EvolDir

May 1, 2008

Month in Review

Forward

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

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

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

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Conferences

Adelaide AustralAsiaGeneticsSoc Jul7-10 DeadlineMay1

Genetics Society of AustralAsia Annual Meeting 7-10 July 2008 http://www.adelaide.edu.au/gsa2008/ Abstract submission deadline: 1 May 2008

This is a reminder that the deadline for early registration and abstract submission to the annual meeting of the Genetics Society of AustralAsia is May 1, 2008.

See you in Adelaide in July.

Jack da Silva University of Adelaide

Jack da Silva <jack.dasilva@adelaide.edu.au>

Amsterdam SexualConflict May15

One-day symposium “Sexual Conflict”

Thursday 15 May 2008

VU University, Amsterdam (The Netherlands)

This year’s annual symposium of the Royal Dutch Zoological Society will focus on sexual conflict throughout the animal kingdom. The aim is to provide an overview of sexual conflict and its implications in separate sex, parthenogenetic and hermaphroditic mating systems. The programme will also include the awarding of the Dutch Zoology Prize 2008 and the society’s annual meeting.

Programme: 10:00 Arrival & Coffee 10:30 Welcome by Nico M. van Straalen (president of the Royal Dutch Zoological Society) 10:35 Introduction by Nico K. Michiels (University Tuebingen, Germany) 10:45 Göran Arnqvist (University of Uppsala, Sweden) - Sexual conflict - an evolving view of interactions between the sexes 11:30 Ken Kraaijeveld (Leiden University, The Netherlands) - Male genes with nowhere to hide; sexual conflict in haplodiploids 12:15 Lunch 12:45 136th Annual meeting of the Royal Dutch Zoological Society (KNDV) 13:30 David J. Hosken (University of Exeter, United Kingdom) - Sexual selection and sexual conflict in flies 14:15 Aaron Goetz (California State University, Fullerton, USA) - Sexual conflict in humans: Evolutionary consequences of female infidelity 15:00 Tea & Coffee 15:30 Dutch Zoology Prize 2008: Laudatio by Gert

Flik (chair of the jury), presentation of award by Nico M. van Straalen 15:45 Joris M. Koene (VU University, Amsterdam, The Netherlands) - Sex and conflict in hermaphrodites: stabbing, piercing and allohormones 16:30 Reception (in the Tuinzaal, W&N building)

Place: VU University, lecture room 12A05 (main building, 12th floor, wing A) De Boelelaan 1105, Amsterdam, The Netherlands For directions see http://www.vu.nl Registration: Admission and lunch are free. Please register by sending an e-mail with the subject "sexual conflict symposium" to desiree.hoonhout@falw.vu.nl before 5 May.

Organised by: Royal Dutch Zoological Society, KNDV (http://www.kndv.nl) Department of Animal Ecology, VU University (http://www.bio.vu.nl/do/)

For details about the meeting: http://www.kndv.nl http://www.bio.uu.nl/˜kndv/PDFs/zoolprijs2008_poster.pdf http://www.bio.uu.nl/˜kndv/PDFs/zoolprijs2008_programme.pdf Dr. Joris M. Koene Faculty of Earth and Life Sciences Vrije Universiteit De Boelelaan 1085 1081 HV Amsterdam THE NETHERLANDS tel: +31 (0)20 5987095 fax: +31 (0)20 5987123 e-mail:joris.koene@falw.vu.nl URL: http://www.jkoene.dds.nl URL: http://www.bio.vu.nl/do/staff/JMKoene.htm joris.koene@falw.vu.nl joris.koene@falw.vu.nl

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Atlanta SystemsBiology Oct18-21

International Launch Conference: Frontiers in Multi-Scale Systems Biology

Introducing the New Integrative BioSystems Institute at Georgia Tech

Georgian Terrace Hotel, Atlanta, Georgia – USA October 18-21, 2008

With this conference, the Georgia Institute of Technology announces and celebrates the launch of its new Integrative BioSystems Institute. Frontiers in Multi-Scale Systems Biology will highlight representative topics of multi-scale systems biology including: genomics; proteomics; metabolomics; molecular inventories and databases; modeling and simulation; high-performance computing; enabling experimental and computational technologies; as well as applications in cancer, neuroscience and the environment.

Confirmed Speakers:

Leonard Anderson, Morehouse School of Medicine

David Bader, Georgia Institute of Technology

Kim Baldridge, UniversitÃt ZÃ¼rich, Switzerland

Gang Bao, Georgia Institute of Technology

Upinder Bhalla, Natâl Centre for Biol. Sciences, India

Charles Boone, University of Toronto

Richard Caprioli, Vanderbilt University

Jennifer van Eyk, Johns Hopkins University

Mark Hay, Georgia Institute of Technology

Sorin Istrail, Brown University

Minoru Kanehisa, Kyoto University, Japan

Peter Karp, SRI International

Jay Keasling, University of California at Berkeley

Douglas Lauffenburger, MIT

Richard E. Lenski, Michigan State University Frank LÃ, Georgia Institute of Technology

Victor de Lorenzo, Natâl Centre of Biotechnology, Spain

Maryann Martone, University of California San Diego

John McDonald, Georgia Institute of Technology

Alfred Merrill, Georgia Institute of Technology

Hirotada Mori, Keio University, Japan

Garry Nolan, Stanford University

Ajay Royyuru, Thomas J. Watson Research Center

Helena Santos, Universidade Nova de Lisboa, Portugal

Michael Savageau, University of California at Davis

Klaus Schulten, University of Illinois

Pamela Silver, Harvard Medical School

Jeffrey Skolnick, Georgia Institute of Technology

Masaru Tomita, Keio University, Japan

Elizabeth Wellington, University of Warwick, U.K.

Raimond Winslow, Johns Hopkins University

The conference will be held in the historic Georgian Terrace Hotel in Atlanta, GA. The conference banquet will be held in the Oceans Ballroom of the Georgia Aquarium, the largest aquarium in the world. During dinner, guest can view beluga whales and various fished through two large aquatic observation windows.

For more information and registration, please visit http://www.ibsi.gatech.edu/frontiers/ Contact: Ms. LaDawn Terry, Georgia Institute of Technology, 313 Ferst Drive, Atlanta, GA 30332-0535; contact@ibsi.gatech.edu

Jessica Gilmore <Jessica.Gilmore@biology.gatech.edu>

CardiffU ParasitesAndSelectionInFish Jul21-25

The Fisheries Society of the British Isles is holding its annual International Symposium at the University of Cardiff, Wales, UK from 21st to 25th July, 2008, entitled:

Parasites as Agents of Selection in Fish: from genes to ecosystems

Parasites are increasingly recognised by biologists as important mediators of ecological interactions and agents of natural and sexual selection in host populations. Fish serve as hosts to a wide range of 'conventional' parasitic organisms (i.e. agents of disease such as viruses, fungi, lice and worms), and have proven to be extremely good models for testing key hypotheses in lab and field research. Furthermore, investment in courtship and parental behaviour risks parasitism by conspecifics that engage in 'sneaky' mating tactics. There is currently considerable interest in the impacts of both 'conventional' heterospecific parasites, and conspecific 'cuckoos' on the fitness of host individuals and the consequences of parasitism for populations and communities. This meeting addresses some of the most relevant and pressing research themes in fish parasitology, behaviour and evolutionary ecology.

Themes include:

Parasites, genes and evolution.

Fitness consequences of infections.

Ecological implications of parasitism.

Host-parasite interactions in altered environments.

Invited speakers: Kevin Lafferty, Mathias Wegner, Steve Feist, Alexandra Grutter, Bernd Sures, Cameron Goater, David Marcogliese, Scott Monks, Martin Reichard, Joern Scharsack and Chris Williams

Conveners: Dr Iain Barber (University of Leicester) and Dr Jo Cable (University of Cardiff).

Early registration deadline: 30 April 2008.

For more information see:

http://www.fsbi.org.uk/2008/index.html Organisational contact: Tricia Ellis-Evans (tricia@paceprojects.co.uk)

Scientific content: Iain Barber (ib50@leicester.ac.uk)

andrew.maccoll@nottingham.ac.uk

CornellU Female mate choice symposium

The upcoming ISBE (International Society for Behavioral Ecology) meeting at Cornell provides an opportunity to organize symposia on the last day of the conference to discuss specific issues in behavioral and evolutionary ecology. I plan to submit a proposal for a symposium on variation in female choice and context-dependent female choice. The goal of this symposium is to highlight this issue to generate increased interest in this field and to bring together people who have interests in this topic. My hope is to generate discussion of this issue, establish which areas are in the greatest need of attention, and provide some direction for future research in this field. The format is not yet fixed, but will most likely be a mixture of contributed talks with significant time for discussion. Ideally talks will highlight new or important findings in this area (selection, choice, cognitive considerations, speciation), develop theory in this area, and/ or provide some perspective for the future. If you are planning to attend the ISBE meeting and would like to contribute to this symposium, please contact me as soon as possible for further information. I'd also like to gauge the level of interest in this topic, so if you would be interested in attending, but not necessarily presenting, I would also appreciate hearing from you.

Thank you,

Alexis Chaine

alexis.chaine@ecoex-moulis.cnrs.fr

Station d'Ecologie Expérimentale du CNRS (USR 2936) Laboratoire Evolution et Diversité Biologique

09200 Moulis

France

Alexis Chaine <alexis.chaine@EcoEx-Moulis.cnrs.fr>

Edinburgh ParasitoidEvolution Jun5-6

Second call for Behavioural Evolution of Parasitoids (BEPAR) workshop, June 5-6, Edinburgh, UK.

We are extremely pleased to make the second announcement of the forthcoming Behavioural Evolution of Parasitoids (BEPAR) workshop “Genetic and Genomic Approaches for Parasitoid Behavioural Evolution”, to be held at the University of Edinburgh, June 5-6 2008.

This ESF-supported workshop aims to bring together parasitoid researchers interested in the behaviour and evolution of parasitoid insects, to explore how new genetic and genomic techniques can inform and enhance our research. Whilst our focus through the invited speakers is on genetic approaches, we wish to encourage as broad a range of participants as possible, including those with little or no genetics background. This way we hope to facilitate interactions between parasitoid researchers using different techniques to answer similar questions, as well as highlight new questions that we need to address. As such, we particularly would like to encourage early-stage researchers to attend.

The invited speakers will cover topics spanning host-parasite interactions, life-history evolution, reproductive behaviour, sex allocation and social behaviour. Confirmed speakers include: Leo Beukeboom, Lex Kraaijeveld, Hans Smid, Amy Toth, Saskya van Nouhuys, Fabrice Vavre and Jack Werren. In addition to the invited speakers, we invite abstract submissions for both spoken and poster presentations.

The workshop has a fee of £120 that will cover accommodation, daytime meals and the workshop fee. There will also be a wine reception at the end of first day. Delegate number is limited to 80. Registration is via the dedicated workshop website, where further details of the locations and accommodation can also be found.

http://www.biology.ed.ac.uk/bepar2008/Home.html The closing date for registrations is May 2nd 2008.

We very much look forward to welcoming you to Edinburgh this June.

David Shuker and the workshop team.

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Bart Pannebakker Institute of Evolutionary Biology School of Biological Sciences University of Edinburgh West Mains Road Edinburgh EH9 3JT Scotland UK e-mail: Bart.Pannebakker(at)ed.ac.uk tel: +44 (0) 131 650 5553 fax: +44 (0) 131 650 6564 http://westgroup.biology.ed.ac.uk/BartP/BartP.html The University of Edinburgh is a charitable body, registered in Scotland, with registration number SC005336.

Bart.Pannebakker@ed.ac.uk
Bart.Pannebakker@ed.ac.uk

Ghent EuroEvoDevo Jul29-Aug1

Second Meeting of the European Society for Evolutionary Developmental Biology in Ghent, 29 July-1 August 2008

The April 15th deadline for registration and abstract submission for this meeting is drawing near.

We have an excellent programme of plenary talks and symposia planned (see below), together with sessions for contributed talks and posters. For further information visit the society website <http:// evodevo.eu/>

You are invited to submit an abstract for a contributed talk or poster. Registration and abstract submission can be achieved electronically via the society website <http:// evodevo.eu/>

Plenary Speakers: Walter Gehring (Basel, Switzerland) - The history of Hox Jane Langdale (Oxford, U.K.) - Evolution of meristems and leaves Angela Nieto (Alicante, Spain) - The Snail gene family in development and evolution Kevin Peterson (Dartmouth, USA) - Molecular palaeobiology Sabine Zachgo (KÃ, Germany) - The evolution of bilateral symmetry in flowers

Symposia and Minisymposia

Adaptive Developmental Plasticity

Organizer(s): Caspar J. Breuker (Oxford), Melanie Gibbs (Louvain-la-Neuve)

Mathieu DenoÃ«l - Costs and benefits of facultative paedomorphosis in newts and salamanders across varied environments Jacintha Ellers - Correlated evolution of phenotypic plasticity: A search for molecular mechanisms Olof Leimar - Adaptive developmental plasticity: the role played by environmental, genetic and maternal cues Mark van Kleunen - Constraints on the evolution of adaptive plasticity

Bioinformatics

Organizer(s): Didier Casane (Paris)

FrÃ©dÃ©ric Bastian and Marc Robinson-Rechavi - Bgee: Integrating homology and ontologies for Representing anatomy in ontologies - standardisation and the challenge of linking species-specific anatomy ontologies comparative Thorsten Henrich - 4DXpress: A platform for cross species expression pattern comparisons Michel Kerszberg and Jean-FranÃLe Garre - Modelling cellular processes to gain insight into developmental signalling FranÃMonÃ©ger - How to construct a virtual organ using MORPHEX tools David Osumi-Sutherland - t.b.a. Nadine PeyriÃ©ras - Embryomics: sequencing in space and time the cell lineage tree of Paracentrotus lividus, Phallusia mammillata and Danio rerio

Canalization, robustness and developmental stability

Organizer(s): Vincent Debat (MNHN Paris), Tom van Dooren (Leiden)

Christian Braendle and Marie-Anne FÃ©lix - Environmental and evolutionary variability of a robust developmental system: Caenorhabditis vulval cell fate patterning Vincent Debat and Tom Van Dooren - Robustness and evolutionary capacitance : on the drift between adaptation and constraint Han Mulder - Estimation and exploitation of genetic differences in environmental variance in animal breeding Rebecca Young - The ontogeny of fluctuating asymmetry in the foraging morphology of shrews

Development as bridge between micro- and macroevolution

Organizer(s): Jukka Jernvall (Helsinki)

Michael Coates - t.b.a. Anjali Goswami - Minding the Gap: Modularity as a link between ontogenetic interactions Johannes Jaeger - Shift Happens: Developmental and Evolutionary Dynamics Jukka Jernvall - A dental bridge between populations, species, and evolution

Evolution and development of segmentation

Organizer(s): Wim Damen (KÃ)

Michael Akam and Carlo Brena - t.b.a. Wallace Arthur - Evolution of segment number in centipedes: heritability, plasticity and speciation Guillaume Balavoine - Annelid segmentation Ariel Chipman - t.b.a. Evelyn Schwager - Differences in anterior and posterior segmentation in spiders

Evolution of axis formation and axial patterning in basal metazoans

Organizer(s): GÃ¼nter Plickert (KÃ), Yulia Kraus (Moscow)

Maja Adamska - Sponge embryos are patterned by a conserved suite of wnt, tgf-beta and hedgehog pathways Alexander Ereskovsky - Epithelial morphogenesis in sponges during sexual and asexual reproduction, growth and regeneration Thomas Holstein - Origin of the metazoan body plan Evelyn Houiliston and Tsuyoshi Momose - The role of localized maternal frizzle signals in axis formation and patterning in Clytia, a metagenetic hydroid Sally Leys - Evolution of germ layers GÃ¼nter Plickert - Lower metazoa and the evolution of axis formation Ulrich Technau - A genome perspective on the evolution of animal complexity

Evolution of head and brain (the arthropod head problem)

Organizer(s): Gregor Bucher (GÃ)

Gregor Bucher - Develomental genetics of the insect head. Graham Budd - The paleontological approach to the arthropod head problem. Wim Damen - Head development in spiders Andrew Economou - The insect intercalary segment: development and evolution Joakim Eriksson - Head development in spiders

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

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Grenoble ConservationGenetics Oct20-23

"Landscape Genetics"

We announce a workshop in LANDSCAPE GENETICS that will address conservation genetic issues in natural populations within a landscape context. The main goal of the workshop is to bring together young researchers working in the field of conservation genetics with landscape ecologists and spatial statisticians to discuss new technologies and statistical methods.

