary & Ecological Genomics will take place at the Station Biologique de Roscoff, Roscoff, France.

Second announcement

Aims: The course, which consists of lectures, tutorials and computer based exercises, aims to highlight the crucial role of marine genomics for the understanding of the marine environment and for an efficient use of its resources. Advanced PhD students and junior postdocs are encouraged to apply. The course consists of the following topics.

Phylogeny & tree of life - sequence analyses, phylogenetic techniques (clustering, Bayesian statistics), molecular clock, case studies

Phylogeography - molecular evolution through networks, phylogeographical techniques, coalescence, population dynamics, case studies

Population genetics - structure, connectivity and gene flow, assignment, effective size and population dynamics, case studies

Genomics - next generation sequencing, database searching, basic skills in data handling and bioinformatics

Functional genomics - genome structure, molecular evolution at the functional level

Comparative genomics - whole genome comparisons, concatenated phylogeny, genome organization, annotating genomic information, co-evolution

Environmental genomics - methods for detecting diversity; detecting adaptive variation; NGS: why and how; case studies. Applications in aquaculture, blue biotech, conservation, fisheries, nutrigenomics and the like will be discussed.

Target group PhD students (at least in their second year) and junior post docs with a solid knowledge in phylogenetics and/or population genetics. Students with an applied background (e.g. aquaculture, blue biotech, fisheries, nutrigenomics) are encouraged to apply.

16 participants will be selected on the following criteria: 1. Relevance of the course for their PhD or post-doc project 2. Background and experience 3. We aim at mixing people with different research backgrounds; not more than one person per institute will be considered. We aim at an equal gender distribution.

The selected persons will be notified at the end of April and have to confirm attendance within 7 days. We will have a waiting list in case of non-confirmations and cancellations.

Teachers Sandie Baldauf, U. Uppsala, SE Simon Creer, U Bangor, UK Yves Desdevises, U Paris 6, FR Jakob Hemmer-Hansen, DTU-Aqua, DK Jeanine Olsen, U Groningen, NL Frédéric Partensky, SB-Roscoff, FR Daniel Vaulot, U Paris 6, FR Filip Volckaert, KU Leuven, BE Mathias Wegner, GEOMAR, Kiel and AWI-Sylt, GE

Organizing committee Jonas Collén, SB-Roscoff, FR Damien Guiffant, SB-Roscoff, FR Matthias Obst, Univ. Gothenburg, SW Jeanine Olsen, Univ Groningen, NL Filip Volckaert, KU Leuven, BE

For information and application please consult http://-meeg2012.sciencesconf.org .The application deadline is April 9th 2012.

Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

SantaBarbara R Jun15

We are pleased to announce an intensive short course on using R to perform comparative methods to be held in Santa Barbara on June 11th to June 15th. This course is funded by the National Science Foundation, and a number of stipends to cover or defray travel, room, and board are available to qualified students and post-docs. Topics covered will include an introduction to the R programming language, tree manipulation, independent contrasts and phylogenetic generalized least squares, ancestral state reconstruction, models of character evolution, diversification analyses, and community phylogenetic analysis. If you are interested please submit your CV along with a short (maximum 1 page) description of your research interests, background, and reasons for taking the course. Admission is competitive, and the best applications come from students with data sets to analyze. International applicants are welcome.

To apply visit http://tinyurl.com/macro-in-R . Application deadline is April 30th.

Individuals from cultural, racial, linguistic, geographic and socioeconomic backgrounds that are currently underrepresented in science are especially encouraged to apply.

Please contact the co-organizers, Michael Alfaro (michaelalfaro@ucla.edu) and Luke Harmon (lukeh@uidaho.edu) with any questions.

Michael Alfaro Sent with Sparrow (http://-www.sparrowmailapp.com/?sig)

michael.lynch.alfaro@gmail.com

SaoPaulo Evolution Aug19-31 reminder

This is a reminder that applications to the Sao Paulo School of Advanced Sciences - Evolution are due by

April 9th. The 80 selected students will have all expenses covered by FAPESP.

SPSAS-evo will be a two-week course, offered August 19-31, 2012, in Ilhabela, São Paulo, Brazil, centered on a range of topics in Evolutionary Biology taught by a host of world class experts conducting cutting-edge research in Evolution. The main goals are to generate authoritative outreach material focused on Evolution and to showcase ongoing research in São Paulo, aiming at attracting the most promising students, post-docs and young faculty to the state of São

Paulo.

There are 80 spots available, the target applicants are graduate students, but a few spots will be filled by outstanding post-docs and undergraduate students. People from all nationalities and backgrounds conducting research in Evolutionary Biology are encouraged to apply. Applications will be evaluated on a competitive basis and selected applicants will have expenses fully covered by FAPESP (except students who already receive FAPESP funding). Application deadline is April 9th. To apply, follow instructions at:

http://www.ib.usp.br/zoologia/evolution Please direct any questions you may have to evolution@ib.usp.br

Speakers: Michael Alfaro (University of California at Los Angeles), André V. L. Freitas (Universidade Estadual de Campinas), Gonzalo Giribet (Harvard University), Alexander W. A. Kellner (Universidade Federal do Rio de Janeiro), Andrew Knoll (Harvard University), Antonio Carlos Marques (Universidade de São Paulo), Mark Q. Martindale (University of Hawai'i), Nancy Moran (Yale University), Howard Ochman (Yale University), Tiago B. Quental (Universidade de São Paulo), Gregory Rouse (Scripps Institution of Oceanography), Marcello G. Simões (UNESP - Botucatu), Antonio M. Solé-Cava (Universidade Federal do Rio de Janeiro), Günter Wagner (Yale University)

