EvolDir

August 1, 2011

Month in Review

Foreword

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

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

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

—— / ——

Conferences

Cairns CoralAdaptation July

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

Dear colleagues,

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

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

With best regards,

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

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

Monica Medina <mmedina@ucmerced.edu>

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

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

MINI-SYPOSIUM ABSTRACT:

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

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

OPENING DATE FOR SUBMISSION OF ABSTRACTS: 1 July 2011

CLOSING DATE FOR SUBMISSION OF ABSTRACTS: 1 October 2011

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

Regards, Chris

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

ColdSpringHarbor NematodeEvolution Apr3-6

Greetings —

We are pleased to announce the 2012 Evolution of Caenorhabditis and Other Nematodes meeting at Cold Spring Harbor!

The meeting will take place April 3-6, 2012. The abstract deadline is January 20, 2012. As per CSHL customs, the majority of oral presentations will be selected from the submitted abstracts (session chairs will present too); the abstracts must present unpublished research.

You can see our draft website at:http://meetings.cshl.edu/meetings/worms12.shtml As you will see on the website, Marie-Anne Félix will serve as our keynote speaker and we have attracted a strong and diverse group of 12 worm evolutionary biologists and genomicists to serve as session chairs. Research presented and discussed at the meeting will include C. elegans and other Caenorhabditis evolutionary biology, the evolution of animal- and plant-parasitic nematode species, and the biodiversity and megagenetics of nematodes. This year, we have also invited two session chairs (Holly Bik, Tom Moens) who will bring expertise and knowledge in marine nematodes. There will also be a strong emphasis on genomics. We have applied to NSF for funding to help support students and postdocs, and plan to pursue additional support from NIH and corporate sources this summer.

There will be one poster session, and we are currently organizing our meeting around six themes that will most likely serve as the themes for the six oral sessions:

Fundamental evolutionary forces Evolution of development and reproductive mode Evolution of parasitism and pathogenesis Metagenomics and biodiversity Computational genomics of Caenorhabditis species Computational genomics of other nematodes

We look forward to seeing your abstracts in January, and everyone in April!

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

---

Edinburgh QuantGenetics Jun17-22

Advance Notice: 4th International Conference on Quantitative Genetics

Edinburgh 17-22 June 2012

http://www.icqg2012.org.uk/ Polygenic variation in quantitative and other complex phenotypes underpins most important traits in human health and disease, agriculture, natural populations and evolution. This conference provides an opportunity to learn about the rapid advances in this field from the worlds leading researchers, as well as to present and discuss your own results. The meeting is being held in the impressive surroundings of the Edinburgh International Conference Centre at the centre of Scotlands historic capital.

Confirmed speakers will include:

Eric Lander (Genetics Society Mendel Medal Lecture) Örjan Carlborg (Genetics Society Balfour Lecture) Goncalo Abecasis, Piter Bijma, Ed Buckler, Mark Blows, Gustavo de los Campos, Richard Durbin, Jarrod Hadfield, Ben Hayes, Matt Hurles, Frank Johannes, Trudy Mackay, Mark McCarthy, Magnus Nordberg, Sergey Nuzhdin, Patrick Phillips, Chris-Carolin Schoen, Nik Schork, Pak Sham, John Storey, Peter Visscher, and Alastair Wilson.

The Conference will be arranged in nine broad sessions: Genetic architecture - Evolutionary quantitative genetics - Variation in the genome - Advances from new numerical methods - Opportunities from technological advances - Emerging areas - Bridging the genotype-phenotype gap - Interactions among individuals and with the environment - Genomic information in prediction.

We shall also select papers for oral presentation from submitted poster abstracts. There will be poster sessions and also opportunities for small symposia to be arranged by participants on Wednesday afternoon or at lunchtimes/early evening.

Chairs who will lead and introduce sessions include David Balding, Marie-Anne Felix, Michel Georges, Greg Gibson, Mark Kirkpatrick, Theo Meuwissen, Derek Roff, Veronica van Heyningen and Bruce Walsh.

To receive further information about the conference and to note interest (pre-registration), please go to http://-www.icqg2012.org.uk/ The deadline for early registration and submission of abstracts for consideration for oral presentation is 3 February 2012.

We look forward to seeing you in Edinburgh in June 2012.

Bill Hill, Lutz Bünger, Chris Haley, Mike Kearsey, Loeske Kruuk, DJ de Koning, Josephine Pemberton, and Alan Wright

– Prof W G Hill Institute of Evolutionary Biology School of Biological Sciences University of Edinburgh West Mains Road Edinburgh, EH9 3JT

e-mail: w.g.hill@ed.ac.uk Phone: +44-(0)131-650 5705 Fax: +44-(0)131-650 6564

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

w.g.hill@ed.ac.uk

Glasgow ConservationBiol Aug28-Sep1

Dear Colleagues,

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

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

Kind regards,

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

–

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

Judit Voros <jvoros@nhmus.hu>

Gottingen PrimateBrainEvolution Dec6-9

VIII. Göttinger Freilandtage Behavioral Constraints and Flexibility

06-09 December 2011 Göttingen, Germany

Because primates have some of the relatively largest brains, advanced cognitive and learning abilities, because they are large mobile animals that have the opportunity to encounter many different microhabitats, and because they may encounter changing conditions or rare climatic crises during their relatively long lives, they may be some of the most behaviorally flexible animals. On the other hand, many aspects of primate behavior are suggestive of the existence of constraints as the result of phylogenetic, cognitive, genetic or epigenetic factors. Because primates are the most difficult taxon for the study of these constraints because the necessary experiments are not possible, a dialogue with colleagues working with other model taxa may therefore advance our understanding of the determinants of mammalian social behavior. The specific aims of this meeting are therefore to bring together students of primate and mammalian behavior and sociality for a comprehensive analysis and synthesis of the factors that either facilitate of constrain behavioral flexibility at all levels of natural organization, ranging from individuals to higher taxa. Confirmed invited speakers include: Louise Barrett, Dan Blumstein, Josep Call, Tim Clutton-Brock, Zoe Donaldson, Kay Holekamp, Jason Kamilar, Andreas Koenig, Dieter Lukas, Denis Réale, Norbert Sachser, Carsten Schradin, Benard Thierry, Jenny Tung and Carel van Schaik.

http://www.soziobio.uni-goettingen.de/Kongresse/-Freilandtage/gft2011/gft2011.php Prof. Dr. Peter M. Kappeler Sociobiology/Anthropology University of Göttingen Kellnerweg 6 D-37077 Göttingen +49-551-397317 http://www.soziobio.uni-goettingen.de/ New Animal Behavior Book: http://www.springer.com/-life+sciences/behavioural/book/978-3-642-02623-2 “Kappeler, Peter” <pkappel@gwdg.de>

Hawaii Biocomputing Jan3-7 Deadline

In response to several requests, we are pleased to announce an EXTENDED DEADLINE for submitting manuscripts for the Microbiome Studies special session at the Pacific Symposium on Biocomputing. Please pass this along to any colleagues who you think may be interested.

New Deadline: 25 July 2011

Here is the revised call for papers:

We invite you to submit manuscripts to be considered for presentation at this special session of PSB. Papers will be published in the peer- reviewed proceedings and indexed in Medline. The objective of this Microbiome Studies special session is to expand our understanding of the composition, structure, and function of microbial ecosystems and their impact on human health and well-being. We particularly encourage studies that apply “next generation” sequencing technologies, and reports of tools that support the analysis and sharing of data from such studies. Problems of specific interest may include, but are not limited to:

Algorithm, statistical, software, and database development for analyzing data from shotgun metagenomics, 16S hypervariable region surveys, and microbial transcriptomics.

Association studies of microbial consortia with human health, agriculture, bioremediation, climate change, and engineering.

Theoretical and simulation studies of microbial ecology, function, and evolution.

The role of microbial consortia in natural ecosystems.

Interactions among different microbial systems and macrobiological systems

Other topics within the subject area are welcome. Note that all submitted papers should make clear their relevance for the study of Microbiome Studies. If unsure whether your paper fits the session theme, please contact one of the co-chairs.

For details, see the special session website: http://-psb.stanford.edu/cfp-ms We invite you to submit your work to this year’s special session!

Submission deadline is 25 July 2011

James A. Foster Jason Moore Jack Gilbert John Bunge

foster@uidaho.edu

Jyvaskyla Coevolution Oct4-7 Reminder

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

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

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

Our keynote speakers will be Dr. Sheena Cotter from Queens’ University (Belfast), Dr. Mario Vallejo Marín from University of Stirling (Scotland) and Dr. Dagmar Voigt from University of Kiel (Germany) in addition to contributions from local professors (a.o. Prof. Johanna Mappes, Prof. Hannu Ylönen).

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

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

tions

Registration deadline is August 31st and deadline for abstract submission is July 31st. Registration fee is 80 Euro. This includes Tuesday dinner and social evening, Wednesday festive dinner, Friday excursion and coffee and tea.

For more information or to register, please visit:

https://www.jyu.fi/bioenv/en/divisions/eko/coeevolution/coevolution-symposium You can also contact us through coevo.symposium@jyu.fi.

Looking forward to meeting you in Jyväskylä!

On behalf of the organizing committee,

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

http://users.jyu.fi/˜savarga/ http://jyu.academia.edu/SandraVarga sandra.varga@jyu.fi

---

KansasCity Genomics Nov4-6

Save the dates

...and plan to attend the 9th Annual "Genes in Ecology, Ecology in Genes" Symposium on November 4, 5, & 6, 2011, in Kansas City. We will convene in the Muehlbach/Marriott Hotel in downtown Kansas City at 6:00 p.m. and conclude on Sunday at noon. Registration will be opening soon!

Ecological Genomics is a field at the interface of ecology, evolution and genomics that seeks to place the functional significance of genes and genomics into an ecological and evolutionary context.

We have an outstanding lineup of speakers for the 2011 Symposium and we encourage you to attend!

PLENARY SPEAKER: Louis Bernatchez - Université Laval

FEATURED SPEAKERS:

Bryon Adams - Brigham Young University Justin Borvitz - University of Chicago Daniel Buckley - Cornell University John Colbourne - Indiana University John Jaenike - University of Rochester Brian Lazzaro - Cornell University Jeremy Marshall - Kansas State University Emilie Snell-Rood - University of Minnesota Victoria Sork - University of California-Los Angeles

POSTER SESSIONS: A poster session will be held on Saturday afternoon. Poster topics should be related to the field of Ecological Genomics. A LIMITED NUMBER OF SUBMITTED POSTER ABSTRACTS WILL BE SELECTED FOR ORAL PRESENTATIONS.

Please share this announcement with colleagues and students who are interested in learning more about the field of Ecological Genomics. If you have questions, please contact Michael Herman or Loretta Johnson.

Funding for this symposium is provided by Kansas State University.

Ecological Genomics Institute Directors:

Dr. Loretta Johnson, johnson@ksu.edu Dr. Michael Herman, mherman@ksu.edu Kansas State University, Division of Biology 116 Ackert Hall, Manhattan, KS 66506-4901 ecogen.ksu.edu

Michael Herman Division of Biology Kansas State University 266 Chalmers Hall Manhattan, KS 66506 Office: (785) 532-6741 Lab: (785) 532-6773 FAX (785) 532-6653 Email : mherman@ksu.edu http://www.k-state.edu/hermanlab Learn about the Kansas State University Ecological Genomics Institute at http://ecogen.ksu.edu mherman@ksu.edu

---

London SexualSelection Dec1-2

Association for the Study of Animal Behaviour Winter Meeting, 1st & 2nd December 2011, The Zoological Society, London.

SECOND CALL FOR ABSTRACTS: Deadline July 31 2011

Why do animals mate with the "wrong" partner?

Organisers David Shuker and Nathan Bailey, University of St Andrews.

Animals often attempt to mate with partners that appear to be of "low quality". Such partners range from apparently low fitness individuals of the opposite sex but of the same species, through to members of the same sex or even members of a different species, from which no fitness benefits should accrue. In this two-day meeting we will explore the evolutionary causes and consequences of seemingly "sub-optimal" mate choice behaviour. There are two questions we hope will be addressed. First, are behaviours such as reproductive interference between species or same-sex matings within species biologically relevant or merely quirky pathologies that offer little insight? Second, to what extent do mate choices in one context (getting the "right" species or sex, or the "sexiest" partner) inform us about mate choice in other contexts?

We hope to stimulate behavioural ecologists to think again about what we expect from mate choice and to consider whether unusual mate choices may help or hinder our view of mating systems and sexual selection. Although mate choice is our focus, we expect the discussion to be wide-ranging and relevant to those interested in animal decision-making, especially context-dependent choice, and individual variation in behaviour more generally.

We delighted that Professor Marlene Zuk (University of California Riverside) and Professor Karin Pfennig (University of North Carolina) will be our plenary speakers.

If you would like to contribute a talk (20 + 5 minutes) or poster to the meeting, please email an abstract (200 words max.) to Dave Shuker at:

david.shuker@st-andrews.ac.uk

The deadline for abstract submission for spoken presentations will be July 31st 2011. Poster presentations may be considered after that date, depending on available space. We hope to provide a preliminary schedule of talks sometime in August.

We are also delighted that Professor Gene Robinson (University of Illinois) will be giving the 2011 Tinbergen Lecture during the meeting, and that Dr Sarah Pryke (Macquarie University) will be giving her Christopher Barnard Award for Outstanding Contributions by a New Investigator talk.

As is traditional, the ASAB Winter Meeting has no fee and does not require registration. However delegates make their own arrangements for travel, accommodation and main meals. For further details and updates about the programme of the conference, and for ideas about accommodation, please visit our website:

http://biology.st-andrews.ac.uk/shuker/ASAB-Winter-Meeting-2011.html Dr David M Shuker NERC Advanced Research Fellow School of Biology University of St Andrews Harold Mitchell Building St Andrews Fife KY16 9TH UK Email: david.shuker@st-andrews.ac.uk

LAB WEBSITE: http://biology.st-andrews.ac.uk/-shuker Tel: +44 1334 463 376 Fax: +44 1334 463 366

dms14@st-andrews.ac.uk

Marseilles 15thEvolBiol Sep27-30 program

The 15th EBM program is available http://sites.univ-provence.fr/evol-cgr Few spots for posters are available

Please note The 16th EBM meeting will take place the last week of september 2012

best regards Pierre

Pierre PONTAROTTI <Pierre.Pontarotti@univ-provence.fr>

NorthCarolina SEPEEG 2011 Oct21-23

SouthEastern Population Ecology and Evolutionary Genetics (SEPEEG 2011) - October 21-23, 2011

We are happy to announce the 37th annual SEPEEG (formally SEEPAGE) meeting, which is hosted this year by The University of North Carolina Chapel Hill. The meeting will take place October 21-23 at The Besty-Jeff Penn 4H center in Reidsville, NC (about 40 minutes north of Greensboro, NC).

http://sepeeg.bio.unc.edu The conference registration fee (which isnt quite final but will be very soon) will cover on-site housing, meals, and entertainment. Keeping with the tradition of SEPEEG, the 2011 meeting will be informal and accommodations will be on the rustic side. Participants may register to give an oral presentation and/or poster. A poster session will be held during the social event after dinner Saturday. A keynote address will be given on Saturday afternoon. Keynote Speaker: Dr. Haven Wiley, University of North Carolina at Chapel Hill

This meeting is a great opportunity for early career scientists to present their work in a congenial setting.

Questions can be emailed to SEPEEG@bio.unc.edu

On Behalf of SEPEEG,

Dr. Corbin D. Jones

Organizer

Corbin Jones <cdjones@email.unc.edu>

Oxford Biogeography Sep23-25 2

The International Biogeography Society will convene its Early Career “Advances in Biogeography” Conference from 23rd to 25th September, 2011, in Oxford, UK. Registration is only GBP40 with IBS membership. The deadline for registration is 31st July 2011. For more information and access to registration, please visit http://www.biogeography.org/-html/Meetings/2011Oxford/index.html . A special opportunity exists to also attend the Oxford University’s Biodiversity Institute Symposium on “Biodiversity conservation beyond protected areas” (21st - 22nd September) which immediately precedes the IBS Early Career Conference. A reduced registration fee (GBP10) is being offered to IBS members who are attending the IBS Early Career Conference; for more information please visit the symposium website http://biosymposium.moonfruit.com/ . A list of presentations accepted for the IBS meeting is available at http://www.biogeography.org/html/Meetings/-2011Oxford/presentations_weeklyupdate.html .Limited spaces for oral presentations and posters are still available.

If you have any questions, please write to the organizing committee at ibsearlycareerconference@gmail.com

Michael Dawson mdawson@ucmerced.edu International Biogeography Society

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

Porto Portugal AncientHumanDNA Nov23-25 reminder

Dear Evoldir Members,

The ***call for abstracts*** concerning the international conference “COMPARING ANCIENT AND MODERN DNA VARIABILITY IN HUMAN POPULATIONS” to be held in Porto (Portugal), November 23-25, 2011 will close the 15th of July, 2011, Do not miss the deadline!

The aim of the conference is to compare the results emerging everywhere about the genetic variability of ancient populations with the modern variability of their supposed descendants, or with populations inhabiting the same region. Research on animal domestication is also welcome! Contemporary ancient DNA technology allows the typing of several specimens and a population genetics approach of ancient and remote populations is now emerging. With this meeting we want to give emphasis to this new dimension of ancient DNA studies that equally challenges scholars working with modern or ancient material.

For more details we invite you to check the following website: http://www.mnhn.fr/mnhn/-ecoanthropologie/Porto2011/Porto2011_index.html Thank you!

Franz Manni and Jorge Rocha, convenors

Franz Manni <manni@mnhn.fr>

Townsville QLD AustralasianEvolutionSociety Sep24-27 registration

Dear Evolutionary Biologists,

I would like to invite you to join us for the 7th Biennial meeting of the Australasian Evolution Society (http://aes.eriophora.com.au/events/evolution11/-index.html) to be held in Townsville, Queensland from 24-27 September 2011. This year our conference will be held jointly with the International Union for the Study of Social Insects (Australian Section).

Registration and abstract submission is now open! For more information, and to register, please go to http:/-/aes.eriophora.com.au/events/evolution11/index.html. Registration includes entry to all sessions, the conference ice-breaker/welcome function, the conference dinner, all lunches, morning and afternoon teas, a conference pack, and membership to the Australasian Evolution Society.

’Evolution & Sociality Conference 2011’ will be held at the Rydges Convention Centre in Townsville, situated within the heart of the restaurant and hotel region of the town and only a short walk to the beach and ferry to Magnetic Island. Pre-conference drinks and registration start on the evening of Saturday 24 September at the Townsville Yacht Club. Presentation sessions will run each day from Sunday 25 September to Tuesday 27 September. The Conference dinner will be held on the evening of Monday 26 September at the Museum of Tropical Queensland.

Finally, please assist us by advertising 'Evolution & Sociality Conference 2011' to your fellow colleagues and students.

We hope you will join us and look forward to seeing you in sunny Townsville in September!

On behalf of the organising committee,

Megan Higgie

Vice-President Australasian Evolution Society

Dr Megan Higgie Lecturer / ARC Australian Postdoctoral Fellow School of Marine and Tropical Biology James Cook University Townsville QLD 4811 Australia

T: + 61 7 4781 5734 E: megan.higgie@jcu.edu.au

"Higgie, Megan" <megan.higgie@jcu.edu.au>

UMunich MetazoanPhylogeny Oct11-14 Registration3

Dear colleagues,

the *registration and poster abstract submission* for the "Deep Metazoan Phylogeny 2011 - new data, new challenges" conference, to be held from October 11-14, 2011 at the University of Munich (Germany) *has been extended to August 1, 2011, 23:59h CEST (UTC + 2)!*

However, ONLY abstract submission for POSTERS are possible until the final deadline!

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

We look forward to welcoming you in Munich in October!

for the organizing team

Gert Woerheide

Prof. Dr. Gert Woerheide Molecular Geo- & Palaeobiology Department of Earth and Environmental Sciences & GeoBio-CenterLMU Ludwig-Maximilians-Universitaet Muenchen Richard-Wagner-Strasse 10 80333 Muenchen Germany

Phone: +49 (89) 2180-6718 Fax: +49 (89) 2180-6601 E-Mail: woerheide@lmu.de www.palmuc.de | www.mol-palaeo.de

Lab publications: www.molecularpalaeobiology.eu www.researcherid.com/rid/C-1080-2008 woerheide@lmu.de

---

WoodsHoleMA NortheastMobileDNA Sept1-3

CALL FOR ABSTRACTS

North East Mobile Genetic Element Meeting - 2011 Swope Center MBL - Woods Hole, MA September 1 -3, 2011

Registration is now open for the 3d North East Mobile Genetic Element Meeting in Woods Hole, MA, September 1 -3, 2011. ÂThe registration deadline is *August 8*: http://ws2.mbl.edu/conference/register.asp?conf=3DMOBILE11 This is an opportunity for investigators from the North East U.S. and nearby institutions in Canada to meet and share the latest research information relevant to mobile genetic elements, their role in genome function and evolution, and mechanisms of transposition.Â The meeting especially offers a chance for junior investigators, postdoctoral fellows and graduate students to present their research work.Â

Meeting abstracts should be submitted separately by e-mail to the organizers, Irina Arkhipova < iarkhipova@mbl.edu > or Bill Reznikoff < breznikoff@mbl.edu >. Please indicate in your message whether you would like to present a talk or a poster.

We scheduled 4 sessions with half hour talks, a poster session, and a two-hour excursion on the MBLâs 50' collecting vessel.ÂPlease contact the meeting organizers directly if you need financial assistance or if you wish to attend the excursion.ÂAll students and postdocs from minority groups traditionally underrepresented in science will have their registration, accommodation, and meals covered from the conference funds. Please inform us by e-mail if you are eligible, and indicate âcheck/money orderâ as the payment method during registration.

We look forward to seeing you in Woods Hole this fall!

Bill Reznikoff

Irina Arkhipova

Co-organizers

Marine Biological Laboratory Woods Hole, MA 02534 USA

iarkhipova@mbl.edu

GradStudentPositions

Australia AdaptationToEnvironmentalChange

Please follow the link to find details for PhD scholarships within the Hawkesbury Institute for the Environment at the University of Western Sydney, Australia.

http://www.uws.edu.au/hie/hie/-scholarships2#HIEHDRS Deadline: 29 July 2011

The HIE is a new multi-million dollar research institute offering comprehensive field and laboratory based facilities for research from genes to ecosystems. Dedicated to answering crucial questions about the impact of environmental change on terrestrial ecosystems, the Institute's multidisciplinary research team is exploring how these ecosystems, and their components, respond to changes in atmospheric CO2 concentration, temperature, drought, land use, fire and biotic invasion.

We are seeking excellent doctoral candidates to undertake research within the broad 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 multitrophic interactions;

- Ecology, physiology, biochemistry and genetics underpinning adaptation of plants to a changing environment.

Applicants should discuss their research aspirations and eligibility with potential supervisors in the Hawkesbury Institute: http://www.uws.edu.au/hie/people Contact the Research Training, Policy and Programs Officer to discuss enrollment and scholarships: Ms Sandra Lawrence: sg.lawrence@uws.edu.au

jeffpowell2@googlemail.com

EastCarolinaU PlantEvolutionaryGenomics

GRADUATE STUDENT POSITIONS: POPULATION GENETICS, PHYLOGENOMICS, AND COMPARATIVE GENOMICS OF LEGUMES AT EAST

CAROLINA UNIVERSITY

Multiple graduate student (Ph.D. or M.S.) positions are available in the laboratory of Dr. Ashley N. Egan in the Department of Biology, East Carolina University. We seek highly motived colleagues to study evolutionary genetics and genomics of the plant tribe Phaseoleae (family Leguminosae/Fabaceae) that includes many species of economic importance (soybean, common bean, jicama, etc). Research interests in our lab include bioinformatics, computational biology, molecular systematics, evolutionary and population genetics, and evolutionary comparative genomics.

Research activities can involve fieldwork in the US and abroad, next-generation DNA sequencing, and phylogenetic, phylogenomic, andcomparative genomic analyses. Opportunities exist for students to develop independent projects making use of considerable 454 transcriptome data collected from several species across phaseoloid legumes. For an outline of current projects and prospective projects in thelab, please go to http://www.ecu.edu/cs-cas/biology/egan_ashley.cfm .

Prospective students with a background in genomics, botany, phylogenetics, and/or population genetics are encouraged to apply. Evidence of robust quantitative/analytical skills, strong work ethic, passion for investigating scientific questions, ability to work in both field and laboratory conditions and collaborative skills will all be vital for the success of potential candidates. Students will be supported by a combination of research and teaching assistantships.

A National Science Foundation funded PhD position is also available to study the phylogenetics, taxonomy, and population genetics of Kudzu, Pueraria lobata, a highly invasive species in the U.S. This work involves extensive fieldwork in Asia and will involve collaborations with several international scientists. Field and prior research experience is a plus. Work will involve DNA extraction and amplification, microsatellite genotyping, next-generation sequencing and analyses, phylogenetic and population genetic analyses and genomics.

Interested applications should send a cover letter with statement of research interests, CV, and transcripts (can be unofficial) to Dr. Ashley Egan (egana@ecu.edu). In addition, please have three references sendletters to the same e-mail address. More information about the department and graduate program admission process can be found at the Department of Biology (www.ecu.edu/biology) and http://www.ecu.edu/cs-cas/biology/applyingforadmission.cfm and, for PhD's, the Interdisciplinary Doctoral Program in Biological Sciences (www.ecu.edu/idpbs) . Application review begins immediately for a start date of fall or winter semester 2011.

Ashley N. Egan, Ph.D. Assistant Professor, Department of Biology North Carolina Center for Biodiversity Howell Science Complex - Mailstop 551 East Carolina University Greenville, NC 27858-4353 Office: N303a/N304 Lab: N304/N305 Phone (252) 328-4244 fax (252) 328-4178

egana@ecu.edu

MichiganStateU LivestockWholeGenomePrediction

Dear colleagues,

Two PhD assistantships, both pertaining to whole genome prediction/selection under heterogeneous environments, are available at Michigan State University. For full descriptions and details, please refer to my website: www.msu.edu/~tempelma. Please distribute this post to potential candidates.

My apologies for any multiple postings.

Sincerely,

Rob Tempelman

Rob Tempelman <tempelma@msu.edu>

Munich Zurich HostParasite

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

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

Two PhD students in Evolutionary Biology

Project title: Host-parasite interactions in hybridizing Daphnia, the role of variable environments

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

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

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

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

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

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

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

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

— / —

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

---

UAdelaide Biodiversity

Environmental Genomics for biodiversity assessment: PhD opportunity at the Australian Centre for Ancient DNA, Adelaide in association with Department of Primary Industries and Resources of South Australia (PIRSA)

A PhD position is available within a large environmental genomics project to apply next-generation DNA sequencing approaches to the analysis of environmental samples and develop a new range of methods to perform biodiversity surveys, taxonomic discovery, and underpin environmental impact reports. The project, which is a $1M Australian Research Council-industry partnership, will employ multiplexed PCR, 2nd/3rd Generation Sequencing, and advanced Bioinformatics and Phylogenetics to develop novel systems for rapid and accurate biodiversity assessment. This PhD will apply environmental genomics approaches to the following areas: Developing new tools for assessing biodiversity from environmental samples; Non-invasive methods to monitor the presence and abundance of threatened species; Investigating the relationship between biodiversity and biotic and abiotic factors, e.g. rainfall, geology, land-use history.

We are looking for a highly motivated graduate student, who enjoys independent and unusual research. An interest in environmental biodiversity is a key requirement, and a background in any of the following would be useful: molecular ecology, molecular biology, genetics, bioinformatics, chemistry/biochemistry. The project is for 3 years, starting in 2011/2012.