The following major topics will be addressed by keynote speakers (Sam Cushman, Bryan K Epperson, Marie-Josée Fortin, Olivier Francois, Olivier Hardy, Rolf Holderegger, Pierre Taberlet, Lisette Waits, Wilfried Thuiller)

- Using Landscape genetic to assess the impact of landscape fragmentation on genetic diversity and genetic connectivity - Using genome scan and landscape genetics to assess genetic basis of local adaptation

The workshop will be held close to Grenoble, France (http://www.st-hugues-de-biviers.org/entreprises/-

entreprises.htm) from the 20-23.10.2008 (arrival Monday 20.10., departure Thursday 23.10.)

We here Call for Applications:

Please provide a title and an abstract of at most one page and add also a short list of your three most relevant publications.

Note that the workshop is limited to 20 participants, and a final selection will be done at the beginning of May.

Grant applications will be chosen based on scientific quality, and priority will be given to applicants who come from countries supporting the ESF programme (Austria, Belgium, Croatia, Czech Republic, Denmark, Finland, France, Hungary, Netherlands, Norway, Spain, Sweden, Turkey).

Funding will cover all local costs (accommodation, meals) and part of the travel costs.

Deadline for registration is April 30th 2008.

Send applications by e-mail to:

Dr. Gernot Segelbacher

gernot.segelbacher@wildlife.uni-freiburg.de <mailto:gernot.segelbacher@wildlife.uni-freiburg.de>

Organizers:

Gernot Segelbacher Stéphanie Manel

Dept. Wildlife Ecology Laboratoire d'Ecologie Alpine, University of Freiburg University Grenoble

–

Dr. Gernot Segelbacher

MPI Ornithology Vogelwarte Radolfzell Schlossallee 2 D-78315 Radolfzell

segelbac@orn.mpg.de

http://www.orn.mpg.de Please consider your environmental responsibility before printing this email

Gernot Segelbacher <segelbac@orn.mpg.de>

Halifax EvolutionaryProtistology Jul21-26 deadlines

Dear EvolDir.

The 17th meeting of the International Society for Evolutionary Protistology (ISEP) is taking place in Halifax, Nova Scotia, 21-26th July. This is a co-meeting with ISOP, with the whole meeting called PROTIST2008.

Registration at 'early' rates, and Abstract Submissions are due by MAY 15. This is a little over three weeks away.

For Registration, and more details on the conference, please visit the meeting website at: https://protist2008.dal.ca/ Alastair G.B. Simpson, PhD Assistant Professor, Department of Biology, Dalhousie University Canadian Institute for Advanced Research

Phone: 902 494 1247 (Country code 1) Fax: 902 494 3736 (Country code 1) Email: alastair.simpson@dal.ca Lab website: http://myweb.dal.ca/asimpso2/home Mail address: Department of Biology Life Sciences Centre, 1355 Oxford St, Halifax, Nova Scotia, B3H 4J1, Canada

UPCOMING PROTISTOLOGY MEETING! PROTIST 2008 - A joint meeting of ISEP and ISOP 21-26 July, 2008, at Dalhousie University Visit https://protist2008.dal.ca/ for details.

Alastair Simpson <Alastair.Simpson@Dal.Ca>

IrvineCA MEEGID IX Oct30-Nov1 Registration

17/04/08

Dear Colleague,

registrations are opened for the 9th International Congress "Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases" (MEEGID IX), to be held at University of California, Irvine, 30th October-1st November 2008. For registration instructions, go to: http://www.th.ird.fr//site_meegid/doc/Registration.pdf. General information on MEEGID IX at: http://www.th.ird.fr//site_meegid/menu.htm See you soon in Irvine!

Michel Tibayrenc, MD, PhD Editor -in-chief Infection, Genetics and Evolution (Elsevier) http://www.elsevier.com/locate/meegid IRD representative in Thailand IRD Representative Office French Embassy 29, South Sathorn Road, Bangkok 10120, Thailand Tel : + (66 2) 627 2190 Fax : + (66 2) 627 2194 Cel: + (66 81) 82 64 056 E-mail : Michel.Tibayrenc@ird.fr Website : http://www.th.ird.fr Michel.Tibayrenc@ird.fr

Irvine Evolution May25

Western Evolutionary Biologists Meeting – Irvine, CA May 25

The Network for Experimental Research on Evolution (NERE) invites evolutionists to attend the 2^nd annual Western Evolutionary Biologists Conference on May 25, 2008.

Registration is free, but mandatory. Registration deadline is May 1. Abstract deadline for talks and posters is May 1.

For more information and registration visit the web-2008 website at: http://www.lifesci.ucsb.edu/web-2008/ NERE will cover transportation to the meeting for NERE members. We encourage graduate students and postdocs to attend. Evolutionists in the University of California System should contact their local Associate Director (see website for more information) to arrange transportation.

At the meeting, NERE will present the 2008 WEBY Award (Western Evolutionary Biologist of the Year), and the winner will present an address (for details on nomination, see NERE website). The 2007 WEBY winner was Al Bennett.

About NERE: See also: http://nere.bio.uci.edu/ NERE, the Network for Experimental Research on Evolution, is a University of California Multicampus Research Program funded and administered through the UC Office of the President and its constituent UC campuses. NERE (pronounced "near") supports collaboration, communication, and graduate education concerned with research on biological evolution. NERE serves as a conduit for interactions between evolutionists within the University of California system and between University of California scientists and the global scientific community.

– Todd Oakley Associate Professor Ecology Evolution and Marine Biology University of California-Santa Barbara Santa Barbara, CA 93106

ph 805-893-4715 http://www.lifesci.ucsb.edu/-eemb/labs/oakley oakley@lifesci.ucsb.edu oakley@lifesci.ucsb.edu

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Manchester EuropeanCommunityGenetics Sep9-10

European Community Genetics workshop 9-10th September 2008, Manchester, UK.

We are organising a two day workshop on Community Genetics supported by The Genetics Society for European researchers to be held at the University of Manchester 9-10th September 2008. The aim of the workshop is to bring together ecologists and evolutionary biologists from Europe to discuss current and future research in the emerging field of Community Genetics. The meeting will be a mixture of invited talks and discussions. The following speakers are confirmed:

Prof. J. Antonovics (The University of Virginia) Prof. A. Gatehouse (Newcastle University) Prof. P. Grime (The University of Sheffield) Dr. G. Iason (The Macaulay Institute) S. Zytynska (The University of Manchester) Dr. J. Ferrari (The University of Oxford) Dr. R. Preziosi (The University of Manchester) Dr. D. Shuker (The University of Edinburgh) Dr. F. Vavre (Université de Lyon) Dr. J. Wolf (The University of Manchester)

If you are interested in attending or would like further information please contact Jennifer Rowntree via email at jennifer.rowntree@manchester.ac.uk

We look forward to hearing from you.

Jennifer Rowntree, Richard Preziosi (University of Manchester), Dave Shuker (University of Edinburgh)

Dr Jennifer Rowntree Preziosi Lab Faculty of Life Sciences University of Manchester Smith Building Oxford Road Manchester M13 9PT

jennifer.rowntree@manchester.ac.uk http://www.preziosilab.org http://-personalpages.manchester.ac.uk/staff/-Richard.Preziosi/jennyindex.html jennifer.rowntree@manchester.ac.uk

MNHN Luxembourg BiodiversityHotspots Mar26-28

International Symposium "Biodiversity Hotspots" March 26-28 2009, MNHN Luxembourg

Dear Sir or Madam, Dear friends of biodiversity research,

in October 2007 we held a very fruitful conference about relict species and/or populations. After this meeting about species survival in restricted regions, we want to invite you for a new symposium about "biodiversity hotspots" (in March 26-28 2009). We will discuss about the evolution, status and conservation of areas with exceptional high species/genetic richness.

All details are given on our symposium-website

www.symposium.lu/hotspots/ We are looking foreward to see you in March 2009!

Sincerely, Jan Habel

– Dr. Jan Christian Habel Musée national d'histoire naturelle Luxembourg 25, rue Münster L-2160 Luxembourg

Tel: ++49 (0)651 2068737

Jan Christian Habel <janchristianhabel@gmx.de>

NHM London MolluscSpeciation Apr25

Advance announcement

A ONE DAY SYMPOSIUM "SPECIATION IN MOLLUSCS"

Friday, 25th April 2008, starting 10.30 am

Venue: The Flett Theatre, Natural History Museum, London, UK (closest entrance on Exhibition Rd)

The Malacological Society of London announces a one day symposium ÂÂSpeciation in MolluscsÂÂ to coincide with the Annual General Meeting of the Society. Talks will be given by invited speakers at the forefront of this field. This meeting will be of interest to evolutionary biologists, biogeographers, students, postdoctoral researchers and researchers.

Provisional Timetable 1030-1040 - Introduction and welcome (Georges Dussart, President Malacological Society, London) 1040-1120 - Menno Schilthuizen (Evolution on a block of rock; snail speciation on tropical limestone karst) 1120-1200 - Ellinor Michel ÂÂ©(Gastropod endemism in African freshwaters: traits, time and topography) 1200-1320 - lunch and AGM meeting 1320-1400 - Jon Todd (Patterns from the fourth dimension of a marine snail radiation) 1400-1440 - Chris Meyer (Dispersal and speciation in a big pond) 1440-1500 - Coffee break & poster session 1500-1540 - Angus Davison (Speciation and gene flow between Japanese snails of contrasting ecology and opposite chirality) 1540-1620 - Emilio Rolan (Ecological speciation of Littorina saxatilis in Galicia) 1620-1750 - Wine reception & poster session

Places are limited, and registration is required. Registration is FREE and includes a wine reception to follow the meeting. Please let us know if you wish to bring a poster, and provide an abstract. Send applications by e-mail to Suzanne Williams (S.Williams@nhm.ac.uk).

The full programme, including abstracts, is attached.

Dr Suzanne Williams Zoology Dept Natural History Museum Cromwell Rd London SW7 5BD United Kingdom Tel: + 44 (0) 207 942 5351 (office) 5774 (lab) Fax: +44 (0) 207 942 5867

http://www.nhm.ac.uk//research-curation/staff-directory/zoology/cv-5597.html Suzanne Williams <s.williams@nhm.ac.uk>

NorthCarolinaStateU BehaviourEvolution Jun4-7

2008 Annual Meeting, American Genetic Association, June 4-7. "Genetics and Genomics of Behavior." Key Lecturer: Mariana Wolfner.

This year's AGA conference will explore current status and future trends in the genetic architecture of behavior, neurogenetic mechanisms of behavior, and evolution of behavior. In addition to a stellar group of invited speakers, there will be an opportunity for platform presentations from participants who submit abstracts.

Competitive scholarships for travel and registration will be available for students and postdoctoral fellows.

Details and registration at www.agasymposium2008.org agajoh@oregonstate.edu agajoh@oregonstate.edu

Paris Zoology Aug26-29

.., we believe that evolutionary biologists can also be interested because we intend to cover verious time and space scales, include the evolutionary scale.

Thank you.

Roger Arditi

The 20th International Congress of Zoology (< http://icz2008.snv.jussieu.fr/ >) will take place in Paris from 26th to 29th August. During this meeting, we organize a symposium in entitled "Interdisciplinary approaches in ecology: from individuals to populations and communities". We greatly encourage ecological and evolutionary zoologists to apply for a presentation (either as an oral communication or as a poster).

Selection of speakers will be based mainly on adequacy to the general theme of the symposium. Therefore, interdisciplinary work as well as approaches dealing with multiscale issues (either temporal or spatial scales, both ecological and evolutionary) will be greatly appreciated.

Please send an abstract before 31st May 2008 to

Nicolas Loeuille (<mailto:nicolas.loeuille@gmail.com>)

The organizers of Symposium S18: Roger Arditi, Jorge Cancela da Fonseca, Nicolas Loeuille

Pr. Roger Arditi <roger.arditi@agroparistech.fr> Ecologie des populations et communautés (USC2031, INRA) Fonctionnement et évolution des systèmes écologiques (UMR7625, CNRS) Université Pierre et Marie Curie (Paris 6), 7 quai Saint Bernard Bât. A, 7ème étage, case 237, 75252 Paris cedex 05, France Tel. +33 1 44 27 26 31. Fax +33 1 44 27 35 16 http://ecologie.snv.jussieu.fr/ Roger Arditi <roger.arditi@agroparistech.fr>

Portugal BarnacleEvolution Sept25-27

Dear all,

I am pleased to announce the Pollicipes International Conference, to be held at Sines Art Center, Portugal, from 25 to 27th September 2008.

Pollicipes species are stalked barnacles that inhabit marine rocky shores and are a very important economical resource intensively exploited in some countries, namely in Portugal and Spain.

This will be a multidisciplinary conference about Pollicipes. Studies from different areas of knowledge are welcome - biology and ecology, evolution, population genetics, morphology, physiology, fishery and management, anthropology, etc.

More information available at www.pollicipes.uevora.pt Please disseminate this notice as widely as possible.

Hoping to see you in Sines,

João Castro

University of Evora Portugal

joananfernandes@gmail.com

Raleigh NC BehaviorGenomics Jun4-7

2008 Annual Meeting, American Genetic Association, June 4-7. "Genetics and Genomics of Behavior." Key Lecturer: Mariana Wolfner.

This year's AGA conference will explore current status and future trends in the genetic architecture of behavior, neurogenetic mechanisms of behavior, and evolution of behavior. In addition to a stellar group of invited speakers, there will be an opportunity for platform presentations from participants who submit abstracts.

Competitive scholarships for travel and registration will be available for students and postdoctoral fellows.

Details and registration at www.agasymposium2008.org agajoh@oregonstate.edu agajoh@oregonstate.edu

RockefellerU Evolution May1-2

On May 1 & 2 we will be having a symposium on evolution here at the Rockefeller University. The symposium will feature 18 speakers from around the world including Jerry Coyne, Ford Doolittle and Svante Paabo.

Arianne Dowdell-Marshall Director of Special Events Rockefeller University 1230 York Ave New York, NY 10065 p: 212-327-8073 f: 212-327-7876

Arianne Dowdell-Marshall <adowdell@mail.rockefeller.edu>

Roscoff France Endosymbioses Oct20-23

Bonjour ! Voici l'annonce d'une école thématique CNRS :

Les endosymbioses trophiques et leur rôle dans l'évolution passée et contemporaine des Eucaryotes

Trophic endosymbioses and their role in past and present Eukaryote evolution

20-23 Octobre 2008, Station Biologique de Roscoff

Site web : http://www.sb-roscoff.fr/ETSymbioses2008/ Je joins l'affiche et le programme prévisionnel - merci de votre attention ! Marc-André

Marc-André SELOSSE

Professeur, Université Montpellier II Centre d'Ecologie Fonctionnelle et Evolutive CNRS, UMR 5175, Equipe Interactions Biotiques 1919 Route de Mende, 34 293 Montpellier cedex 5, France Tel. 33(0)4 67 61 32 31; Fax 33(0)4 67 41 21 38 Tel. mobile 33(0)607 1234 18

Editeur du New Phytologist (http://www.newphytologist.org/) Editeur associé de Symbiosis (http://people.bu.edu/iss/ Symbiojournal.html).