Kind regards,

Dan

Daniel J. G. Lahr, PhD Post-doctoral Research Associate DZ-USP

Dan Lahr <dlahr@ib.usp.br>

Seattle StatGenetics Jul9-27 AdditionalInstructors

SISG is pleased to announce that Michael Goddard, Professorial Fellow at the University of Melbourne, will be one of the co-instructors for Module 22, Plant and Animal Association Mapping. Mike Goddard is well-known for his contributions to the statistical aspects of animal genetics. His 2012 papers include “Quantification of Inbreeding Due to Distant Ancestors and Its Detection Using Dense Single Nucleotide Polymorphism Data” Genetics 190:283 and “Uses of Genomics in Livestock Agriculture” Animal Production Science 52:73. Details at http:www.biostat.washington.edu/-SISG/ Bruce Weir <bsweir@u.washington.edu>

Seattle StatGenetics Jul9-27 ScholarshipAppl

The deadline is April 13 for scholarship applications for the 2012 Summer Institute in Statistical Genetics in Seattle, July 9-27. Details at the “Summer Institutes” tab at http://www.biostat.washington.edu Registration is also open for Statistical Genetics summer courses at the University of Edinburgh, June 13-29. Details at the “Summer Institutes” tab at http://www.biostat.washington.edu Bruce Weir <bsweir@u.washington.edu>

SouthWestResStn AntEvolution

Hi there,

There's a new course being offered at the South Western Research Station that might be of interest to evolutionary biologists working on social insects.

This is the link: http://research.amnh.org/swrs/ants-southwest Really hope you could help spread the word on this by posting it in the announcement section on your website.

Thanks for your consideration,

Charissa

– Charissa de Bekker

Marie Curie Postdoctoral Research Fellow Department of Biology & Entomology Center for Infectious Disease Dynamics Penn State University charissa de bekker <amd32@psu.edu>

UCopenhagen ModellingSpecies

Dear colleagues,

The Center for Macroecology, Evolution and Climate at the University of Copenhagen organizes the second edition of the International PhD course on Species Distribution Models. This PhD course will cover:

* Ecological and evolutionary theory on species distributions and species niches * Methodological issues (calibration, forecasting, validation, etc) * Training in SDM software * Applications of SDMs to a broad range of questions from global change biology to phylogeography

More information: http://macroecology.ku.dk/teaching/int_phd_course/

Best regards

David Nogués-Bravo

Dr. Katharine A. Marske

Postdoctoral Researcher Center for Macroecology, Evolution and Climate Department of Biology University of Copenhagen DK-2100 Copenhagen Ø Denmark +45 35 32 13 34

KAMarske@bio.ku.dk

UWashington ViralEvolution Jul9-11

A course on Evolutionary Dynamics and Molecular Epidemiology of Viruses will be held at the University of Washington in Seattle July 9-11, 2012.

Instructors: Philippe Lemey and Marc A. Suchard

The course is part of the Summer Institute on Statistics and Modeling of Infectious Diseases, a collection of short courses from July 9-25, 2012.

Tuition scholarships are available for students and postdocs.

Some travel money is available for U.S.-based students and postdocs. Deadline to apply for scholarhips is April 13, 2012, but we will consider applications after that date if necessary.

People can enroll in one 2.5-day course or several.

More Information is available at http://depts.washington.edu/sismid Co-listed with Summer Institute in Statistical Genetics: http://www.biostat.washington.edu/suminst Course description: This module covers the use of phylogenetic and bioinformatic tools to analyze pathogen genetic variation and to gain insight in the processes that shape their diversity. The module focuses on phylogenies and how these relate to population genetic processes in infectious diseases. In particular, the module will cover Bayesian Evolutionary Analysis by Sampling Trees (http://beast.bio.ed.ac.uk/). This software will be used in class exercises that are mainly focused on estimating epidemic time scales, reconstruction of changes in viral population sizes through time and inference of spatial diffusion of viruses. Evolutionary processes including recombination and selection will also be considered.

M. Elizabeth Halloran MD MPH DSc

Professor Center Stat. & Quant. Infect. Dis. (CSQUID) Vaccine and Infectious Disease Institute Hutchinson Research Center

and

Department of Biostatistics University of Washington 1100 Fairview Ave N, M2-C200 Seattle, WA98109-1024 USA

Phone: 206-667-2722 Fax: 206-667-4378

M Elizabeth Halloran <betz@fhcrc.org>

Valencia HPC for NGS May21-22

http://bioinfo.cipf.es/courses/hpc4ngs Next Generation Sequencing has brought unprecedented volumes of data to the bioinformatics arena. Cost reduction in NGS forecasts massive adoption of these technologies by the genome research community. High Performing Computing might be a necessary choice for an efficient processing and analysis of this daunting amount of data. The HPC4NGS SeqAhead workshop presents recent advances in the application of High Performing Computing solutions for NGS. The workshop covers HPC developments for assembly, mapping, RNA-seq, variant analysis, and more and it is targeted to bioinformaticians and computer scientists with interest in NGS.

Organizes: COST Action SeqAhead Local organizers: Ana Conesa, Ignacio Medina, Joaquín Dopazo Venue: Centro de Investigación Príncipe Felipe, Valencia, Spain Registration fee: 70â¬*(includesmaterial, lunchandcoffeebreaks)Registration :* *http : //bioinfo.cipf.es/courses/registration/hpccourseFurtherinfo : aconesa@cipf.es*

– Ana Conesa, PhD. Head Genomics of Gene Expression Lab Bioinformatics and Genomics Department Centro de Investigaciones Príncipe Felipe Avda. Autopista Saler, 16 46012 Valencia (Spain) Phone: +34 96 328 96 80

aconesa@cipf.es bioinfo.cipf.es/aconesa www.blast2go.org Ana Conesa <aconesa@cipf.es>

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.