International Students wishing to study at The University of Adelaide in 2012 should check the available scholarship opportunities (http://www.adelaide.edu.au/-graduatecentre/scholarships/postgrad/international/) as they provide payment of full tuition fees plus an annual living allowance of approximately AUD$21,000 tax free. Note the closing date for international scholarship enrolment is 31st August, 2011 or 31st October for Australian/NZ applicants. Please contact the following supervisors and provide your CV/resume:

Prof. Alan Cooper (alan.cooper@adelaide.edu.au)

Dr. Laurence Clarke (laurence.clarke@adelaide.edu.au)

Australian Centre for Ancient DNA School of Earth & Environmental Sciences THE UNIVERSITY OF ADELAIDE SA 5005 AUSTRALIA

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

http://www.adelaide.edu.au/acad/ laurence.clarke@adelaide.edu.au

---

UAdelaide Bioinformatics

Bioinformatics for Environmental Genomics: PhD opportunity at the Australian Centre for Ancient DNA, Adelaide in association with Biomatters (N.Z.)

A PhD position is available within a large environmental genomics project to develop bioinformatic techniques to perform biodiversity surveys, taxonomic discovery, and forensic analyses using next- generation sequencing data. The project, which is a $1M Australian Research Council-industry partnership, will employ advanced bioinformatics and phylogenetic techniques to develop novel systems for rapid and accurate biodiversity assessment. This PhD will develop and apply novel bioinformatic approaches in the following areas: Biodiversity analysis of environmental genomic data from projects covering forensics, Antarctic biodiversity, water systems (natural and water supplies), and terrestrial ecosystems; Multigene comparative analysis of bio- and phylogenetic relationships between sites; Developing software for the Geneious bioinformatics workbench to analyse large complex environmental datasets.

The successful candidate will be hosted at Biomatters, Auckland for part of the project to facilitate training in software development for the Geneious platform.

We are looking for a highly motivated graduate student, who enjoys independent and unusual research. An interest in environmental biodiversity is a key requirement, and a background in any of the following would be useful: bioinformatics, programming, statistics/ mathematics, genetics, molecular biology. The project is for 3 years, starting in 2011/2012.

International Students wishing to study at The University of Adelaide in 2012 should check the available scholarship opportunities (http://www.adelaide.edu.au/-graduatecentre/scholarships/postgrad/international/) as they provide payment of full tuition fees plus an annual living allowance of approximately AUD$21,000 tax free. Note the closing date for international scholarship enrolment is 31st August, 2011 or 31st October for Australian/NZ applicants. Please contact the following supervisors and provide your CV/resume:

Prof. Alan Cooper (alan.cooper@adelaide.edu.au)

Dr. Laurence Clarke (laurence.clarke@adelaide.edu.au)

Australian Centre for Ancient DNA School of Earth & Environmental Sciences THE UNIVERSITY OF ADELAIDE SA 5005 AUSTRALIA

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

http://www.adelaide.edu.au/acad/ laurence.clarke@adelaide.edu.au

---

UAntwerp EvolutionaryParasitology

The Biology departement of the Faculty of Sciences has an opening available (closing date 7th August 2011) for a full-time

Ph.D. scholarship in Evolutionary Parasitology

The Evolutionary Ecology Group has a long tradition in fundamental and applied population biology of vertebrates, with a particular emphasis on patterns and processes of dispersal and gene flow. A major interest of the group is the spatial ecology of host-parasite interactions and infectious diseases. This PhD project focuses on transmission mechanisms and population structure of nidicolous ticks in relation to the ecology and spatial behaviour of their avian hosts. The project is tightly linked to a long-term population study of hole-breeding great and blue tits. The study combines molecular approaches (microsatellite analyses, molecular host identification) with laboratory and field observations on behaviour and ecology of parasites as well as hosts.

We are looking for an enthusiastic and highly motivated student with a strong interest in Evolutionary Parasitology. Candidates should have a Master degree in Biology or an equivalent degree in life sciences with a sufficient background in population ecology, evolutionary biology and parasitology. Candidates should have excellent study grades. Students in their graduation year can also apply.

We offer a Ph.D. scholarship for two years, with one possible extension of two years after a positive evaluation. Starting date is 1st October or November 2011. Applications shoquld be done using the mandatory online application form. More information can be found at

http://www.ua.ac.be/main.aspx?c=3D*VACATURES&n=3D26394&ct=3Dc025734&e=3D268736 Or go to www.ua.ac.be/mobility > vacancies

For more information, contact erik.matthysen@ua.ac.be

erik.matthysen@ua.ac.be

UArkansas 2 MiteSystematics

Graduate Assistantships: Systematics of North American water mites (no mite experience necessary)

Two NSF-funded PhD positions are available to work on a systematic revision of North American water mites in the family Torrenticolidae with Dr. Ashley Dowling at the University of Arkansas in the Department of Entomology. The project starts in January 2012 and is in collaboration with Dr. Andrea Radwell (Univ. of Arkansas) and Dr. Ian Smith (Canadian National Collection).

Water mites (Acari: Hydrachnidiae) are among the most numerous, diverse, ecologically important - and unknown - groups of arthropods in freshwater ecosystems, however, there are very few water mite experts worldwide, and even fewer trained in modern systematics. The objective of this PEET project is to revise, monograph, and disseminate data on a North American water mite family, Torrenticolidae, while training two PhD students in water mite systematics using modern taxonomic and phylogenetic methods.

Research will include 1) field collection in the North American Rocky Mountains, Yukon and Alaska, the Sierra Nevada Mountains in California, and Appalachian Mountain drainages in Georgia and Florida; 2) species descriptions focusing on a digital workflow and cybertaxonomic methods to speed up the time from discovery to dissemination of data; and 3) a full phylogenetic revision of Torrenticolidae based upon molecular and morphological data.

Previous experience with mites is not required for work on this project. We are primarily looking for students with a good background in biology and a strong interest in systematics and natural history. Students should be self motivated and possess a desire to become an expert in a group very few know much about.

For more information about the project or the graduate assistantships, please contact Ashley Dowling at 479-575-2482 or adowling@uark.edu. Information about the University of Arkansas can be obtained at http://www.uark.edu and the Department of Entomology at http://entomology.uark.edu/. The PhD positions are fully funded and include student stipend, healthcare and tuition at the University of Arkansas.

Ashley Patrick Gregg Dowling <adowling@uark.edu>

UBasel 2 FishEvolution

Open PhD positions at the University of Basel to study pattern and process in evolutionary radiations of fossil and living actinopterygian fishes

The group of Walter Salzburger at the University of Basel in Switzerland (http://evolution.unibas.ch/-salzburger/) invites applications for two PhD positions. The successful candidates will work in a Swiss National Science Foundation supported research project (Sinergia) about patterns and process in evolutionary radiations of fossil and living actinopterygian fishes, concentrating on the speciation and phylogeny of extant fish species flocks. The project is a collaboration between M. Snchez (http://www.msanchezlab.net/), H. Furrer (http://www.pim.uzh.ch/de/index.php) and W. Salzburger.

We are looking for highly motivated, open-minded, and creative students, who are interested in evolutionary biology in general and in adaptive radiation and speciation in particular. Successful candidates will have research experience in at least one of these areas: evolutionary biology, fish biology, phylogenetics, population genetics, comparative anatomy, and/or morphometrics.

The working language in the SalzburgerLab is English. Basel is a highly attractive city in beautiful surroundings at the boarder between Germany, France and Switzerland, with a multinational population, and many educational, cultural and other recreational opportunities.

To apply, please send a single PDF file merged from the following parts: CV including publication list, a statement of your research interests and motivation, and two academic references. Please include the word SinergiaSalzburger2012 in the subject line. The application deadline is September 1, 2011. The positions are available in fall of 2011, at a negotiable starting date.

Many thanks and kind regards,

Prof. Walter Salzburger (e-mail: walter.salzburger@unibas.ch)

Marcelo Snchez <m.sanchez@pim.uzh.ch>

UGuelph MarineInvertBiodiversity

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

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

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

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

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

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

Stipend funding is available at NSERC network rates.

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

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

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

UHawaii SnailSystematics

We have National Science Foundation funding to support a graduate student at the PhD level to work on systematics, evolution and conservation of Hawaiian land snails. For full details and application instructions please go to http://www.hawaii.edu/cowielab/HLS_GA_notice.htm –

Kenneth A. Hayes, Ph.D. University of Hawaii Center for Conservation Research and Training 3050 Maile Way, Gilmore 408 Honolulu, HI 96822 Tel: (808) 956-0956 Fax: (808) 956-2647 Email: khayes@hawaii.edu or hayesk@si.edu

khayes@hawaii.edu

UInnsbruck IntegrativeBiodiversity

MOLECULAR ECOLOGY, INSTITUTE OF ECOLOGY, UNIVERSITY OF INNSBRUCK

PhD position

Update: This position was originally announced via EvolDir on June 17, 2011, with a very short deadline of four days. We have decided to prolong the application deadline until August 10, 2011. Applications already submitted remain valid and do not need to be re-sent.

The University of Innsbruck, Austria, seeks to hire at the PhD student level in the area of molecular ecology. The position is a 3-years position at the Molecular Ecology Group of the Institute of Ecology, starting from 1 October 2011.

The Molecular Ecology Group uses the exciting opportunities offered by the advance in molecular biology, to study ecology as a snap-shot of evolving biodiversity. Data from multiple sources are integrated to enhance the success of biodiversity research. The research focuses on terrestrial animals.

Responsibilities

1. participation in an interdisciplinary and integrative biodiversity research project on Palaearctic Tetramorium ants, i.e., addressing of population genetic, phylogeographic, phylogenetic and taxonomic questions relating to the delimitation of cryptic species, and the evolution and evolutionary ecology of cryptic diversity

2. application of molecular genetic lab techniques (e.g. mtDNA but also nuclear sequence loci, following their NGS-based development) and associated inference methods (e.g. gene flow analysis, phylogenetic reconstruction, phylogeographic analysis), morphometrics and relevant statistical methods, and possibly further disciplines (e.g., near-infrared spectroscopy, ecological niche modelling)

3. preparation of manuscripts

4. participation in the PhD program of Innsbruck University

5. teaching of a maximum of 2 hours per semester, if there is demand in the faculty

Selection criteria

A. completed study of biology, MSc level

B. demonstrated research experience in population genetics, phylogeography, phylogenetics or taxonomy of arthropods

C. keen interest in evolution and ecology, and a high level of motivation

D. ability to work effectively as part of a multidisciplinary team

E. flexibility in the course of progressing research

F. ability to work independently

G. ability to work under pressure

H. good knowledge of oral and written English

PhD supervisor

Birgit C. Schlick-Steiner

Salary

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

Further reading

Schlick-Steiner et al 2010 Annual Review of Entomology 55: 421-438

Schlick-Steiner et al 2006 Molecular Phylogenetics and Evolution 40: 259-273

Schlick-Steiner et al 2007 Trends in Ecology and Evolution 22: 391-392

Steiner et al 2010 Zoologischer Anzeiger 249: 223-254

Moder et al 2007 Journal of Zoological Systematics and Evolutionary Research 45: 82-87

Steiner et al 2006 Myrmecologische Nachrichten 8: 175-180

Schlick-Steiner et al 2007 Biological Journal of the Linnean Society 91: 247-255

Klarica et al. 2011 Journal of Chemical Ecology 37: 549-552

Steiner et al 2008 Diversity and Distributions 14: 538-545

How to apply

To apply, please submit, by E-mail to <fss-technik@uibk.ac.at>, with cc to <birgit.schlick-steiner@uibk.ac.at>, and with the subject line "Chiffre: BIO-6591 - Bewerbung um ein wissenschaftliche Stelle": a cover letter (including a reference to "Chiffre: BIO-6591"), systematic point-by-point replies as to your readiness for the responsibilities and how you meet the selection criteria, brief statement of research interests, list of relevant methods successfully applied thus far, complete curriculum vitae, complete list of publications, and

facultatively up to three pdf files of published work. Also, if possible, arrange for two letters of recommendation to be sent to <birgit.schlick-steiner@uibk.ac.at>

Applications must be written in German or English. The deadline for receipt of all applications is August 10, 2011.

The (legally binding) announcement in German can be found at:

http://www.uibk.ac.at/service/c101/-mitteilungsblatt/2010-2011/33/mitteil .pdf

The research institution and its environment

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

More information needed?

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

Birgit C. Schlick-Steiner Professor of Molecular Ecology

Institute of Ecology University of Innsbruck Technikerstr. 25 A-6020 Innsbruck, Austria Phone: +43 512 507-6120 Fax: +43 512 507-6190

— / —

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

---

UNewcastle OrganelleEvolution

Early stage researcher (PhD fellowship) to study the evolution and functions of the minimal mitochondria (mitosomes) of parasitic microbial eukaryotes: Newcastle upon Tyne, UNITED KINGDOM We are seeking to fill a fully funded PhD fellowship in molecular evolutionary biology for the Marie Curie Initial training Network ³Symbiomics ' Molecular Ecology and Evolution of Bacterial Symbionts². Symbiomics is funded by the European Framework Program 7 Marie Curie Actions with the purpose of offering Early Stage Researchers the opportunity to improve their research skills, join established research teams and enhance their career prospects.

Description: Many parasitic microbial eukaryotes possess highly reduced organelles related to mitochondria called mitosomes that have lost many of the pathways and proteins, including those used for energy generation, that make mitochondria essential components of human cells. Mitosomes are thus excellent model systems for understanding the limits of mitochondrial reductive evolution and for identifying the truly essential features of these eukaryotic organelles of ancient endosymbiotic origin. The research and training: The project will be primarily based in the laboratory of Martin Embley and Robert Hirt (Institute for Cell and Molecular Biosciences) at Newcastle University. The early stage researcher will receive training in comparative bioinformatics of parasite genomes to formulate hypotheses of mitosome evolution, functions and host-mitosome interdependencies, and training in molecular cell biology and advanced imaging techniques to test those hypotheses experimentally. The successful candidate will join a multidisciplinary and multinational group working at Newcastle on various aspects of parasite biology and evolution. Co-supervision by Prof Thomas Schweider, including secondment to the University of Greifswald, will be used to provide synergistic training in the proteomics of purified mitosomes. The Symbiomics network includes 14 leading research groups and participants from the private sector, and will provide additional training through a combination of local and network-wide activities that will include research secondments, workshops and courses, soft skills training, network and project meetings, regular thesis committee meetings, and mentoring. At the end of the training the students will have the skills they need for successful careers in academia or industry in a broad range of disciplines.

Benefits: The contract duration will be 36 months for the PhD position. The salary will be in accordance with the EU FP7 Marie Curie ITN regulations and will consist of salary, mobility allowance, a career exploratory allowance and contribution to participation expenses.

Requirements: Master degree or equivalent in a biological sciences subject Applicants should have training and research experience in microbiology, molecular biology, or related disciplines. Very good knowledge of English in writing and speaking is required. Applicants must satisfy the eligibility criteria for Marie Curie Initial Training Networks. For PhD positions, the students should have an MSc or equivalent degree that enables them to begin their PhD studies. Researchers must not have resided or carried out their main activity (work, studies, etc.) in the country of the host organization for more than 12 months in the 3 years immediately prior to their recruitment.

Application To apply, please submit, by E-mail to <martin.embley@ncl.ac.uk>, a cover letter including your rational for applying for this post and how you meet the selection criteria, a CV including the names of at least two referees. Applications must be written in English. The deadline for receipt of all applications is August 23, 2011.

Dr. T. M. Embley Professor of Evolutionary Molecular Biology & Royal Society Wolfson Research Merit Award Holder Institute for Cell and Molecular Biosciences Lab/office M2.041 (2nd floor Cookson Building). Framlington Place Newcastle University NE2 4HH UK

Tel 0191 222 7702 Fax 0191 222 7424

University Home page:

http://www.ncl.ac.uk/camb/staff/profile/-martin.embley New Lab Webpage:

http://www.ncl.ac.uk/microbial_eukaryotes/ Take a look at our Molecular Systematics course Web Page - it is also available in down-loadable (powerpoint) format:

http://bioinf.ncl.ac.uk/molsys

martin.embley@ncl.ac.uk

URegensburg PlantEvolutionaryGenomics

regensburg CENTRE for BIOCHEMISTRY AND BIOPHYSICS.

Department of cell biology and Plant biochemistry.

*Ph.D. position in Evolutionary Genomics of Plant Reproductive Isolation *

We are looking for a candidate for a Ph.D. position to investigate the genetic und developmental mechanism behind the process of reproductive isolation in plants. The project involves a comparative analysis of the transcriptome of several species within the genus Arabidopsis using Next Generation Sequencing methods. The candidate genes identified in this analysis will be functionally characterized *in vivo* using molecular, genetic, cell biological and biochemical techniques for their role in reproductive isolation and plant defense.

This project is part of a consortium involving several workgroups across Germany and Switzerland. As part of this network the PhD candidate will interact on a regular basis within a diverse group of experts in plant reproductive biology, bioinformatics and genomics. Moreover, the PhD student will be offered a structured PhD program within the Regensburg International Graduate School of Life Sciences (RIGeL). Regensburg is an attractive university town in south-eastern Germany (Bavaria). The universities and city of Regensburg are proud of a recent poll by international scholars rating Regensburg as the âbest place to live and study in Europeâ.

We are looking for a motivated and well-organized student who holds a Master of Sciences in Biology or equivalent and has experience in molecular biology, especially in molecular plant sciences. We look for candidates who are interested in plant developmental biology, plant pathology and who are able to work and think methodically and independently. Candidates should have excellent communication skills in English and have fun working in a team.

For informal enquiries and additional information on this position please send an e-mail to Dr. Mariana Mondragon-Palomino. To apply please send in a single PDF file your curriculum vitae, the contact information of two recent references and a statement of research interests. The position is immediately available and will remain open until an appropriate candidate is identified.

*Contact: *

Dr. Mariana MondragÃ³n-Palomino

Phone +49 941 943-4909 Telefax +49 941 943-3352 Universitätsstraße 31 D-93053 Regensburg

mariana.mondragon@biologie.uni-regensburg.de http://www.biologie.uni-regensburg.de/Zellbiologie/-index.html www.biologie.uni-regensburg.de Mariana Mondragon <mariana.mondragon@biologie.uni-regensburg.de>

UWesternSydney Evolution

Doctoral Scholarships Hawkesbury Institute for the Environment, University of Western Sydney, Australia Advancing research on ecosystem function and environmental change

The new Hawkesbury Institute for the Environment (HIE) offers comprehensive state of the art field- and laboratory based facilities for research from genes to ecosystems. Dedicated to answering crucial questions about the impact of environmental change on terrestrial ecosystems, the HIE's multidisciplinary research team is exploring how these ecosystems and their components respond to changes in atmospheric CO2 concentration, temperature, drought, land use, fire and biotic invasion. HIE is located on the Richmond Campus, at the foot of the Blue Mountains close to Sydney.

We are seeking excellent doctoral candidates to undertake research within the areas of the HIE: * 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 interactions, including vertebrate and insect ecology, herbivory, multitrophic and symbiotic interactions; * Ecology, physiology, biochemistry and genetics underpinning adaptation of plants and insects to a changing environment.

Approaches will include laboratory, controlled environment and field- based experiments as well as computer modelling and simulation in the intersection of integrative physiology, genomics, ecology and evolution. During the course of the project, you will have access to leading International and Australian scientists for supervision, consultation and advice. There is a possibility of the successful candidate spending a period of time at collaborating 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's web site for information about English language requirements at www.uws.edu.au/international/-admissions/english_lan- guage_requirement

What does the scholarship provide? * Tax free stipend of $32,860 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 should contact and discuss their research aspirations and eligibility with potential supervisors in the Hawkesbury Institute http://www.uws.edu.au/hie/people prior to application. * Contact the Research Training, Policy and Programs Officer to discuss enrolment and scholarships: Ms Sandra Lawrence: sg.lawrence@uws.edu.au

How to apply: Submit an application form, research proposal and CV by the APPLICATION CLOSING DATE 29 JULY 2011. Details of what to include in your research proposal can be found at http://www.uws.edu.au/research/-future_research_students/apply#Requirements The application form can be downloaded from the web: www.uws.edu.au/research/scholarships Dr Markus Riegler Insect Symbiosis Lab Hawkesbury Institute for the Environment University of Western Sydney

Locked Bag 1797 Penrith NSW 2751 Australia email: m.riegler@uws.edu.au office: +61-(0)2-4570 1229 fax: +61-(0)2-4570 1314 www.uws.edu.au/hie/markusriegler M.Riegler@uws.edu.au

Jobs

CaliforniaStateU LA ConservationGenetics

Assistant Professor, Conservation Genetics

The Department of Biological Sciences, California State University, Los Angeles, seeks to fill a tenure-track position in Conservation Genetics beginning Fall, 2012. A Ph.D. in Conservation Genetics or related field is required, with a minimum of one year related post-doctoral experience. The candidate is expected to teach undergraduate and graduate courses, participate in course and program development, establish an externally funded research program in an area of conservation genetics and involve undergraduate and Master^{1}s students in the research. While any organismal focus will be considered, preference will be given to candidates whose research focuses on a plant system. Submit curriculum vitae, statement of research plans, statement of teaching philosophy, transcripts, three letters of recommendation and the University^{1}s Application for Academic Employment form http://www.calstatela.edu/univ/hrm/docs/forms/Empl_applic_academic.pdf to Search Committee ' Conservation Genetics, Department of Biological Sciences, California State University, Los Angeles, 5151 State University Drive, Los Angeles, CA 90032 (nmcquee@calstatela.edu). Review of completed applications will begin October 17, 2011 and continue until position is filled. EO/Title IX/ADA Employer.

Thanks again and let me know if there is some problem with this. Nancy McQueen

– Nancy L. McQueen, PhD Professor of Microbiology and Chair Department of Biological Sciences 5151 State University Drive Los Angeles, CA 90032 Telephone: 323 343-2052 nmcquee@calstatela.edu

Nancy McQueen <nmcquee@exchange.calstatela.edu>

Crete IMBG 2 Bioinformatics

Two positions in Bioinformatics/Computational Biology

The Institute of Marine Biology and Genetics (IMBG) of the Hellenic Centre for Marine Research (HCMR), invites applications for two (2) experienced researchers in the field of Bioinformatics - Computational Biology. These positions are funded by the EU-FP7 "MARBIGEN" project "Supporting research potential for MARine BIodiversity and GENomics in the Eastern Mediterranean"(www.marbigen.org). This project aims at supporting IMBG excellence in the fields of biodiversity and genomics, by integration of phenotypic, community ecology and genomic approaches within an evolutionary context. It includes upgrading existing and acquiring new equipment for automated 3D phenotyping, genomic data production and bioinformatics, taking advantage of the knowledge and experience existing in excellent research entities of the EU though exchanges of researchers, the organization of workshops and seminars, and hiring incoming experienced scientific personnel.

IMBG is located in Crete, Greece (http://www.hcmr.gr/listview2.php?id=102), 15 km east of the city of Heraklion by the seashore. Its focus is on studying biodiversity at all levels of biological organization, from genes to ecosystems. It leads the Greek national network for biodiversity research (related to ESFRI infrastructure "LIFEWATCH"), is a member of the national network for genomic research, and participates in the pan-European ESFRI infrastructure "EMBRC" (European Marine Biological Resource Centre).

Specifically, experienced researchers are to be recruited for the following positions:

1. Bioinformatician / Computational Biologist with interest / experience in applying genomic approaches in organismic and population biology. Ability in analysis of next generation sequencing data, gene annotation and genome assembly will be considered.

2. Bioinformatician with experience in genomics and metagenomics of microbial organisms. Experience in analysis of data, produced by next generation sequencing will be considered.

Candidates must have a PhD in a related field and at least three years of postdoctoral experience, a demonstrated record of significant research and the potential to make substantial contributions as independent investigators. The fellows are expected to be involved in running projects of the Institute but also to develop new research projects and to interact with the multidisciplinary research environment of the host Institute.

Applications should consist of a)a cover letter detailing previous experience, research interests and motivation for applying, b)an academic CV and c) contact information for three referees (including e-mail address), which should be submitted electronically to magoulas@her.hcmr.gr until September 10, 2011.

The expected starting date for the positions is in October 2011. Gross salaries will be 4500 euro per month and duration of contracts will be initially one year, extendable for one further year.

For more info please contact Dr. Giorgos Kotoulas <kotoulas@her.hcmr.gr>

We are committed to increasing the proportion of female researchers at IMBG/ HCMR and strongly encourage applications from female candidates.

Dr. Antonios Magoulas

Director, Institute of Marine Biology and Genetics Hellenic Centre for Marine Research (HCMR) P.O. Box 2214, 710 03 Heraklion, Greece Tel. +30 2810 337801 Fax +30 2810 337870

kasapidi@her.hcmr.gr

EastCarolinaU LabTech EvolGenetics

Lab Technician - Molecular evolutionary genetics Department of Biology East Carolina University Greenville, NC

We seek a highly motivated lab technician to join the lab of Dr. Ashley N. Egan at East Carolina University, an active lab investigating population genetics, evolutionary genomics, and phylogenetics of legume and invasive species. For an outline of current and prospective projects in the lab, please go to http://www.ecu.edu/cs-cas/biology/egan_ashley.cfm . Applicants must have experience with PCR and DNA sequencing and/or microsatellite genotyping. Responsibilities include DNA extractions, sequencing and genotyping of plant samples, database entry and archiving and other duties as required.

Minimum Qualifications: Bachelor's or Master's Degree in an appropriate field such as Biological Sciences, Molecular Biology, or Genetics, PLUS demonstrated research experience that included performing DNA extractions and PCR, and facility with standard computer software programs. Experience with microsatellite genotyping and/or DNA sequencing is required. Applicants should be US citizens. Preference will be given to applicants with a Master's degree or demonstrated experience in the field. This is a full time 1-yr position to start September 2011. Applications are being accepted immediately and will be reviewed until the position is filled.

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

Ashley N. Egan, Ph.D. Assistant Professor, Department of Biology North Carolina Center for Biodiversity Howell Science Complex - Mailstop 551 East Carolina University Greenville, NC 27858-4353 Office: N303a/N304 Lab: N304/N305 Phone (252) 328-4244 fax (252) 328-4178 egana@ecu.edu

---

FrenchGuiana 3yr ResAssist PlantPopGenetics

Research assistant 36-month temporary contract

Duration: 36 months

Employer: INRA

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

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

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

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

The research assistant will:

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

- Annotate the above libraries

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

- Apply the markers to the fingerprinting of plantation trees

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

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

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

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

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

Ivan Scotti ivan.scotti@ecofog.gf

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

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

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

GriffithU ResFellow AdeliePenguins

Dear Professor Golding,

Please find below, a second job ad I would like to appear on your site for the position of Research Fellow (Ancient DNA - Adelie Penguins):

Research Fellow (Ancient DNA - Adelie Penguins)

Reference: 492715 Element: Environmental Futures Centre Work type: Fixed term (3 years)

Overview: The successful applicant will work at Nathan Campus as a member of a team to conduct research into the area of ancient DNA with the aim to recover DNA sequences from both modern and ancient animal tissues that will assist with the management and completion of the Human Frontier Science Project.

This is a fixed term (3 years), full time position based at the Nathan campus, Queensland, Australia.

The role: The successful applicant will have a unique opportunity work in collaboration with international research teams on genomic studies of Adelie Penguins in Antarctica. The position may involve fieldwork in Antarctica over the summer months.

Applicants will work in a state-of-the-art ancient DNA facility as well as modern molecular biology laboratories. This facility is equipped with a dedicated 454 DNA sequencer and a real-time PCR facility. Laboratory technologies will include PCR amplification of DNA, cloning, the construction of libraries for second generation DNA sequencing, quantitative PCR and DNA capture methods.

The person: Completion of a relevant Doctoral degree such as Molecular Biology or Biochemistry. Expertise in second-generation DNA sequencing and DNA capture technologies is required. In addition, ancient DNA experience and some bioinformatics expertise would be an advantage. An ability to work with a multi disciplinary team including mathematicians, archaeologists, geologists is necessary.

Salary range: Research Fellow, Grade 1: AUD $59,533 - $70,030 per annum. Salary package including 17% employer superannuation contribution: AUD $69,654 - $81,935 per annum.