Publications : www.cefe.cnrs.fr/coev/MA_Selosse.htm ma.selosse@wanadoo.fr

StonyBrookU Darwin2009Celebration Nov5-9

Darwin 2009 Celebration at Stony Brook University and AMNH Stony Brook University is pleased to announce a special outreach and scholarly event to celebrate the 150th anniversary of the publication of Charles Darwin's Origin of Species in 1859. The meeting will take place 5-9 November 2009. The scholarly meeting will feature more than twenty invited speakers from a wide range of disciplines in evolutionary biology and allied fields, with a structure that will facilitate the open discussion of scientific and intellectual issues surrounding evolution. The outreach events are being organized in collaboration with the American Museum of Natural History and will include public lectures as well as teachers' workshops. Registration will open soon. Visit our web site at http://darwin09.org to learn more about these events, with contact information and further details about the meeting.

– Jeffrey Levinton Distinguished Professor Department of Ecology and Evolution Stony Brook University Stony Brook NY 11794-5245

tel (631) 632 8602 fax (631) 632 7626 Marine Biology Web Page http://life.bio.sunysb.edu/marinebio/mbweb.html Research Web Site http://life.bio.sunysb.edu/marinebio/levinton.main.html Jeffrey Levinton <jeffreylevinton@gmail.com>

UIowa Evolution of Sex Jun16-19 Update

Final UPDATE:

1. General registration is still open. Space remains available for poster presenters and attendees, but it is limited. Please register as soon as possible at:

http://ccg.biology.uiowa.edu/sexrec/regform2.php 2. Information on Venue, Travel and Accommodation is available at:

http://ccg.biology.uiowa.edu/sexrec/venue.php 3. The final schedule of 45 talks is available at:

http://ccg.biology.uiowa.edu/sexrec/SexRecSchedule.pdf 4. A list of confirmed attendees is available at:

http://ccg.biology.uiowa.edu/sexrec/attendees.php ______ General Announcement:

³EVOLUTION OF SEX & RECOMBINATION: IN THEORY AND IN PRACTICE²

June 16-19, 2008, at the University of Iowa, Iowa City, USA.

http://ccg.biology.uiowa.edu/sexrec The Roy J.

Carver Center for Comparative Genomics and the Department of Biology at the University of Iowa will host an international conference on the evolution of sex & recombination. This conference will immediately precede the 2008 Evolution meeting taking place in nearby Minneapolis, Minnesota (June 20-24).

Talks will be given by invited speakers at both the junior and senior level. Contributed talks and posters will be given by conference attendees at all levels of seniority.

Topics include: -Advantages of sexual reproduction -Experimental evolution of sex -Estimating recombination rates -Mating types & sex determination -Linkage, selection & population size -Sex chromosomes -Sex & pathogenesis -Sexual selection -Sexual conflict

Confirmed invited speakers: Aneil Agrawal University of Toronto Philip Awadalla University of Montreal Doris Bachtrog University of California, San Diego Graham Bell McGill University Bill Birky University of Arizona Rhona Borts University of Leicester Christina Burch University of North Carolina-Chapel Hill Bernardo Carvalho Universidade Federal do Rio de Janeiro Brian Charlesworth University of Edinburgh Nick Colegrave University of Edinburgh Tim Cooper University of Houston Ursula Goodenough Washington University-St. Louis Joe Heitman Duke University Michael Hood Amherst College Alex Kondrashov University of Michigan Curt Lively Indiana University Michael Lynch Indiana University David Mark Welch MBL, Woods Hole Stephanie Meirmans University of Bergen Andy Peters University of Wisconsin-Madison Steve Proulx Iowa State University Bill Rice University of California, Santa Barbara Isa Schön Royal Belgian Institute of N.S. Marcy Uyenoyama Duke University Jerry Wilkinson University of Maryland Cliff Zeyl Wake Forest University

An additional 19 contributed talks have also been selected from among faculty, post-doc and graduate student applicants.

A symposium issue to be published in Journal of Heredity is being planned and all presenters will have the opportunity to contribute a paper to the issue.

Enquiries are encouraged (including potential sponsors) and should be directed to the organizers: sexrec@uiowa.edu

On behalf of the organizing committee, thanks.

We hope to see you in Iowa City in June!

John Logsdon –

John M. Logsdon, Jr., Ph.D. Associate Professor Director, Roy J. Carver Center for Comparative Genomics University of Iowa Department of Biology 319 335 1082 office 310 Biology Building 319 335 1083 lab Iowa City, IA 52242-1324 319 335 1069 FAX

email <john-logsdon@uiowa.edu> web < http://ccg.biology.uiowa.edu > < http://euplotes.biology.uiowa.edu >

UMinnesota Evolution 2008 Jun20-24 deadline3

The deadline for submission of Evolution 2008 presentation titles has been extended to April 10, 2008.

Please visit http://www.evolution2008.org for more information.

This is the annual meeting of the Society for the Study of Evolution, the Society of Systematic Biologists, and the American Society of Naturalists.

Participant registration should be completed by May 1, 2008 to qualify for discounted rates.

We look forward to welcoming you to Evolution 2008 and are eager to answer your questions to make your participation a productive and memorable experience. Questions may be directed to Heather Dorr (cceconf3@umn.edu <mailto:cceconf3@umn.edu).

On behalf of the societies, the organizing committees, and the University of Minnesota, thank you for your participation.

George Weiblen Evolution 2008 Program Coordinator Associate Professor, Department of Plant Biology Herbarium Curator, Bell Museum of Natural History

George Weiblen <gweiblen@umn.edu>

Uppsala QTL-MAS May15-16

QTL-MAS conference/workshop focusing on fine mapping, genome-wide association studies and genomic selection. To be held in Uppsala, Sweden on 15th-16th May.

Dear All,

Due to the large number of applicants, there is now only a very limited number of places available at QTL-MAS XII for people not presenting an analysis of the data set. Registration will close on Friday April 25th. Those analysing the data set will still be able to register but also must do so by 25th April.

Best wishes

Lucy Crooks, organising committee QTL-MAS XII.

Lucy Crooks <qtlmas12@computationalgenetics.se>

URennes AdaptiveDynamics Jun4-6

Workshop Adaptive Dynamics of Parasitoids

Invitation for contributed speakers

Where : Biological Staion at Paimpont When : 4-6 juin 2008 Organised by :

Jacques van Alphen and Joan van Baaren (UMR CNRS 6553 ECOBIO), Université de Rennes 1, as part of the project COMPAREVOL (http://comparevol.univ-rennes1.fr/) Funded by : BEPAR (ESF), Université de Rennes 1, Agrocampus Rennes, CNRS, Rennes métropole

Description of the workshop: The workshop is an initiative of the ESF Network BEPAR (http://bepar.sophia.inra.fr/). The workshop will bring together leading scientists in the field of adaptive dynamics with experts on parasitoid behavioural ecology, in the aim to advance our understanding of the evolution of parasitoid diversity by adaptive speciation by host and habitat shifts. It second aim is to study how behvavioural ecological theory can be merged with adaptive dynamics to study host shifts in parasitoids in adaptive dynamics models rich in behavioural details. (i) scientific summary Much of the theory developed for understanding and predicting the evolution of behavioural and life-history traits of parasitoids is based on simplified optimization approaches, which are applicable only if selection is frequency-independent. In contrast, empirical ecological research reveals the ubiquity of frequency-dependent selection pressures on almost all lifehistory traits of interest. Such frequency dependence occurs whenever selection depends on the phenotypic composition of a population, which is the rule in natural systems Even, when frequency dependent selection is taken into account for by using a game theoretical approach, the environment is generally considered to be static. Adaptive dynamics theory can resolve this mismatch between theory and the real world. Adaptive dynamics is a recent body of theory, which is quite successful in modelling evolutionary processes that are difficult to analyze with classical game theoretical models or population genetic models. The method takes into account that an evolutionary change in an organism causes also a change in the way the organism experiences its environment. This allows an evolving population to escape from a fitness valley and reach a new fitness maximum. The method is particularly successful in explaining evolutionary branching and hence in modelling speciation events. Hymenopteran insect parasitoids are disputably the second most species-rich group of insects after the coleopterans, with an estimated number of species well in excess of 200,000. The presence of species rich genera with sympatric species specialized in exploiting different but related host species, host plants or different habitats, suggest that ecological speciation by host or habitat shifts plays an important role in evolutionary radiation and speciation of parasitoids. A key to understanding host and habitat shifts in parasitoids is the foraging behaviour of female parasitoids. Parasitoid foraging behaviour is under strong natural selection because each step in a sequence of behavioural decisions has consequences for the number of offspring produced during adult lifespan. Parasitoids must first find the habitat of its host, often by attraction to olfactory cues, next they must search the host habitat to find a host. After encountering a host the parasitoid must decide if she accepts or rejects the host, and if a host is accepted how many eggs should be laid and which sex the offspring should have. Finally, parasitoids must decide how long to continue searching in a particular host habitat. A rich literature of deductive behavioural ecological models predicts the optimal decisions for each of these steps in a particular environment and there is ample empirical evidence showing that parasitoid foraging behaviour is often close to the predicted optimum for that environment. Moreover, comparative studies based on independent contrasts between phylogenetically close species have provided further evidence that parasitoid foraging behaviour is adaptive. Behavioural ecological evidence, thus, suggests that a parasitoid female choosing a different habitat to search for hosts, or accepting a new host species, would have a high probability decreasing her fitness and hence that host and habitat shifts would be difficult. In contrast, adaptive dynamics theory shows how selection originating from local ecological interactions may drive surprisingly rapid adaptive radiations. However, adaptive dynamics models so far lack the behavioural details of interest to behavioural ecologists. The evolutionary dynamics of parasitoid biodiversity, in particular ecological speciation by host or habitat shifts has so far received little attention. By combining the expertise of parasitoid behavioural ecologists with that of adaptive dynamics theorists, the

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UToronto PlantGenomics Jun23-26

6th Canadian Plant Genomics Workshop Monday 23rd - Thursday 26th June, 2008 Toronto, Ontario, Canada

The 6th Canadian Plant Genomics Workshop will bring together Canadian researchers and internationally-renowned scientists to explore recent advances in genomics research and how these advances are being integrated within the plant sciences. The workshop will examine the latest developments in genomics; insights into the processes and pathways that control plant development, metabolism, or interactions with the environment and other organisms; and new opportunities for biotechnology and biofuels.

The deadline for submitting an abstract and for early-bird registration for the 6th Canadian Plant Genomics Workshop is fast approaching: April 18th.

Please consider submitting an abstract as we would like to have a large pool of high-quality abstracts from which to choose oral presentations for the workshop. Registration and abstract submission may be made on the CPGW2008 conference website at http://cpgw2008.cagef.utoronto.ca/ . Program - Confirmed Plenary Speakers

Philip Benfey (Dept. of Biology, Systems Biology Group, Duke) Justin Borevitz (Dept. of Ecology and Evolution, Chicago) Clint Chapple (Dept. of Biochemistry, Purdue) Xuemei Chen (Dept. of Botany and Plant Sciences, UC Riverside) Sean Cutler (Center for Plant Cell Biology, UC Riverside) S. Dinesh Kumar (Molecular, Cellular & Developmental Biology, Yale) Sheng Yang He (MSU-DOE Plant Research Laboratory) Tim Hughes (Centre for Cellular and Biomolecular Research, U. Toronto) Ralph Quatrano (Dept. of Biology, WUSTL) Doris Wagner (Dept. of Biology, University of Pennsylvania)

On behalf of the National and Local Organizing Committees, I look forward to seeing you in Toronto.

Please forward this email to colleagues who may be interested in attending and/or post the attached flyer in your institute.

Thank you,

Nick Provart (CPGW2008 conference chair)

Nicholas Provart, PhD Assistant Professor, Plant Cyberinfrastructure & Systems Biology Director, Graduate Program in Genome Biology and Bioinformatics Member, Centre for the Analysis of Genome Evolution and Function Rm 3051, Dept. of Cell and Systems Biology, Uni. Toronto 25 Willcocks St., Toronto, ON. M5S 3B2. CANADA

Tel. (+1) (416) 978-7141, Fax. (+1) (416) 978-5878 URL. http://www.csb.utoronto.ca/faculty/provart/ Arabidopsis Tools. http://www.bar.utoronto.ca email. nicholas.provart@utoronto.ca TTC. Spadina LRT, Willcocks St

Nicholas Provart <nicholas.provart@utoronto.ca>

WinchesterUK ALifeXI Aug5-8

Artificial Life XI

The Eleventh International Conference on the Simulation and Synthesis of Living Systems 5th - 8th August 2008, Winchester, UK www.alifexi.org IMPORTANT DATES

- 25 April 2008: Abstract submission deadline - 9 May 2008: Camera ready deadline - 5-8 August 2008: Conference dates

CALL FOR SUBMISSIONS

The deadline for abstract submissions to ALIFE XI is approaching.

Abstracts are limited to 500 words reporting a mature piece of work with relevance to artificial life. Every submission will be subject to full peer review and all accepted submissions will be allocated an oral presentation slot and published by MIT Press in a single online open-access proceedings volume (the first of its kind). The best 15-20 submissions will have the opportunity to be reworked for publication in special issues of the MIT Press journal Artificial Life.

Please note that: we are interested in abstract submissions from across the entire remit of artificial life, including relevant research in physics, chemistry, biology, economics, social science, and philosophy. If your research addresses problems such as adaptive, autonomous or collective behaviour, self-organisation, coevolution, metabolism, or development in natural or engineered systems, then please consider attending the conference, which is shaping up to be a very exciting meeting. Our keynote speakers represent some of the most exciting topics in science today, and we are committed to making the meeting accessible to as many interested researchers as possible, whatever their home discipline and financial or geographic situation.

OVERVIEW

Artificial life investigates the fundamental properties of living systems through simulating and synthesizing biological entities and processes in artificial media. Summer 2008 will see the international ALife conference hosted by the University of Southampton, UK, bringing the meeting to Europe for the first time in its 21-year history. Over the last two decades, some of the highly speculative ideas that were discussed at the field's inception have matured to the extent that new conferences and journals devoted to them are being established: synthesising artificial cells, simulating biological networks, exploiting biological substrates for computation and control, and deploying bio-inspired engineering are all now cutting-edge practice.

The ALIFE XI conference provides an opportunity for those working across these topics to get together and exchange ideas and results. To this end, the conference will present a selection of the best current work in the field, highlight new directions for investigation, and present high-profile keynote speakers.

Papers are welcome in all areas of the field, including: . Synthesis and origin of life, self-organization, self-replication, artificial chemistries . Evolution and adaptation, evolutionary dynamics, evolutionary games . Coevolution, major evolutionary transitions, levels of selection, ecosystems . Development, differentiation, and regulation; generative representations . Synthetic biology . Self-organizing technology, self-* computing and computational ecosystems . Unconventional and biologically inspired computing . Bio-inspired robots and embodied cognition, autonomous agents, evolutionary robotics . Collective behaviour, communication, cooperation . Artificial consciousness; the relationship between life and mind . Philosophical, ethical, and cultural implications . Mathematical and philosophical foundations of ALife, new and creative syntheses

Several artificial life "themes" have been proposed as live research topics around which conference sessions may organise. See www.alifexi.org/themes for full details.

LOCATION

The conference will be held in Winchester, a beautiful historic city in southern England known for its 11th-century cathedral and 12th-century castle. Winchester is set in forested countryside about an hour south-west of London and Heathrow airport, and a few miles from the host institution, the University of Southampton.

IMPORTANT DATES

- 25 April 2008: Abstract submission deadline - 9 May 2008: Camera ready deadline - 5-8 August 2008: Conference dates

ORGANIZATION

Seth Bullock (chair), Jason Noble, Richard Watson, Mark Bedau

HOST INSTITUTION

School of Electronics and Computer Science, University of Southampton, UK

CONTACT

For further information about the conference program, travel, accommodation, and local arrangements, please see www.alifexi.org. For questions about the submission and reviewing process, please email submissions@alifexi.org. For all other questions, contact questions@alifexi.org.