Further information: Obtain the information package and application requirements by visiting http://jobs.griffith.edu.au/jobSearch.asp For position queries, contact Professor David Lambert, Environmental Futures Centre on +61 (0) 7 3735 5298.

For application queries, contact Mr Chris Delannoy, Recruitment Officer on +61 (0) 7 3735 3505.

To apply please visit http://jobs.griffith.edu.au/jobSearch.asp All applications must be submitted online.

Closing date: 5 August 2011 4.30 pm AEST.

Regards

Wayne Beech Recruitment Consultant | Recruitment CARE Centre | HR Services Office of Human Resource Management I Griffith University 1.26 Bray Centre (N54), Nathan Campus, QLD, 4111 Ph: (07) 3735 5093 I Fax: (07) 3735 5371 l http://www.griffith.edu.au/ For Office of HRM Service Standards, click here “Griffith University - EOWA Leading Organisation for the Advancement of Women 2010. Committed to an organisational culture in which women participate as equals at all levels”.

Email: w.beech@griffith.edu.au

Wayne Beech <w.beech@griffith.edu.au>

GriffithU ResFellow AncientDNA

Research Fellow (Ancient DNA - Sacred Ibis)

Reference: 492714 Element: Environmental Futures Centre Work type: Fixed term (3 years)

Overview: The successful applicant will work at Nathan Campus as a member of a team to conduct research into the area of ancient DNA with the aim to recover DNA sequences from both modern and ancient animal tissues that will assist with the management and completion of the Human Frontier Science Project.

This is a fixed term (3 years), full time position based at the Nathan campus, Queensland, Australia.

The role: The successful applicant will have a unique opportunity work in collaboration with international research teams on genomic studies of Sacred Ibis mummies from ancient Egypt. The position may involve fieldwork in Egyptian catacombs.

Applicants will work in a state-of-the-art ancient DNA facility as well as modern molecular biology laboratories. This facility is equipped with a dedicated 454 DNA sequencer and a real-time PCR facility. Laboratory technologies will include PCR amplification of DNA, cloning, the construction of libraries for second generation DNA sequencing, quantitative PCR and DNA capture methods.

The person: Completion of a relevant Doctoral degree such as Molecular Biology or Biochemistry. Expertise in second-generation DNA sequencing and DNA capture technologies is required. In addition, ancient DNA experience and some bioinformatics expertise would be an advantage. An ability to work with a multi disciplinary team including mathematicians, archaeologists, geologists is necessary.

Salary range: Research Fellow, Grade 1: AUD $59,533 - $70,030 per annum. Salary package including 17% employer superannuation contribution: AUD $69,654 - $81,935 per annum.

Further information: Obtain the information package and application requirements by visiting http://jobs.griffith.edu.au/jobSearch.asp For position queries, contact Professor David Lambert, Environmental Futures Centre on +61 (0) 7 3735 5298.

For application queries, contact Mr Chris Delannoy, Recruitment Officer on +61 (0) 7 3735 3505.

To apply please visit http://jobs.griffith.edu.au/jobSearch.asp All applications must be submitted online.

Closing date: 5 August 2011 4.30 pm AEST.

Regards

Wayne Beech Recruitment Consultant | Recruitment CARE Centre | HR Services Office of Human Resource Management I Griffith University 1.26 Bray Centre (N54), Nathan Campus, QLD, 4111 Ph: (07) 3735 5093 I Fax: (07) 3735 5371 l http://www.griffith.edu.au/ For Office of HRM Service Standards, click here "Griffith University - EOWA Leading Organisation for the Advancement of Women 2010. Committed to an organisational culture in which women participate as equals at all levels".

Email: w.beech@griffith.edu.au

Wayne Beech <w.beech@griffith.edu.au>

NESCent WebDesign

User Interface Design and Web Application Developer

The National Evolutionary Synthesis Center (NESCent) seeks a creative and enthusiastic individual to design user interfaces and web applications for scientific applications that manage, analyze, visualize and share data in support of evolutionary research. The incumbent will work as part of a small informatics team in close collaboration with domain scientists.

NESCent (http://nescent.org) is an NSF-funded center dedicated to cross-disciplinary research in evolutionary science. Our informatics team works closely with visiting and resident scientists to support their custom software and database development needs (http://informatics.nescent.org), and collaborates broadly with other biodiversity informatics projects. All NESCent software products are open-source, and the Center has a number of initiatives to actively promote collaborative development of community software resources. Above all, we are enthusiastic about our work, about the mission of the Center, and about the contribution of informatics to that mission.

Job description: The incumbent will design and develop user interfaces and web applications for databases and other software tools for sponsored scientists and staff. The job responsibilities include all stages of the software development process, including requirements gathering, design, implementation, release packaging and documentation, as part of a small team (typically 2-3 individuals). We expect the incumbent to present their work at conferences and contribute to publications with scientific collaborators; interact regularly with visiting and resident scientists, other members of the informatics team and Center staff; and generally serve as an expert resource for Center personnel. The position provides opportunities for professional development and encourages research into new technologies. Most informatics staff work at our Durham NC offices, located adjacent to Duke University, but we support a wide range of technologies for virtual communication with off-site staff and collaborators.

Salary range: $70,000 - $80,000, depending on education and experience

Required Qualifications: * Demonstrated success collaborating with clients on custom software solutions * Experience with various stages of the software development cycle * Expertise in development and testing of user interface designs * Excellent communication skills, both virtual and face-to-face

Preferred Qualifications: * M.S. or Ph.D. in Computer Science, Bioinformatics or related field * Demonstrated interest in science, particularly biology * Expertise in dynamic and interactive web technologies (JavaScript, CGI) * Expertise in rapid application development and respective programming technologies and languages (e.g., modern scripting languages and web-application frameworks such as Python/Django, Ruby/Ruby-on-Rails, and Perl/Catalyst). * Expertise in graphic design * Expertise in data visualization and/or scientific data integration * Expertise in software usability design and assessment * Expertise in web service (SOAP, REST, XML, JSON) and semantic web technologies * Fluency in Java programming * Prior experience in relational database programming (PostgreSQL or MySQL) * Experience with open-source, and collaborative, software development

How to apply: Please send cover letter, resume and contact information for three references to Dr. Karen Cranston, Training Coordinator and Bioinformatics Project Manager (karen.cranston@nescent.org); Please also complete the online application at the University of North Carolina HR website: http://bit.ly/r9HQ8r. Informal inquires or requests for additional information may be directed to Dr. Cranston by email or phone (+1-919-613-2275). Closing date is August 15, 2011.

–

Karen Cranston, PhD Training Coordinator and Informatics Project Manager nescent.org

Karen Cranston <karen.cranston@nescent.org>

PrincetonU EvolutionaryBiolPrincetonU EvolutionaryBiol

ASSISTANT PROFESSORSHIP ECOLOGY, EVOLUTION AND/OR BEHAVIOR

Princeton University's Department of Ecology and Evolutionary Biology plans to hire individuals at the level of tenure-track Assistant Professor. We have broad interests in ecology, evolution, behavior, functional biology, conservation biology, disease and biogeochemistry; a common appreciation of theory, natural history and evolutionary thinking unites the Department. We seek applicants who pursue research that aims for significant conceptual and/or empirical integration across traditional disciplinary boundaries and who have a strong commitment to teaching. It is possible that an appointment may be joint with the Princeton Environmental Institute, especially if the applicant's research focuses on problems of global or environmental change.

Applicants should write a vision statement, no longer than two pages, that outlines the conceptual dimensions of one or more major unsolved problems in their field and how their approach will contribute to solving them. The vision statement should be more than a summary of the applicant's prior and current research.

Applications, including the vision statement, curriculum vitae, three reprints and contact information for three references should be addressed to Simon Levin, Search Committee Chair, and submitted online via http://jobs.princeton.edu. Screening of applications will begin 12 September 2011.

Princeton University is an equal opportunity employer and complies with applicable EEO and affirmative action regulations.

(Direct link to the online posting of Job Req #0110466: https://jobs.princeton.edu/applicants/jsp/shared/-position/JobDetails_css.jsp?postingId=182122)

Diane Carlino Department Manager Ecology and Evolutionary Biology Princeton University 104A Guyot Hall 609-258-5810 dcarlino@princeton.edu

Diane Carlino <dcarlino@Princeton.EDU>

RutgersU Genomics

Position Description A full-time bioinformatics staff position is available immediately in the Bhattacharya Group (see http://dblab.rutgers.edu/) at Rutgers University (New Brunswick, New Jersey, USA) to carry out genomic and bioinformatic research on a variety of basic and applied research projects. The position is associated with the newly established Genome Cooperative (for details, see http://dblab.rutgers.edu/-

genome_cooperative/).

This individual will report to Bhattacharya and other Cooperative members and will support and perform collaborative research work in molecular biology and genomics using bioinformatic approaches. Duties include: (1) to perform analysis of genome data using existing computational tools and to interpret and present data and results to collaborators, (2) to train other lab members in the use of specialized tools for genome research, and (3) to contribute to manuscript and grant preparation. Ideal candidates will have a computational biology/genomics background with significant research experience, proven scripting skills (PERL/Python), as well as experience with relational databases (mysql or similar) and publicly available genome resources.

Requirements The position requires a bachelor's degree in a biological or computer science or an equivalent combination of education and/or experience. Working knowledge and experience in molecular evolution, genomics, phylogenetics, high-performance computing and/or UNIX environment, are highly desirable. Knowledge of web design, server management and/or programming languages (C/C++/Java) is a plus.

Rutgers, The State University of New Jersey, is a leading national public research university. It is the only public university in New Jersey in the Association of American Universities, a group comprising North America's 61 leading research universities. The Protein Data Bank (PDB; http://www.pdb.org/) is hosted at Rutgers.

APPLICATION DEADLINE: September 15, 2011. Position will remain open until filled.

SALARY is offered based on qualification and experience.

Any queries should be addressed directly to Debashish Bhattacharya (bhattacharya@aesop.rutgers.edu). To apply, please send the following items to the same email address: (1) a cover letter stating potential start date (2) a curriculum vitae, including contact information for at least two references, and (3) a brief statement of research interest and career goals

Rutgers is an equal opportunity/affirmative action employer.

Debashish Bhattacharya Professor Department of Ecology, Evolution and Natural Resources Institute of Marine and Coastal Sciences Foran Hall 102 Rutgers University, New Brunswick, NJ 08901, USA Telephone: (732) 932-8193

bhattacharya@aesop.rutgers.edu

SaudiArabia Biodiversity

The Red Sea Research Center at KAUST (rsrc.kaust.edu.sa) is seeking qualified candidates for positions as Lab Manager, Lab Technician and Field Technician. We have active projects in Marine Microbiology, Coral Genomics, Coral Reef Ecology, Biodiversity, Marine Ecology, and Fisheries Ecology in the Red Sea. Please reply to rsrc.director at kaust.edu.sa with a statement of interest and CV. Information about KAUST can be found on the general website (http://www.kaust.edu.sa).

Lab Manager: To manage genetics/microbiology research laboratory operations, team management, maintaining research consumable supplies, and be able to assist with faculty, staff, and student research projects, including visiting scientists and researchers.

Major Responsibilities: Maintenance of lab environment and performing or organizing equipment service; ordering of lab equipment and consumables to ensure continuous operations, and to follow up with suppliers and Procurement where needed; completion and submission of safety training and all other administrative reports to relevant departments; to attend and/or participate in Center meetings and individual lab meetings as requested; to coordinate administrative duties for general Center technicians to ensure smooth and continuous lab operations, including leave scheduling; to oversee and coordinate the general daily operations of the lab including liaising for scientists and researchers visiting the Center.

Competencies: Fluent in English, both spoken and written; excellent written and verbal communication skills; experience writing formal and scientific reports.

Qualifications: An undergraduate degree in biology, genetics, marine biology, or related/relevant discipline. Undergraduate degree or higher in a relevant discipline.

Minimum of 3 years experience working in a biological research laboratory with preference for genetics or microbiology experience, with at least 1 year experience in team or major project management; preferably will have experience with all or most of the following instruments, equipment, or techniques: Polymerase Chain Reaction (PCR), Quantitative Polymerase Chain Reaction (qPCR), bioanalyzer, incubation chambers, fluorescence microscopes, liquid handling robots, ultracentrifuge, liquid nitrogen handling, DNA extraction and amplification, freeze dryers.

Lab Technician: To assist with lab research as well as maintain diverse research projects in collaboration with local & international scientists. Some opportunity may exist for independent projects.

Major Responsibilities: Preparation of samples for laboratory analysis and/or culture; preparation, optimization, and analyses of PCR reactions; maintenance of lab environment and performance of minor equipment maintenance; ordering of lab equipment and consumables to ensure continuous operations, and to follow up with suppliers and Procurement where needed; to attend and/or participate in Center meetings and individual lab meetings as requested; to assist with general daily operations of the lab including liaising for scientists and researchers visiting the Center; help oversee students experiments in the lab if required by faculty; DNA isolation; RNA isolation; PCR and cloning; operation of qPCR, bioanalyzer incubation chambers, fluorescence and other microscopes, liquid handling robots, ultracentrifuge, liquid nitrogen handling, freeze dryers, and next-generation library preparation (Illumina and 454)

Competencies: Fluent in English, both spoken and written; excellent communication skills; experience writing formal and scientific reports; broad knowledge of tropical marine life / ecosystems as well as global conservation issues; experience living/working abroad for prolonged periods.

Qualifications: Undergraduate degree in biology, genetics, marine biology, or related/relevant discipline; minimum of 1 year of experience working in a biological research laboratory with preference for genetics or microbiology experience; experience living abroad; experience working in college or university also an advantage; good understanding or fluency in Arabic an advantage, but not required.

Field Technician: To assist with field research as well as maintain diverse research projects in collaboration with local & international scientists. Some opportunity may exist for independent projects.

Major Responsibilities: Preparation of samples for laboratory analysis, including sample preservation and cataloging; sample collections in the field; dissection and processing of field samples; maintenance of lab environment and performance of minor equipment maintenance; ordering of field equipment and consumables to ensure continuous operations, and to follow up with suppliers and Procurement where needed; to manage inventory of Center field gear; to attend and/or participate in Center meetings and individual lab meetings as requested; to assist with general daily

— / —

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

TexasAMU Evolutionary-MarineMolecularBiology

Dear Evoldir members,

We are searching for a marine molecular biologist. Although the exact area of specialty is open, evolutionary biologists and population geneticists using cutting-edge molecular techniques to address questions of relevance to marine systems are welcome to apply! I'm not on the search committee, so please contact Paul Zimba the search committee chair. His address is at the end of the ad below.

Deb Overath

Details:

Assistant Professor: Marine Molecular Biology The rapidly growing Marine Biology Program in the Department of Life Sciences of Texas A&M University-Corpus Christi invites applications for a tenure-track Assistant Professor of Marine Molecular Biology. The successful candidate will specialize in the use of cutting-edge molecular approaches to address marine biological research problems. This position will further expand and complement our existing program (www.marinebiology.tamucc.edu). The preferred start date is January 2012, but no later than September 2012. A competitive startup package will accompany this position.

Job Duties: The successful candidate will be expected to develop a vigorous, externally-funded research program, supervise graduate students, and teach undergraduate and graduate courses supporting the Biology B.S. and M.S. Programs, Marine Biology M.S. Program, and, particularly, the joint Interdisciplinary Ph.D. Marine Biology Program. Preferred Qualifications: Candidates must have a Ph.D. degree in a biological (or closely related) discipline.

Texas A&M University-Corpus Christi is a rapidly growing research university located on the Gulf of Mexico overlooking Corpus Christi Bay. With over 10,000 students, it offers a wide array of academic programs with 18% of the students enrolled in graduate programs. Applications are particularly encouraged from individuals with active, federally-funded research programs and strong external collaborations who can take advantage of our modern research laboratories and equipment, including those associated with our core molecular and microscopy facilities. Ample opportunities exist for collaboration with researchers from the Department of Life Sciences as well as from the University's strong portfolio of marine-oriented research institutions such as the Harte Research Institute for Gulf of Mexico Studies (http://harteresearchinstitute.org), Center for Coastal Studies (http://ccs.tamucc.edu) and Conrad Blucher Institute (http://www.cbi.tamucc.edu/). Our unique location provides many opportunities for marine-related research including proximity to extensive bays and estuaries along the Gulf of Mexico.

With a population of ~300,000, Corpus Christi has numerous urban conveniences while maintaining a small-town atmosphere. Located in South Texas, Corpus Christi is close to popular destinations, including Padre Island National Seashore, San Antonio and Austin. Apply online at https://islanderjobs.tamucc.edu. Application must include a cover letter describing qualifications, research and teaching interests, curriculum vitae, and the names and phone numbers of four or more references.

The position will remain open until filled with preference given to applicants submitting all requested documentation by August 15, 2011. Contact Information: Dr. Paul Zimba, Search Chair, Paul.Zimba@tamucc.edu

R. Deborah Overath, Ph.D. Assistant Professor of Biology Local Program Director Hispanic Leaders in Agriculture and the Environment Department of Life Sciences (ST 312) 6300 Ocean Drive, Unit 5800 Texas A&M - Corpus Christi Corpus Christi, TX 78412

Phone: (361) 825-2467 Cell: (361) 876-4542 Fax: (361) 825-2742

"Overath, Deborah" <Deborah.Overath@tamucc.edu>

UCalifornia Berkeley ProfessorMuseumDirector

Professor of Integrative Biology and Director of the Museum of Vertebrate Zoology. The Department of Integrative Biology and the Museum of Vertebrate Zoology at the University of California, Berkeley invite applications for a joint tenuredfaculty appointment in the evolutionary biology of vertebrates. We view vertebrate evolutionary biology broadly, and the successful candidate's research expertise might thus include (but not be limited to) the areas of systematics, biodiversity informatics, comparative phylogenetics, evolutionary genomics, conservation biology, evolutionary ecology, and evolutionary and ecological dynamics in relation to environmental change. The successful candidate will be expected to maintain a dynamic, field collections-based, extramurally funded research program, and will have an inspired vision for the future of the MVZ and museum-based research more generally. Candidates must have a strong interest in undergraduate and graduate teaching and will be expected to contribute to instruction in general and specialized courses. A commitment to expanding and utilizing museum collections in research, education, and outreach is required. The MVZ and IB are highly interested in candidates who have engaged in service towards increasing the participation of individuals from groups historically under-represented in higher education. For further information about the MVZ and IB, please visit our websites (http://mvz.berkeley.edu/ and http://ib.berkeley.edu/). For information regarding confidentiality, please refer to: http://apo.chance.berkeley.edu/evalltr.html . Please submit application materials describing relevant qualifications and experience for the position, a curriculum vitae, statements of research interests, teaching philosophy and outreach to underrepresented groups, a vision statement for the MVZ, and the names and contact details for three references. Applications should be submitted electronically via http://ls-ourunit.berkeley.edu:80/candidate/selRegister.php?i=576 or via email to: VertEvol.IB.MVZ@gmail.com.

If electronic submission is not possible, materials must be sent by regular mail to:

Vertebrate Biology and MVZ Director Search Committee Department of Integrative Biology 3040 Valley Life Sciences Building University of California, Berkeley Berkeley, CA 94720-3140 USA

Applications must be received electronically or postmarked by September 7th, 2011.

Berkeley is committed to addressing the family needs of faculty, including dual career couples and single parents. The University of California is an Equal Opportunity/Affirmative Action Employer.

Debra Downey <dmdowney@berkeley.edu>

UCalifornia SantaBarbara ResTech DrosEvolGenomics

The Ecology, Evolution, and Marine Biology Department at UC Santa Barbara is currently recruiting an intro-level Lab Technician to join the team of Dr. Thomas Turner.

Information on the Turner lab is available here (labs.eemb.ucsb.edu/turner). The Lab Technician will perform several general duties relating to ongoing projects on the evolutionary functional genomics of behavior in Drosophila, including maintenance of Drosophila populations and high-throughput quantification of behaviors. Broader participation in research projects is possible for motivated and qualified applicants. To apply online go to jobs.ucsb.edu, and search positions for job #20110242.

Thomas Turner Assistant Professor Department of Ecology, Evolution, and Marine Biology University of California, Santa Barbara Web: labs.eemb.ucsb.edu/turner/

thomas.turner@lifesci.ucsb.edu

UCambridge TempLectureship HumanEvolution

Temporary Lectureship in Human Evolutionary Genetics

Division of Biological Anthropology, Department of Archaeology and Anthropology

Start date: 15th September 2011

Limit of tenure applies*

Applications are invited for a Temporary Lectureship in Human Evolutionary Genetics. The successful candidate will be expected to contribute to the teaching and examination of the undergraduate and graduate courses, administration in Biological Anthropology, and to research activities. Some teaching will be specifically in the area of Evolutionary Genetics.

Applicants should hold a PhD in the relevant field, have some experience of university teaching and research and share an interest in multi-disciplinary approaches to human evolution.

The pensionable stipend will be £36,715 pro rata. This post is part-time (80%).

Further particulars of the post can be found here:

Applications should consist of a University application form, a covering letter, a CV with a full list of publications, and a one page statement of research and teaching interests, as well as the names and addresses of three referees who can be contacted. The application form (CHRIS/6) needs to have parts 1 & 3 completed: it is found at http://www.admin.cam.ac.uk/offices/hr/forms/chris6/ or can be obtained from Mrs Jane Clare, Administrative Secretary, Department of Archaeology and Anthropology, University of Cambridge, Pembroke Street, Cambridge CB2 3QY. Please submit one hard copy of your application to Mrs Clare and also send one single pdf file of the whole application to her at jc478@cam.ac.uk.

Deadline for applications: 15th August 2011. Interviews are planned for early September.

*Limit of tenure: 12 months

The University values diversity and is committed to equality of opportunity.

The University of Cambridge only advertises their own and college vacancies on this website; we do not advertise any external vacancies.

The University has a responsibility to ensure that all employees are eligible to live and work in the UK.

Toomas Kivisild <tk331@cam.ac.uk>

UChester ConservationGenet ResAssist

UNIVERSITY OF CHESTER APPLIED SCIENCES -BIOLOGY CONSERVATION GENETICS RESEARCH ASSISTANT FIXED TERM CONTRACT UNTIL 31ST JULY 2012 21 HOURS PER WEEK £19,261 - £21,021 PER ANNUM, PRO RATA

A vacancy has arisen for an experienced and motivated research assistant, to carry out genetic analysis on a number of conservation genetics projects. The results will be used to directly manage endangered species both in captivity and in the wild. Current projects include working on Asiatic lions, Scottish wildcats, pygmy hippos, chimpanzees and forest elephants. The project is for 3 days per week and 12 months initially.

The successful candidate will have previous experience of high throughput microsatellite genotyping and mitochondrial sequencing, as well as a proven ability to work with a range of sample materials (blood, tissue, feather, faecal). This is an exciting opportunity for the right candidate.

Candidates may download further details and an application form from our website at www.chester.ac.uk/-jobs/ or send an A4 SAE to HRM Services, University of Chester, Parkgate Road, Chester CH1 4BJ quoting reference number HRMS/10172.

Closing date: Wednesday 10th August 2011, 12 noon.

Many thanks Samantha Fenn HR Adviser

Telephone: 01244 512 044

Samantha Fenn <s.fenn@chester.ac.uk>

UCollege London 2 EvolutionaryBiol

Two Job Vacancies: Closing date: 31 July 2011

University College London, Department of Genetics, Evolution and Environment

1. Reader<http://en.wikipedia.org/wiki/-Reader_(academic_rank)> or Professor in Evolutionary and Comparative Biology 2. Reader<http://-en.wikipedia.org/wiki/Reader_(academic_rank)> or Professor in Ecology and Biodiversity

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

We invite applications from world class research scientists for two positions available in the areas of Evolutionary and Comparative Biology and Ecology and Biodiversity.

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

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

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

Further information about this post, together with application details, can be found at http://-www.ucl.ac.uk/gee/jobs Informal enquiries concerning the position in Evolution and Comparative Biology can be made to Prof Max Telford (m.telford@ucl.ac.uk)

Informal enquiries concerning the position in Ecology and Biodiversity can be made to Dr David Murrell (d.murrell@ucl.ac.uk)

Max Telford Professor of Zoology Department of Genetics, Evolution and Environment, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel: +44 (0)20 7679 2554 (Internal: 32554) Fax: +44 (0)20 7679 7096 http://www.ucl.ac.uk/biology/academic-staff/-telford/telford.html a new open access journal EvoDevo: http://www.evodevojournal.com/ Telford & Littlewood: Animal Evolution. OUP< http:/-/ukcatalogue.oup.com/product/9780199570300.do >

Software to align Nucleotide sequence according to Amino Acid translation TranslatorX< http://-www.translatorx.co.uk >

Files and software for downloading:< http:/-/web.mac.com/maxtelford/iWeb/Work/-Downloads.html >

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

Xenoturbella You Tube video< http://-uk.youtube.com/watch?v=3DyJXNcoxL2Xs >

The Linnean Society of London< http://-www.linnean.org/ >

m.telford@ucl.ac.uk

ULiverpool Bioinformatics

Team Leader: Computational Biology/Bioinformatics

Much of this job will involve the analysis of genetic variation from next-gen sequence and so a evolutionary/population genetics background relevant, provided accompanied by good computing skills.

The Centre for Genomic Research is a leading laboratory for the application of genomic technologies and bioinformatic analyses. Supported by the University, MRC and NERC, it is applying cutting-edge technologies to environmental, biomedical and comparative genomic research. Providing guidance and oversight to a team of bioinformaticians, you will have the primary responsibility of developing and implementing next-generation sequencing analyses. In addition, you will also be responsible for providing direction to the development of the CGR and ensure that the CGR remains at the forefront of developments in computational biology. The post is available for 3 years initially.

More details at: http://www.liv.ac.uk/working/-job_vacancies/research/R-5736551.htm Dr Steve Paterson Institute of Integrative Biology University of Liverpool Liverpool L69 7ZB, UK Tel (+44) 151 795 4521 Mob (+44) 151 794 7668 Fax (+44) 151 795 4408 Email s.paterson@liv.ac.uk

S.Paterson@liverpool.ac.uk

UMaryland ResAssist PopGenetics

A Faculty Research Assistant position in population genetics and genomics is available to work with Dr. Stephen Keller at the Appalachian Laboratory (AL) of the University of Maryland Center for Environmental Science (UMCES). The focus of the research is on using genetic data to understand the impacts of changing environmental conditions on natural populations, including effects on population size, structure, connectivity, and adaptation (http://skeller.al.umces.edu/).

Duties and responsibilities: This position will focus primarily in the lab on generating molecular genetic data for evolutionary analysis. The position may also involve computational data analyses, growth and maintenance of plants in the greenhouse, ecological field work, ordering of lab supplies and maintaining lab equipment, contributing to manuscript preparation, and assisting undergraduate and graduate students.

Qualifications: A B.S. or B.A. in the natural sciences is required by the time of appointment. Candidates should be proficient in standard molecular biology methods such as DNA/RNA extraction, electrophoresis, primer design, PCR, DNA sequencing, genotyping, restriction digests, etc. A positive attitude, excellent organizational skills, and a strong quantitative background are regarded favorably.

The position is available starting in late September or early October, and can be filled at either half-time (20hrs/wk) or full-time (40 hrs/wk). An excellent benefits package is available, including health, dental, and retirement. Candidates should apply by emailing a letter of interest, their CV, and contact information for three references to porndorff@umces.edu.

The close date for this position advertisement is 7/31/2011.

More information about AL, located in the central Appalachian region of western Maryland, can be found athttp://www.umces.edu/al. UMCES is an Affirmative Action/Equal Opportunity Employer.

kelle913@umn.edu

UMichigan EvolutionaryBiol

Diarmaid Ó Foighil Professor, Ecology & Evolutionary Biology Director, Museum of Zoology The University of Michigan 1109 Geddes Avenue Ann Arbor, MI 48109-1079 Ph. 734 647 2193

EVOLUTIONARY BIOLOGY and EVOLUTIONARY ECOLOGY

University of Michigan

The Department of Ecology and Evolutionary Biology at the University of Michigan invites applications for a TENURE-TRACK POSITION (open rank) in evolution. We seek outstanding individuals with research and teaching interests in any area of evolutionary biology or evolutionary ecology. Particular foci of interest include evolutionary or ecological genetics and genomics, evolutionary theory, phylogenetics, and evolution of morphology, function, and behavior. Also strongly encouraged are research programs that take advantage of the outstanding collections of the Museum of Zoology, Herbarium, and Museum of Paleontology. For further information, see website:http://-eeb.lsa.umich.edu.< http://eeb.lsa.umich.edu./ >

To apply, please see website:http://-www.lsa.umich.edu/eeb/applications/, and arrange to have three letters of recommendation submitted through the same website. Review of applications will begin on 10 September 2011. Women and minorities are encouraged to apply and the University is supportive of the needs of dual career couples. The University of Michigan is an Equal Opportunity/Affirmative Action Employer.

"O'Foighil, Diarmaid" <diarmaid@umich.edu>

UOklahoma CollectionAssistant

FULL-TIME POSITION AVAILABLE COLLECTION ASSISTANT IN THE DEPARTMENT OF RECENT INVERTEBRATES SAM NOBLE OKLAHOMA MUSEUM OF NATURAL HISTORY

The Department of Recent Invertebrates is looking to fill a full-time position that will provide assistance to the Curator, Collection Manager, and Student Collection Assistant with a grant-funded project to catalog, digitize (electronic data capture), and verify specimen information for entomological specimens in the collection.

Typical job functions include: - Creating catalog records in a database that includes specimen information from specimen labels and associated materials - Generating and installing specimen labels - Following established protocols and standards for project tasks - Maintaining records of workflow for assessments of project benchmarks

See Job Requisition Number 12028 on the OU Human Resources website (http://jobs.ou.edu/hr) for additional information, and required education, skills, and proficiencies.

Salary: $10.25 per hour Benefits: Yes Hours per week: 40

For further information, contact Dr. Janet K. Braun (jkbraun@ou.edu, 325-0801) or Dr. Katrina L. Menard (kmenard@ou.edu, 325-8534)

Dr. Katrina Menard Collections Manager of Recent Invertebrates Sam Noble Oklahoma Museum of Natural History University of Oklahoma Kmenard@ou.edu (405) 325-8534

"Menard, Katrina L." <kmenard@ou.edu>

UOttawa EvolutionaryBiol

*Tenure-track faculty position, Department of Biology, University of Ottawa, CANADA

Note that the position advertised below is open to any field of biological research and those with evolutionary interests are encouraged to apply. Preference will be given to candidates who could contribute to the teaching of field biology.

—

THE UNIVERSITY OF OTTAWA invites applications for a tenureâtrack faculty position in the Department of Biology. Candidates must have a solid research program and the ability to contribute to our teaching in field biology. Exceptional candidates with interests in other areas of Biology may also be considered. Appointments will normally be at the Assistant Professor level although appointment at a higher rank may be possible. Candidates must have a PhD, a strong publication record, and good communication and teaching skills. The University of Ottawa is North Americaâs largest bilingual university; the successful applicant must be able to teach effectively in both French and English.

The candidate will join a vibrant, research-intensive Department (www.biology.uottawa.ca) of 40 faculty members with strengths in bioinformatics, cellular/molecular biology, conservation, ecology, evolution, and physiology. The Department is also home to interdisciplinary initiatives through the laboratory facilities of the Center for Advanced Research in Environmental Genomics (www.careg.uottawa.ca) and the Institute of the Environment (www.ie.uottawa.ca). The successful candidate will participate in undergraduate and graduate teaching in the Biology, Biopharmaceutical Sciences, Biomedical Sciences, and/or Environmental Sciences programs.

Before September 30, 2011, applicants should send a cover letter detailing their linguistic abilities, a curriculum vitae, a 2-page description of their proposed research program, a 1-page statement of teaching interests and philosophy, and the names and contact information of 3 referees.

All documents should be arranged in the above order and sent as a single PDF file, named by the candidateâs last and first names, to biochair@uottawa.ca.

All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. Equity is a University of Ottawa policy; women, Aboriginal peoples, members of visible minorities and persons with disabilities are encouraged to apply.

The University of Ottawa is proud of its 160-year tradition of bilingualism. Through its Official Languages and Bilingualism Institute, the University provides training to staff members and to their spouses in their second official language. At the time of tenure, professors are expected to have the ability to function in a bilingual setting.

http://www.academiccareers.uottawa.ca/node/349 — –

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

---

USFWS Washington ConservationGenetics

Position/Title: Interdisciplinary Geneticist or Fish Biologist

Agency/Location: U. S. Fish & Wildlife Service, Longview, WA

Responsibilities: Takes the lead in genetic data collection, analysis, and report writing for a variety of projects working with different fish species and genetic analysis methods (e.g. to address questions of population structure, population assignment, and species and sex identification). Provides overall technical coordination and uses genetic methods to estimate the relative reproductive success of hatchery and natural origin Pacific salmon in the wild. Performs statistical analyses and generates graphical representations of study results, and incorporates these data into written reports, scientific publications, and oral presentations.

Qualifications: Master's degree or equivalent work experience. Extensive work experience in: the principles, theories, and techniques of molecular and population genetics in order to determine pedigree relationships based on multi-locus genotypic data; genetic analytical and statistical techniques for determination of parentage, genetic variation within and among populations, population assignment, population structure, and hybrid status; and demonstrated oral and written communications skills.

Salary: $47,448.00 - $61,678.00 /year (GS-9 on the Federal pay schedule).

Closing Date: July 29, 2011

Contact: USAJOBS at http://www.usajobs.gov. USFWS, Abernathy Fish Technology Center web site: http://www.fws.gov/aftc. Applicants MUST follow the application process described in the vacancy announcement to receive consideration. Below is the link to the full text job opportunity announcement.

Interdisciplinary Fish Biologist (Genetics), GS-0440/0482-09, VIN FS-484722-KB11

Denise Hawkins Regional Geneticist U.S. Fish & Wildlife Service Abernathy Fish Technology Center 1440 Abernathy Creek Rd. Longview, WA, 98632 Phone: (360)425-6072 x339 Fax: (360)636-1855

Denise_Hawkins@fws.gov

UStAndrews ResFellow Evolution

48-month Independent Research Fellowship, University of St Andrews, Scotland

The School of Biology at the University of St Andrews is seeking to appoint an enthusiastic independent research fellow (IRF). The successful candidate will have or develop an innovative and high-profile research programme in the biological sciences. The School has a number of research strengths, but of key relevance for Evoldir subscribers are those in Evolution, Behaviour and Ecology, spanning molecules through to whole organisms. Ideally the IRF will conduct research complementary to the School's current research expertise, for instance as encompassed by the Centre of Evolution, Genes and Genomics, the Scottish Oceans Institute, and the Institute for Behavioural and Neural Sciences.

You will have a degree in the life sciences and will hold a relevant PhD. We are looking to appoint an early career stage researcher who is in the process of developing their own research programme, and who will prove successful in attracting funding for their research and publishing high-quality research findings in top-ranking international journals. Candidates with existing or pending fellowships are strongly encouraged to apply.

This is a 48-month appointment with an anticipated start date of 01 November 2011 or as soon as possible.

Informal enquiries to Prof Mike Ritchie, email: mgr@st-andrews.ac.uk

Formal applications MUST be made through the University's Human Resources application procedures. Please look for application reference CD7082 at https://www.vacancies.st-andrews.ac.uk/-welcome.aspx CLOSING DATE: Friday 15th July 2011

Dr David M Shuker NERC Advanced Research Fellow School of Biology University of St Andrews Harold Mitchell Building St Andrews Fife KY16 9TH UK Email: david.shuker@st-andrews.ac.uk

LAB WEBSITE: http://biology.st-andrews.ac.uk/-shuker Tel: +44 1334 463 376 Fax: +44 1334 463 366

dms14@st-andrews.ac.uk

UTuebingen FullProf PlantEvoEcology

The Biology Department of the Faculty of Science at Tübingen University, Germany, invites applications for the position (starting April 1st, 2012) of

Full Professor (W3) for Plant Evolutionary Ecology

The successful candidate will pursue an internationally high-end research agenda in the field of evolutionary biology, or the ecology of plants or fungi. Teaching obligations cover botany, ecology and/or evolution of plants.

We are seeking individuals whose research interests will focus on whole organisms. Possible research areas include organismic interactions, evolutionary ecology, community ecology and applied ecology and evolution. We envisage a largely experimental approach, supplemented by theoretical or molecular methods. Active participation in the exciting research environment provided by the Evolution and Ecology Forum Tübingen (EvE) is expected which enables collaborations within the Departments of Biology and Geosciences and with the Max-Planck-Institute for Developmental Biology. Furthermore, collaborations with the Tübingen Center for Plant Molecular Biology (ZMBP) would be desirable.

A formal requirement for appointment is the "Habilitation" or equivalent scientific and educational experience.

The University of Tübingen is committed to strengthen the proportion of women in research and teaching, and strongly encourages applications of qualified female scientists.

Applicants with disabilities who possess equivalent qualifications will be given preferential treatment.

Applications including a statement of interest, curriculum vitae, list of publications, teaching experience and visions of future research should be sent by e-mail to the Dean of the Faculty of Science, University of Tübingen, Germany (dekanat@mnf.uni-tuebingen.de) until August 31, 2011.

Any questions? -> Heinz Koehler, heinz.koehler@uni-tuebingen.de -> Katja Tielboerger, katja.tielboerger@uni-tuebingen.de

(Submitted by Nico Michiels, nico.michiels@uni-tuebingen.de)

Nico Michiels <nico.michiels@uni-tuebingen.de>

Other

AFLP repeatability issue

Dear all,

I work with insect genomic DNA using AFLP for my M.Sc. thesis, and I'm having problems with repeatability - my duplicates (starting from restriction-ligation) have an error rate of about 30%.

error rate = Jaccard distance between a pair of duplicates = [#(1,0) + #(0,1)]/[#(1,0) + #(0,1) + #(1,1)], where 1 is "peak present" and 0 is "peak absent"

Based on what I can gather from the literature, a Jaccard distance of 30% is about normal. However, my concern is that almost all the unrepeatable peaks have high fluorescence intensity in one duplicate, while are absolutely nonexistent in the other (instead of just being small badly-shaped bumps that can't be properly scored by the software).

I hope that someone who has experience in AFLP can illuminate me on the following questions: if you've done the calculation, what is the Jaccard distance you usually get for duplicates starting from restriction-ligation? For those peaks that are unrepeatable, do you ever get tall peaks in one duplicate and absolutely flat baseline at the corresponding bp in the other duplicate? If so, how do you deal with them?

I've tried using fresh reagents (except for the stock solutions of primers). And selective PCR has been very repeatable - I don't know about the other steps. Please see below for the AFLP protocol I'm following. I'm also happy to share the .fsa files (or a screenshot if preferred) of the duplicates if anyone wants to see them.

Many thanks for any assistance, Yue - yuy965@mail.usask.ca

My AFLP protocol: 1. Restriction: 250 ng of DNA, 1.5 ug of BSA, 1x NEBuffer4, 5 Units of EcoRI and 5 Units of MseI (both from NEB). Total reaction volume = 30 uL. Incubated at 37 C for 3 hrs. 2. Ligation: 1x NEBuffer4, 5 uM of EcoRI adaptor, 5 uM of MseI adaptor, 60 cohesive end units of T4 DNA ligase (from NEB), 1 mM of ATP. A total volume of 10 uL to be added to the restriction products. Final volume = 40 uL. Incubated at 12 C for 16 hrs, then 65 C for 20 min to inactivate enzymes. 3. Pre-selective PCR: I use Qiagen Type-it Microsatellite PCR Kit without Q solution, 0.5 uM final concentration for each primer, 2.5 uL of 1:20 dilution of restriction-ligation products. Final reaction volume = 10 uL. 95 C for 5 min, followed by 22 cycles of (95 C for 30 sec, 56 C for 90 sec, 72 C for 60 sec), followed by 60 C for 30 min. 4. Selective PCR: Qiagen Type-it PCR Kit, 0.5 uM for each primer, 1 uL of 1:20 dilution of pre-sel products. 95 C for 5 min, followed by a touchdown phase of 13 cycles of (94 C for 30 sec, 65 C for 60 sec, 72 C for 60 sec) with 0.7 C reduction per cycle, followed by 12 cycles of (94 C for 30 sec, 56 C for 30 sec, 72 C for 60 sec), followed by 60 C 30 min. Run on ABI 3130x and scored using GeneMapper.

yuy965@mail.usask.ca

Biogeography teaching exercises answers

Below are the answers I received. Thanks to all who replied, sorry for the delay in reposting. - Sarah Gilman

—–

Peter Unmack <peter.mail2@unmack.net>: I have a lab written up based on Mega and phylogeny. It is all very self contained / explained. This was based on mega version 4, I haven't checked the details on what changes would need to be made to make it compatible with version 5 (you can still download both versions). http://www.megasoftware.net/ From memory it takes around 1.5-2 hours or so to work through.

Cheers Peter

I've taught some "phylogeography" short courses in the past, and I've posted my labs as PDFs here:

http://filogeografia.dna.ac/labs.html I hope 1 or 2 might be useful for you. Be aware some are a bit old, but the newest were updated in 2009. Some assume a specific data set, but most are general enough to be applied to any DNA sequence data matrix. Feel free to use or modify these labs to your own needs.

I recently started to use GIS in conjunction with phylogeography/biogegraphy hypothesis testing, and I found this paper really useful (link above), because it tests several interesting hypothesis and also comes with tutorials to replicate their study. http://www.sciencedirect.com/science/-article/pii/S1055790311000480 I have posted the materials for a phylogeny exercise I have done with high school students and high school teachers at http://www.eebweb.arizona.edu/Grads/mherron/-Darwin/Darwin.html .This may be aimed a bit low, but I'm sure it could be adapted for advanced undergraduates.

I would be very grateful for a summary of your responses.

I don't have any prepared resources, but am aware of several on-line resources that might help. First, you could use genbank (at NCBI) and let them choose organisms and genes, then conduct a phylogenetic reconstruction. For element occurrence data, you might try NatureServe. I don't know how much that helps, but they're ideas for starters. If you choose to pursue either one and have questions, I'd be happy to help sort them out.

Getting beginners up and running with GIS is tricky, b/c current Arc software is so complex. In my Conservation Biology course I use DIVA-GIS, which is free and downloadable - and there's a tutorial in this book:

Gibbs, Hunter, and Sterling. 2008. Problem-solving in conservation biology and wildlife management, 2nd ed. Blackwell.

Might be some other good stuff in there - I think the table of contents is available on-line.

The tutorial took some re-working on my part but works OK - takes 3 weeks of 3 hour labs to do (1 as tutorial for novices, 2 to do the exercise).

What textbook do you plan to use? Lomolino is very comprehensive and fairly affordable (still $100, but you get a lot for that) but has a jillion typos. We played "find the typo" in my class...

I'd be interested in what other exercises people submit - my Biogeography class is lecture-only.

My students were expected to find out if the plants from family Apiaceae that are edible or used as spices form a monophyletic group. We used the GenBank search command '"apioid superclade" rpl16 not genome' to obtain the sequences. They were analysed in RAxML. The students found researching food fascinating and the subsequent discussion about interpretation of the phylogeny yielded one of the most fruitful discussions in my course.

I'm not sure if this is what you're looking for, but I had an interesting project in an Evolution class that went something like this:

We were given about 15 cactus species and told to construct a phylogeny based on their morphology. We were to determine which characteristics we wanted to use. If you wanted to be sneaky, you could add in a non-cactus species that looked like a cactus (my entire class was fooled!).

You could probably use other organisms, but cactus is really easy to work with. Hope this helps!

—

Sarah Gilman, Ph.D.

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

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

SGilman@jsd.claremont.edu

Bullet ant samples

Bullet ant (Paraponera clavata) samples requested for molecular work.

As a postdoc in Dr. Corrie Moreau's lab at the Field Museum I have recently developed microsatellite primers for the bullet ant, Paraponera clavata. I am particularly interested in two questions:

(i) the phylogeography throughout the distribution range of the species, (ii) whether colony structure changes throughout the distribution range of the species.

For question (i) one individual per colony would be helpful from as many colonies as possible. For question (ii) I would need 12-15 workers from a single a colony from as many colonies as you are able to get that number of works - these colonies could also be used for question (i).

Any and all samples, regardless of the preservation method, would be greatly appreciated (please send specimens to the address below). Please feel free to contact me or Corrie Moreau with questions.

Stefanie Kautz Department of Zoology Field Museum of Natural History 1400 South Lake Shore Drive Chicago, IL 60605 USA

Corrie Saux Moreau, Ph.D. Assistant Curator, Division of Insects Department of Zoology Field Museum of Natural History 1400 South Lake Shore Drive Chicago, IL 60605 USA Office: (312) 665-7743 Fax: (312) 665-7754 cmoreau@fieldmuseum.org http://fieldmuseum.org/users/corrie-moreau *** NOTE NEW LAB WEBSITE: www.moreaulab.org ***

Corrie Moreau <cmoreau@fieldmuseum.org>

CapeVerde VoluntaryFieldAssist

Field Assistant in Cape Verde, North Africa ? Sept to Dec 2011

We are seeking 1 Voluntary Field Assistant for a field-based project on mating system evolution in the Republic of Cape Verde. The assistant is required from 15 September until 15 December 2011. The position is funded, except the assistant has to cover his/her journey to (and from) Maio, Cape Verde.

The project We are investigating mating system and parental care of Kentish plover Charadrius alexandrinus in Cape Verde by monitoring colour-ringed individuals. This is an all-year resident population and many individuals are already ringed from previous years.

The place The study sites are in Maio Island, Cape Verde, at the Salina Porto Ingles and nearby lagoons (see the Bradt Guide to Cape Verde Islands). Accommodation on the islands is in an apartment, with occasional water and electricity. The island has spectacular wildlife, including endemic birds, corals and marine mammals; it is a beautiful and inspiring place to work. However, the island is a small and isolated place with basic commodities, the weather can be harsh, and a great deal of walking and cycling are required.

The job The fieldwork will run from 15 September to mid December 2011. It will be unsupervised, and will involve ? among other tasks ? searching for plover nests and marked plovers and their families, taking behavioural observations and monitoring nest survival. It will also involve capturing, ringing and bleeding adults and young.

The candidates This is a voluntary post ? applicants must be willing to pay for their own transport to Maio. Once in Maio, however, accommodation, basic food and expenses associated with research will be covered. In addition, 100 Euro per month may be offered to the deserving Assistant. Phone calls and internet costs will not be covered.

You will be a keen birder with sharp eyes and plenty of experience in trapping, handling and ringing birds. Clean driving licence is essential. You must be personable and happy to engage with locals to explain the project; some Spanish or Portuguese is helpful. You must be physically fit, hard-working and meticulous, and have a proven ability to work independently.

As you will appreciate from its description, the project will involve many different challenges. A proven ability to collect high-quality data is essential (i.e. a good degree in a biological subject or equivalent experience), and you should be prepared to type up your data in the evenings! You must have a positive attitude and an ability to look after yourself ? this means cooking your own meals, dealing with logistics, and most importantly being capable of organising your own work for a long period of time.

If you like chatting on the phone, or feel the need to text and email people all the time, this position is not for you. The cost of living is high, and fancy food is expensive.

Costs It is possible to fly through Lisbon from the UK that costs about £700. Internal flights from Praia to Maio should be under £100 one way, and the Praia-Maio ferry costs about £15.

Interested? Please send a current CV with an email stating why you feel you are a strong candidate to me (Professor Tamas Szekely) at T.Szekely@bath.ac.uk. Application deadline: 31st July 2011. Interviews will be carried out as the applications coming in, and an offer will be made by 6th August 2011.

I will also need the contact details (email and telephone) of two referees. If you have any questions, please direct them to me at the same email address, or call me at +31 50 363 8085.

Professor Tamas Szekely Professor of Biodiversity Dept of Biology and Biochemistry, University of Bath, Bath BA2 7AY, UK 01225 383676 (phone), 01225 386779 (fax), T.Szekely@bath.ac.uk (email) http://www.bath.ac.uk/bio-sci/biodiversity-lab/index.htm NEW: Social Behaviour: Genes, Ecology and Evolution Edited by Tamas Szekely, Allen J Moore & Jan Komdeur Cambridge University Press, 2010 http://www.cambridge.org/gb/knowledge/isbn/item5708507/?site_locale=en_GB bssts@bath.ac.uk

Data assessment

Would anybody like to explain or give me some guidance on: - conducting preliminary data assessment for an assignment test - what assumptions should be considered regarding the test and how to test the assumptions ?

any suggestion, clue or reference will be highly appreciated.

Thank you very much.

Regards

sena

Sena A Subrata <sena.subrata@wildlife.uni-freiburg.de>

DNA pH meter

I am looking for any recommendations for a pH meter that will measure DNA pH in very small sample sizes - any suggestions very welcome - the cheaper the better.

Alan Forrest A.Forrest@rbge.ac.uk

– The Royal Botanic Garden Edinburgh is a Charity registered in Scotland (No SC007983)

Alan Forrest <A.Forrest@rbge.ac.uk>

Drawing Multiple Gene Trees answers

Thanks to everyone for your quick responses!!

Responses to Draw Multiple Gene Trees:

Lars Arvestad's PrIMETV draws embedded trees: http://prime.sbc.su.se/ The authors provide a web-based version as well, which is very easy to use. I was able to draw the individual gene trees within the same species tree, then merge all the images in Adobe Illustrator.

DensiTree http://www.cs.auckland.ac.nz/ ˜ remco/DensiTree/DensiTree.html I used this program to illustrate the trees (>8000) produced by a Bayesian run. Very effective for showing the major patterns plus their relative occurrences.

Other Suggestions I did not try:

Dendroscope

http://topiaryexplorer.sourceforge.net/ Check out ms by R. R. Hudson:

http://home.uchicago.edu/ ˜ rhudson1/source/mksamples.html Jaime Elizabeth Blair, PhD Assistant Professor of Biology Franklin & Marshall College Lancaster PA 17604 Office (717) 291-3959 jaime.blair@fandm.edu http://edisk.fandm.edu/jaime.blair Jaime Blair <jaime.blair@fandm.edu>

Draw multiple gene trees

I am looking for a way to draw multiple gene trees within a given species tree, similar to Mesquite's contained trees. Does anyone know of software that will do this, preferably with Nexus formatted trees as input? Thank you! Jaime Blair

–

Jaime Elizabeth Blair, PhD Assistant Professor of Biology Franklin & Marshall College Lancaster PA 17604 Office (717) 291-3959 jaime.blair@fandm.edu http://edisk.fandm.edu/jaime.blair Jaime Blair <jaime.blair@fandm.edu>

Genephor SSCP gels

I have been using a Genephor electrophoresis apparatus (Amersham, then GE Healthcare) to identify alleles of polymorphic loci since 2005, with much success. From around June 1, I have not been able to obtain new gels and then found out that GE has discontinued them, even though the apparatus and the supplies are still listed in their catalog as of today (July 25). It has not been possible to obtain any indication of whether GE is hoping to provide them again. Have other users found alternatives?

Any help will be greatly appreciated!

André Lachance

André Lachance <lachance@uwo.ca>

Help MasterBayes

Hi all,

I am A PhD student in aquaculture and genetic from Chile. Actually I am doing one paternity analisis with microsatellite markers, I did it with colony2 but now I would like compare my results with Master Bayes, lamentably I am very new in R and I can not run the package with R. I would appreciate any comment.

Thanks in advance Regards Rodrigo

Atte. Rodrigo Badilla. Marine Biologist Candidato a Doctor en Acuicultura. Laboratorio de Genetica Marina. ULPGC, España Celular:62202469 http://www.gi.ulpgc.es/iusa2/es/node/146 rodrigo.badilla@gmail.com

Herbarium DNA Survey

This is a notice to welcome contributions to the Synthesys herbarium DNA project. Synthesys is a European Union funded project which aims to create an integrated European infrastructure for researchers in the natural sciences. This project aims to collate published and unpublished techniques used by scientists to extract DNA from herbarium specimens across land plants, and their relative success for any given taxon.

Emails have already been sent out to selected researchers, but if you have experience of extracting DNA from herbarium samples please do let us know your experiences by completing the questionnaire on Survey Monkey.

Survey accessed at: http://www.surveymonkey.com/s/VDFPYNL Information obtained will be stored on a publically available online database, and published in a high impact review paper. All contributions will be acknowledged by reference to you by name and/or paper citation as you wish.

Please feel free to forward the survey to colleagues and collaborators who may have additional information. If you have any queries, please feel free to contact me.

Many thanks,

Alex Woodcraft

Alex Woodcraft Herbarium DNA researcher Jodrell Laboratory, Royal Botanic Gardens, Kew Richmond, Surrey, TW9 3DS, United Kingdom Tel: +44 (0)20 8332 5372; fax: +44 (0)20 8332 5371

A.Woodcraft@kew.org

Hybridlab software

Dear all,

I need to use the software Hybridlab by Nielsen et al. Nielsen, E. E., Bach, L. A. and Kotlicki, P. (2006), Hybridlab (version 1.0): a program for generating simulated hybrids from population samples. Molecular Ecology Notes, 6: 971-973. It should be available at: http://www.difres.dk/ffi/uk/populationgenetic/hybridlab/index.asp but the link seams to be broken. Maybe one could provide me with the program file? I would be very grateful.

Best regards, Aleksandra Biedrzycka

Institute of Nature Conservation Polish Academy of Sciences Al. Mickiewicza 33 31-120 Kraków tel. 12 370 35 51

biedrzycka@iop.krakow.pl

Introns evolution

Dear all

Does anyone knows which models of evolution can we use for introns ? Microsatellites such as Infinite Allele Model (IAM) and Stepwise Mutation Model (SMM) or Sequence models like GTR, HKY, etc... Thank you very much. Best regards

– Goncalo Silva PhD student

BEE - Biogeographical Evolution and Ecology CCMAR/CIMAR-LA- Centre of Marine Sciences of the University of Algarve

Adress: Universidade do Algarve, Campus de Gambelas, Faculdade de Ciências e Tecnologia, Edifício 7, lab. 2.51, 8005-139 Faro, Portugal

Mobile: +351 966647732 Fax: +351 289800051

Goncalo Silva <gfsilva@ualg.pt>

Introns evolution 2

Dear all,

I would like to reformulate my question regarding introns evolution since the answers I got didn't clarify my doubt, I guess I didn't explain it very well...

I'm studying the genetic variation of an intron of a single species and I would like to know which models of evolution I can use for this sequence alignment. I'm not sure that introns mutate under the same models as mitochondrial DNA or nuclear coding regions. I can have two types of "changes": nucleotide mutations and indels. Developed nucleotide evolutionary models (JC, HKY, GTR, etc...) included information such as base frequencies, Gamma distribution, substitution rates or number of parameters and introns should fit on nucleotide evolutionary models. However, introns have indels that not represent any function or have no meaning (as far as I know). Moreover, these indels seems to appear randomly, more or less like microsatellites size changes. From my data, I can't understand if the step between 3 and 5 bp gap is a gap of 4bp and I'm not sure if it has to be like that. Are intron gain/loss of nucleotides random? If so, I can code indels like microsatellites (lenght size), but I will loose mutations information. Does anyone knows which evolutionary models are more appropriate for introns? Thank you very much.

Goncalo Silva PhD student

BEE - Biogeographical Evolution and Ecology CCMAR/CIMAR-LA- Centre of Marine Sciences of the University of Algarve

Adress: Universidade do Algarve, Campus de Gambelas, Faculdade de Ciências e Tecnologia, Edifício 7, lab. 2.51, 8005-139 Faro, Portugal

Mobile: +351 966647732 Fax: +351 289800051

Goncalo Silva <gfsilva@ualg.pt>

Memorial for Bill Jordon

Dr Bill Jordan Memorial Evening

27th July, 2011

Mappin Pavilion, ZSL London Zoo

Dr Bill Jordan, Senior Research Fellow at the Institute of Zoology, passed away on 25th May.