– Seth Bullock Science & Engineering of Natural Systems School of Electronics and Computer Science University of Southampton, SO17 1BJ

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YaleU Evolution in Health Apr17

The second of two Yale Symposia on Evolution in Health and Disease will take place April 17th at the Yale School of Medicine, New Haven, Connecticut.

Admission is free. No registration is required. A reception will be held in the Medical History Library following the Symposium courtesy of the Department of Obstetrics and Gynecology.

Please call this opportunity to the attention of faculty, postdoctoral fellows, graduate students, and advanced undergraduates by forwarding this email to them.

You can get details on the program at the symposium web site:

http://www.yale.edu/evomedsymposia For the organizing committee,

Stephen C. Stearns Edward P. Bass Professor of Ecology and Evolutionary Biology

Other members of the organizing committee:

Durland Fish, Professor of Epidemiology and Public Health Charles Lockwood, Professor of Obstetrics, Gynecology, and Reproductive Sciences Stephen Malawista, Professor of Medicine Paul Turner, Associate Professor of Ecology and Evolutionary Biology

Stephen Stearns <stephen.stearns@yale.edu>

GradStudentPositions

BangorU MolEvol

There are currently opportunities for NERC-funded postgraduate studentship programs within the Molecular Ecology and Fisheries Genetics Laboratory, Bangor University (MEFGL http://biology.bangor.ac.uk/research/mefgl/) in the following areas:

Using 454 mitogenomics to elucidate a higher level spider phylogeny - Dr S Creer in collaboration with Dr. Sara Goodacre (Nottingham University), Prof. Greg Hurst (University of Liverpool), Dr. Miquel Arnedo (Universitat de Barcelona) and Dr. Susan Masta (Portland State University).

Life history correlates of personality traits and their plasticity across multiple environmental conditions - Dr D Croft

The Molecular Ecology and Fisheries Genetics Laboratory (MEFGL) is a leading research division within the School of Biological Sciences' (SBS) Molecular Ecology and Evolution Group, one of the largest research areas within the University. A central part of our work is the application of molecular markers such as microsatellites, AFLPs, single nucleotide polymorphisms (SNPs) and sequence data (454 and Sanger) to fundamental evolutionary and ecological questions relating to the origins, levels, distribution and ecological significance of genetic variation in wild populations.

The MEFGL, together with other members of the Molecular Ecology & Evolution Group, has recently moved into the purpose-built research suite embedded within the newly built £8 million Environment Centre for Wales (ECW). The new facility provides open-plan office space for up to 28 postgraduate and postdoctoral researchers, alongside dedicated PCR, sequencing, bioinformatic, and main laboratory facilities.

Eligibility - Eligibility is restricted to European Union (EU) nationals only. UK citizen candidates must have, or expect to receive a 2.1 degree or higher, or a 2.2 degree with a masters qualification. Non-UK EU nationals who have spent the previous three years in the UK undergoing education (undergraduate study or masters) are also eligible to apply. For further guidance, please consult the NERC website.

Closing date is soon: 21st April 2008

Application forms and further information from: Mrs. Karen Goodwin, School of Biological Sciences, Bangor University, Gwynedd LL57 2UW, UK.

Tel: 01248 382430 Fax: 01248 370731

email: studentship.enquiries@sbs.bangor.ac.uk

– Si Creer Post Doctoral Research Fellow Molecular Ecology and Fisheries Genetics Group School of Biological Sciences University Wales, Bangor Bangor Gwynedd LL57 2UW UK

e-mail: s.creer@bangor.ac.uk Tel: +1248 382302 Fax: +1248 371644 Home Page: http://biology.bangor.ac.uk/ ˜ bssa0d/ “S.Creer” <bssa0d@bangor.ac.uk>

BrockU MolEvolution GeneticInfoSystems

Graduate student position in molecular evolution of genetic information systems

Genetic information is stored in the cell in the form of DNA, which the cell cannot access directly. Instead, DNA information undergoes extensive, multistep processing before it can be acted upon to direct cellular functions. One of these processes, alternative mRNA splicing, not only transmits genetic information but also enhances it by generating multiple alternative genetic messages from the same gene. The cell expands considerable amount of resources to generate these alternative messages and while some are essential for the proper functioning and development of the cell, the significance of others is subject of great debate since their function in the cell is unclear. Are they errors tolerated by the cell or do they represent an as yet unknown type of genetic information or a novel regulatory process?

Graduate student positions are available, either MSc or PhD, to evaluate the significance of alternative messages by comparing their production in a variety of animals including primates, other mammals, birds, fish, and amphibians. Our guiding principle is that if alternative messages are functionally important then we will be able to trace their evolutionary development and uncover evidence of their role in the various animals we will investigate.

Student financial support is available for Canadian citizens and landed immigrants.

For additional information, please contact:

Dr. Adonis Skandalis Dept. Biological Sciences Brock University St. Catharines, Ont. L2S 3A1 adonis.skandalis@brocku.ca

Miriam Richards <miriam@brocku.ca>

DalhousieU FishComparativePhylogeography

PhD position in Comparative Phylogeography/Conservation Genetics of Patagonian or northern fishes

Support for a PhD position is expected to become available at Dalhousie University (Halifax, Nova Scotia, Canada) for research in comparative phylogeography and conservation genetics of fish in Patagonia or in the north. The student will develop a research project that uses molecular genetic and phenotypic approaches to examine issues in phylogeography, adaptive radiation and/or conservation genetics. The successful candidate should have experience with molecular techniques and should have a strong interest in population genetics and statistics. Fieldwork in Patagonia will take place in collaboration with scientists from Argentina and Chile. The position is expected to start in the 2008/2009 academic year, pending funding approval and is contingent upon acceptance to the Department of Biology graduate program. Potential applicants may consult: Ruzzante et al 2006 ME 15:2949-2968; Palstra et al 2007 ME 16:4504-4522; and Ruzzante et al 2008 ME available online.

If interested please send an e-mail application including CV, names and addresses of two to three referees and a statement describing the reason(s) for your interest in this research to: Daniel E Ruzzante, Associate Professor and Canada Research Chair in Marine Conservation Genetics, Department of Biology, Dalhousie University, Halifax, Nova Scotia, Canada, B3H 4J1.(email: daniel.ruzzante@dal.ca, http://myweb.dal.ca/ ˜ ruzzante)

Daniel Ruzzante, Associate Professor Canada Research Chair in Marine Conservation Genetics Department of Biology, Dalhousie University, Halifax, Nova Scotia, Canada, B3H 4J1 phone: (902) 494-1688 fax: (902) 494-3736 e-mail: daniel.ruzzante@dal.ca

http://myweb.dal.ca/ruzzante http://-/patagonia.byu.edu Canada Research Chairs http://www.chairs.gc.ca ruzzante <Daniel.Ruzzante@Dal.Ca>

ETH Zurich HostParasite Coevolution

A 3 year PhD position is available in the Experimental Ecology group (headed by Paul Schmid-Hempel), Institute of Integrative Biology (IBZ) at ETH Zurich to study Red Queen dynamics during host-parasite coevolution under the supervision of Mathias Wegner. We use the Red Flour beetle Tribolium castanaeum and its microsporidian parasite Nosema whitei as a model system to experimentally study the short term evolution of recombination rate of the host. Depending on the scientific interest of the candidate, the work can include experimental evolution, experimental manipulation of recombination rate by artificial selection and RNA interference, and determination of host genetic factors influencing resistance and measurement of population genetic parameters during coevolution. The applicant ideally has some background in molecular and evolutionary biology (especially population genetics). Applications and enquiries should be sent to Mathias Wegner (mathias.wegner@env.ethz.ch) by 10th May 2008 and contain a short summary of their motivation and relevant experience, along with their CV, and contact information for 2-3 references. Salary is according to SNF (Swiss National Fund) guidelines.

– Mathias Wegner Institute of Integrative Biology Experimental Ecology Universitätstrasse 16 ETH-Zentrum, CHN J12.1 CH-8092 Zürich

http://www.eco.ethz.ch/people/assistants/-wegnerm/ mathias.wegner@env.ethz.ch mathias.wegner@env.ethz.ch

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GrenobleFrance PhylogeneticDiversity

Dear colleagues, Could you please circulate this announcement to any potential candidate? Best regards,

Centre National de la Recherche Scientifique (CNRS) Laboratoire d?Ecologie Alpine (LECA) Grenoble, France

Description

The functional Traits and Dynamic of Ecosystems (TDE) group is looking for a highly motivated PhD student or postdoc associate to take part in the ANR funded project DIVERSITALP (Forecasting the impacts of global changes on French Alpine Flora: distribution of specific, functional and phylogenetic diversities, simulations and conservation strategies). Although there is now convincing evidence of ongoing climatic change and its impacts of life on Earth, one major limitation impeding the use of models for implementing sound management plans and adaptation strategies to forthcoming global changes is that the mechanisms structuring the distribution of species, functional and phylogenetic diversities are loosely known. This is particularly the case in Alpine ecosystem. The PhD student or postdoc will have to investigate the mechanisms that shape plant community structure in the Alpine Region by quantifying the relative importance of niche-based processes (habitat filtering vs competitive exclusion) and neutral processes. To do so, mechanisms of plant communities? assemblage and biodiversity maintenance will be studied in the light of species? environmental niche (climatic, soil, topographic), functional traits (? and ? niche traits) and phylogenetic relationships. Theoretical models will have to be constructed and tested on existing data. Experimental studies using mesocosmes could be envisaged.

Supervision Dr. Wilfried Thuiller Dr. Sébastien Lavergne

Education MSc/PhDin ecology, community and theoretical ecology or related discipline

Qualification Strong background in community ecology, phylonenetic analyses and species co-existence models. Strong motivation for theoretical and applied studies. Excellent English writing skills. Willingness to work in a team. Excellent knowledge of statistics and mathematics under R and Scilab plateforms.

Duration 3 years for a PhD 2 years for a Postdoc

Collaborators to the project Dr. Nicolas Mouquet (Univ. Montpellier, France) Dr. David Mouillot (Univ. Montpellier, France) Dr. Jérome Chave (Univ. Toulouse, France)

Deadline for application September 2008.

Contact person Send your application, including CV, names of three reference persons and a brief statement to:

Dr. Wilfried Thuiller (wilfried.thuiller@ujf-grenoble.fr) Dr Sébastien Lavergne (sebastien.lavergne@ujf-grenoble.fr) Laboratoire d'Ecologie Alpine, UMR-CNRS 5553 Université J. Fourier BP 53, 38041 Grenoble Cedex 9, France Tel: +33 (0)4 76 63 54 53

– Dr. Wilfried Thuiller Laboratoire d'Ecologie Alpine, UMR-CNRS 5553 Université J. Fourier BP 53, 38041 Grenoble Cedex 9, France Tel: +33 (0)4 76 63 54 53 Fax: +33 (0)4 76 51 42 79

Email: wilfried.thuiller@ujf-grenoble.fr Home page: http://www.will.chez-alice.fr Website: http://www-leca.ujf-grenoble.fr/equipes/tde.htm –

Sebastien Lavergne Laboratoire d'Ecologie Alpine, UMR-CNRS 5553 Universite Joseph Fourier BP 53, 38041 Grenoble Cedex 9, France tel +33 (0)4 76 63 54 50 fax +33 (0)4 76 51 42 79 http://www-leca.ujf-grenoble.fr/membres/lavergne.htm sebastien.lavergne@ujf-grenoble.fr

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IrelandNatlBotanicGarden FernConservation

PhD Studentship Conservation Biology of the Threatened Killarney Fern (*Trichomanes speciosum*) in Ireland

National Botanic Gardens, Glasnevin and Trinity College, Dublin.

Trichomanes speciosum is categorized as Endangered in Ireland, and is listed in Annex II of the EU Habitats Directive. The aims of this fully funded project are to contribute to the conservation management of this species by assessing clonal growth, reproduction and population differentiation. This will require the development of appropriate field monitoring methods, site characterization, assessment of population sizes, use of molecular markers to provide population genetic information, and the development of conservation management guidelines for the species.

The research will be co-supervised by Dr Noeleen Smyth (National Botanic Garden, Glasnevin) and Dr Steve Waldren (Botany Department, Trinity College Dublin)

Conditions of the award: Applicants should have a first or upper second class primary degree, or an MSc, in a appropriate discipline (Botany, Environmental Science). Familiarity with molecular techniques, field survey work, and an ability to drive are all highly desirable, as well as a capacity for both individual research and intergration into team work. The starting date for the position is October 2008.

Amount of the award: Successful candidates will receive a stipend of 16,002 per year for up to three years. Fees for postgraduate students from the EU will be fully covered by the project. There will be opportunities to earn some extra money teaching and demonstrating on undergraduate courses and invigilating examinations.

Application procedure: submit a current CV, a letter containing a statement of interest, and the names and contact details of two referees to Dr N. Smyth (National Botanic Garden, Glasnevin, Dublin 9, Ireland. Phone: +353-1-8040327, Email: noeleen.smyth@opw.ie, from whom further details may be obtained.

Closing Date: 10th May 08.

colin.kelleher@gmail.com

LundU AlgaEvolution

The University of Lund announces the following vacancy:

POSTGRADUATE SCHOLARSHIP in Evolution, within the discipline of Limnology

Invasion patterns a bloom-forming alga

The position will be part of the Research School in Genomic Evolution at Lund University, with placement at the Department of Evolution, Section of Limnology, Faculty of Science.

The Research School in Genomic Evolution is an integrated part of the Centre for Genomic Evolution (CGE). Genomic evolution is a new interdisciplinary research field on the interface between ecology, evolutionary and molecular biology, and genomics. A long-term goal is to achieve an integrated understanding of the molecular, evolutionary and ecological mechanisms and processes that are involved in the generation of the immense diversity of form, and function that characterizes living organisms. Clearly these processes operate at different levels of biological organization, and at different temporal and spatial scales. Further information about CGE and the research school could be found at http://www.ekol.lu.se/research/genomic-ecology . Reference Number: 110 Last application date: 15 May 2008 Starting date: As soon as possible Information: Karin Rengefors, Ph. +46 46 222 84 27 e-post: Karin.Rengefors@limnol.lu.se Worker's unions at the University of Lund: ST, SACO and SEKO

Project Description: This project involves studying the population genetic structure of a nuisance microalga, in relation to its invasion and dispersal patterns. It thus has both a basic science approach as well as an applied aspect. The background is that a large number of Nordic lakes have become invaded or dominated by the noxious microalgal species Gonyostomum semen (Raphidophyte) during the past decades. This phytoplankton species forms intense blooms and expels slimy threads that cause skin irritation to bathers as well as clogging of filters, thereby reducing the recreational value of lakes and water quality. It is unclear whether the species has been spreading to new lakes or simply become more abundant due to changes in the environment. This position will involve using DNA techniques to determine genetic profiles for Gonyostomum strains, and subsequently population structure as well as geographical patterns.

This position is suitable for students interested in approaching evolution questions with molecular tools. The project will involve traveling to sampling locations in Sweden and neighboring countries, which is why a driver's license is necessary. The daily work will be very lab-oriented, including culturing of algae and molecular analyses.

Qualifications: Requirements for this position are an MSc or comparable degree in evolution preferably with an aquatic evolution specialization. The successful candidate will have experience in PCR techniques. A driver's license is required, as is good knowledge of written and spoken English.

Regulations concerning appointment as a full doctoral student can be found in HF 5 Chap 1-7§§and SFS 1998:80. Also consult the admission regulations at http://www.science.lu.se/o.o.i.s/2319 . An educational stipend is awarded for the first 18 months of full-time study, following which time the student is appointed as a full doctoral student. Regulations concerning educational stipends for doctoral students can be found in SFS 1995:938 and 1998:81. Regulations concerning appointment as a full doctoral student can be found in HF 5 Chap 1-7§§and SFS 1998:80.