For a tribute to Bill's life, see http://www.zsl.org/science/ioz-staff-students/jordan,1078,AR.html

The Zoological Society of London will be holding an evening to celebrate Bill's life, at London Zoo, Regent's Park from 6.00-7.30 pm on 27th July at the Mappin Pavillion.

Please note that there will be a formal part to the proceedings at 6:30pm, when some of Bill's friends and colleagues will say a few words. The evening will continue at the Zoo Sports and Social Club from 7:30pm onwards (directions will be given at the end of the formal part of the evening).

Entrance will be via the Prince Albert Gate, referenced on the map attached and car parking will be available from 5:30pm until 11:30pm in the main car park.

Please let Amelia Scudamore (amelia.scudamore@zsl.org) know if you'd like to attend, or if you have any questions or queries.

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

Methods for multilocus genotypes

Dear All,

I'm curious if anyone could suggest ways to generate multilocus genotypes from the following of data. The ultimate aim is to analyze the data with phylogenetic, population genetic and allele frequency spectrum methods to probe population histories.

We're planning to conduct next-gen (454) amplicon sequencing (20-40 loci) on a microsporidia (/Nosema bombi/) pathogen of bumble bees. Prior to this, we used a genome enrichment method to discover polymorphic loci and enable primer design. The samples are /Nosema /spores taken directly (not cultured) from the the guts of bees ($n > 100$). All spore sequences for a particular locus from a single bee will be barcoded with the ID for that bee.

Because there are likely to be multiple strains of /Nosema /in each bee, alleles (belonging to each strain) may be in linkage disequilibrium. /Nosema/ is thought to be largely clonal, but they may reproduce sexually occasionally (the jury is still out on this).

Given enough depth of sequence coverage at each locus, I'm wondering if there're ways to generate multilocus genotypes of each strain (with some sort of probability) using LD or index of association information?

Many thanks in advance.

Haw Chuan Lim Postdoctoral Research Associate Dept of Entomology 320 Morrill Hall University of Illinois 505 S Goodwin Ave Urbana, Illinois 61801 USA Tel: (217)333-2170 Fax: (217)244-3499 Website: http://sites.google.com/site/bigriverforest/ hawclim@life.illinois.edu

microsat NGS

Dear all,

I was wondering if any of you have information on sequencing microsatellite repeats (amplicons) on a 454 platform.

Essentially, I would like to get some information on the accuracy when sequencing microsatellite amplicons. Do you get the two alleles (e.g. heterozygotes) in equal proportions or do you get a distribution of several repeat lengths due to pcr-errors? If so, what kind of coverage (50x, 100x) do you need to estimate the "correct" alleles? And is there any difference between di-, tri, tetra or penta-repeats as you would expect?

I would be gratefull if any of you could point me to some papers on this topic or share your experience. Thanks!

Note: I do not ask for info on how to use 454 seq to develop new microsats as there are plenty of papers on that.

Koen

kdegelas@gmail.com

NESCent K12EvolutionEducation Proposals

K-12 Evolution Education for Underrepresented Minorities: Request for Proposals

Deadlines: September 1, 2011 or January 1, 2012

NESCent - The National Evolutionary Synthesis Center (Durham, NC)

As part of NESCent's ongoing efforts to increase diversity in evolutionary science, the center is sponsoring a range of targeted activities in the general area of K-12 Evolution Education for Underrepresented Minorities. We are seeking to support one or more Catalysis Meetings, Working Groups or other synergistic activities that lead to the creation of new programs, activities or initiatives designed to increase exposure to, and participation in evolutionary science by K-12 minority students who are historically underrepresented in the discipline.

In particular, proposals that are significantly interdisciplinary, and that demonstrate a mix of senior and emerging researchers, including graduate students, are encouraged. Competitive proposals will not only define the target audience(s) and outline strategies for developing innovative activities, but will include detailed plans for implementation and assessment. Proposals should also indicate how activities and programs align with state and/or federal education standards.

NESCent invites researchers to submit proposals for two kinds of meetings:

Catalysis Meetings: These one-time meetings bring together ~30 scientists from diverse disciplines to focus on a major question or research area in evolutionary science. These meetings typically last for 3-5 days.

Working Groups: Working Groups involve small groups of scientists (10-12 participants) collaborating intensively on the analysis or synthesis of data, models or both, to address a major question in evolutionary science. The working groups will typically meet 3-4 times over two years, with each meeting lasting 3-5 days.

Synergistic Activities: We also strongly encourage linkages among our science programs (see URL below). We invite proposals that plan synergistic activities between two or more of the following: working groups, catalysis meetings, postdoctoral fellows, sabbatical scholars, short-term fellows, and graduate students. Proposals for each of these must be submitted separately; they should include a clear statement of linkage between proposals (including clear identifications in each of the separate proposals of which proposals are linked).

NESCent will not support collection of new data or field research, but encourages the mining of public and private databases. NESCent is committed to making data, databases, software and other products that are developed as part of NESCent activities available to the broader scientific community.

To learn more about the various types of proposals, and the proposal process, please visit https://www.nescent.org/science/proposals.php, or contact Dr. Allen Rodrigo (a.rodrigo@nescent.org) or Dr. Jory Weintraub (jory@nescent.org).

Jory Weintraub <jory@nescent.org>

NESCent RequestProposals Meetings

Evolution and the Social Sciences: Request for Proposals

Deadline: September 1, 2011 or January 1, 2012

Proposals are now being accepted for meetings, working groups, and other synergistic activities, which explore the intersection of the evolutionary and social sciences at the US National Evolutionary Synthesis Center (NESCent).

We welcome proposals that seek to understand the value of evolutionary thinking in a particular social science, or conversely, how social science can inform evolutionary studies of human (and perhaps, other species) biology. In particular, proposals that are significantly interdisciplinary, and that demonstrate international participation and a mix of senior and emerging researchers, including graduate students, are encouraged. Minority participation is also an important consideration in evaluation.

NESCent invites researchers to submit proposals for two kinds of meetings:

Catalysis Meetings: These one-time meetings bring together ~30 scientists from diverse disciplines to focus on a major question or research area in evolutionary science. These meetings typically last for 3-5 days.

Working Groups: Working Groups involve small groups of scientists (10-12 participants) collaborating intensively on the analysis or synthesis of data, models or both, to address a major question in evolutionary science. The working groups will typically meet 3-4 times over two years, with each meeting lasting 3-5 days.

Synergistic Activities: We also strongly encourage linkages among our science programs (see url below). We invite proposals that plan synergistic activities between two or more of the following: working groups, catalysis meetings, postdoctoral fellows, sabbatical scholars, short-term fellows, and graduate students. Proposals for each of these must be submitted separately; they should include a clear statement of linkage between proposals (including clear identifications in each of the separate proposals of which proposals are linked).

NESCent will not support collection of new data or field research, but encourages the mining of public and private databases. NESCent is committed to making data, databases, software and other products that are developed as part of NESCent activities available to the broader scientific community.

To learn more about the various types of proposals, and the proposal process, please visit https://www.nescent.org/science/proposals.php, or contact Dr. Allen Rodrigo (a.rodrigo@nescent.org) or Dr. Craig McClain (cmcclain@nescent.org).

Craig R. McClain, Ph.D. Assistant Director of Science National Evolutionary Synthesis Center 2024 W. Main St. Suite A200 Box 104403 Durham, NC 27705 919-668-4590

cmcclain@nescent.org

Associate Editor for Journal of Biogeography: http://www.wiley.com/bw/journal.asp?ref=0305-0270 Deep-Sea News: http://deepseanews.com/ National Evolutionary Synthesis Center: http://www.nescent.org/-

Research Homepage: http://craigmcclain.com/ McClain Craig <cmcclain@nescent.org>

Software MEGA5

We announce the release of MEGA5 (Molecular Evolutionary Genetics Analysis version 5). MEGA5 is a biologist-friendly software with a graphical user interface for comparative analysis of molecular sequence data. MEGA provides utilities for mining online databases, building sequence alignments and phylogenetic trees, as well as many widely used statistical analyses such as tests of selection, variance estimation, and bootstrap confidence tests.

The newest addition in MEGA5 is a collection of Maximum Likelihood (ML) analyses for inferring evolutionary trees, selecting best-fit substitution models (nucleotide or amino acid), inferring ancestral states and sequences (along with probabilities), and site-by-site estimation of evolutionary rates. ML algorithms in MEGA5 compared favorably with other software packages in terms of computational efficiency and the accuracy of the estimates of phylogenetic trees, substitution parameters, and rate variation among sites. MEGA5 is intended for the Windows platform, and it has been configured for effective use on Mac OS X and Linux desktops. It is available FREE of charge from www.megasoftware.net .

A detailed description of MEGA5 and new results are now published in MBE (2011; doi:10.1093/molbev/msr121). A preprint PDF is available from: www.kumarlab.net/pdf_new/-TamuraKumar11.pdf .

The full complement of features implemented in MEGA5 includes:

[1] Sequence Alignments: Direct DNA, codon, and protein alignments; both manual and automated alignments with trace file Editor. Built-in automated aligners: CLUSTALW and MUSCLE.

[2] Select Best Fit Substitution Model (ML); Substitution Models (+F With and Without Empirical Frequencies; REV = Reversible). Rate Variation and Base Compositions: Gamma rates (G) and Invariant sites (I) models; Incorporate Compositional Heterogeneity. DNA: General-Time- Reversible (GTR), Tamura-Nei, Hasegawa-Kishino-Yano, Tamura 3- Parameter, Kimura 2-Parameter, Tajima-Nei, Jukes-Cantor; Codons: Nei- Gojobori (original and modified), Li-Wu-Lou (original and modified); Protein: Poisson, Equal-Input, Dayhoff (+F), Jones-Taylor-Thornton (+F), Whelan-And-Goldman (+F), Mitochondrial REV (+F), Chloroplast REV (+F), Reverse Transcriptase REV (+F)

[3] Estimate Substitution Pattern (MCL, ML); Estimate Rate Variation among Sites (ML); Estimate Transition/Transversion Bias (MCL, ML); Estimate Site-by-Site Rates (ML) [4] Infer Phylogenetic Trees (NJ, ML, ME, MP); Phylogeny Tests (Bootstrap & Branch-length tests); Branch-and- Bound Exact Search (MP); Heuristic Searches (ML, ME, MP), including Nearest-Neighbor-Interchange (NNI), Close-Neighbor-Interchange (CNI), and Max-Mini.

[4] Compute Distances: Pairwise and Diversity; Within- & Between-Group Distances; Bootstrap and Analytical Variances; Separate distances by Site Degeneracy, Codon Sites; Separation of Distances in Transitions and Transversions; Separate Nonsynonymous and Synonymous Changes

[5] Tests of Selection: For Complete Sequences or Set of Codons; Sequence Pairs or Groups (Within & Between)

[6] Ancestral Sequences: Infer by ML with Relative Probabilities for states or by MP (all parsimonious pathways); both DNA and Protein

[7] Molecular Clocks: Tajima's 3-Sequence Clock Test; Likelihood Ratio Test (ML) for a Topology; Estimate Branch Lengths under Clock

Sudhir Kumar Center for Evolutionary Medicine & Informatics (CEMI) Biodesign Institute & School of Life Sciences Arizona State University Tempe, AZ 85287-5301, USA

s.kumar@asu.edu s.kumar@asu.edu

Software optiFLP

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

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

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

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

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

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

University of Innsbruck Molecular Ecology Group 6020 Innsbruck, Austria

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

Software TreeComparision

Dear Community,

We just made available two new tools at: www.exelixis-lab.org/software.html Simon Berger designed a simple visual tree comparison tool that allows you to highlight differences between two and up to four trees. This may be useful when you want to compare a Bayesian versus a ML tree or if you have different ML trees that are not statistically significantly different from each other.

Denis Krompass has designed a stand-alone GUI for the RAxML Evolutionary Placement Algorithm described in:

S.A. Berger, D. Krompaß, A. Stamatakis: "Performance, Accuracy and Web- Server for Evolutionary Placement of Short Sequence Reads under maximum-likelihood". In Systematic Biology 60(3):291-302, 2011.

This is a stand-alone graphical user interface (that also offers visualization and reference tree building) which will make using the Evolutionary Placement Algorithm for short reads really easy.

Many thanks to Denis and Simon for implementing all this.

Alexis

alexandros.stamatakis@gmail.com

PostDocs

BostonU TeachingEvolutionToChildren

Post-Doctoral Fellow

Child Cognition Lab, Department of Psychology, Boston University

The Child Cognition Lab at Boston University (PI: Deborah Kelemen, PhD) invites applications for a 1-2 year post-doctoral research position. The post-doctoral fellow will play a leadership role in the everyday management of existing grant-funded projects on the teaching of natural selection to elementary school children and the development of teleological reasoning. Responsibilities will include: facilitating relationships with schools and teachers; conducting and supervising research and data collection with young children in the lab / classroom; development of age-appropriate instructional and assessment materials; development and implementation of qualitative data coding protocols; quantitative data analysis; co-supervision of a large team of research assistants; writing reports for funding agencies; presentations at conferences; authorship (under PI guidance) of publications in peer-reviewed journals.

Job requirements:

Doctoral degree in science/ biology education or evolutionary biology; background in quantitative and qualitative research; strong experimental design and statistical analysis skills (SPSS preferred); experience supervising research assistants; evidence of independent, creative scholarship; strong authorship /writing skills, and publication productivity in peer-reviewed journals. Developmental psychology knowledge and/or prior experience working with young children and in schools strongly preferred (e.g. elementary school teaching experience a bonus).

Review of applications will begin 20 July 2011 and continue until the best candidate is found. Please submit a cover letter, CV, and a list of 3 professional references to childlab@bu.edu

Direct any inquiries to Becca Seston (Lab Manager, Child Cognition Lab) at childlab@bu.edu.

Check www.bu.edu/childcognition for information about the Child Cognition Lab.

Deborah Kelemen, Ph.D. Associate Professor Boston University Department of Psychology 64 Cummington Street Boston MA 02215

Email: dkelemen@bu.edu Office Phone: (617) 353-2758 Child Cognition Lab Phone: (617) 358-1738 Fax: (617) 353-6933 URL: http://www.bu.edu/childcognition debkelemen@gmail.com

---

Brussels AfricanPlantEvolution

*Postdoc on evolutionary genetics / ecology of African plants in Brussels *

The team of Dr Olivier Hardy at the Université Libre de Bruxelles (Belgium) is seeking a candidate for a 16 months postdoctoral position to work on evolutionary genetics / evolutionary ecology of central African plant species. The candidate should have experience in population genetics, phylogeography, phylogenetics and/or community ecology modeling. Some laboratory experience in molecular genetics is required. Experience with tropical plants and/or next-generation sequencing techniques is a plus. The candidate will contribute to new projects funded by the Belgian National Fund for Scientific Research (FNRS). One project is entitled "Population dynamics of trees and herbaceous species characteristic of central African rain forests in relation to past human and climate perturbations", and the other "Organization of plant biodiversity across African rain forests at different levels of integration using genetic markers: phylogeography, DNA barcoding, and phylogenetic structure of communities". The research project of the candidate will be flexible and adapted to his/her previous experience. The candidate will be based in Brussels, will have access to a molecular lab and could realize field missions in Africa. Candidates must have a PhD obtained less than 6 years ago and cannot be of Belgian nationality or be residing in Belgium for more than 2 years (conditions imposed by the FNRS grant). Interested candidates should send their CV to Olivier Hardy (ohardy@ulb.ac.be) as soon as possible (deadline 31 August 2011). More details about the projects will be provided. The FNRS grant can start by end 2011 or early 2012. The monthly net salary is ca. 2000 euros. The team lead by Olivier Hardy (cf. http://ebe.ulb.ac.be/ebe/Hardy.html) is currently composed of 4 postdocs and 4 PhD students. Research topics focus on African rainforests and include phylogeographic studies of several forest dwelling tree, herbaceous and epiphyte (orchids) species; population and quantitative genetics of some timber tree species; studies on seed and pollen dispersal; development of DNA barcoding approaches for plant species; (phylo)diversity patterns of tree communities and plant-environment relationships. Most field work occurs in Cameroon, Gabon or Benin in collaboration with local researchers. Olivier Hardy also performs modeling studies in population genetics and community ecology, and develops software for data analyses.

Some recent publications of the team:

Micheneau C, et al. (2011) Cost-effective method for the development of microsatellite loci: a case study with /Pericopsis elata/ (Fabaceae). /American Journal of Botany /(in press)

Réjou-MéchainM, Hardy OJ (2011) Properties of similarity indices under niche-based and dispersal-based processes in communities. /The American Naturalist/ 177: 589-604.

Koffi KG; Hardy OJ, Doumenge C, Cruaud C, Heuertz M (2011) Diversity gradients and phylogeographic patterns in a widespread African tree typical of mature rainforests, /Santiria trimera/ (Burseraceae). /American Journal of Botany/ 98: 254-264.

Parmentier I, et al. (2011). Predicting alpha diversity of African rain forests: models based on climate and satellite-derived data do not perform better than a purely spatial model. /Journal of Biogeography /38: 1164-1176.

Debout GDG, Doucet J-L, Hardy OJ(2011)Population history and dispersal ecology inferred from spatial genetic structure of a Central African timber tree, /Distemonanthus benthamianus/ (Caesalpinioideae). /Heredity /106:88-99.

Duminil J, Heuertz M, Doucet J-L, Bourland N, Cruaud C; Gavory F; Doumenge C, Navascués M, Hardy OJ (2010) CpDNA-based species identification and phylogeography: application to a complex of African tropical tree species. /Molecular Ecology/ 19: 5469 5483.

Daïnou K, Bizoux J-P, Doucet J-L, Mahy G, Hardy OJ, Heuertz M (2010) Forest refugia revisited: SSRs and cpDNA sequences support historical isolation in a wide-spread African tree with high colonization capacity, /Milicia excelsa/ (Moraceae). /Molecular Ecology/ 19:4462-4477.

Ley A, Hardy OJ (2010) Species delimitation in the Central African herbs /Haumania/ (Marantaceae) using georeferenced nuclear and chloroplastic DNA sequences. /Molecular Phylogenetics and Evolution/ 57:859 867.

Navascués M., Hardy O. J., Burgarella C. (2009) Characterization of demographic expansions from pairwise comparisons of linked microsatellite haplotypes. /Genetics/ 181: 1013-1019.

Hardy O. J. (2008) Testing the spatial phylogenetic structure of local communities : statistical performances of different null models and test statistics on a locally neutral community. /Journal of Ecology/ 96: 914 926.

Hardy O. J., B. Senterre (2007). Characterising the phylogenetic

— / —

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

Cornell GermlineStemCellGeneEvolution

POSTDOC AT CORNELL UNIVERSITY WITH CHIP AQUADRO AND DANIEL BARBASH FUNCTIONAL ANALYSIS OF EVOLUTIONARY DIVERGENCE IN GERMLINE STEM CELL REGULATORY GENES IN DROSOPHILA

My colleague Daniel Barbash and I are searching for a postdoctoral researcher to work on an NIH-funded project to investigate the evolutionary causes and functional consequences of rapidly evolving germline stem cell regulatory genes in Drosophila species, including genes such as Bam and Bgcn (Mol Biol Evol. 23: 655-62, (2006); Mol Biol Evol. 24: 182-91 (2007)). We are particularly interested in candidates who are interested in applying developmental, biochemical, genetic and molecular evolutionary approaches to testing hypotheses generated from population genetic analyses. Starting date is ~ Jan. 2012 but is flexible. Please contact Chip Aquadro for further information at CFA1@cornell.edu. Our labs and the Cornell community provide an excellent research, training and living environment with fantastic, interactive colleagues and excellent laboratory facilities and resources.

Chip Aquadro (http://mbg.cornell.edu/cals/mbg/-faculty-staff/faculty/aquadro.cfm) Daniel Barbash (http://mbg.cornell.edu/cals/mbg/faculty-staff/-faculty/barbash.cfm) Department of Molecular Biology and Genetics, Cornell University, Ithaca, NY Cornell Center for Comparative and Population Genomics (http://3cpg.cornell.edu)

cfa1@cornell.edu

CornellU CanineGenomics

Dr. Adam Boyko's laboratory at Cornell University is focused on studying the rapid evolution and diversification of dogs and genetic basis of complex traits and disease. A postdoctoral position is available to develop and apply genomic methods for understanding canine evolution and biology. Specific subprojects include: developing bioinformatic approaches for discovering variants underlying complex phenotypes and disentangling complex demographic history; collection and genetic analysis of indigenous "village dog" populations throughout the world; and understanding the influence of natural versus artificial selection in shaping standing genetic variation and the genetic architecture of quantitative traits in dogs. The applicant should have a Ph.D. in biology, bioinformatics, statistics or related field, proficiency in computer programming, and experience in computational genomics. The fellow can expect to be part of cutting-edge studies involving genome-wide association studies, next-generation sequencing, and RNA-seq in dogs, with ample opportunities for collaboration with researchers in Biomedical and Clinical Sciences and for developing independent research projects. To apply, send a CV, cover letter, statement of research interest and contact information for 3 references to Dr. Adam Boyko: boyko at cornell dot edu. Review of applications will begin August 31. Informal inquiries are welcome, and start date is negotiable.

arboyko@gmail.com

CornellU PopulationGenomics

Postdoctoral Position in bioinformatics/population genomics at Cornell University

A POSTDOCTORAL POSITION is available to develop bioinformatic tools for improved SNP genotyping and population genetic/phylogeographic analysis using next generation sequence data from non-model species (i.e., no reference genome). The candidate will be expected to participate in both methods development and data analysis. Projects involving existing data include a sensitivity analysis of SNP genotyping accuracy from Illumina genotype-by-sequence (GbS) data both with and without benefit of a reference genome; phylogeography and coalescent analysis of whole genome pathogen SNPs based on GbS, and transcriptome assembly for SNP calling and RNA-seq. The candidate will be jointly supervised by Kelly Zamudio (Ecology and Evolutionary Biology; http://www.eeb.cornell.edu/zamudio/KZ_Home/-Welcome/Welcome.html) and Matt Hare (Natural Resources; http://www.dnr.cornell.edu/cals/dnr/-people/faculty.cfm?netId=mph75); interactions also will be facilitated with pertinent genomics labs at Cornell (Siepel, Keinan, Aquadro, Clark) and with personnel at the Computational Biology Services Unit at Cornell.

Qualifications: a Ph.D. in computer science, genetics, evolutionary biology, or comparative genomics; strong population genetics knowledge and demonstrated expertise in analyzing large population-level data sets; programming skills. Preference will be given to applicants with demonstrated ability to develop creative solutions to bioinformatic challenges.

Applications will be reviewed starting August 15 and the position can begin as soon as a suitable applicant is chosen. Funds for this position come from the Atkinson Center for a Sustainable Future (http://www.sustainablefuture.cornell.edu/grants/AVF/) and the Cornell Center for Comparative and Population Genomics (http://3cpg.cornell.edu/). The position is available for one year with the possibility of extension pending approval of funds.

To apply, send (PDFs preferred) CV, a short statement of interest and qualifications, and contact info for three references to Dr Matt Hare: mph75 at cornell dot edu. Informal inquiries are welcome.

About Cornell

Cornell is home to a large, active community of researchers interested in evolutionary genomics and population genetics (see http://3cpg.cornell.edu/), and has a strong campus-wide emphasis on sustainability studies (see http://www.sustainablefuture.cornell.edu). General information on postdoc life at Cornell is available from the Office of Postdoctoral Studies at Cornell (http://www.postdocs.cornell.edu/). Cornell University is an affirmative action/equal opportunity employer.

Dr. Matthew Hare Associate Professor Department of Natural Resources 213 Bruckner Hall Cornell University

mph75@cornell.edu

EPFL Lausanne ComputationalPopGen

Postdoctoral Positions in Computational & Theoretical Population Genetics

Two postdoctoral positions are available in the Jensen Lab in the School of Life Sciences at the Ecole Polytechnique Federale de Lausanne (EPFL).

Research in the Jensen Lab focuses on adaptation in natural populations - and includes theory, methodological and statistical development, and data analysis. Current and on-going projects range from the development of approximate Bayesian statistics for the joint inference of recurrent hitchhiking and demographic parameters, to Neanderthal genomics, to direct measures of the distribution of fitness effects of new mutations using experimental yeast data. Additional information may be found on the lab web page: http://jensenlab.epfl.ch Requirements for this position include a PhD, a strong background in population genetics, and experience in programming and statistical analysis. The positions are open until filled, though review of applicants will begin on September 01 - thus, in order to ensure full consideration, applications are encouraged prior to that date. Applicants should email a CV, contact information for three references, and a brief statement of research interests to: jeffrey.jensen@epfl.ch

Starting dates are flexible, and salary is commensurate with experience (starting postdoc salary is 81,100 CHF / euro 63,300 / $93,800 per year.)

The EPFL provides an intellectually engaging research community at the interface of biology, computer science, mathematics and statistics; additionally supported by a strong population genetics community across western Switzerland. EPFL is an extremely international campus, with over half of the faculty alone coming from abroad (with all lab and campus interactions being conducted in English). Campus is located on the southern edge of Lausanne, along the shores of Lake Geneva, and at the foot of the Alps. http://sv.epfl.ch/ jeffrey.jensen@epfl.ch

ETH Zurich MolEvolution

Postdoc fellowship / Ph.D. studentship / IT-Programmer

Successful candidates will have a strong background in bioinformatics, computer science, statistics, and/or computational biology. Fluency in a major scripting language, and experience in software development is a must. Some background in biology is desirable, but interest in biology and bioinformatics is required. Candidates should be highly motivated and have the ability to work independently. As the research will involve a mix of disciplines, candidates with experience in several fields will be preferred (bioinformatics, genetics, protein structure, computational science, mathematics, physics, statistics).

ETH Zurich boasts excellent facilities for studying and recreation. The working language in the group is English, which is also widely used in Switzerland. CBRG is a member of the Swiss Bioinformatics Institute (SIB) and benefits from SIB training courses and networking. Zurich is located less than one hour from the Alps, and is a small but vibrant city offering one of the best living standards in teh world. Zurich is well connected to major European cities and has a large international community.

Salary and social benefits are very competitive.

To apply please send a single PDF to Dr Maria Anisimova (maria.anisimova@inf.ethz.ch) containing:

**CV (with publication list if applicable)

**Scanned academic transcripts (list of grades in university courses)

**Three references

In addition, Postdocs and PhD students are asked to submit:

** A short statement of research interests, mentioning research topics of master/diploma theses (not exceeding two pages)

** Reprints of up to 3 representative publications, if available.

When applying, please mention the type of position you are seeking in the subject of your email. The position is open until filled (quick response is recommended).

maria.anisimova@inf.ethz.ch

GriffithU 2+2Grad AncientDNA

Australian Postdoctoral and PhD scholarships in ancient DNA: Expressions of Interest

Two postdoctoral positions are available in the Ancient DNA Laboratory at Griffith University in Brisbane, each for a period of three years. Expertise in second-generation DNA sequencing and DNA capture techniques is preferable. In addition, ancient DNA experience and some bioinformatics expertise would be an advantage. The successful applicants will work on genomic studies of Sacred Ibis mummies from ancient Egypt (as part of a Human Frontier Science project). Alternatively funding is also available for a project dealing with the recovery of genomes of modern and ancient Adélie penguins (as part of an ARC Linkage research project). The former may involve fieldwork in Egyptian catacombs and the latter in Antarctica over summer months. Postdoctoral minimum salary is $67,547 RF 1.4 but remuneration will depend on experience and qualifications.

Two PhD scholarships (3 years) are also available to work on the above projects. These provide a unique opportunity for students to work in collaboration with an international team of researchers. Applicants will work in a state-of-the-art ancient DNA facility as well as modern molecular biology laboratories based at the Nathan campus of Griffith University in Brisbane. These laboratories comprise a dedicated 454 DNA sequencer and a real time PCR facility. PhD scholarships pay $22,860 living expenses. Course costs do not apply for Australian or New Zealand students.

A description of the laboratory's research can be found at http://www.griffith.edu.au/professional-page/david-lambert Curriculum vitae and a covering letter should be sent to: Prof David Lambert Griffith School of Environment and School of Biomolecular and Physical Sciences Griffith University Nathan 4111, Australia Email d.lambert@griffith.edu.au.

Prof David Lambert PhD FRSNZ Professor of Evolutionary Biology Griffith University N55 -2.13H (office) N34 2.05 (Laboratory) 170 Kessels Road, Nathan Qld 4111 Australia

Phone +61 7 373 55298 (Office) Phone +61 7 373 57262 (Lab) Fax +61 7 373 57459 Email d.lambert@griffith.edu.au

David Lambert <d.lambert@griffith.edu.au>

KansasStateU ModelingPlantNetworks

Postdoctoral Research Scientist: Computational Modeling of Plant Gene Networks

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

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

Application Process The position will be for an initial period of 3 years, at a starting salary of $42,000 - 45,000 per annum. The candidate will report to Dr. Sanjoy Das. Review of applications will begin on July 15, 2011 and continue until the position is filled. Applicants should submit curriculum vitae with a list of three references in pdf format to plantmodelpostdoc@gmail.com (cc: sdas@ksu.edu and/or welchsm@ksu.edu). Further details will be available at: www.ece.ksu.edu/~sdas EEO/AA Policy Kansas State University is an equal opportunity employer and actively seeks diversity among its employees. Background check required.

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

Chassy Nichols <chassy@ksu.edu>

MPI Plon Stickleback Coevolution

Postdoctoral position in host-parasite co-evolution in sticklebacks

The Department of Evolutionary Ecology of the Max Planck Institute for Evolutionary Biology at Plön, Northern Germany, studies the evolution of sex and mate choice. Both sexual reproduction and mate choice may be strategies in the co-evolutionary arms race between hosts and parasites. With the model organism three-spined stickleback we study with methods from immunology, immunogenetics, molecular biology, parasitology, behavioural ecology and population/field ecology whether mate choice continuously optimises the resistance of the offspring against ever changing natural parasites in lab and field experiments. We further study whether this process can maintain the enormous polymorphism of the MHC-immunogenes of vertebrates through parasite mediated balancing selection. With its pleiotropic role in parasite resistance and mate choice the MHC provides an exceptional tool to study host-parasite co-evolution and ultimately understand the maintenance of sexual reproduction. Furthermore, because they occur in rivers, lakes and the Baltic Sea, sticklebacks offer an intriguing opportunity to investigate immunogenetic local adaptation and the role of MHC in speciation (http://www.evolbio.mpg.de/).

The position is part of our interdisciplinary research program. The position is primarily devoted to research, but there is the possibility to teach an advanced course in our International Max Planck Research School (http://imprs.evolbio.mpg.de/). The position is open for two years with potential prolongation. The successful candidate has research experience in evolutionary biology and brings any complementary expertise and skills to our team. She/he shares our enthusiasm for studying host-parasite co-evolution experimentally in a competitive field. Our institute offers an international environment with English spoken in the labs. It offers an excellent infrastructure allowing for the most recent techniques.

Plön is in the middle of the Schleswig-Holstein lake-district within a very attractive and touristic environment near the Baltic Sea, close to the university towns of Lübeck and Kiel. Hamburg and Lübeck are the closest airports.

Applicants should send a CV, list of publications, statement of research interests, and contact information of 3 referees as a single PDF to Manfred Milinski (milinski@evolbio.mpg.de). Review of applications will continue until the position is filled.

The Max Planck Society is an equal opportunity employer.

– Britta Baron Max-Planck-Institute for Evolutionary Biology phone ++49(0)4522-763-253 August-Thienemannstrasse 2 fax ++49(0)4522-763-310 24306 Ploen email baron@evolbio.mpg.de Germany http://www.evolbio.mpg.de Britta Baron <baron@evolbio.mpg.de>

NewYorkU PlantGenomics

POSTDOC IN PLANT EVOLUTIONARY/ECOLOGICAL SYSTEMS BIOLOGY

A postdoctoral scientist position to study rice evolutionary/ecological systems biology is open in the laboratory of Michael Purugganan at the NYU Center for Genomics and Systems Biology. Applicants should have (1) a strong background in plant molecular biology/systems biology, (2) experience in experimental and computational analyses of genome-wide gene expression and (3) interest in plant evolutionary and ecological genomics. Interested parties can email an inquiry and their CV to mp132@nyu.edu

Michael Purugganan Dorothy Schiff Professor of Genomics

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

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

---

Ottawa FungalTaxonomyGenomics

POSTDOCTORAL FELLOWSHIPS IN FUNGAL TAXONOMY AND GENOMICS. Keith Seifert is looking for two post-docs, one interested in the identification of microfungi, and the other interested in participating in a genome project, for two-year positions in Ottawa, Canada. The first position is funded by the A.P. Sloan Foundation. A large and diverse collection of 6000-7000 strains isolated by a dilution-to-extinction method from a global survey of house dust needs to be characterised for comparison with existing pyrosequencing data (see Amend et al. 2010. PNAS 107: 13748-13753). The second position is funded by Agriculture and Agri-Food Canada and other sources, and will require expertise in the bioinformatics around genome characterization, with the goal of developing real-time PCR assays for an economically important fungal species. Please contact Keith at keith.seifert@agr.gc.ca if you are interested.

Keith A. Seifert Research Scientist | Chercheur scientifique Biodiversity (Mycology and Microbiology) | Biodiversité (Mycologie et Microbiologie) Agriculture and Agri-Food Canada | Agriculture et Agroalimentaire Canada 960 Carling Avenue | 960 Carling Avenue Ottawa, Ontario | Ottawa (Ontario) K1A 0C6

keith.seifert@agr.gc.ca

Telephone |Téléphone: 613-759-1378 Facsimile | Télécopieur: 613-759-1701 Teletypewriter | Téléimprimeur 613-773-2600

“Seifert, Keith” <Keith.Seifert@AGR.GC.CA>

OxfordU 1yr ComparativeGenomicsSoftware

Mathematics, Physical and Life Sciences Division

DEPARTMENT OF STATISTICS

POSTDOCTORAL RESEARCH ASSISTANT

Fixed term appointment of 1 years’ duration

Grade 7: Salary £29,099 -£35,788 p.a

(Grade 6: Salary £25,854 - 30,870 p.a for a non-doctoral applicant)

READVERTISEMENT

The Research Project: “COGANGS” - Comparative Genomics and Next Generation Sequencing - Software Development for Annotation of very large number of genomes

Applications are invited for a full-time Postdoctoral Research Assistant to commence as soon as possible. This is a fixed-term post (1 year initially, with a possibility of extension for a further year) funded by the European Union. Candidates should have a relevant background and research experience in computer science/mathematics or a related field. The project involves collaboration between CLC Bio, BIOBASE, deCODE Genetics, Renyi Institute, University of Göttingen, and Novel Computing Systems in Biology and Professor Jotun Hein (Oxford, UK) to work on the development of software.

The successful applicant will be expected to have a doctorate in a relevant subject area or equivalent research experience in a relevant scientific field is an advantage, but not a prerequisite. Biologists with a demonstrated ability to work on large software development projects will also be considered.

Applications are to be submitted electronically. Please read the “Person Specification and Job Description” before preparing your application. You will need to upload a supporting statement, Curriculum Vitae, list of publications, details of teaching experience, statement of research interests and names and contact details of two referees.

Informal enquiries to: the Administrator (email: jobs@stats.ox.ac.uk) quoting reference: 100573

To apply for this role and for further details, including the job description and selection criteria, please click on the link:

https://www.recruit.ox.ac.uk/pls/hrisliverecruit/erq_jobspec_version_4.jobspec?p_id=100573 Only applications received before 12:00 noon, UK time on Friday 5 August 2011 can be considered.

Interviews to be held on Friday 12 August

Christine

—

Christine Stone Administrative and Personal Assistant Department of Statistics, University of Oxford 1 South Parks Road Oxford OX1 3TG Tel: +44 (0)1865 272866/60 Fax: +44 (0)1865 272595

Christine Stone <cstone@stats.ox.ac.uk>

Paris CaenorhabditisViral Coevolution

Postdoc position, Félix lab, Paris, France Co-evolution of Caenorhabditis and viral pathogens

A postdoctoral position is available for three years in the laboratory of Marie-Anne Felix, at the Ecole Normale Supérieure, Paris, France.

For interested candidates, please send a letter of motivation, a Curriculum Vitae and a list of three referees to: Marie-Anne Félix e-mail: felix@ijm.univ-paris-diderot.fr

The team is presently located in the Jacques Monod Institute in Paris and will be moving in the fall to the Department of Biology at the Ecole Normale Superieure: http://www.ibens.ens.fr/spip.php?rubrique2 Marie-Anne Felix <felix@ijm.univ-paris-diderot.fr>

Paris GeneticStatistics

Postdoctoral position in Genetic/Statistics Position are available at AgroParisTech and Le Moulon Plant Genetics Lab located in Paris (France).

*Subject:* Genome wide association study between structural variation, agronomical traits variation and heterosis in maize

Context:*_ The project aims at demonstrating the efficiency of combining innovative genome sequencing methods, microarrays, bioinformatics, statistics and association mapping to accelerate the identification and the use of structural variants in maize breeding. The Moulon Plant Genetics laboratory main scientific interest is to decipher the genetic determinism of complex traits. For this purpose, they develop complementary strategies based on QTL detection with linkage and association genetics approaches. The MIA lab (AgroParisTech) is a statistical group involved in bioinformatics application. They are interested in the general problem of breakpoint detection, particularly for large scale comparative genomic hybrididization (CGH) analysis. In the context of the ANR CNV-Maize project, both laboratories join efforts to address the effect of structural variation on complex traits in plants, considering maize as a model.

*_Program:_ * The post-doc will work first with the MIA lab (AgroParisTech) in order to devise suitable statistical methods for pangenomic CGH array signal analysis. Next the post-doc will apply these methods to the data from the 300 inbred lines covering the maize diversity hybridized on the pangenomic CGH array and perform association studies between the structural variants and some agronomic traits in the Moulon Lab. *

Background: *The applicant should have a strong background in genetics and/or in applied statistics; typically a PhD in one of these fields. The person will be in charge of the statistical analysis of high-density CGH profiles and of their interpretation. He/she will collaborate with both geneticists from Le Moulon and statisticians from AgroParisTech. She/he will also contribute to develop new methods for the specific aim of the project, in particular to take into account specificities of CNV to develop original association genetics models. To achieve these tasks, she/he will benefit from the expertise of the two teams and will therefore collaborate in an inter-disciplinary context.A strong background statistics and/or statistical quantitative genetics is required. A strong experience in programming is also highly desirable.

*_Localization:_ *The UMR AgroParisTech / INRA Applied Mathematics and Computer Sciencesâ(MIA lab) is located in center of Paris (http://www.agroparistech.fr/mia/). The UMR INRA/Univ. Paris XI/CNRS/AgroParisTech “GÃ©nÃ©tique VÃ©gÃ©tale du Moulon” (Moulon lab) is located in the south of Paris (30km) and close to the University of Paris XI (http://moulon.inra.fr/). Both labs are located along the express train RER B.

Salary:*_ 1900 per month including health insurance

(2200 before taxes).

Contacts:*_ StÃ©phane Robin (robin@agroparistech.fr); StÃ©phane Nicolas (snicolas@moulon.inra.fr; Emilie Lebarbier (emilie.lebarbier@agroparistech.fr)

Applications should be sent and should include a CV, a statement of research interests, and names of referees.

References:*_ Picard F < http://www.ncbi.nlm.nih.gov/pubmed?term=%22Picard%20F%22%5BAuthor%5D >, Lebarbier E < http://www.ncbi.nlm.nih.gov/pubmed?term=%22Lebarbier%20E%22%5BAuthor%5D >, Hoebeke M < http://www.ncbi.nlm.nih.gov/pubmed?term=%22Hoebeke%20M%22%5BAuthor%5D >, Rigaill G < http://www.ncbi.nlm.nih.gov/pubmed?term=%22Rigaill%20G%22%5BAuthor%5D >, Thiam B < http://www.ncbi.nlm.nih.gov/pubmed?term=%22Thiam%20B%22%5BAuthor%5D >, Robin S < http://www.ncbi.nlm.nih.gov/pubmed?term=%22Robin%20S%22%5BAuthor%5D >.

(2011) Joint segmentation, calling, and normalization of multiple CGH profiles. /Biostatistics,/ doi:10.1093/biostatistics/kxq076 Ducrocq S., Madur D., Veyrieras J.B., Camus-Kulandaivelu L., Kloiber-Maitz M., Presterl T., Ouzunova M., Manicacci D., Charcosset A. (2008) Key impact of Vgt1 on flowering time adaptation in maize: Evidence from association mapping and ecogeographical information.

— / —

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

PennsylvaniaStateU Craniofacial EvoDevo

Post doctoral position at The Pennsylvania State University Department of Anthropology

Position: Post doctoral associate Focus: craniofacial development and anatomy, craniosynostosis, morphometrics, image analysis, developmental genetics

We are looking for excellent post doctoral researchers to work on a large collaborative project concerning the genetics of craniosynostosis and normal craniofacial development. Craniosynostosis is a common malformation, defined as the premature fusion of one or more calvarial sutures with an incidence of 3 to 5 per 10,000 live births in all racial populations. Although substantial advances have been made in understanding the clinical and molecular aspects of syndromic craniosynostosis caused by single gene mutations, knowledge of associated phenotypic variability, its developmental basis, modifiable and genetic risk factors, and outcomes is limited. The project, funded by the National Institutes of Craniofacial and Dental Research of NIH, seeks to understand the developmental basis of craniosynostosis and shed light on the interaction of skeletal and neural tissue in the development and evolution of neurocranial shape. The data needed to obtain our stated goals require the collection of morphometric (landmark coordinate and other types of 3D measures) data from large samples of micro-computed tomography (CT) scans of embryonic mouse skulls with known genetic mutations and micro-magnetic resonance images of their brains. The post doctoral associate will be responsible for the collection of the cranial data sets from the micro-CT images, but will be involved in other aspects of the project including the collection of alternate skeletal data sets, the study of embryonic neural and skeletal development, quantitative analysis of morphological and genetic data, meetings among collaborators, manuscript preparation, and further grant writing. Experience in one or more of the following specialties is required: developmental biology and genetics, image analysis, craniofacial anatomy, morphometrics, molecular laboratory methods. We are looking for someone deeply interested in applying modern technologies and methods to the understanding of the developmental processes involved in the production of the head as well as craniofacial evolution. Applicants should send a current curriculum vita, a statement of research interest and experience, and a list of three references to Joan Richtsmeier via e-mail: jta10@psu.edu. Earliest start date: September 1, 2011. Institution: The Pennsylvania State University (http://www.psu.edu) Location: State College, PA (http://www.statecollege.com). Salary: commensurate with experience at NIH levels. Duration of appointment: one year with 2 additional years possible depending upon funding. For more information on the lab and the project see: http://getahead.psu.edu Penn State is committed to affirmative action, equal opportunity and the diversity of its workforce.

“Faye L. Maring” <fmaring@la.psu.edu>

Plouzane France PhytoplanktonDiversity

Postdoctoral position

A Â« phytochips Â» : a new tool to study the toxic phytoplankton diversity in the bay of Seine.

The aims of this project is to develop a new molecular tool as alternative means to provide fast, safe and complete identification of Harmful Algal Bloom (HAB) species. Monitoring of phytoplankton is actually based on the microscopic identification and counting of the cells of interests. It is time consuming, tedious and no challenging. Microarray or Phylochips have been chosen since this technology allows a genetic identification of the target organisms. It can be used to achieve simultaneous detection of phytoplankton species and to estimate the number of taxons in the seawater samples. This study is a part of the project called âComancheâ, which one of the objectives is to study the origin of the toxic algae blooms and to investigate their impact on the scallop fisheries in the Bay of Seine. In this area, recurrent toxic events, ASP (Amnesic Shellfish Poisoning) and DSP (Diarrheic Shellfish Poisoning) events occur in the eastern Channel affecting the scallop fishery. The identification of the Pseudo-nitzschia species is crucial to evaluate the potential risk of samples since all of the species belonging to this genus do not produce phytotoxin. The determination of these species requires an electronic microscopy analysis, which is inappropriate for extensive monitoring. This novel Phylochip will allow us to discriminate the toxic species within Pseudo-nitzschia genus, to quantify the biodiversity of phytoplankton and follow their dynamic and distribution in bay of Seine as well.

Key words : Microarray, Biodiversity, Pseudo-nitzschia, Dinophysis, Phylochips, Phytoplankton.

- Expertises : PhD candidate with a strong background in microarray technique, bioinformatics and statistics expertises. Knowledge in phytoplankton ecology is not necessary, but will be appreciated.

- Investigators : : Informal enquires to Dr. Catherine Dreanno (Catherine.dreanno@ifremer.fr) and to VÃ©ronique Le Berre Anton (veronique.leberre@insa-toulouse.fr)

-Funding : Ifremer- ANR 18 months

- Location : Laboratoire ou Service et UnitÃ© dâaccueil : Service Interfaces et Capteurs, UnitÃ© Recherches et DÃ©veloppement Technologiques, Ifremer, centre de Brest, 29280 Plouzane, France. And Laboratoire d'IngÃ©nierie des SystÃmes Biologiques et des ProcÃ©dÃ©s (LISBP) UMR INSA/CNRS 5504/INRA 792 INSA - 135, avenue de Rangueil 31077 Toulouse, France.

Caution the candidate will work in these two laboratories.

Web site : To apply for this position, please send a letter of intent and a CV to Dr. Catherine Dreanno (Catherine.dreanno@ifremer.fr) or visit our web site : http://wwz.ifremer.fr/institut/Travailler-a-l-Ifremer/-Bourses-de-recherche/Bourses-post-doctorales-2011-2012, before September 12th 2011.

–

Dr. Catherine DREANNO (PhD)

Service Interfaces & Capteurs IFREMER BP 70 29280 PlouzanÃ©, FRANCE Tel : (+33) 02.98.22.40.99

http://www.ifremer.fr/ic/ Catherine DREANNO <Catherine.Dreanno@ifremer.fr>

RutgersU Bioinformatics

POSITION DESCRIPTION: A full-time postdoctoral position is available immediately in the Bhattacharya Group (http://dblab.rutgers.edu/) at Rutgers University (New Brunswick, New Jersey, USA) to carry out computational and bioinformatic research on prokaryote evolution, specifically on the early evolution of redox enzymes with respect to diversification of life during the Great Oxidation event.

Duties and responsibilities include (1) developing (improving existing) automated pipeline for large-scale phylogenetic/phylogenomic analysis of prokaryote proteins, (2) formulating and testing biological hypotheses relevant to prokaryote evolution (e.g., horizontal gene transfer), (3) co-supervising postgraduate student(s) and being highly proactive in generating high-quality, high-impact journal publications, and (4) presenting research findings at national/international meetings/conferences.

This position is part of a three-year project funded by the Gordon and Betty Moore Foundation (http://-www.moore.org/) to uncover how the metal-containing enzymes responsible for the critical electron transfer reactions that turn basic elements (e.g. H, O, C, S, and N) into biologically active molecules have evolved. Funding will be used to develop bioinformatic approaches to produce independent evolutionary relationships based on protein sequence/structure and to generate hypotheses for how the bio-catalyzed electron transfer reactions arose and now function. The collaborative team consists of experts within various departments at Rutgers in the fields of genome evolution, protein structures, microbiology, biochemistry, and geoscience.

QUALIFICATIONS: Ideal candidates will have a computational biology/genomics background with over two years of full-time research experience, proven scripting skills (PERL/Python), as well as experience with relational databases (mysql or similar) and publicly available genome resources.

Working knowledge and experience in molecular evolution, genomics, phylogenetics, high-performance computing and/or UNIX environment, are highly desirable. Knowledge of web design, server management and/or programming languages (C/C++/Java) is a plus.

The successful applicant will be highly organized, have strong interpersonal skills, and demonstrate high-level ability to write in clear, grammatically correct English.

GROUP DESCRIPTION: Our group has a long-term interest in genome evolution of microbes, specifically among algae and protists, with a heavy focus on plastid origin, endosymbiosis, and organellogenesis. The lab is equipped with an Illumina GAIIx sequencer for generating genomic, transcriptomic, and epigenomic data, with excellent in-house high-performance supercomputing facilities and pipelines for routine genome assemblies, annotation and large-scale phylogenomic analyses. The candidate will have complete access to the facilities and the opportunities to be involved one or more of the many projects currently underway. Recent publications: Science 2011, 332:714; Curr Biol 2011, 21:328; Biol Direct 2011, 6:12; Plant Physiol, 2011 155:1561.

Rutgers, The State University of New Jersey, is a leading national public research university. It is the only public university in New Jersey in the Association of American Universities, a group comprising North America's 61 leading research universities. The Protein Data Bank (PDB; http://www.pdb.org/) is hosted at Rutgers.

APPLICATION DEADLINE: September 15, 2011. Position will remain open until filled.

SALARY is offered based on qualification and experience.

Any queries should be addressed directly to Debashish Bhattacharya (bhattacharya@aesop.rutgers.edu). To apply, please send the following items to the same email address: (1) a cover letter stating potential start date (2) a curriculum vitae, including contact information for at least two references, and (3) a brief statement of research interest and career goals

Rutgers is an equal opportunity/affirmative action employer.

Debashish Bhattacharya Professor Department of Ecology, Evolution and Natural Resources Institute of Marine and Coastal Sciences Foran Hall 102 Rutgers University, New Brunswick, NJ 08901, USA Telephone: (732) 932-8193

bhattacharya@aesop.rutgers.edu

SangerInst ComputationalGenomics

Postdoctoral Fellow: Computational Genomics

Genomics of gene regulation

A postdoctoral position is available in Computational Genomics at the Wellcome Trust Sanger Institute under the leadership of Dr Daniel Gaffney. The long-term goal of the lab is to understand how genetic change influences gene regulation, using a combination of statistical and experimental approaches. The specific project is flexible, and the successful applicant will be expected to develop their own interests, but current research themes include

(i) Regulatory and gene expression variation in humans (ii) The impact of regulatory change on disease susceptibility and evolution (iii) Comparative genomics and molecular evolution of gene regulatory regions

We welcome candidates with a background in Biology and strong quantitative skills. Candidates from Physics, Statistics or Computer Science with strong interests in computational biology and/or population genetics are also encouraged to apply. Excellent programming skills, experience with very large data sets and an ability to work as part of a team are essential. Our lab also has access to wet-lab facilities and personnel - as part of their research, the successful candidate will also have the opportunity to generate novel high-throughput data sets and to test hypotheses in an experimental setting.

Essential Skills

PhD in a relevant subject area (Computational Biology, Population Genetics/Genomics, Computer Science, Physics) Excellent programming skills (C, C++, Perl, Python, or R) Strong statistical and quantitative skills Ability to communicate ideas and results effectively Ability to work well with other team members Independent research goals and objectives

Ideal Skills

Experience with analysis of -omics data sets Previous experience with genetics of gene regulation, QTL analysis

Other information

Although genetic variation in gene regulation is thought to play an important role in evolution and disease, the pathway from regulatory mutation, via gene expression to phenotype is still poorly understood. Understanding this pathway will be an essential component in the application of genomics to personalized medicine. The Sanger Centre offers a world-class academic environment, access to cutting edge sequencing facilities and extensive expertise in genome analysis and human genetics. As such, we are in a prime position to begin to address some of these fundamental questions. The ultimate goal of our lab is to be able to predict the impact of new mutations on gene regulation and to understand how such changes impact phenotype. To achieve this, we combine of sequence and genome analysis, comparative genomics and population level, expression QTL-mapping.

This is a 3 year fixed-term position. The closing date for this position is 10th August 2011. Salary range is £28,280 to £34,778 dependent on experience.

Postdoctoral Fellows are typically in their first or second postdoctoral position as part of a period of early career research training. Successful applicant(s) who have submitted their PhD thesis and are awaiting their PhD award to be confirmed will be placed on a transitional pay point, currently £26,103. On confirmation applicants will be moved on to the pay scale above.

This position is initially for a fixed term of 3 years. Applications can be made on the Sanger jobs website at: https://jobs.sanger.ac.uk and follow the link for "Postdoctoral Fellow - Computational Genomics - Genomics of Gene Regulation"

For further information please contact Daniel Gaffney on dg13@sanger.ac.uk and visit the lab website at:

http://www.sanger.ac.uk/research/faculty/dgaffney/ Daniel Gaffney Career Development Fellow Wellcome Trust Sanger Institute Wellcome Trust Genome Campus Hinxton, Cambridge, CB10 1SA UK

Tel: ++44 (0) 122 349 6866

Daniel Gaffney <dg13@sanger.ac.uk>

Stuttgart PlantPopulationGenomics

We are looking for a

POSTDOCTORAL SCIENTIST

to work on a project within the DFG-funded German Priority Program "Adaptomics - Evolutionary Plant Solutions to Ecological Challenges". The project involves the population genomic analysis of the two endemic plant species Arabidopsis pedemontana and Arabidopsis cebennensis to study the relationship between genetic diversity, reproductive system and natural selection in species with small distribution ranges and small effective population sizes. Investigating the interplay of genetic drift and natural selection in response to environmental change will be a central focus of the work and will be done by genome resequencing, genetic mapping, and additional methods. The project will be carried out in close collaboration with the group of Marcus Koch (University of Heidelberg) and other partners in the priority program.

Highly motivated candidates with a Ph. D. degree, a background in botany, population/conservation genetics or evolutionary biology, and a record of scientific publications are welcome to apply. The ideal candidate has experience with population genetic simulations and statistical analysis, scripting skills (e.g., R or Python) and a good knowledge of modern genomics methods. The project requires the ability to coordinate and to conduct field work in the Piemontese Alps (Italy) and the Cevennes (France) together with local botanists.

The successful applicant will be appointed for three years. The salary will be according to the German government salary scale (TV-L E13) and depends on previous experience, age and marital status. The University of Hohenheim is an equal opportunity employer. Women and members of minority groups are strongly encouraged to apply.

We are located on a beautiful campus in the South German city of Stuttgart with a rich cultural life and a nice surrounding. There is a critical mass of researchers in Hohenheim wo work on plant population and quantitative genetic analysis (mostly in a plant breeding context) for interaction and collaboration. Further information about our group can be obtained from http://-

evoplant.uni-hohenheim.de or the address below.

Please send your application (Cover letter, CV, list of publications, letter of research interests, addresses of at least two references) until 15 September 2011 as a single PDF document with the subject line “Adaptomics” by email to Bärbel Hessenauer (baerbel.hessenauer@uni-hohenheim.de).

Dr. Karl Schmid Professor of Crop Biodiversity and Breeding Informatics Institute of Plant Breeding, Seed Science and Population Genetics Fruwirthstrasse 21 D-70599 Stuttgart, Germany Phone: +49 711 459 23487

karl.schmid@uni-hohenheim.de

SyracuseU Speciation

Postdoctoral Position in Ecological Speciation.

A postdoctoral position to study ecological speciation in yucca moths is available in the laboratory of David Althoff at Syracuse University. Specifically, the role of host plant use in the evolution of morphological and reproductive traits will be combined with analyses of genetic structure to test hypotheses about the process of speciation. The position will require field studies, behavioral experiments, insect rearings, and use of molecular tools to analyze genetic structure. Daily tasks will include insect cultivation, morphological measurements, behavioral assays, and collection and analysis of population genetic data.

The position will be awarded for one year with the possibility of renewal for additional years. The ideal candidate will be proficient in studying insect behavior, microsatellite and sequencing techniques, population genetic analyses, and willing to travel for extended periods for field studies and collections. Additionally, the person should be willing to train undergraduates and assist in other on-going projects in the lab.

Applicants should send an e-mail to dmalthof@syr.edu explaining their interest in the position, a CV, and the names and contact information for at least two references. The position will begin after September 1, 2011.