Those who hold an educational stipend or a doctoral student appointment must first be accepted for postgraduate study. To be accepted, a student must be judged to have the competence necessary to complete a course of postgraduate study.

In addition to pursuing postgraduate studies, the doctoral student may also perform other duties - including research, teaching and administration - according to the specific regulations.

The university strives for a more even gender representation within postgraduate education.

Applications: Applications are made on a specific application form found on the web site: http://www.science.lu.se/o.o.i.s/2319 . The application must reach the Registrar, Kansli N, Lund University, Box 118, SE-221 00 Lund, Sweden, not later than May 15th, 2008. All submitted documents must be attested as to their authenticity.

Kerstin Johannesson-Andersson

Administrator

Karin Rengefors, PhD Associate Professor Limnology, Dept. of Evolution Evolution Building, Lund University SE-22362 Lund, Sweden Phone: +46 46 222 8427, Fax: +46 46 222 4536 Homepage: http://www.limnol.lu.se/index.asp Karin Rengefors <Karin.Rengefors@limnol.lu.se>

LundU DamselflySpeciation

Clinal variation, hybridization and speciation in calopterygid damselflies

A PhD-fellowship is available for three years to study the ecology and genetics of a hybrid zone between C. splendens and C. xanthostoma in southern France. The candidate is supposed to spend 50 % of his research time in France and 50 % in Sweden. The project is part of collaboration between the Department of Ecology at Lund University (Sweden) and CNRS at Toulouse (France), aimed to foster European research collaboration.

Field work and experiments will mainly be performed between May and August in France, and laboratory work, data analyses and theoretical work in Sweden. The candidate is expected to perform field experiments (mate presentations, phenotypic manipulations) alongside with spatial analyses of phenotypic variation in key phenotypic traits, such as the degree of wing melanisation between and within these species. These field studies will be performed across the hybrid zone south of the Loire River as well as along altitudinal gradients up in to the Pyrenees. There will also be opportunities for the candidate to investigate other issues such as the importance of plastic mate preferences in maintaining sexual isolation and species boundaries. Field facilities are provided by CNRS in Moulis, and laboratory facilities by the Department of Ecology at Lund University.

We are seeking a highly motivated, independent student who is willing to work both in the field and in the laboratory. Strong collaborative and communicative skills are needed, and knowledge in French is helpful, but not necessary. Previous experience with field work in evolutionary ecology, molecular work, statistics and/or modelling will be considered an advantage. A strong interest in theoretical aspects of ecology and evolutionary biology are essential.

Please send letter of interest for this PhD-opportunity o the following address:

Erik Svensson Section for Animal Ecology Department of Ecology Lund University SE-223 62 Lund, SWEDEN

Fax: +46 46 222 47 16 Phone: +46 46 2222 38 19 E-mail: erik.svensson@zooekol.lu.se

Send curriculum vitae, copies of exams, letters of recommendation (optional), the names and contact information of 1-2 reference persons and a short letter where you explain your background and why you are interested in this position no later than no later than May 15 2008.

For general information about the research affiliation in Sweden see: http://www.biol.lu.se/zooekologi/epb/people-en/es-en/es-lab-en.htm Representative publications linked to the Swedish research group and to this project: http://www.biol.lu.se/zooekologi/epb/people-en/es-en/es-pub-en.htm Information about the French research affiliation: http://www.ecoex-moulis.cnrs.fr/ Erik Svensson Professor (Animal Ecology) Department of Ecology Lund University SE-223 62 Lund SWEDEN

Phone: +46 46 222 38 19 Fax: +46 46 222 47 16

Erik.Svensson@zooekol.lu.se

MarieCurie 9 Speciation

SPECIATION: A Marie Curie Initial Training Network

Nine 'Early-stage researcher' positions are expected to be available, for 3 years in each case, starting in the autumn of 2008. ESR will register for a PhD degree in one of the 4 partner universities: Sheffield (UK), Jyvaskyla (Finland), Groningen (The Netherlands) and St Andrews (UK).

We anticipate projects in the following areas (lead supervisors):

1.1 Genetic incompatibilities and the evolution of reproductive barriers between allopatric Drosophila populations (Anneli Hoikkala/Maaria Kankare, Jyvaskyla) 1.2 Genetics and genomics of prezygotic isolation in Nasonia (Leo Beukeboom/Louis van de Zande, Groningen) 1.3 Genetics of reproductive isolation in grasshopper hybrid zones (Roger Butlin, Sheffield) 2.1 The role of sexual selection in the evolution of reproductive isolation (Rhonda Snook, Sheffield) 2.2 Genetics and genomics of song preference in Drosophila (Mike Ritchie, St Andrews) 3.1 Modes of speciation and diversity patterns (Franjo Weissing/Leo Beukeboom, Groningen) 3.2 Variation in developmental mode and divergence in Pygospio and Littorina (Emily Knott, Jyvaskyla) 3.3 The genetic basis of variation in reproductive diapause in Drosophila montana (Anneli Hoikkala/Maaria Kankare, Jyvaskyla) 3.4 The genetic basis of variation in reproductive diapause in Nasonia vitripennis (Leo Beukeboom/Louis van de Zande, Groningen)

For further information and details of how to apply, please see http://speciation.group.shef.ac.uk/itn or contact the Coordinator, Roger Butlin (r.k.butlin@sheffield.ac.uk)

Roger K Butlin Professor of Evolutionary Biology

Animal and Plant Sciences University of Sheffield Western Bank Sheffield S10 2TN UK

Tel. +44 (0)114 2220097 FAX +44 (0)114 2220002

r.k.butlin@sheffield.ac.uk

NatlUIreland PostglacialBiogeography

PhD Studentship: Postglacial biogeography of Ireland's rare arctic-alpine carnations.

Applications are invited for a 3 year PhD project investigating the biogeography and genetic diversity of rare arctic-alpine plants on Ireland's Western Seaboard. Arenaria ciliata and Minuartia recurva occur on a few high mountains sites in Ireland, with their closest sister populations over 1,000km away in the Alps and Iberia respectively. This project will use a variety of molecular marker methods including AFLP and chloroplast haplotype analysis to build a putative postglacial migration model explaining how and why these and 6 other related Caryophyllaceae species came to have their current distributions. This project is ideally suited to a candidate with strong field experience of the European flora and expertise in molecular markers/ DNA sequencing. Over the course of the project summer field collections will be made in Ireland, Britain, Scandinavia, Iberia and the Alps. The post carries a stipend of euro16,000 per annum, with additional funds to cover university fees, travel to conferences and advanced training in population genetics/ molecular ecology methods.

The start date for the Project is June/ July 2008. The studentship will be based at the Molecular Ecology Laboratory, NUI Maynooth, in collaboration with National Botanic Gardens, Glasnevin, Dublin (Dr Colin Kelleher). The National University of Ireland, Maynooth is located in a small university town 30km from Dublin and hosts one of the leading biological science clusters in Ireland. Applications, including a personal statement, up to date CV and the contact details of 3 referees should be sent to conor.v.meade at nuim.ie. or posted to:

Dr Conor Meade Molecular Ecology Laboratory Department of Biology NUI Maynooth Co. Kildare, Ireland.

This project is funded by the Science Foundation Ireland Research Frontiers Programme.

Conor Meade <conor.v.meade@may.ie>

NewZealand SystemsBiology

One of the great challenges of the post genomic era is to understand how the interaction of complex biological processes is coordinated within cells. By combining experimental approaches with mathematical modelling we can provide novel insights into the regulation of biological processes and predict the potential consequences of altering substrate levels and pathways.

This PhD project will focus on modelling the production of different steroid hormones during pregnancy. The ultimate goal of this project is to create a mathematical model that describes the regulation of and complex interaction among intermediate substrates in the foetal and placental steroid hormone synthesis pathways. The mathematical model is expected to improve our understanding of how changes in the levels of intermediate substrates affect the different steroid synthetic pathways that are operating in the placenta and in the foetus. This will help us to understand how placenta and foetus co-ordinate the synthesis of the different hormones necessary for pregnancy success and provide insight into how perturbations of steroid metabolism ultimately affect the viability of the foetus and, subsequently, the long-term health of the offspring.

The student will be part of a multidisciplinary international team. This theoretical project will use biological expertise and data generated in the laboratories of AgResearch's Reproductive Technologies Group (Hamilton, New Zealand) and from INRA in Jouy en Josas, France.

The successful candidate will extend his/hers skills in mathematical modelling and computer simulations to describe the performance of complex systems and obtain experience in epigenetics and systems biology. These are highly sought-after skills in the interface between mathematics, physics and the life sciences.

We are seeking enthusiastic and talented graduates who wish to take advantage of this exciting opportunity to contribute to the development of systems biology in New Zealand. We would particularly like to hear from applicants with at least a second honours degree in a subject with a strong applied mathematics content such as physics, mathematics, statistics or engineering and a demonstrated interest in biology or biochemistry; experience with mathematical modelling in the life sciences is an advantage. Good written and verbal communication skills and a high level of motivation and commitment are required.

This PhD is funded by the National Research Centre for Growth and Development (NRCGD) and is based at AgResearch's theoretical biology group in Hamilton, NZ.

The position is open until a suitable candidate has been found.

Contact tanya.soboleva@agresearch.co.nz or anette.becher@agresearch.co.nz for further details.

S. Anette Becher, D.Phil. Section Manager - Bioinformatics, Mathematics & Statistics T +64 3 489 9028 M +64 29 489 9081 E Anette.becher@agresearch.co.nz

AgResearch Limited Invermay Agricultural Centre Puddle Alley, Private Bag 50034, Mosgiel, New Zealand T +64 3 489 3809 F +64 3 489 3739 www.agresearch.co.nz Farming Food and Health. First Te Ahuwhenua Te Kai me te Whai Ora. Tuatahi

anette.becher@agresearch.co.nz

NHM Paris IslandSpeciation

Call for applications 2008: PhD Opportunity at the Natural History Museum, Paris.

Contact: J.-N. Labat (labat@mnhn.fr), UMR 5202 'Origine, Structure & Evolution de la Biodiversité', Muséum National d'Histoire Naturelle, Paris, France.

*Endemism and speciation in a mega diverse island ecosystem: the /Arthroclianthus///Nephrodesmus/ (Leguminosae) species complex in **New Caledonia***

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Project summary

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The /Arthroclianthus///Nephrodesmus/ (Leguminosae, tribe Desmodieae) species complex, endemic to New Caledonia, displays striking morphological and ecological diversities. The distinction between within-species and among-species variability is difficult. Twenty-four species are currently described, but 42 morpho-species (37 for /Arthroclianthus/, 5 for /Nephrodesmus/) have been detected in a preliminary survey. Several aspects will be considered:

1) Systematics: the student will establish a molecular phylogeny (using both organelle and nuclear DNA markers) in order to distinguish the major clades, reconstruct the genealogical relationships among taxa, estimate the date of appearance and timing of diversification in the different clades, and propose a biogeographic scenario.

2) Evolution of floral morphology: on the basis of the molecular phylogeny, the student will examine the evolution of reproductive characters and assess the correlation between reproductive morphology and ecology. The two genera differ in their species diversity, which may be linked to the apparition of a pollination syndrome in /Arthroclianthus/: whereas all other species of the tribe are insect-pollinated, these species are suspected to be bird-pollinated. The correlation between rapid speciation and bird-pollination was previously observed in other genera of the family (e.g. /Chadsia/ and /Pyranthus/).

3) Genetic diversity: because the species are very closely related, the within-species genetic diversity will have to be considered in order to delimit taxa and study their relationships. Moreover, events of reticulate evolution are stongly suspected and speciation may still be on-going. A fine-scale genetic study will therefore be performed within small groups of species that will be circumscribed based on the molecular phylogeny.

4) Taxonomy and conservation : based on molecular data and morphological observations, species delimitation will be re-evaluated. The student will subsequently use Geographical Information System (GIS) in order to characterize the IUCN conservation status of all taxa under study. This will be particularly important since the /Arthroclianthus/ and/ Nephrodesmus/ mainly occur in sclerophyllous forests, which have suffer a drastic range contraction (only 1% of their initial range remains) and maquis, which is under huge human pression (mining activity and its related urbanization).

Scientific context

This PhD project will be performed within the broad framework of the program “BIONEOCAL: Phylogenetic and population studies of the emergence of endemism in New Caledonia”, funded by the French National Agency for Research (ANR). This project fits the main research areas of the UMR 5202 'OSEB', and the PhD student will therefore have many opportunities to collaborate and share experience with other members of the team.

Co-advisors: Myriam Gaudeul (MNHN) & Jérome Munzinger (IRD, Nouméa)

Selection criteria

This work will require intensive field work, observations on herbarium specimens, molecular analyses in the lab, statistical treatments and writing publications. We seek for a highly motivated candidate with a solid background in evolutionary biology and systematics, including phylogenetics and population genetics. Molecular skills (DNA extraction, PCR, cloning) will be appreciated. The ideal candidate will be enthusiastic, organised and be able to work both independently and in collaboration with others.__

Application Process

A limited number of 3-year PhD fellowships are being opened. Interested candidates must first contact J.-N Labat (labat@mnhn.fr <mailto:labat@mnhn.fr>) and provide a CV before mid-May 2008. The candidate will subsequently have to send a full written application before 11 June, and to defend his application orally in front of the Doctoral program College (auditions held the 30 June, 1st and 2nd July 2008).

See in french at : http://www.mnhn.fr/museum/front/medias/enSup/13468_sujet_JN_Labat.pdf About the application process (in french):

http://www.mnhn.fr/museum/foffice/science/science/Enseignement/ecoleDoctorale/somthese/fiche.xsp?ARTICLE_ARTICLE_ID=9200&idx=-4&nav=liste

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RhodesU WeevilPopulations

Master's Bursary Available

A bursary is available for a Master's student in the Department of Zoology and Entomology at Rhodes University to develop and analyse microsatellite markers in the weevil, Porthetes hispidus. P. hispidus is host specific to the cycad Encephalartos friderici-guilielmi and is probably its primary pollinator. This cycad is distributed mostly around the Cathcart-Queenstown district of the Eastern Cape and is found as isolated colonies separated by a range of distances with one or two isolated populations occurring near Kokstad, KwaZulu Natal. Population genetic structure in this weevil could be mediated by distance between populations of its host plant, host and population fidelity, or extinction-recolonisation dynamics, among other factors. This project aims to determine levels of genetic variation and patterns of genetic structure in this weevil, as well as gain insight into its mating system. Though the project is primarily lab based there may be some opportunity for field work as it will be useful to sample from populations that have not yielded weevils in past collecting trips. A keen interest in evolutionary biology and some background in molecular biology would be valuable attributes for candidates for this bursary. Submit CV and brief statement of interests to:

Dr. Doug Downie Department of Zoology and Entomology Rhodes University Grahamstown 6140 South Africa d.downie@ru.ac.za 046 603-8086

d.downie@ru.ac.za

StockholmU EvoDevo

A 4-year PhD-position in Evolutionary Ecology is available at the Department of Zoology, Stockholm University, Sweden. Main supervisor Dr. Karl Gotthard. The subject of the project is "Evolution of developmental plasticity in insects" and last date for applying is May 2.

Evolution of developmental plasticity in insects

Developmental plasticity that leads to alternative phenotypes depending on environment is often controlled by developmental switches/ thresholds. Such switches integrate environmental and genetic effects on phenotypes and are important mechanisms for the evolution of adaptive plasticity. This project will explore the evolution of developmental plasticity by mechanistic and genetic studies of developmental switches, as well as studies of how the expressed phenotypic variation influences fitness in realistic ecological settings. The project focuses on larval development in butterflies of the genus Pararge and deals with developmental switches of two different types (life cycle and color dimorphisms) that are sensitive to different environmental cues. The prospective student will perform breeding and selection experiments to estimate the level of developmental coordination and genetic architecture of the switch mechanisms. He/She will also test the potential adaptive value of developmental switches by performing laboratory and field experiments that investigate fitness consequences of variation in phenotype (life history traits and larval color morphs) in realistic environments. The exact details of the Ph.D. project are open for discussion.