Thank you,

David

David Althoff Assistant Professor Dept. of Biology Syracuse University 107 College Place Syracuse, NY 13244 Office: 315.443.1096 FAX: 315.443.2012 plantecology.syr.edu/althoff/

David M Althoff <dmalthof@syr.edu>

TexasAMU 2 Bioinformatics Genomics

Two Post Doctoral positions available in the Department of Veterinary Integrative Bioscience at Texas A&M University. Please see the descriptions below.

POSITION #1 TITLE: Post-Doctoral Research Associate in Bioinformatics LOCATION: Texas A&M University, College Station, TX SALARY: Commensurate with experience CLOSING DATE: Open until filled DURATION: Two years with a possibility of extension depending on performance and funding

DESCRIPTION: The Chowdhary & Cai lab (http://vetmed.tamu.edu/labs/cytogenics-genomics & http://www.genomezoo.net) is seeking a joint appointment post-doc that will apply the latest bioinformatics tools towards understanding equine diseases (including laminitis, recurrent airway obstruction, and stallion subfertility), phenotypes, and evolution of equids. The Chowdhary lab is focusing on characterizing genetic factors involved in major equine diseases, sexual development, and reproductive disorders. The approaches applied include genetic association analysis using the equine SNP chip, microsatellites, copy number variation tiling array, re-sequencing of candidate genes, gene expression microarrays, next-generation sequencing, protein expression analysis, RT-PCR, RH mapping, karyotyping, and FISH. In addition, the lab is also working on describing the PAR and the MSY of the equine Y chromosome including gene loss, gain, function, and the roles Y genes play in stallion fertility. The Cai lab focuses on the interaction between the genotype and phenotype using computational genomics to identify the causal variants underlying genetic disorders and complex traits of different organisms. Projects will focus on applying next-generation sequencing to follow up associations found with more traditional methods. The work is funded by USDA-CREES, USDA-NIFA, American Quarter Horse Foundation, and Morris Animal Foundation.

We seek a motivated postdoc that is interested in applying the latest bioinformatics tools to understand the genomic factors that play a role in diseases and phenotypes of horses, and other important domestic, agricultural, and wild animals. The post-doc will be required to write manuscripts and proposals, and will have opportunities to develop additional projects in line with their areas of interest. The successful applicant will work as part of a multidisciplinary team and will develop skills in bioinformatics, genomics, and translational medicine.

REQUIREMENTS: Ph.D. in a relevant biological discipline with previous research experience using genomic bioinformatics tools. Knowledge of both genomics and computational analysis of genomic data is required, as is familiarity with Linux, Python, Matlab, and Perl, and the ability to write scripts. Excellent writing, communication skills, and the ability work as part of a team are also required. Previous work with large data sets, SNP analysis, and next-generation sequencing data is preferred. Knowledge and experience with horses, other domestic animals, or wildlife is also preferred.

TO APPLY: For inquiries or to apply, email Dr. Jan Janecka (jjanecka@cvm.tamu.edu) a (1) a 1-page cover letter with as summary of your primary research experience and interests, (2) your CV, (3) and contact information for three references.

Bhanu P. Chowdhary Associate Dean for Research and Professor Department of Veterinary Integrative Biosciences Texas A&M University College Station, TX 77843 - 4458 Tel. 979-845-5092

POSITION #2 TITLE: Post-Doctoral Research Associate in Genomics LOCATION: Texas A&M University, College Station, TX SALARY: Commensurate with experience CLOSING DATE: Open until filled DURATION: Two years with a possibility of extension depending on performance and funding

DESCRIPTION: The Chowdhary lab (http://vetmed.tamu.edu/labs/cytogenics-genomics) is seeking a post-doc that will use the latest genetic tools towards understanding equine diseases (including laminitis, recurrent airway obstruction, and stallion subfertility), phenotypes, and evolution of equids. The Chowdhary lab is focusing on characterizing genetic factors involved in major equine diseases, sexual development, and reproductive disorders. The approaches applied include genetic association analysis using the equine SNP chip, microsatellites, copy number variation tiling array, re-sequencing of candidate genes, gene expression microarrays, next-generation sequencing, protein expression analysis, RT-PCR, RH mapping, karyotyping, and FISH. In addition, the lab is also working on describing the PAR and the MSY of the equine Y chromosome including gene loss, gain, function, and the roles Y genes play in stallion fertility. Projects will integrate diverse methods, but focus on applying

— / —

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

---

UBarcelona ArtificialSelection

POSTDOC OPPORTUNITY IN BARCELONA

Our group is interested in analyzing the impact of artificial selection and of domestication on genomewide nucleotide diversity. We are looking for a motivated and dynamic postdoc to work in statistical and population genetics issues arising from Next Generation Sequencing (NGS) data. Broadly, there are two topics on which the postdoc could focus:

-Use of realistic simulations to model complex demographic and selective scenarios to mimic, eg, the usefulness of genomic selection, SNP ascertainment bias or the power of different tests to identify selection.

-Development of software to seamless carry out diverse variability tests from NGS data.

We will pay special attention to livestock or domestic plants, where artifical selection has been strong. In addition, we are carrying diverse studies to to unravel the adaptation of pigs to extreme climates using new sequencing technologies or to identify genes related to meat quality also in pigs, so ample opportunities also exist to get involved in analyzing real data from livestock.

The postdoc will join a multidisciplinary group with expertises in quantitative, population and molecular genetics. The work will be developed in a new center in Agrigenomics (www.cragenomica.es)within the campus of Universitat Autonoma of Barcelona (www.uab.es).

Initially, the position is for one year with possible extensions, salary will be commensurate with CV. Experience in NGS data analyses is not required but we do ask for good programming skills. We require the candidate is competitive at the national level to be eligible for a Juan de la Cierva or similar postdoc. This means that the PhD should NOT have been obtained earlier than 2008 and should have a good publishing record.

Interested persons please email CV, letter of motivation and of interests, and name and email of at least two scientists who can provide references.

–

Miguel Perez-Enciso ICREA professor Centre for Research in Agricultural Genomics (CRAG) and Facultat de Veterinaria UAB Campus Universitat Autonoma Barcelona Bellaterra E-08193 Spain Tel: +34 935636600 ext 3346 Fax: +34 935636601 miguel.perez@uab.es http://www.icrea.cat/Web/ScientificStaff/Miguel-Perez-Enciso-255 http://bioinformatics.cragenomica.es/numgenomics/ Sociedad Espanyola de Genetica: http://www.segenetica.es/ Miguel Perez-Enciso <miguel.perez@uab.cat>

UBath HoneyBeeEpidemiology

A two-year postdoctoral position at the University of Bath in evolutionary genetic aspects of European Foul Brood (EFB) in honey bees.

Deadline: Monday 25, July

Applicants must have a PhD in evolutionary genetics, and / or experience with infectious disease modelling. Applicants are likely to be closely considered if they have previous experience in the following fields: apiculture, genetic modelling of processes involving admixture, spatial genetic modelling, epidemiology and bioinformatics. A strong record of publication and a passion for cutting-edge research is highly desired. Standard experience with molecular biology and bioinformatics techniques would be highly desirable.

For details about the position and application procedures, see the following:

https://www.bath.ac.uk/jobs/Vacancy.aspx?ref=JK608 Dr. Nick Priest (n.priest@bath.ac.uk) Lecturer in Evolutionary Genetics Dr. Ed Feil (e.feil@bath.ac.uk) Reader in Microbial Evolution Department of Biology & Biochemistry Bath, UK

N.Priest@bath.ac.uk

UBritishColumbia ForestPathogen PopulationGenomics

Population genomics of forest pathogens Department of Forest Sciences University of British Columbia Supervisors: Richard Hamelin and Kermit Ritland

A post-doctoral fellowship is available in the area of population and evolutionary genomics of forest fungal pathogens. You will participate in the following projects. (1) De-novo whole-genome sequencing of one species each of Pucciniales (rusts), Oomycetes (cankers and root diseases) and Dothydeomycetes (cankers and blights). (2) Genome resequencing of representative strains within these taxa. In these first two projects the role will be supportive, as this sequencing will be handled by the Genome Sciences Center in Vancouver, and the strains will be collected and cultured by others in the project. The major roles for you will then be: (3) Identifying genome-wide SNPs and haplotype profiles for each strain, and the use of such data for inferring the origin of pathogen introduction, mapping of migration routes, and identifying genomic regions involved with pathogenicity using evolutionary comparisons. (4) Development of new approaches for inferring migrational history of taxa, and inferring the sexual history of these fungi with genome-scale data.

Applicants should have a background in population genomics which involves strong computational or statistical skills. By no means is this position restricted to people with fungal experience; the methods transcend this kingdom and applicants who have worked with any organism are welcomed, as long as population genomics skills are present. Experience with fungi will broaden your perspective of the diversity of life. You will also have the opportunity to interact with several other students and post-docs in this project. This project involves the Canadian Forest Service, Forest Products Innovations, and Canadian Food Inspection Agency, so you will be exposed to a diversity of end-users. It should be noted that the other major component of this project is defining sets of genes at various hierarchical levels that can be translated to the important application of detection and monitoring of these pathogens. You may be interested in participating in this activity.

To apply, submit a CV, a cover letter and names and contact information of three referees to Kermit Ritland (kermit.ritland@ubc.ca). The start date can be immediate or until January 1, 2012, and the duration can be up to 3 years, pending satisfactory initial reviews of progress. This project is funded by Genome BC and Genome Canada, with matching from the Canadian Forest Service.

"Ritland, Kermit" <kermit.ritland@ubc.ca>

UCambridge HumanEvolutionaryGenetics

Post-Doctoral Research Associate Department of Archaeology and Anthropology Salary: £27,319 Limit of tenure: 30 months Department of Archaeology and Anthropology is pleased to announce a full time Research Associate Fellowship with the effect from 1 September 2011 or soon after that date. The Research Associate would be funded by a grant from the ERC titled, An inter-disciplinary approach for identifying evolutionary active regions in the human genome. The project involves research on the variation of human genome in populations from various climate zones. It will combine evidence from Humanities and Natural Sciences to build realistic models of population dispersals over the past 100 thousand years and using high-throughput genotyping and second generation sequencing methods will attempt to reveal regions in the genome that have been affected by natural selection due to environment and life style differences. Applicants should have, or must be expecting to complete, a Ph.D. in Population Genetics, Bioinformatics or related field before they take up this position. A good knowledge of models, methods, and theory in human population genetics and working experience with genomic data bases is required. In addition, programming skills, experience with computer simulations and familiarity with analysis tools designed for genome-wide genotype and second generation sequencing data will be an advantage. Informal inquiries may be addressed to Dr. Toomas Kivisild at tk331@cam.ac.uk Applications consisting of a full CV, letter of application and a signed CHRIS/6 application cover sheet (Parts 1 and 3 only) with the names and contact details of two referees should be sent to Mrs. Jane Clare, Department of Archaeology and Anthropology, Pembroke Street, CB2 3DZ, e-mail: jc478@cam.ac.uk to arrive no later than August 15 2011. A CHRIS/6 application cover sheet can be downloaded from www.admin.cam.ac.uk/offices/hr/forms/chris6/ Interviews will take place on 26th August 2011. Closing date: 15 August 2011. The University values diversity and is committed to equality of opportunity. The University of Cambridge only advertises their own and college vacancies on this website; we do not advertise any external vacancies. The University has a responsibility to ensure that all employees are eligible to live and work in the UK.

PhD Studentship in Human Evolutionary Genetics Department of Archaeology and Anthropology Limit of tenure: 36 months

Department of Archaeology and Anthropology is pleased to announce a PhD studentship in Human Evolutionary Genetics to start in October 2011. The three-year studentship is available as part of an ERC funded project entitled,

An inter-disciplinary approach for identifying evolutionary active regions in the human genome.

Start date: October 1st, 2011

Supervisor: Dr. Toomas Kivisild, Dept. Biological Anthropology, University of Cambridge

Co-supervisor/Advisor: Dr. Chris Tyler-Smith, WT Sanger Institute

The project involves research on the variation of human genome in populations from various climate zones. It will combine evidence from Humanities and Natural Sciences to build realistic demographic models of population differentiation and dispersals over the past 100 thousand years and using high-throughput genotyping and second generation sequencing methods will attempt to reveal regions in the genome that have been affected by natural selection due to environment and life style differences.

Applicants should have a Masters degree and/or the equivalent of at least a high 2:1 UK honours degree in one of the following areas: Population Genetics, Bioinformatics, Computational Biology or similar field. Programming skills, experience with computer simulations and familiarity with analysis tools designed for genome-wide genotype and second generation sequencing data will be an advantage.

Funding: The studentship provides a starting stipend of £19,619 pa which is expected to cover all college and University composition fees and basic maintenance costs for the duration of the studentship. The studentships are open to all home and EU students. Non-EU applicants can only be considered if they already have the means to cover the fees differential for overseas students.

Informal inquiries may be addressed to Dr. Toomas Kivisild at tk331@cam.ac.uk

Applications consisting of a full CV, letter of application and a signed CHRIS/6 application cover sheet (Parts 1 and 3 only) with the names and contact details of two referees should be sent to Mrs. Jane Clare, Department of Archaeology and Anthropology, Pembroke Street, CB2 3DZ, e-mail: jc478@cam.ac.uk to arrive no later than August 15

2011. A CHRIS/6 application cover sheet can be downloaded from www.admin.cam.ac.uk/offices/hr/forms/chris6/

— / —

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

UChicago PopulationGenetics

Postdoc position, University of Chicago

A postdoctoral position is available in Molly Przeworski's lab at the University of Chicago. Current work in the group focuses on the causes and consequences of variation in recombination, as well as on a wide range of topics in evolution and population genetics; for more information, see http://przeworski.uchicago.edu/. The successful candidate will have considerable latitude to design his/her project.

Applicants for the position must have a background in theoretical population genetics or come from a quantitative field (such as statistics or computer science) and have a demonstrated interest in genetics and evolution. Strong programming and bioinformatics skills are essential. Informal inquiries as well as applications (including a CV, copies of relevant publications and two letters of recommendation) should be emailed to Molly Przeworski at mfp@uchicago.edu. The starting date is negotiable but could be as early as fall 2011.

The group shares space and weekly lab meetings with those of Jonathan Pritchard and Matthew Stephens and enjoys close ties with other members of the Human Genetics and Ecology & Evolution departments, notably Anna Di Rienzo, Dick Hudson and Carole Ober. Moreover, it benefits from the large and outstanding community of researchers in population genetics, statistics and genomics at the University of Chicago.

Molly Przeworski Howard Hughes Medical Institute Dept. of Ecology & Evolution and Dept. of Human Genetics University of Chicago

molly.przew@gmail.com

UEdinburgh BacterialEvolution

Research Fellow in Bacterial Evolutionary Genomics

£29,972 - £35,788

A research fellow position is available in the Laboratory for Bacterial Evolution and Pathogenesis at The Roslin Institute, University of Edinburgh with Dr J. Ross Fitzgerald. The 3 year BBSRC-funded project will investigate the evolution of virulence in Staphylococcus aureus, the major human and animal pathogen using a comparative next generation sequencing approach. Depending on the background of the successful candidate, a combined approach including phenotypic and virulence analysis may be employed to understand the genetic and functional basis for host-adaptation. Overall, the project will aim to identify and characterise the evolution of new virulent clones of S. aureus affecting humans and animals with a long term goal of designing ways for preventing or controlling infections. The candidate will have experience of handling next generation sequences for comparative genomic and evolutionary analyses. In addition, experience in molecular microbiology would be a distinct advantage. The Roslin Institute is a new world-class centre for biomedical research of relevance to both animal and human health with a strong focus on infectious diseases. The Institute has state of the art research facilities for imaging, proteomics, and genomics, including next-gen sequencing (Illumina, HiSeq). Within the University of Edinburgh the project will also involve collaborations with the Institute for Evolutionary Biology and other research groups within Edinburgh Infectious Diseases. Please contact Ross.Fitzgerald@ed.ac.uk for more information or informal discussion.

Relevant selected references:

Guinane et al and J. Ross Fitzgerald. 2010. Evolutionary genomics of Staphylococcus aureus reveals insights into the origin and molecular basis of ruminant host adaptation. Genome Biol Evol 2:454-66

Lowder BV, et al and J. Ross Fitzgerald. 2009. Recent human-to-poultry host jump, adaptation, and pandemic spread of Staphylococcus aureus Proc Natl Acad Sci U S A. 106:19545-50

– J. Ross Fitzgerald, Ph.D., Laboratory for Bacterial Evolution and Pathogenesis, The Roslin Institute and Centre for Infectious Diseases, University of Edinburgh, Easter Bush, Midlothian EH25 9RG, Scotland, UK

Email: Ross.Fitzgerald@ed.ac.uk Tel: +44 (0)131 6519235 http://www.roslin.ed.ac.uk/ross-fitzgerald/ – The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

Ross Fitzgerald <Ross.Fitzgerald@ed.ac.uk>

UGhent Bioinformatics

Dear all,

We have a job opening for a postdoctoral scientist in Bioinformatics who will be involved in the integrative analysis of RNA-seq data and growth phenotype data.

Please forward to any interested colleagues.

Kind regards, Stefanie De Bodt

(our apologies for multiple posting)

Postdoctoral Scientist Bioinformatics

The Department of Plant Systems Biology, VIB, University Ghent (www.psb.ugent.be) is an internationally renowned and dynamic research institute that employs molecular genetics, genomics and bioinformatics to unravel developmental processes in plants. The Systems Biology of Yield group, headed by Prof. Dirk Inzé, is focusing on the integration of multiple data sources (genomics, transcriptomics, phenotyping) to investigate the complex regulation of plant growth in relation to the environment.

- Job description: We want to recruit an enthusiastic postdoc in bioinformatics/systems biology. With the advent of sequencing technologies, we are now able to exploit the natural variation of plants to study growth and development in the model species Arabidopsis thaliana as well as the crop species Zea mays (corn). You will be involved in the integrative analysis of RNA-seq data and growth phenotype data. The successful applicant will be working in close collaboration with our experimental team, to develop and apply computational methods to analyze inhouse generated data.

- Profile: You have a PhD degree in Bioinformatics, Computational Science or in Biotechnology/Biochemistry/Bioengineering or equivalent. You have a good knowledge/experience in programming (one or more of the following: Perl/Python, R, SQL, Java and/or C++), proficiency in Unix/Linux. Experience with next-generation sequencing and/or microarray data analysis, genome-wide association mapping, machine learning and/or network inference is a plus Strong background in statistics is a plus Good knowledge of plant biology is a plus You speak English fluently. You have good communication skills and like to work in a team. You can work independently and like to take initiative.

- The contract will be for a period of 3 years. We offer a diverse job in a young international team, an open and informal work atmosphere and in modern facilities. The institute is located in the vibrant university city of Ghent.

- Start date: as soon as possible, the position remains vacant until a suitable candidate is found.

- Application: Send your letter of motivation, your CV and references to Christine Tiré (christine.tire@psb.vib-ugent.be). Further information can be obtained by contacting Stefanie De Bodt (stefanie.debodt@psb.vib-ugent.be).

Stefanie De Bodt, PhD

VIB Department of Plant Systems Biology, UGent Technologiepark 927 B-9052 Gent Belgium Tel: 32 (0)9 3313692 Website: http://www.psb.ugent.be Stefanie De Bodt <stefanie.debodt@psb.vib-ugent.be>

UMaryland AlgalBiodiversity

Community Phylogenetics and Green Algal Biodiversity

We seek highly motivated postdoctoral researchers to participate in two NSF-funded, collaborative research projects studying biodiversity and systematics in green algae, working in the laboratory of Dr. Charles Delwiche at the University of Maryland College Park. We are using high-throughput sequencing of expressed sequences to study phylogenetics, ecology, and evolution in green algae. These studies will collect very large sequence datasets that will entail substantial challenges in informatics and analysis. The successful candidates will work at the cutting edge of research in biological diversity, and will have the opportunity to explore the interconnections between evolutionary history, cellular metabolism, and community function. Willingness to work in a highly collaborative environment including postdocs, graduate students, and undergraduates will be essential. There will also be opportunities for the candidate to pursue his or her own research program within the broad context of the grant proposal, and in collaboration with the PI, lab, and outside collaborators.

Two positions are open, one to be filled immediately, and one to be filled in Fall/Winter, 2011. Both positions require a Ph.D. in the biological sciences, bioinformatics, or a related field, and preference will be given to candidates having experience with algal/plant biodiversity, RNA biology, high-throughput sequencing, and/or sequence analysis. An initial commitment of one year will be expected, and can be extended upon mutual agreement to at least three years. Benefits include vacation, health insurance, and retirement contributions. Opportunities for career development will be available as a part of the project and through the broader University environment. The University of Maryland is located in College Park, a suburb of the Washington, D.C. Metropolitan Area, and provides a vibrant cultural and academic environment with easy access to a vast array of Federal research facilities.

The starting date is flexible and will remain open until filled, but for best consideration applications should be received no later than July 30. Informal inquiries are encouraged, prior to formal application. To apply formally, please send the following:

1. A curriculum vitae 2. Names of 3 referees willing to provide a letter of recommendation upon request 3. A brief statement of how your research goals fit with research on algal biodiversity, systematics, and evolutionary biology.

Email applications are preferred, and should be sent to: aaalgeee@gmail.com

todd.oakley@lifesci.ucsb.edu

UMontana PlantEvolutionaryGenetics

A postdoctoral position is available in the lab of Lila Fishman at the University of Montana. We study the genetic mechanisms underlying selfish evolution, adaptation, and speciation in *Mimulus* (monkeyflowers): < http://dbs.umt.edu/research_labs/fishmanlab/ >. The postdoc will focus on a project investigating the mechanisms and consequences of female meiotic drive in yellow monkeyflowers.

Female meiotic drive, in which homologous chromosomes compete for access to the single product of female meiosis, is predicted to be a ubiquitous evolutionary force and may account for fundamental features of plant and animal chromosomes. The *Mimulus* meiotic drive system (see Fishman & Saunders 2008, Science 322, 1559), which is polymorphic within and among species, represents a rare opportunity to empirically test controversial hypotheses about selfish chromsomal evolution. The overall project includes cytogenetic experiments to test whether female meiotic drive is centromeric in origin and mechanism, genetic mapping of drive modifiers, molecular evolution studies of drive-associated loci, and field/greenhouse experiments to fully characterize the costs of drive. These projects are facilitated by newly available genome resources, including a full reference genome (of drive line) and numerous resequenced lines/populations. The postdoc's primary responsibility will be conducting the genetic mapping, molecular evolution, and cytogenetic components of this integrative project. The postdoc will also be encouraged to develop independent research projects on selfish evolution, speciation or adaptation within the emerging model genus *Mimulus*, and to participate in outreach and training activities.

The successful candidate will have excellent laboratory and analytical skills in cytogenetics, genetics, and/or genomics/bioinformatics, as well as demonstrated writing ability and a strong interest in evolutionary processes.

The postdoc position will be based at the University of Montana in beautiful Missoula, MT (halfway between Yellowstone and Glacier National Parks), but may also involve periods of work in collaborating labs. Funding is available for two years, subject to review after the first year, with an annual salary range of $35,000-38,000 (plus benefits) depending on qualifications. Preferred start date: December 2011, but flexible.

HOW TO APPLY:

Position open until filled. Screening of applications will begin August 15, 2011.

For more information about the position and application process, please contact Dr. Fishman directly (lila.fishman@mso.umt.edu).

To apply, please submit a letter of interest, CV, and list of three references via the listing on the UM Employment page (* https://umjobs.silkroad.com/*)

ADA/EOE/AA/Veteran's Preference As an Equal Opportunity/Affirmative Action employer, we encourage applications from minorities, veterans, and women. Qualified candidates may request veterans' or disabilities preference in accordance with state law

– Lila Fishman, Ph.D. Associate Professor Division of Biological Sciences University of Montana Missoula, MT 59802

office: 406 243-5166 cell: 406 274-4996 fax: 406 243-4184

lilafishman@gmail.com

UMontreal HumanPopulationGenomics

Postdoc: Human Genomics and Population Genomics, University of Montreal A postdoctoral position is available in the population and evolutionary genomics laboratory at the University of Montreal of Philip Awadalla (http://www.philip-awadallalab.org/). Researchers will be involved in the development of methods and collection/analysis of data generated in our ongoing studies of human genomics and disease. The successful candidate will be trained in population or statistical genetics, or have strong computational or statistical skills. Postdoctoral research scientists can work on interesting projects of their choosing related to the labs' general research interests or our current projects.

Possible/related projects include: 1) Next-generation tools and development of model and non-model based methods to study the role of common and rare genetic variants responsible for a number of human traits or disorders, mostly related to child health (cancer, immunodeficiencies, etc.). 2) Next-generation genomics applications for studying the critical co- regulatory factors associated with humans and malaria, sampled from populations globally. A "population biology" approach to identifying key genes and gene networks associated with infection and resistance in both humans and pathogens. 3) Molecular and statistical genomics projects examining the severity of sickle-cell disease in Africa and the North and South America. 4) Genetic and genomic epidemiology of endophenotypes from a deeply phenotyped Quebec cohort of 20,000 participants ages 40-69 - CARTaGENE (www.cartagene.qc.ca). CARTaGENE is an infrastructure for population genomics research. This resource will contribute to the development of better diagnosis, treatment and disease prevention programs.

Interested individuals with a Phd should please write to Philip Awadalla (philip.awadalla@umontreal.ca).

philip.awadalla@umontreal.ca

UParisSud Radionuclide adaptation

Postdoc position to model the spread of radionuclides from fires in areas affected by Chernobyl and the consequences for human health, ecology and biodiversity

Description: We seek applications for a Postdoctoral Fellow position to model radionuclide redistribution as a consequence of fires that occur in the vicinity of Chernobyl. The disaster at the Chernobyl power plant in 1986 released more than 130 PBq of radioactivity, with most deposited in nearby areas of Ukraine, Belarus and Russia. Approximately half of this material still remains after natural decay of radionuclides. More than 10,000 km2 were heavily contaminated, and most human activity including forestry ceased in these areas, causing accumulation of firewood for the last 25 years. Because climate change has in addition caused an increase in temperatures and a decrease in precipitation, there is an increased risk of forest fires. Such fires are disproportionately located in contaminated areas as revealed by satellite images. Forest fires produce radioactive smoke that can be transported and subsequently deposited in densely populated areas such as Kiev and Moscow, depending on wind direction and patterns of rainfall. Such redistribution of radioactivity could have dramatic consequences for public health, but also animals and plants, and for the possibility to grow crops and practice farming in large areas that are not contaminated today. The objective of this Postdoctoral Fellowship is to assess the consequences of different kinds of forest fire (minor fires, intermediate fires that affect 30% of the area, worst case scenario of the entire area being affected by fire) on re-distribution of radioactive material. The project will use a state of the art earth system model in which a fire model, SPITFIRE, has been embedded. We will model climate change, risk and distribution of forest fires and determine risk of deposition of radioactive material transported by smoke. We will calculate radioisotopes concentration and deposition fields from which exposure doses can be derived. This will allow health experts to quantify public health and biological consequences of such re-distribution of radioactive material. At an early stage in this work a workshop will bring together fire experts, health experts and ecologists to assess the current state of understanding and the uncertainties associated with modeling fires and radionuclides. The position is for 24 months, and we would like the candidate to start at or close to September 1st 2011.

Candidate background: We seek candidates that have a thesis, a superior ability to write papers, and familiarity with numerical modeling. The applications should include a resume, a statement of research interests and the names of at least two references including e-mail addresses and telephone numbers.