I am looking for an independent student with a strong interest in evolutionary theory and experience of empirical work in any of the fields of evolutionary ecology, behavioral ecology, quantitative genetics, and life history evolution. Experience of experimental work using insects will be considered an asset.

The Department of Zoology at Stockholm University, Sweden offers a very strong research environment in evolutionary ecology, excellent lab and field station facilities as well as a stimulating scientific atmosphere that encourages students to develop independent scientific ideas. There are several research groups working on evolutionary ecology of insects and good opportunities for collaborations within the department.

The formal instructions for applying is found at the Stockholm University web pages at:

http://www.su.se/content/1/c6/03/89/02/-468_0856_08.pdf For more information about the position contact Karl Gotthard (karl.gotthard@zoologi.su.se)

Karl Gotthard Department of Zoology Stockholm University 106 91 Stockholm Sweden Tel: +46 8 16 40 48 Fax: +46 8 16 77 15 Web page: http://www.zoologi.su.se/research/gotthard/-index.html karl.gotthard@zoologi.su.se

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StockholmU EvolutionaryGenetics

One PhD position in Evolutionary Genetics (dnr 11/08)

at the Department of Genetics, Microbiology and Toxicology (GMT), Stockholm University.

Research area: We are looking for a doctoral student who is broadly interested in evolutionary genetics of animals, ranging from population/conservation genetics to aspects of molecular evolution relevant to our understanding of animal evolution. The main focus of our research group is the use of evolutionary genetics, mainly below the species level, to understand ecological, evolutionary and population processes in marine mammals. Please refer to our web-site (Research Groups: Per Palsböll at www.gmt.su.se < http://www.gmt.su.se >) for more details on our research and publications.

The doctoral candidate will be educated in evolutionary/population genetics of natural animal populations and supervised by Prof. Per Palsböll, and Dr. Martine Bérubé.

Qualifications: A highly motivated person with a strong background in animal evolutionary genetics and practical laboratory experience (PCR, DNA sequencing etc.). Proficiency in English as well as quantitative and programming skills is of additional and considerable merit. The position is open to all nationalities.

Application: The application has to include your curriculum vitae, a copy of your University grades, one copy of your main undergraduate thesis work, names and address/contact details of two referees, in addition to other documents that you feel is important to your application. A summary of your motivation and suitability for this PhD programme should be included as well along with a proposal for a possible doctoral project that will fit in the ongoing research of our laboratory.

Terms of employment: The research education is a 48 months paid position. The position is financed by a fellowship for the first years, and subsequently as a regular doctoral position for the remainder of the PhD-program.

Stockholm University, which is located in the capital of Sweden, has a very strong research environment in evolutionary biology and excellent facilities as well as a stimulating scientific atmosphere. There are many research groups working on evolutionary questions in the Departments of Zoology and Botany as well as at the nearby Museum of Natural History and the Technical University.

For further details, please contact Per Palsböll (Per.Palsboll@gmt.su.se), telephone: +46 (0)8161998.

The closing date (postmark) for applications is May 2nd 2008. Please quote reference number dnr 11/08.

Completed applications should be sent by regular mail (not e-mail) to:

Anette Storbacka

PhD position in Evolutionary Genetics (dnr 11/08) Department of Genetics, Microbiology and Toxicology Stockholms Universitet, Svante Arrhenius väg 16, 106 91 STOCKHOLM

Union representatives at Stockholm University are Bo Ekengren, SACO, tel: +46 (0)8162661, Lisbeth Häggberg, ST, tel: +46(0)8164017, and Gunnar Stenberg, SEKO, tel: +46(0)703164341.

Per J. Palsbøll, Professor Department of Genetics, Microbiology and Toxicology Stockholm University, 106

91 Stockholm, Sweden

Visiting address: Svante Arrheniusväg 16, Room E545 Office phone: +46 (0)8 16 1998 Mobile phone: +46 (0)73 5182364

Per J Palsboll <Per.Palsboll@gmt.su.se>

TrinityCollege Bioinformatics

Dear Evoldir

A 3-year PhD studentship is available to study gene expression in bees parasitised by a nematode worm. The project will be supervised by Dr Mark Brown (Trinity College Dublin), Dr Seirian Sumner (Institute of Zoology, London) and Professor Mark Blaxter (University of Edinburgh) and will involve a combination of parasitological, next-generation sequencing, quantitative-PCR, and bioinformatic analysis.

The position is open to EU citizens. The ideal applicant will have (or be expecting to attain) a 1st or 2:i honours degree (or equivalent) in Genetics or Biology, preferably with experience in RNA work and good quantitative skills. The position will start on 01.10.08 and will involve working in Ireland and the UK. Requests for further information and applications (a CV, cover letter and names of 2 academic referees) should be made to Mark Brown (mabrown@tcd.ie). The deadline for applications is 15.05.08.

Trinity College Dublin(www.tcd.ie) is Ireland's premier university (ranked 13th in Europe and 53rd in the World). The School of Natural Sciences (www.tcd.ie/-naturalscience) has a thriving research environment, with particular strengths in ecology, evolution, gene expression and parasitology. The project is funded by Science Foundation Ireland under its Research Frontiers Programme.

Mark JF Brown, MA (Oxon), PhD, FTCD Lecturer in Zoology Department of Zoology School of Natural Sciences Trinity College Dublin Dublin 2 Ireland

tel: +353 (0)1 896 1627 fax: +353 (0)1 677 8094 email: mabrown@tcd.ie web: http://www.tcd.ie/-Zoology mabrown@tcd.ie

UAarhus PopulationGenetics

Ph.D. position: Landscape population genetics and the role of organic farming.

In connection with a newly started project under DARCOF a Ph.D. position is available in landscape population genetics and the role of organic farming.

The project is a 3 year AGSoS co-financed Ph.D.-project at the University of Aarhus, Denmark

The purpose of the Ph.D. project is to analyse the landscape genetics of the ground beetle and the field vole from nearby conventional and organic farms in order to identify the microevolutionary processes of gene flow and drift within the two kind of farming methods to address the role of organic farms as gene resource. Hence, to a) analyse the amount of genetic diversity and possible reduction of genetic diversity (bottleneck) in the two species on organic and conventional farms, b) analyse the genetic population structure of the two species and c) to estimate the spatial scale and direction of dispersal.

Information on application procedures and the project can be found at :

http://www.nat.au.dk/13184

or by contacting

Professor Volker Loeschcke (volker.loeschcke@biology.au.dk) University of Aarhus, Ecology and Genetics, Depart. of Biological Sciences, Ny Munkegade, Build. 1540, DK-8000 Aarhus C, Denmark.

Senior Researcher Liselotte Wesley Andersen (lwa@dmu.dk) University of Aarhus, National Environmental Research Institute, Dept. of Wildlife Ecology and Biodiversity, Grenåvej 14, 8280 Rønde, Denmark

lwa@dmu.dk

UBritishColumbia MolecularBreeding

Graduate student assistantship in molecular breeding and functional foods

University of British Columbia, Vancouver, BC, Canada

One graduate student assistantship is currently available in the laboratories of Dr. Steven Lund and Dr. David Kitts for prospective students interested in a career in plant genomics and molecular genetics. The project entails biochemical genomics and molecular breeding for improved antioxidant capacity in raspberry fruits. The successful applicant will have an opportunity to receive training in metabolite analyses via LC-MS, TEAC and ORAC free radical assays, gene cloning, bioinformatics, and DNA marker discovery. The successful applicant will also work closely with the collaborating small fruits lead geneticist at the Pacific Agri-food Research Centre (Agassiz, BC), Chaim Kempler. More information can be found online at: http://www.landfood.ubc.ca/wine/lund/FuncFood.html

The position is available immediately for commencing dissertation research. Students graduating this Spring are encouraged to apply now. It is not too late to be accepted to the UBC Graduate School for September 2008, either through the UBC Genetics Graduate program or the Plant Science Graduate program in the Faculty of Land and Food Systems. To begin the application procedure, please send your CV and a copy of your transcript(s) to:

Steven T. Lund, Ph.D. University of British Columbia Wine Research Centre 241 - 2205 East Mall Vancouver, BC V6T 1Z4 Canada

or electronically: stlund@interchange.ubc.ca

UCalgary PlantMacroevolution

MSc/PhD opportunity in Plant Macroevolution at the University of Calgary.

I am looking for a highly motivated student for 2008/2009 at the PhD or MSc level who is interested in the evolution of plant sexual systems, plant speciation, and/or pollination. Projects can be tailored to the student's specific research interests and can involve theory, comparative phylogenetic analysis and/or field work in the Canadian Rockies or the Gulf Islands. The ideal candidate will have a strong background in plant identification and/or phylogenetic theory. For more information, see: < http://homepages.ucalgary.ca/~jvamosi/ >. Guaranteed funding of at least $20,000 CAD/year for 4 years (PhD) or 2 years (MSc) is available through a combination of teaching and research assistantships. Candidates with strong GPAs will be eligible for several provincial funding sources, in addition to federal sources available to Canadian citizens.

Requirements: Potential applicants must have a minimum GPA of 3.20 (on a four-point system). For students entering an MSc, this is based on the last two years of the undergraduate degree consisting of a minimum of 10 full-course equivalents. For those entering a PhD with an MSc, the overall GPA from the MSc will be considered. Canadian citizens will be given first priority, but applications from qualified international candidates will also be considered. Please note that proficiency in the English language is required for graduate programs at the University of Calgary. To inquire, submit (via email) a cover letter with a brief review of your research experience, interests, resume, transcripts, and names of three academic references to: Dr. Jana C. Vamosi, Department of Biological Sciences, University of Calgary, 2500 University Dr NW, Calgary AB T2N 1N4, jvamosi@ucalgary.ca.

jvamosi@ucalgary.ca jvamosi@ucalgary.ca

UEastAnglia Evolution of reproductive success

NERC CASE PhD studentship, 2008

The making of a successful male: an integrated study of male reproductive success in a pest insect.

Start: October 2008.

Location: School of Biological Sciences, University of East Anglia, Norwich, NR47TJ and Oxitec Ltd, Abingdon, OX14 4RX.

Supervisors: Tracey Chapman, Matt Gage (http://www1.uea.ac.uk/cm/home/schools/sci/bio) and Luke Alphey (CASE partner) (http://www.oxitec.com/).

Aim: To take a broad approach to integrate the understanding of fundamental, evolutionarily-important traits in insect pest control.

Summary: Male reproductive success comprises pre- and post-mating components that are rarely subject to integrated study. This studentship will address this, and apply pure and applied research approaches to a pest of significant economic importance for which transgenic insect technology is well advanced. We have applied experimental evolution to the Mediterranean fruit fly (medfly) and now seek to determine reproductive fitness and divergence in male reproductive traits. We predict that males evolving under increased sexual competition will evolve more effective courtship and significantly higher post-mating competitiveness. This will reveal the traits that make a successful male medfly, and also whether pre- or post-mating traits are more strongly selected. The student will pursue this work at a novel molecular level by utilising the expertise of the CASE partner to conduct a targeted transcriptional analysis of important male reproductive proteins in the evolved lines. The project will extend into the applied domain by testing whether pre- and post-mating traits in evolved lines and in transgenics produced for a novel method of insect control, vary predictably in their response to the key environmental variable of nutritional status. The results will reveal potential trade-offs and the likely efficacy of the control strains under varying conditions.

Training: The student will join the Evolution, Ecology and Biodiversity Group at UEA (http://bioweb2.bio.uea.ac.uk/research/themes/-organismsenvironment/eeb.html). The School of Biological Sciences at UEA (http://www.uea.ac.uk/-bio/) provides an excellent Ph.D. research and training environment in a Grade 5 research department. The CASE partner Oxitec employs 24 research staff and is an exciting and challenging environment in which to work. It is at the forefront on a world-wide scale in the development of insect transgenesis. The link with Oxitec will therefore provide invaluable insight and experience for the student into work in the commercial world, and will offer technical expertise of the highest standard.

Eligibility: Applicants should have a strong degree in biological sciences or genetics. The full award is available only to residents of the UK, or those satisfying NERC eligibility requirements (http://www.nerc.ac.uk/funding/available/postgrad/-eligibility.asp). The award includes a standard NERC stipend supplemented by 1000GBP per annum by the CASE partner. The student will spend years 1 and 3 at UEA and year 2 with the CASE partner.

Applications: Informal enquiries to Tracey Chapman (tracey.chapman@uea.ac.uk). Formal applications should be made via the Faculty of Science Post-Graduate Office (scipg@uea.ac.uk), see http://-biobis.bio.uea.ac.uk/Resproject/how_to_apply.html for full details. There is no formal closing date and the position will remain open until filled.

“Chapman Tracey Dr (BIO)” <Tracey.Chapman@uea.ac.uk>

UIceland PopulationGenetics

Ph.D. position

A three year Ph.D. doctoral position in population genetics is available at the Population genetics laboratory, Institute of Biology, University of Iceland. Possibility of part-time teaching as Teaching Assistant (TA) which would extend study to four years.

Subject: Natural selection and population structure in Atlantic cod

Project Description: The question of population structure and the influence of locus-specific natural selection, in the abundant Atlantic cod is still debated. The main objective is twofold. First, to develop and apply DNA sequence variation of both introns and exons of several randomly chosen nuclear loci Atlantic cod Gadus morhua to answer questions of population structure in Icelandic cod. Second, to develop and analyze DNA sequence variation of several genes showing locus-specific effects important for functional differentiation within and among local populations. This will allow us to better sort out the effects of history, locus-specific effects (natural selection, mutation, assortative mating and recombination) and genome-wide effects (such as random genetic drift, population structure, gene flow and inbreeding).

The distinction between locus-specific and genome-wide effects is crucial in population genomics and genetics, addressing both questions of demography, ecology and function of the organism.

I am looking for an independent student with a strong interest in population/evolutionary genetics and molecular biology.

Qualifications: Requirements for this position are an MSc or a B.Sc. with distinction. Experience in molecular biology (PCR, sequencing, cloning, etc) and population genetics and evolutionary biology and statistics and data analysis is an advantage.

A condition of appointment is that a prospective student must qualify and must apply for admittance and be admitted for graduate studies at the Faculty of Science (http://www.raunvisindi.hi.is/id/1007496). Application forms for admittance are here: http://-www2.hi.is/solofile/1013017 At this time prospective candidates should submit a brief statement of research interests, CV, copies of undergraduate and postgraduate transcripts, copies of research papers, and names and contact information of two referees to:

Professor Einar Arnason einararn@hi.is Institute of Biology University of Iceland Askja # 346 office 354-525-4613 Sturlugata 7 lab 354-525-4606 101 Reykjavik fax 354-525-4069 Iceland

einararn@hi.is

ULund 3 SexualSelection Speciation

Internships available at the University of Lund in Sweden

Internships are available for students interested in evolutionary ecology in general, and sexual selection and speciation in particular

We are looking for highly motivated and enthusiastic students, with a strong interest in ecology and evolution, and who are prepared to work independently, both in the field and the laboratory. Students will work in close collaboration with PhD-students and postdocs at the Department of Animal Ecology in Lund (Sweden). Studentships are available for two projects (more details below):

1) Calopteryx damselflies

2) Ischnura damselflies

Fieldwork will take place between early June and late July (2 months). It would be of advantage if the student has a driver's license. Time and length of stay can be agreed on personal preferences. We provide housing and travel costs (for students coming from outside of Sweden). The working language of the group is English. If you are interested, please send us an e-mail announcing your interest no later than the 31 March 2008.