Contacts: Yves Balkanski Anders Moller IPSL/LSCE Lab. Ecologie, Systematique (Lab. des Sciences du Climat et de et Evolution l'Environnement) LSCE UMR 8212 CEA-CNRS-UVSQ UMR 8079 CNRS-Universite Paris-Sud XI-AgroParisTech L'Orme des Merisiers - Bat 712, Bat 362 Universite Paris-Sud XI Point Courrier 132 F-91191 Gif sur Yvette Cedex F-91405 Orsay Cedex T +33 1 6908-7725 yves.balkanski@lsce.ipsl.fr anders.moller@u-psud.fr http://www.researcherid.com/rid/A-6616-2011 http://129.175.106.17/pages_perso/-spip.php?article47&lang=fr Anders Møller Laboratoire Ecologie, Systematique et Evolution UMR 8079 CNRS-Université Paris-Sud XI-AgroParisTech Batiment 362 Université Paris-Sud XI F-91405 Orsay Cedex http://www.ese.u-psud.fr/pages_perso/-spip.php?article47〈=en Anders Pape Moller <anders.moller@u-psud.fr>

Uppsala AmbrosiaGeneticDiversity

Swedish University of Agricultural Sciences

Faculty of Natural Resources and Agricultural Sciences Department of Crop Production Ecology, Uppsala Post doctoral position within the project Genetic diversity and invasiveness in Ambrosia artemisiifolia

Ambrosia artemisiifolia, a native plant from North America, has been recognized as the most serious weed in large parts of eastern Europe. It constitutes a health problem causing allergic reactions and is difficult to control in agricultural production. Studies of genetic diversity would form a base for future investigations of the potential for this species to adapt to North European conditions, and e.g. indicate whether its spread is restricted by the critical photoperiod for initiation of flowering.

The position will be based at the department of Crop Production Ecology, but you will be working in a group of researchers from three departments, with expertise in molecular biology, plant ecology and weed biology. In addition, you will be a part of the scientific environment within a larger research programme, Adaptability of invasive weeds and pests.

Duties: The post doc position will focus on the genetic diversity in A. artemisiifolia as a base for future studies of its invasive potential. We expect the candidate to have an interest in genetics and ecology with good knowledge in molecular genetic methods. She/he will be working with the characterisation of phenotypic and genotypic diversity in populations of A. artemisiifolia from North America, Middle East and Europe. The first phase will include scanning of phenotypic variation as regards photoperiod requirement, and neutral genetic variation. Future plans include a follow-up of these studies by identification of quantitative trait loci (QTL) for variation in photoperiod requirements.

Qualifications: Prerequisites for the position include i) a PhD in field relevant to population genetics or molecular ecology, and ii) demonstrated skill in molecular genetic methods, preferably experience in working with QTL. To be appointed as a post doc, the applicant should have been awarded her/his PhD no more than three years at the time of application.

Form of employment: The position encompasses a two-year period (24 months). Extent: 100% Starting date: By agreement

Further information: Lars Andersson Professor +46(0)18 673366 Lars.Andersson@slu.se

and:

http://www.slu.se/sv/for-dig-som/lediga-anstallningar/ mikael.lonn@sh.se

---

UStellenbosch AfricanAntelope

UStellenbosch MolecularCytogeneticsAfricanAntelope

A postdoctoral fellowship is available immediately in the Robinson lab to study molecular cytogenetic relationships of bovids, and African antelope in particular. The Bovidae are noteworthy for the dominance of Robertsonian (Rb) chromosomal fusions in shaping the genomes of many species. Our recent work on this group shows the use of these rearrangements in determining evolutionary relationships is problematic, and that homoplasy predominates in the chromosomal dataset. In sharp contrast, variation in the morphology of the X chromosome appears to hold considerable promise for resolving some of the persistent problems associated with the classification of this group of mammals.

We propose to: (i) Identify intrachromosomal rearrangements of the X chromosome using high density BAC mapping and analysis by microdissected painting probes and FISH. (ii) Develop high-resolution comparative maps that define the borders and orientation of rearranged segments in a species-rich taxonomic sample, and test these data for defining evolutionary relationships among species of the subfamilies and tribes of Bovidae.

A strong background in molecular and classic cytogenetic techniques including chromosomal preparation, fluorescent in situ hybridization/chromosome painting, karyotyping, the use of Cytovision or other image analysis platforms and experience with cell culture is required. A strong interest phylogenetics would be an advantage.

Applicants should provide a CV, statement of research experience and names of three academic referees to:

Professor Terry Robinson (E-mail: tjr@sun.ac.za) Department of Botany & Zoology Stellenbosch University Private Bax X1 Matieland 7602 South Africa http://-www.sun.ac.za/botzoo

Tel: +27 21 808 39 55 Fax: +27 21 808 24 05

"Robinson, TJ, Prof <tjr@sun.ac.za>" <tjr@sun.ac.za>

UZurich FishEvolution

Open postdoctoral position at the University of Zurich to study pattern and process in evolutionary radiations of fossil and living actinopterygian fishes

The Evolutionary Morphology and Palaeobiology of Vertebrates group at the Palaeontological Institute and Museum of the University of Zurich (http://-www.msanchezlab.net/) invites applications for a postdoctoral position. The successful candidate will work in a Swiss National Science Foundation supported research project (Sinergia) about patterns and processes in evolutionary radiations of fossil and living actinopterygian fishes, concentrating on the speciation and phylogeny of a basal Triassic clade. The project is a collaboration between M. Snchez, H. Furrer (http:/-/www.pim.uzh.ch/de/index.php) and W. Salzburger (Basel, http://evolution.unibas.ch/salzburger/).

We are looking for an individual who has received his or her PhD within the last five years, who is highly motivated and can work independently on the project. A successful candidate will have substantial research experience in at least one of these areas: phylogenetics, comparative anatomy, morphometrics and skeletochronology. The selected candidate will be expected to help in teaching and writing a proposal for funding. The position offers a highly competitive salary of up to three years on annually renewable contracts.

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

To be considered, please send a single (!) PDF file merged from the following parts: CV including publication list, a statement of research interests not exceeding three pages, and three academic references. Please include the word SinergiaSnchez2012 in the subject line. The application deadline is August 15, 2011. The position is available in fall of 2011, at a negotiable starting date.

Many thanks and kind regards,

Prof. Marcelo Snchez (e-mail: m.sanchez@pim.uzh.ch)

Marcelo Snchez <m.sanchez@pim.uzh.ch>

YaleU SexualSelection

*Postdoctoral Position Available To Study Sexual Selection and Social Interactions*

A NSF-funded postdoctoral position is currently available in the lab of Suzanne Alonzo (PI) at the Department of Ecology and Evolutionary Biology at Yale University to develop theory on how individual social or behavioral interactions affect evolutionary dynamics, with a focus on reproductive and social traits. The postdoctoral researcher will work independently and in collaboration with the PI to determine the precise questions to be addressed. A Ph.D. in evolution, ecology, or mathematical biology is required. A background in sexual selection, social evolution or evolutionary ecology is preferred. Applicants should have a background in evolutionary or ecological theory and have previous experience developing mathematical models. Individuals with experience with inclusive fitness methods, adaptive dynamics, game theory or quantitative genetics are especially encouraged to apply. The position is currently open and can start as soon as possible.

Application deadline is July 31, 2011. Position will remain open until filled.

In the cover letter, applicants should describe their theoretical background and experience with mathematical modeling and evolutionary theory explicitly. Please submit a curriculum vita, brief statement of research interests, up to 3 relevant manuscripts and contact information for 3 references to Suzanne H. Alonzo by email (Suzanne.Alonzo@Yale.edu). Applicants should also give their earliest potential start date

Yale University is an Equal Opportunity/Affirmative Action Employer. Men and women of diverse racial/ethnic backgrounds and cultures are encouraged to apply.

"Suzanne H. Alonzo" <suzanne.alonzo@yale.edu>

WorkshopsCourses

Adelboden Switzerland TheoryCooperation Aug11-13

CUSO Workshop on 'The Theory of Cooperation' August 11-13, 2011 Adelboden, Switzerland

Dear colleagues,

The behavioural ecology group at the University of Bern is organizing a workshop on 'The Theory of Cooperation', which is to be held on August 11 - 13, 2011, in Adelboden, Switzerland. This meeting is funded by the Conférence Universitaire de Suisse Occidentale (CUSO), and the Doctoral Program in Ecology and Evolution of the western Swiss Universities. Students from the affiliated institutions can apply for full reimbursement of travel/participation and accommodation costs. Interested students (MSc, PhD), postdocs and researchers from other institutions are very welcome to attend this workshop as well; we can usually admit about 25 non-CUSO participants. A preliminary program with the list of speakers, further information about the workshop and instructions on how to register can be found on:

http://behav.zoology.unibe.ch/index.php?pp=-3D56&p=3D67 The deadline for registration is July 15. We would appreciate your help in forwarding this announcement to students in your group who would potentially be interested in participating.

Best wishes, Sander van Doorn Michael Taborsky

Institute of Ecology and Evolution Ethological Research Station Hasli Wohlenstrasse 50a CH-3032 Hinterkappelen Switzerland http://behav.zoology.unibe.ch/
sander.vandoorn@iee.unibe.ch

Barcelona StatisticalGenetics Aug22-26

The course is filling fast, but we have a few more open spaces. Applications will be accepted until all spaces are filled

STATISTICAL GENETICS SHORT COURSE 22-26 August 2011

Barcelona, Spain Hosted by Centre Nacional d'Anàlisi Genòmica (CNAG)

http://www.genetics.ucla.edu/courses/statgene email: statgene@mednet.ucla.edu

We are offering a five full-day intensive workshop on state-of-the-art statistical methods for detection of genetic loci for complex traits.

Each day will include hands-on computer exercises using statistical genetics computer programs, especially the Mendel software package, with its new graphical front-end.

We will cover the general theory behind the methods as well as emphasize the practical aspects needed to give the best chances of success. The Course is designed to assist people who will be performing statistical analyses to discover the genetic basis of complex traits. The methods covered are appropriate to both human and non-human populations. Topics will include:

* Statistical Reviews * Genetic Study Design * Quality Control and other data issues * Haplotyping * Analysis of Qualitative and Quantitative Traits including: - Parametric and Non-Parametric Linkage (NPL) analysis - Methods for Large Pedigrees - Genome-Wide Association Studies (GWAS), or smaller scale, including: + Case/Control or Random Sample + Family-based Designs + Complex Pedigrees derived from Inbred Strains * Ethnic Admixture Analysis * Gene Co-Expression Network Analysis * Rare Variant Analysis Methods Applicable to SNP or Genome Sequence Data

Participants in the Course need no prior experience with these methods or programs. Participants will be required to bring a laptop computer to run the analysis exercises.

The Course features instructors from the Statistical Genetics Group of the UCLA Department of Human Genetics and other leading genetic researchers: - Kenneth Lange - Simon Heath - Steve Horvath - Jeanette Papp - Janet Sinsheimer - Eric Sobel - Hua Zhou

The cost of the course, which includes lunch and snacks every day and a group dinner on Thursday, is:

900 EUR for students from non-profit institutions 1200 EUR for postdocs, staff, and faculty from non-profit institutions 1600 EUR for individuals from for-profit institutions

Transportation and lodging are not included.

The course will be held 22-26 August 2011 in Barcelona, Spain.

For more information, including the simple application process, please visit http://www.genetics.ucla.edu/courses/statgene Please email statgene@mednet.ucla.edu for more information or to submit the simple application material.

JanetS@mednet.ucla.edu

CSHL ComputationalComparativeGenomics Nov9-15

Course announcement:

Cold Spring Harbor COMPUTATIONAL & COMPARATIVE GENOMICS

November 9 - 15, 2011 Application Deadline: July 15, 2011

INSTRUCTORS: William Pearson, University of Virginia, Charlottesville, VA< Lisa Stubbs, University of Illinois, Urbana, IL

This course presents a comprehensive overview of the theory and practice of computational methods for the identification and characterization of functional elements from DNA sequence data. The course focuses on approaches for extracting the maximum amount of information from protein and DNA sequence similarity through sequence database searches, statistical analysis, and multiple sequence alignment. Additional topics include:

* Alignment and analysis of "Next-Gen" sequence data * The Galaxy environment for high-throughput analysis * Identification of conserved signals in aligned and

unaligned sequences * Regulatory element and motif recognition * Integration of genetic and sequence information in biological databases * The ENSEMBL genome browser and BioMart

The course combines lectures with hands-on exercises; students are encouraged to pose challenging sequence analysis problems using their own data. The course is designed for biologists seeking advanced training in biological sequence and genome analysis, computational biology core resource directors and staff, and for scientists in other disciplines, such as computer science, who wish to survey current research problems in biological sequence analysis. Advanced programming skills are not required.

The lecture/lab schedule for the 2010 course can be found at http://fasta.bioch.virginia.edu/cshl Speakers in 2011 course will include:

Aaron Mackey, U. of Virginia, Next-Gen analysis pipelines

Bert Overduin, European Bioinformatics Institute, UK, ENSEMBL and BioMart

Frances Ouelette, Ontario Cancer Research Institute, Databases for Biological Function

William Pearson, U. of Virginia, Similarity Searching, Multiple Alignment

Lisa Stubbs, U. of Illinois, Urbana, Genome browsing, Comparative genomics

James Taylor, Emory, Galaxy and genome analysis pipelines

The primary focus of the computational and comparative genomics course is the theory and practice of algorithms used in computational biology, with the goal of using current methods more effectively and developing new algorithms. Students more interested in the practical aspects of software development are encouraged to apply to the course on Programming for biology. Students who would like in-depth training in the analysis of next-generation sequencing data (e.g., SNP calling and the detection of structural variants) should apply to the course on Advanced Sequencing Technologies & Applications.

—

To apply to the course, fill out and send in the form at:

http://meetings.cshl.edu/course/-courseapp_instr.shtml William Pearson <wrp@virginia.edu>

Edinburgh RADSequencing Sep6-7

3rd UK RAD SEQUENCING MEETING

12.30 6th September 2011 to 17.00 7th September 2011

John McIntyre Conference Centre Edinburgh, UK

Registration: www.radseq.info The 3rd UK meeting on RAD (Restriction-site Associated DNA) Sequencing will be held in Edinburgh on the 6th and 7th of September 2011.

RAD Sequencing is a novel method for sequencing thousands of genetic markers in tens of individuals from any organism using next-generation sequencing. This meeting, the third RAD meeting organized by the GenePool Sequencing and Bioinformatics Facility in Edinburgh, will bring together expert RAD-Seq practitioners and researchers either currently using RAD-Seq or planning to use it.

Dr. Paul Etter and Dr. Julian Catchen, RAD-Seq experts from the University of Oregon, where the method was invented, will be attending the meeting to present and discuss their newly published RAD-Seq protocols and software. We will also hear from a range of researchers making use of RAD-Seq in the UK and beyond.

To register and submit an abstract for the meeting, please visit www.radseq.info For enquiries, please contact genepool-meetings@ed.ac.uk.

Supported by the UK Natural Environment Research Council.

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

John Davey <john.davey@ed.ac.uk>

Manchester Morphometrics Nov7-Dec16

Dear colleagues

I am pleased to announce this year's morphometrics course from the University of Manchester. This year's course will run in the six weeks from 7 November to 16 December 2011.

The course information can be found on the following we site: http://www.flywings.org.uk/MorphoCourse Course content: * Data acquisition: the kinds of data and the equipment used to collect them. * Definitions of size and shape * Geometric methods to characterise shape from a configuration of landmark points (Procrustes superimposition) * Statistics of variation, scatter plots, basic multivariate statistics * Principal component analysis * Measurement error and outliers * Shape transformations and 'warping' – the thin plate spline * Analysis of outline shapes * Distinguishing between groups (taxonomy, clinical diagnosis, etc.) * Allometry and size correction * Influence of external factors on shape (ecomorphology, dose- response studies) * Symmetric forms and measurement of asymmetry. * Morphometric inferences on developmental processes, morphological integration, modularity * Genetics of shape: analyses of resemblance between relatives, QTL analyses. * Phylogeny: reconstructing the evolution of shape

Practice examples: As far as possible, practical exercises are provided to accompany the course content. These practice exercises consist of data sets and explanations on how to run the respective analyses using the MorphoJ software (http://www.flywings.org.uk/-MorphoJ_page.htm). Participants who already have their own data are encouraged to use those and to discuss them as part of the course. I hope there will be a bit of a 'workshop' feel to the course unit.

Group work: Participants will work in small groups to prepare web presentations of possible morphometric studies (blogs or wikis prepared by the groups). This activity stimulates discussion and provides a broad overview of the broad range of questions that can be addressed with morphometric methods.

The fee for the course is GBP 260.00 (I'm afraid it's gone up again slightly from last year – this is out of my control).

All prospective participants need to pre-register for the course. The deadline for this is the *18 September 2011*.

For further details and the pre-registration form, see the course web page: http://www.flywings.org.uk/-MorphoCourse Best wishes, Chris

Christian Peter Klingenberg Faculty of Life Sciences The University of Manchester Michael Smith Building Oxford Road Manchester M13 9PT United Kingdom

Telephone: +44 161 275 3899 Fax: +44 161 275 5082 E-mail: cpk@manchester.ac.uk Web: http://-www.flywings.org.uk Skype: chris_klingenberg

cpk@manchester.ac.uk

Montana ConGen Sep27-Oct1

ConGen COURSE IN MONTANA - 2nd Announcement

To benefit of a low-fare fee register until 15th July. Applications for 2011 edition are yet open but few places are left!

5th ConGen- Population Genetics Data Analysis Course: Recent Approaches for Estimation of Population Size, Structure, Gene-flow, Selection Detection focusing on conservation and beyond

27-Sep/1-Oct 2011, Flathead Lake Biological Station, Montana, USA

Objective: To provide training in conceptual and practical aspects of data analysis for the conservation genetics of natural and managed populations. Emphasis will be on interpretation of output from recent novel statistical approaches and software programs. The course also will allow daily discussions among young researchers and top-researchers to help develop the next generation of conservation geneticists, and to identify developments needed to improve data analysis approaches. This course will cover analysis methods including the coalescent, Bayesian, approximate Bayesian, and likelihood-based approaches.

Who should apply: Ph.D. students, post-docs, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. Applicants must have a basic background in population genetic data analysis, including testing for Hardy-Weinberg proportions and gametic disequilibrium. Participation will be limited to 25 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own data to analyze (for example graduate students at the end of their degree program).

Deadline for application is 30 July, 2011

Course/Workshop Format: For each subject, we provide 30-45 minutes of background, theory, discussion and introduction to concepts. Immediately following, we will conduct data analyses together for 30-60 minutes using relevant software programs and real data sets. Evening hands-on computer sessions and housing together of instructors and students in the same location will allow for extensive exchange and facilitate learning.

Confirmed Instructors/Speakers

Fred Allendorf Robin Waples Oscar Gaggiotti Gordon Luikart Jonathan Pritchard Mike Schwartz Mark Miller Tiago Antao Ted Cosart Paul Hohenlohe David Tallmon Albano Beja-Pereira

For detailed information see http://popgen.eu/-congen2011/ congen@popgen.eu

Albano Beja-Pereira <albanobp@fc.up.pt>

Montreal FounderEffects Oct11

ICHG Satellite Workshop

Populations of the New World: impact of founder effects on health

http://ichg2011popworkshop.yolasite.com/

Tuesday, October 11th, 2011, 8:00 am to 4:00 pm

Salle Saint Antoine (9th floor), Westin Hotel, 270 St. Antoine West, Montreal, QC

Located across the street from the Montreal Convention Center

PROGRAM & SPEAKERS

1st Session: Genetics and genealogies

Marie?\Hélène Roy?\Gagnon (U. of Montreal) & Helene Vézina (U. of Quebec (Chicoutimi)) Genomic and genealogical investigation of the French Canadian founder population structure

Philip Awadalla (U. of Montreal) Interrogating the Genomic and Environmental Control Points of Chronic Disease in a Prospective Aging Quebec Cohort ?\ CARTaGENE

Agnar Helgason (deCODE Genetics) Using IBD segments to study admixture and population structure in Iceland

2nd Session: Amerindian Health Issues

David Reich (Harvard U.) The Genetic History of Native Americans

Robert Hanson (NIDDK, NIH) Genetic Studies of Diabetes Mellitus in Pima Indians

Laura Arbour (U. of British Columbia) Predicting risk for sudden death: The power of clinical and basic science with communities

3rd Session: Admixtures

Nelson B. Freimer (UCLA) Mapping Disease genes in Latin American founder populations

Carlos D. Bustamante (Stanford U.) Population genetics and genomics of admixture in the Americas

Rick Kittles (U. of Chicago) Genetic Histories of Africans in the New World

John Novembre (UCLA) Admixture and Recombination in African?\Americans

4th Session: Selection and adaptation

Anna Di Rienzo (U. of Chicago) Adaptations to local environments in Native Americans

David Goldstein (Duke U.) Identifying pathogenic mutations in whole genome sequence data

Meeting organizers: Damian Labuda & Guy Rouleau, U.of Montreal

Meeting secretary: Ron Lafreniere

PRE?\REGISTRATION WILL BE REQUIRED SINCE ATTENDANCE WILL BE LIMITED TO 80 PARTICIPANTS DUE TO ROOM LIMITATIONS. PLEASE CONTACT RON LAFRENIERE AT RON.RMGA@GMAIL.COM TO REGISTER OR FOR FURTHER INFORMATION.

Damian Labuda <damian.labuda@umontreal.ca>

Portugal TeachingEvolution Sep27-30 2

Dear all,

This is the 2nd call for applications to the Faculty Institutes for Reforming Science Teaching (FIRST) IV-like Workshop being held at CIBIO-UP next fall, now with some changes in eligibility criteria for applicants.

Key elements of FIRST IV include active learning, assessment, and diversity in teaching. FIRST IV-like workshop aims at bringing together professionals interested in teaching and science communication, providing teaching skills and connecting the participants to the FIRST IV network on teaching.

As such, FIRST IV-like workshop is indicated for all those who are interested in science communication or science education at any level or target audience.

Some details are given bellow or you can visit the webpage http://popgencibio.org/web/ We hope to see you in September!

Please share this e-mail with who might be interested.

Kind regards, Rita Campos Rui Faria

Important dates: Registration: July 1 - July 17 2011 Notification of acceptance: July 23 2011 Confirmation of registration (payment): July 23 - 29 2011 Course: September 27 - 30 2011

Instructor: Diane Ebert-May, Professor Department of Plant Biology Michigan State University http://www.plantbiology.msu.edu https://www.msu.edu/~first4/ https://www.msu.edu/course/bs/110/ebertmay/ Registration: Merge the completed application form with all the required materials to create the final application file, which will include: - Application form with the fields completed - Statement explaining your reason for applying to FIRST IV and expected outcomes from your participation in relation to your career goals - Curriculum Vitae - Statement of Teaching Philosophy

Please name your completed application file: LastnameFirstname_FIRSTIVCIBIOapp.pdf

Email the finalized application to ritacampos@mail.icav.up.pt

Price: 360 euros

The course fee includes lunch, morning and afternoon coffee-breaks, room and instructional materials. Shared rooms are entitling to a discount. If you don't need housing, please contact us after being accepted to attend the workshop.

rita.ml.campos@gmail.com

Portugal TeachingEvolution Sep27-30 3

Dear colleagues,

We would like to recall that the deadline to apply to the workshop FIRST IV at CIBIO is approaching (23h59m of July 17).

Faculty Institutes for Reforming Science Teaching (FIRST) IV Workshop aims at bringing together professionals interested in teaching and science communication, providing teaching skills and connecting the participants to the FIRST IV network on teaching.

FIRST IV-like workshop is open to graduate students, posdocs and faculty and also to science communicators and educators.

You can find more information at WEB Program page: http://popgencibio.org/web/ We would also appreciate if you could forward this e-mail to your colleagues and within your research groups and institutions.

Best regards Rita Campos Rui Faria

rita.ml.campos@gmail.com

Trento Italy ConsPopulationGenetics Sep20-22 DeadlineExt

Workshop: POPULATION GENETICS FOR ANIMAL CONSERVATION III 20-22 September 2011, Trento, Italy.

DEADLINE FOR REGISTRATION AND ABSTRACT SUBMISSION HAS BEEN POSTPONED TO JULY 15th

All relevant information, including registration and abstract forms, can be found at: http://pgac3.fem-environment.eu/ Brief description The Third edition of the workshop will be focussed on a well-recognized, yet unsolved issue in conservation genetics: how to bridge the gap between scientists and end-users, i.e. non-scientists such as policymakers, administrators, or park rangers that are directly involved in animal conservation and would like to design, implement and/or apply management and conservation plans using the most modern strategies and tools

Therefore, this workshop intends addressing this gap by focussing on five main themes identified as top priorities during a recent survey conducted by the European consortium ConGRESS of 100 end-users from across Europe:

1) Identifying units for conservation 2) Population connectivity and isolation 3) Reconstructing past population dynamics 4) Detecting and planning translocations and reintroductions 5) Genetic diversity and adaptation Each theme will be tackled in one 2-hour session (with lectures from invited speakers and contributions

from attendees) with final-day round tables discussions where scientists and end-user will have the opportunity to examine, vis-a-vis, unresolved issues and possible solutions.

PGAC III hopes to bring together researchers from different fields (e.g. population genetics, ecology, conservation biology and related) and end-users with basic scientific knowledge and a strong desire to know more about applying population genetics tools to their particular conservation problem. The major aim will be to promote an effective interaction, using a common language, to fully exploit the potential of population genetics as applied to animal conservation.

Invited speakers: Giorgio Bertorelle (University of Ferrara, Italy) Josef Bryja (Academy of Sciences, Czech Republic) Mike Bruford (University of Cardiff, UK) Oscar Gaggiotti (Universit J Fourier, Grenoble, France) Rus Hoelzel (University of Durham, UK) Jacob Hoglund (University of Uppsala, Sweden) Craig Moritz (University of California, Berkeley, USA) Richard Nichols (Queen Marys College, UK) Craig Primmer (Univeristy of Turku, Finland) Gernot Segelbacher (University of Freiburg, Germany) Hans Siegismund (University of Copenhagen, Denmark) Per Sjogren-Gulve (Swedish Environmental Protection Agency) Carles Vil (CSIC, Spain) Raj Whitlock (University of Liverpool, UK)

The Scientific Committee: Giorgio Bertorelle, University of Ferrara, Italy Mike Bruford, University of Cardiff, UK Heidi Hauffe, Fondazione Edmund Mach, S. Michele all'Adige, Trento, Italy Cristiano Vernesi, Fondazione Edmund Mach, Viote del Monte Bondone, Trento, Italy

Cristiano Vernesi Department of Biodiversity and Molecular Ecology Research and Innovation Centre - Fondazione Edmund Mach address: Centro di Ecologia Alpina, Viote del Monte Bondone - 38040 Trento - Italy tel +390461939523 - fax +390461948190 - skypename: cvernesi

Please, consider your environmental responsibility before printing this email

Cristiano Vernesi <vernesi@cealp.it>

UCalifornia Berkeley BayesianPylogeny Aug15-19

SYMPOSIUM / WORKSHOP on Bayesian inference of phylogeny

There will be a mini-symposium on Bayesian inference of phylogeny to be held on the UC Berkeley campus from August 15th to 19th. There will be two days of talks (August 15th and 16th) on various aspects of Bayesian inference as it applies to the phylogeny problem. The following three days will be a workshop for people interested in developing for the RevBayes program. RevBayes implements an R-like language for specifying complex evolutionary models and (attempts) to perform solid statistical estimation of a model's parameters.

Where: UC Berkeley (e-mail John Huelsenbeck for details about the room location) When: August 15 - 16 (talks), August 17 - 19 (workshop on RevBayes for interested developers) How: RSVP John Huelsenbeck (johnh@berkeley.edu) if you intend to attend.

Confirmed speakers include: Michael Jordan (UC Berkeley), Ian Holmes (UC Berkeley), Jeff Thorne (NCSU), Fredrik Ronquist (Swedish Natural History Museum), Jeet Sukumaran (KU), Sebastian Hoehna (Stockholm University), Tracy Heath (UC Berkeley), and John Huelsenbeck (UC Berkeley).

John Huelsenbeck University of California, Berkeley Department of Integrative Biology 3060 VLSB # 3140 Berkeley, CA 94720-3140

E-mail: johnh@berkeley.edu Phone: (510) 502-5887

johnh@berkeley.edu

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterword

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.