1) Detailed project description: Calopteryx damselflies

Main Coordinator: Maren Wellenreuther

Calopteryx splendens and C. virgo are two damselfly species that occur throughout most parts of Europe, and are commonly found along rivers and small freshwater streams. In Sweden, these two damselfly species can either occur in mixed sympatric populations or in distinct allopatric populations. Previous work from our lab has shown that the strength and direction of selection on morphological characters differs between sympatric and allopatric populations. Other ecological factors, such as predation by birds, has also been shown to further act as a selective force on these populations.

Our fieldwork aims to quantify the relative strength and direction of these selective forces on damselfly populations in nature. Our study populations are within a short distance from Lund (1-4 hours by car), and we will visit several populations repeatedly during the field season in June and July. At each population, we will first record the basic data to describe the ecological setting of the population (density of heterospecifics and conspecifics, forest cover, etc.), and then a subsample of the population will be caught (approx. 20 individuals) and stored in nets. At a subset of these populations we will also conduct experiments to investigate the factors (mainly morphological) affecting mating propensity in these species. To do this, we will tether damselflies with a string of cotton to a bamboo stick and will then present the tethered damselfly to potential mates. The response of these potential mates to the tethered damselfly will be recorded. After the experiment, all damselflies will be placed in nets. All caught damselflies (from the random sub-samples and the experiments) will be transported back to the University in Lund, where we subsequently measure the morphological characters. Finally, the ecological and morphological data will get entered into a database and analysed.

In July, it is planned to drive to Finland, and to work for 2 weeks on the damselfly populations near Jyväskylä. This work will be conducted in collaboration with Katja Tynkkynen at the University of Jyväskylä.

2) Detailed project description: Ischnura project

Main Coordinator: Tom Gosden

Heritable colour polymorphisms within species have proven to be useful model systems to investigate a variety of important questions in evolutionary biology, such as genetics, developmental biology and the ecology of frequency-dependent selection. However, a relatively unexplored research area with important implications for such polymorphisms is population and species divergence in mate preferences. If both colour and mate preferences are heritable traits, which is often the case, then sexual selection theory predicts that non-random mating should lead to the build-up of genetic correlations between colour and mate preference, through the formation of linkage disequilibrium between loci for these different traits. Such a genetic correlation can lead to rapid population divergence in mate preference and sexual isolation between allopatric populations as a by-product of locally varying sexual selection pressures.

By examining several populations of the female limited colour polymorphic species of damselfly Ischnura elegans, it will be possible to explore population divergence in male and female mate preference, intersexual conflicts between males and females and investigate the role of such conflicts in the maintenance of different morphs and population morph frequency dynamics. The female morphs consist of one androchrome (male coloured) and two gynochromes, (infuscans and infucans-obsoleta). See Picture

Through a regular population survey that has been ongoing since the summer

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

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UMunich EvolEcolSystematics 2

Reminder: Deadline for non-EU students 30th of April *Master Program in Evolution, Ecology and Systematics in Munich*

The University of Munich (LMU) offers a 2-year, international master program for highly motivated students from Germany and abroad with a background in biology or a related subject. All courses are offered in English. The program started in October 2007 with 11 students from North America, South-America and Germany. Applications are now welcome to start in October 2008.

The EES Master program contains many innovative elements such as a mentoring program, integrated skills courses and individual research training. We also apply a feedback and revision system instead of simple grading. Classes are small and students have a lot of contact to the teachers. Thanks to funding by the Volkswagen Foundation, students can apply for their own research and travel money and for money to invite international speakers. Unfortunately, we cannot provide grants to cover costs of living. Students pay appr. 500 Euro tuition fees per semester.

Application deadlines in 2008: 30th of April (for non-EU students) and 30th of June (for EU-students and others who don't need a visa to study in Germany).

For more information, please have a look at our website (http://www.eeslmu.de) or contact me by e-mail.

Best wishes, Pleuni Pennings

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Pleuni S. Pennings

* Program Coordinator of the Munich Graduate School for Evolution, Ecology, and Systematics

* Postdoc in theoretical evolutionary biology

Evolutionary Biology, Department Biologie II University of Munich (LMU) Großhaderner Str. 2 D-82152 Planegg-Martinsried

Tel: 0049 89 2180 74 234 http://www.eeslmu.de/eeswiki http://www.biologie.uni-muenchen.de/ou/theopopgen/index.htm pennings@lmu.de

pennings@zi.biologie.uni-muenchen.de

UMunich Phyloinformatics

PhD Position in Phyloinformatics Ludwig-Maximilians-University Munich The Exelixis Lab Teaching and Research Unit Bioinformatics Department of Computer Science

Exelixis Lab is the name for a new group which is funded under the auspices of the Emmy-Noether program by the German Science Foundation (DFG). The group is headed by Alexandros Stamatakis (http://icwww.epfl.ch/~stamatak/).

The main research focus is on computational methods for Evolutionary Biology and in particular:

1. on developing models, algorithms, and tools for Evolutionary Biology. 2. on using High Performance Computing techniques and developing programming models for emerging parallel architectures, such as multi-core CPUs or the IBM CELL, for problems in Evolutionary Biology.

The lab offices are situated in the University Premises (Amalienstr., Schwabing) in downtown Munich with a rich cultural life within minutes of walking to recover from a hard day's work or continue coding in a different environment. The net salary for this PhD position is around 1,500 EUR per month and the starting date should be in September/October 2008.

Applicants may expect close supervision and collaboration with other group members. There are no teaching obligations, but PhD students can participate at teaching activities if they like to. Candidates should have a diploma or master's degree in CS or Bioinformatics and outstanding programming skills in C or C++. They should also have a strong background in algorithmic design and mathematical modeling. Background knowledge in Biology, High Performance Computing techniques, and processor architectures is not required, but will be a plus.

To apply for this position, you should send a CV, including a full listing of grades covering all courses taken during your university studies, potentially a list of publications, two letters of recommendation as well as the names and contact details of the two referees, a PDF of your master's or diploma thesis, and the source code of the largest piece of software you have written so far in C or C++ via email to stamatakis@bio.ifi.lmu.de. This position will remain open until filled.

– Dr. Alexandros Stamatakis, Junior Research Group Leader

The Exelixis Lab Teaching and Research Unit Bioinformatics Department of Computer Science Ludwig-Maximilians-University Munich

Tel: +49 162 8541515 (Mobile) +49 89 21804066 (Office) Skype: stamatak Email: stamatakis@bio.ifi.lmu.de WWW: icwww.epfl.ch/ ˜ stamatak

stamatakis@bio.ifi.lmu.de stamatakis@bio.ifi.lmu.de

UNewOrleans EvolutionaryEcology

UNIVERSITY OF NEW ORLEANS

A Ph.D. fellowship in Evolutionary, Physiological or Behavioral Ecology is available in the laboratory of Dr. Simon Lailvaux in the Department of Biological Sciences at the University of New Orleans beginning Fall 2008. The Louisiana State Board of Regents fellowship provides support for four years at an annual stipend of $23-25,000 and includes a full tuition waiver. Areas of current research in the lab include the behavioral and functional ecology of Anolis lizards, quantitative genetics of performance and sexual signaling in insects, and ectotherm thermal biology. Students must apply for admission to the Ph.D. program in Conservation Biology. For more information on the Department, faculty research interests, and other resources, please see the departmental website: http://biology.uno.edu/ Please note that this particular fellowship is only available to US citizens. Interested applicants should contact:

Dr. Simon Lailvaux Department of Biological Sciences University of New Orleans Email: slailvaux@gmail.com

slailvaux@gmail.com

UOslo CodGenomics

POSITION AS DOCTORAL RESEARCH FELLOW (PhD stipendiat) in FUNCTIONAL GENOMICS

available at the Centre for Ecological and Evolutionary Synthesis (CEES), Department of Biology, Faculty of Mathematics and Natural Sciences, University of Oslo.

The position is available for a period of 4 years with 25% compulsory work.

A position as doctoral research fellow to work on the functional genomics and sequencing of the cod genome is now available. The position is affiliated to EMBIO, the steering board for Molecular Life Sciences at the University of Oslo. The successful PhD candidate is expected to work closely with a postdoc/researcher who is financed by the Norwegian Research Council through the FUGE program and is part of the GenoFisk marine platform where we are aiming at sequencing the full genome of several individuals of Atlantic cod. The results will be used to characterize genetic variability within major stocks and populations of Atlantic cod, and other related species for comparisons. We have access to facilities for experimental studies (breeding/rearing) of cod and are equipped to do gene expression analysis through our 454 sequencer.

The CEES, where the candidate will be working, is an interdisciplinary research group within the Department of Biology that combines the skills of population ecologists, evolutionary biologists, geneticists, and statisticians. It has a strong international flavour, and currently employs 17 faculty, 34 postdocs/researchers, 27 PhD students, 25 master students and 33 official international collaborators. The CEES has been awarded status as centre of excellence by the Norwegian Research Council, and is well funded. Information about the centre can be found at: http://www.cees.uio.no For further information please contact: Professor Nils Christian Stenseth, phone: +47 22854584, e-mail: n.c.stenseth@bio.uio.no. Professor Kjetill S Jakobsen phone +47 22854602, e-mail: k.s.jakobsen@bio.uio.no.

Deadline for application: 2 May 2008 REF. NR.: 2008/5168

Please read the full announcement, including instructions on how to apply, at: http://www.cees.uio.no/about/vacancies/phd-functional-020508/ tore.wallem@bio.uio.no

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UOslo Microbial MolEvol

DOCTORAL RESEARCH FELLOWSHIP

Four year PhD position in molecular evolution with 25% compulsory work available from 1. June 2008 at the Microbial Evolution Research Group (MERG), Department of Biology, Faculty of Mathematics and Natural Sciences, University of Oslo

In this project the community structure of mycorrhizal fungi and other fungal root symbionts associated with an alpine plant species will be analyzed. One of the main aims is to analyze which factors that determine the diversity and composition of fungal root symbionts, implementing both experimental and empirical inferences.

The candidate will work together with a group of researchers in the Microbial Evolution Research Group (MERG) and outside. The research program MERG has status as a Strategic Research Initiative at the University of Oslo. The vision of MERG is to develop an internationally leading and dynamic multidisciplinary research environment focusing on ecological, evolutionary and systems biology research on prokaryotic and eukaryotic microbes, their communities and interactions.

The candidate will be expected to participate in both field work, generating data, perform data analyzes, to work cooperatively with other lab members and outside collaborators and to actively publish and present results. 25% of the working time is allocated to duties besides research and project work, and typically includes lecturing and co-supervision of master students. The ideal candidate will be enthusiastic, highly motivated, and independent and should have a background in the area of focus.

Candidates must have a master's degree (or equivalent) within microbial ecology, evolutionary biology, molecular evolution or a related discipline. It will be advantageous to have experience in one or more of the following fields; mycology, molecular DNA techniques (PCR, sequencing, cloning, etc.), molecular biology, phylogeny, population genetics, bioinformatics and experimental evolution.

Please contact Assoc. Prof. Håvard Kauserud at the address below for more details.

The purpose of the fellowship is research training leading to the successful completion of a PhD degree. The fellowship requires admission to the research training programme at the Faculty of Mathematics and Natural Sciences. The applicants must have obtained undergraduate (cand.mag., i.e. B.Sc. level) and postgraduate (cand.scient. or siv.ing., i.e. M.Sc. level) degrees. This represents approximately five years of full time studies after completion of European Upper Secondary School/International Baccalaureate. For more information see: http://www.matnat.uio.no/english/research/research_edu/education.html . Appointment to a research fellowship is conditional upon admission to the Faculty's research training programme. An approved plan for the research training must be submitted no later than one month after taking up the position, and the admission approved within three months.

See the following URL for further details and guidelines for appointment to research fellowships at the University of Oslo: http://www.uio.no/admhb/reglhb/personal/tilsettingvitenskapelig/ansettelsesvilkar/guidelines-researchfellow.xml The University of Oslo (UiO) wishes to achieve a more equal distribution of scientific employees between the sexes. Female applicants are encouraged to apply.

UiO has an agreement for all employers, aiming to secure rights to research results a.o

Contact Person:

Associate professor Håvard Kauserud, tlf. +47 99697116, e-mail: haavarka@bio.uio.no.

Pay grade: 43 - 48 (NOK 325 600,- - 355 000,- equals ca 41 215,- - 44 937,-) depending on qualifications and seniority).

Application deadline: 30. april 2008

Ref. No.: 2008/2967

Application (including statement about relevance of qualifications), CV (marked Ref. No. 2008/2967), copy of certificates and scientific papers should be sent (in 3 sets) to: Faculty of Mathematics and Natural Sciences, attn. Senior Executive Officer Bente Schjoldager, P. O. Box 1032 Blindern, N-0315 Oslo, Norway. Applicants may be called in for an interview.

Application papers will not be returned.

havard.kauserud@bio.uio.no
havard.kauserud@bio.uio.no

USussex JMaynardSmith Studentship

John Maynard Smith PhD Studentship

The University of Sussex seeks applications for the prestigious John Maynard Smith PhD studentship to be held in the laboratory of Adam Eyre-Walker. The Eyre-Walker lab has a number of projects running which involve a mixture of statistical analysis of DNA sequences and population genetic theory. These projects are largely targeted towards understanding the process of mutation and the effects that mutations have on fitness. Current projects involve investigating cryptic variation in the mutation rate, developing methods to infer the distribution of fitness effects, investigating the effects of transposable elements on gene expression evolution and estimating effective population sizes. Further details can be found at http:// www.lifesci.sussex.ac.uk/-home/Adam_Eyre-Walker/Welcome.html . The studentship is available for 3 years from this October and carries a stipend of approx. £12000. The studentship is only available to citizens of EU countries. Enquiries should be addressed to Adam Eyre-Walker (a.c.eyre-walker@sussex.ac.uk) by the closing date of May 4thth.

a.c.eyre-walker@sussex.ac.uk a.c.eyre-walker@sussex.ac.uk

UZurich Experimental and Computational evolution

PhD thesis in experimental evolution/evolutionary bioinformatics

A three-year Ph.D. studentship in evolutionary biology is available in the laboratory of Andreas Wagner at the University of Zurich. Applications will be considered for both experimental and computational projects. The Wagner lab at the University of Zurich studies biological evolution on all levels of organization, from genes, genomes, and genetic networks to whole organisms. Ongoing projects range from laboratory evolution experiments in yeast to human population genomics. A sample of our research can be found at http://www.bioc.uzh.ch/wagner/.** Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and /or fundamental organizational principles of life.

A successful candidate for an experimental project will have substantial research experience with microbiological and molecular biological techniques, acquired in research projects with an evolutionary orientation. Experience in performing microarray experiments will be a plus. A successful candidate for a computational project will have a strong background in bioinformatics and computational biology. Fluency in a major scripting language such as perl, and experience in software development is a must. Also necessary is a strong background in biology. Applications without a demonstrated interest and research history in evolutionary biology will not be considered further.

We are looking for an individual with a Masters Degree or equivalent, who is highly self-motivated and can work independently. The working language in the laboratory is English. German skills, although helpful, are not essential.

Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file merged from the following parts to jobs_aw@bioc.uzh.ch <mailto:jobs_aw@bioc.uzh.ch>: CV including publication list (if available), a scanned academic transcript (list of grades in university courses), a statement of research interests not exceeding two pages, and three references. Please include the word ?EXPCOMP? in the subject line. The application deadline is April 28.

–

Christiane Gujan Administrative Assistant of Prof. A. Caflisch and Prof. A. Wagner Zurich University Institute of Biochemistry Winterthurerstrasse 190 CH-8057 Zurich Switzerland

Tel. 0041 (0)44 635 55 49 Fax 0041 (0)44 635 68 62

Christiane Gujan <gujan@bioc.uzh.ch>

Jobs

AlbertEinstein ComputationBiology

Department of Systems and Computation Biology

Albert Einstein College of Medicine of Yeshiva University

Multiple Tenure Track Faculty Positions

The Albert Einstein College of Medicine, one of the leading medical schools in New York City, is seeking to fill multiple tenure track faculty positions in the newly formed Department of Systems and Computational Biology. Established in April 2008, the major goal of the new department is to advance our understanding of living systems by developing theoretical, computational and experimental approaches to study complex biological systems.

The College has 750 medical students, 325 graduate students and 360 post-doctoral fellows in training and boasts a strong research faculty covering broad areas of experimental biology, offering outstanding opportunities for collaborative interactions. The opening in late 2007 of the 200,000 square foot Center for Genetic and Translational Medicine at Einstein locates computational, systems and experimental scientists in physical proximity to foster interdisciplinary communication and collaboration. Highly competitive start-up packages are available.

We seek outstanding scientists with broad experience and demonstrated collaborative interactions with experimental or clinical investigators. Candidates should have strength in a physical, mathematical or computational field at the Ph.D. or equivalent level. Experience applying these skills to a biological or biomedical area (demonstrated through publications or support) is also desirable. Areas of interest include, but are not limited to: Modeling cellular processes, such as signaling, transcriptional regulation and immune response; Pathway analysis; Genetic networks; Functional proteomics and genomics; Evolution of structure and function; Computational neuroscience; Mathematical and computational modeling of complex traits and diseases.

Applicants should send a letter of interest, C.V., statement of research and teaching interests, and names of three referees, in electronic format to:

Systems and Computational Biology Search Committee

Albert Einstein College of Medicine

Jack and Pearl Resnick Campus

1300 Morris Park Ave. Price Center, Rm. 153

Bronx, New York 10461

E-mail Address: FacultySearch@scb.aecom.yu.edu

Subject line should be: SCB Faculty Search

EOE

– Aviv Bergman, Ph.D. Founding Professor & University Chairman Dept. of Systems and Computational Biology Albert EInstein College of Medicine 1300 Morris Park Ave. Price Center 153 Phone: 718-678-1063 Fax: 718-678-1018 E-mail: aviv@aecom.yu.edu

Aviv Bergman <aviv@aecom.yu.edu>

Angers France PopulationBiology

ASSISTANT PROFESSOR IN POPULATION BIOLOGY

National Institute of Horticulture (INH)

Angers, France

The National Institute of Horticulture (http://www.inh.fr/) invites applications for a tenure track position in population biology applied to plant protection. The position is at the Assistant Professor level. Expected starting date is January 1, 2009.

For complete job description, visit

http://www.emploi-scientifique.info/esf_view_offre.php?id_offre=2307&retour_cand=1XXX The candidate is expected to teach and contribute to the education and training of undergraduate and graduate students. Research will be conducted in collaboration with the UMR BiO3P (http://www.rennes.inra.fr/umrbio3p/). Our team is interested in the evolution of plant-animal interactions as a basis for more sustainable pest and crop management.

Ph.D. required and a post-doctoral experience is desirable.

Deadline for application is June 6, 2008.

Please direct questions to: Josiane .LeCorff@inh.fr

Josiane.LeCorff@inh.fr

AustralianMuseum Sydney 4 Biodiversity EvolBiol

Four research scientist positions at the Australian Museum, Sydney (permanent or 3 year fixed-contract)

INVERTEBRATE BIODIVERSITY RESEARCHERS (marine molluscs, terrestrial/freshwater gastropods, bryozoans or ostracods)

INDO-PACIFIC FISH BIODIVERSITY RESEARCHER

CORAL REEF ECOSYSTEM RESEARCHER

The Australian Museum is Australia's first and most distinguished museum of natural history with a long tradition of excellence in scientific research. Based in Sydney (consistently rated in the top 10 most liveable cities in the world), the Museum is completing a $45 million dollar refurbishment that includes state-of-the art research and collections facilities.

Total starting remuneration package up to the value of $108,353 p.a. including salary ($74,527-$98,190), employer's contribution to superannuation and annual leave loading.

Up to four positions are available (permanent or 3-year fixed contract). Details of the positions can be found at:

http://www.amonline.net.au/display.cfm?TypeName=3DJobs Inquiries: Dr Brian Lassig +61 (02) 9320 6297 or email brian.lassig@austmus.gov.au <mailto:brian.lassig@austmus.gov.au> or Dr Les Christidis +61 (02) 9320 6237 or email les.christidis@austmus.gov.au <mailto:les.christidis@austmus.gov.au>

Applications marked 'confidential' should be sent to the Human Resources Officer, Human Resources Unit, Australian Museum, 6 College St, SYDNEY NSW 2010 or email hr@austmus.gov.au <mailto:hr@austmus.gov.au>

Closing date: Friday 23 May 2008.

Nathan Lo

Australian Museum

6 College Street Sydney NSW 2010 Australia

t 61 2 9320 6346 m 0424 468 285 f 61 2 9320 6486

Nathan.Lo@austmus.gov.au
Nathan.Lo@austmus.gov.au

CNRS France WallLizardSelection

Field assistant for work in France:

Are you interested in working in the French Pyrenees this summer? I am seeking help from a field assistant in a study of genetic diversity and natural selection in wall lizards in the south of France. Work will be daily and demanding. The interested applicant should be highly motivated, personable, and ready for an intense but rewarding field experience in the beautiful French countryside and Pyrennean hill country.

Rooms are covered by the CNRS, but the assistant will need to arrange their own travel to Toulouse and will need to provide their own meals. French students are particularly encouraged to apply as a working knowledge of the French language is preferable.

Please email Brittny Calsbeek:

bstarfor@uvm.edu

Brittny Calsbeek <bstarfor@uvm.edu>

DukeU SummerUndergraduate YeastEvolutionaryGenet

Summer Undergraduate Research Opportunity Yeast Evolutionary Genetics Duke University

Description We are seeking two undergraduate students to participate in an 8-10 week summer research experience. Students will be participate in an NSF funded project to study how genetic variation affects gene regulation and signal transduction in budding yeast. Students will learn to use basic genetic and molecular biology techniques (gene knockouts, PCR, quantitative PCR, etc) to characterize intra- and interspecific differences in gene network function.

Rising junior or senior undergraduate students with previous experience in a molecular or microbiology lab are preferred. Applicants must be US citizens. Applications are encouraged from students from underrepresented groups.

Contact To apply for this position please email a cover letter, CV/resume and the names and contact information for three references to: paul.magwene@duke.edu

For more information see: http://biology.duke.edu/-magwenelab/ Paul Magwene Assistant Professor Department of Biology Duke University

pmmagic@gmail.com

GeorgetownU LabTech DNAFacility

Laboratory Technician Position, Shared DNA Sequence Facility Manager

A part or full-time research assistant position is available in the Biology Department at Georgetown University, Washington, DC in the laboratory of Dr. Matthew B. Hamilton (http://www9.georgetown.edu/faculty/hamiltm1/).

The position involves operation of an ABI 3100 sequencer for researchersin the Dept. of Biology as well as assisting in population and conservation genetics research. Duties include oversight of lab andinstrument operations, collecting microsatellite and DNA sequence data, placing orders for supplies, and assisting with undergraduate and graduate laboratory training. The ability to trouble-shoot instrument problems, effectively schedule instrument time, help instrument users and work with independence is essential. Strong organizational and computer skills are required. On-going research projects in the laboratory include studies of genotype-disease associations in humans, tests of the molecular clock in plant species, and a study of temporal genetic variation in striped bass.

Individuals who have recently completed an undergraduate degree in biology and are seeking further exposure to scientific research beforegraduate study are especially encouraged to apply. Highly motivated individuals will have the opportunity for intellectual engagement in population genetics and molecular evolution research projects and the opportunity to co-author publications. The last two individuals who held the position are now enrolled in prestigious doctoral programs.

This position is available on or about July 21, 2008 for one year with continuation contingent on performance and availability of funds. Minimum requirements are a Bachelor's degree and experience in ecology, evolution, genetics or a related field. Previous laboratory experience with molecular genotyping and/or DNA sequencing is preferred. Salary will be commensurate with experience and includes benefits.

Please send a resume or CV and cover letter summarizing research interests and experience as well as three references with full contact information. Applications will be accepted until the position is filled.

Georgetown University is an equal opportunity/affirmative action educator and employer.

Matthew B. Hamilton, PhD Associate Professor Georgetown University Department of Biology, Reiss 406 37th and O Streets NW Washington, DC 20057 202-687-5924 (office) 202-687-5662 (fax) hamiltm1 at georgetown dot edu http://www9.georgetown.edu/faculty/hamiltm1/ “Matthew B. Hamilton” <hamiltm1@georgetown.edu>

IndianaU ResAssoc EvolutionaryGenetics

Research Associate in Evolutionary Genetics

The Moyle Lab, Department of Biology, Indiana University, Bloomington has an opening for a full time Research Associate starting as early as June 2008. We conduct research in plant evolutionary genetics, focusing on the genetic basis of reproductive isolating barriers and adaptive differentiation (http://www.bio.indiana.edu/~moylelab/). We seek a friendly, self-motivated, meticulous, and intellectually curious individual with a Bachelor’s or Master’s degree in Biology or related field. Research laboratory experience is strongly desired, although training will be provided. Good candidates might include recent college graduates with some relevant experience that wish to spend a bridge year before graduate studies.

The position involves 1/4 time lab management and 3/4 time research. Lab management responsibilities include ordering supplies, maintaining equipment, supervising work-study students, and overseeing lab functioning. Research responsibilities involve assisting lab members with molecular bench work (e.g. DNA and RNA extraction, genotyping, qPCR, sequencing), greenhouse-based phenotyping/QTL mapping, and plant maintenance and crosses. Some prior experience with histology and/or plant embryology would be wonderful. Initial projects will be supervised, although individually-developed projects are possible with greater experience. Salary will be commensurate with education and experience, and full benefits are included.

Submit letter of interest, resume and contact information for 3 references via email to Dee Verostko (dverostk@indiana.edu), using ’Moyle Research Associate’ as the subject line. The position is available immediately and will remain open until suitable candidates are identified. Direct inquires about the position to Leonie Moyle (lmoyle@indiana.edu). Some past and ongoing lab research projects can be found at: http://www.bio.indiana.edu/facultyresearch/faculty/Moyle.html Indiana University is an Equal Opportunity/Affirmative Action Employer.

lmoyle@indiana.edu lmoyle@indiana.edu

LinneanSociety London ExecSecretary

Job Title : EXECUTIVE SECRETARY Sector: Not for profit Job Hours: full time Organisation: The Linnean Society of London Salary: 35,000 - 40,000 (depending on experience)

The Linnean Society of London is seeking someone to drive forward its strategic goals and build on recent Linnaean Tercentenary achievements. The Society’s mission is the cultivation of Natural History in all its branches, notably systematics, plant and animal taxonomy, evolution and the history of biology. It is the worlds oldest extant Biological Society with an international Fellowship. It has an active scientific meetings programme, is actively delivering on-line resources and publishes three international scientific journals and the Linnean newsletter.

You will need a science degree (or equivalent) with a background in Natural History, excellent communication skills and a sound understanding of the academic research environment. Above all, you will be able to demonstrate the drive and ability to make things happen. You will represent the Society at a broad range of meetings and play an active role in fundraising for significant projects that advance the Societys long-term strategy and work to develop new initiatives. Experience in an academic or educational environment and knowledge of museum collections, scientific publications and libraries would be advantageous. Evidence of initiative, administrative and management experience commensurate with managing the activities of an organisation with 12 staff would be valuable. Further details and full job description are available on www.linnean.org Closing date for applications is Monday 12 May 2008.

Mark Wilkinson <mw@bmnh.org>

Mauritania CetaceanFieldAssist

RESEARCH ASSISTANT NEEDED FOR CETACEANS FIELD WORK IN NORTHWEST AFRICA

Hello, I am recruiting one research assistant for a period of approximately three weeks (May and beginning of June) to conduct cetacean research in Mauritania, which is located in Northwest Africa bordering the Sahara desert. The works consists of patrolling the whole Mauritanian coast, from the Parc National du Banc d'Arguin to the border with Senegal, in a 4-wheel drive and collect as much data and biological material as possible.

DUTIES of the research assistant: - be prepared to work long hours under the sun and for consecutive days; - assist with dissections if stranded animals are found; - assist in the collection of all kinds of biological material; - assist with Morphometric analysis of delphinid skulls; - collect plankton and fish samples; - participate in the laboratory activities.

REQUIREMENTS: - Background in biology, marine and environmental sciences or a related field; - Speak French is a plus (not essential) and a second language, such as Portuguese, Spanish or English; - Preferably have previous field experience (not mandatory) - Be prepared to live and work in a very simple manner, as Mauritania is a country with few resources and considered to be quite poor.

There is NO COMPENSATION for this work as it is entirely a VOLUNTEER position. The successful research assistant will be responsible for its own transportation to Nouakchott and living expenses (approx. 10-15 /day) during the time of the volunteering. This research position is ideal for people who want to gain some hands-on experience in the field of cetacean research and that might even want to pursue a future career in this field of expertise. This person should also like to travel and get to know other cultures.

TO APPLY: send an e-mail to one of the following addresses: anapinela@ub.edu or ana.pinela@gmail.com and attach a copy of your CV and a motivation letter briefly explaining why you're interested in this volunteer position.

Details related to the field work will be passed on to the successful candidate on plane fairs, accommodation, live style and costs, etc., as well as information on cetaceans that inhabit Mauritanian waters (bibliographic material).

To those of you, who read until the end THANK YOU FOR YOUR INTEREST!

Cheers,

Ana Pinela PhD Candidate Universitat de Barcelona Facultat de Biologia Dept. Biologia Animal (Vertebrados) Av. Diagonal 645, 1st floor 08028 Barcelona Spain Tel: +34 93 402 1453 Fax: +34 93 403 5740

ana_pinela@hotmail.com

NatlUIreland EvolutionaryBiology

Lectureship in Zoology

National University of Ireland, Galway is seeking a high-caliber zoologist for a permanent faculty position at the rank of lecturer (above the bar). While specific area of research is open, preference may be given to candidates working on either evolutionary/developmental biology, or ecology. Candidates should have a PhD and postdoctoral research and teaching experience.

Further information on the post and how to apply is available on NUIG's website: http://www.nuigalway.ie/news/vacancies.php?v_id=3D1757 Salary will be in the range of â¬64, 663 − â¬85, 562p.a.Informationonthedepartmentisavailableat : http : //www.nuigalway.ie/zoologyDeadlineforapplicationis30May

– Uri Frank Department of Zoology, School of Natural Sciences & Martin Ryan Marine Science Institute National University of Ireland, Galway University Road Galway Ireland Phone: +353-91-492334 Fax: +353-91-525005 Http://www.nuigalway.ie/zoology/frank

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NewYorkU ResTech CelegansVariation

Research Technician, Rockman Lab, New York University

The Rockman Lab at NYU's Center for Genomics and Systems Biology (http://biology.as.nyu.edu/object/-facilities.gsb.html) seeks a motivated, self-directed world-beater as full-time research technician. In this new lab, we will be discovering and characterizing the molecular and evolutionary causes of natural phenotypic variation (http://www.princeton.edu/ ˜ mrockman). Our primary research organism is C. elegans.

The Center for Genomics and Systems Biology is part of the Department of Biology, located in the heart of Greenwich Village in Manhattan. With an ongoing growth trajectory, NYU Biology is developing into a major locus for evolutionary biology. The collaborative and collegial research environment is ideal for work in evolutionary functional genomics. New York University is an equal opportunity employer.

Applicants should have molecular biology skills and a willingness to develop new methods as needed. Worm-handling experience is a plus. Preferred start date is May or June, 2008. Please contact Matt Rockman, mrockman at princeton.edu.

mrockman@Princeton.EDU mrockman@Princeton.EDU

NHM London EvolutionaryMycology

POSITION AS ASSOCIATE PROFESSOR/FULL PROFESSOR IN MYCOLOGY

is vacant at the Section of Botany, Natural History Museum University of Oslo, Norway.

The Natural History Museum (NHM), University of Oslo, is the largest of its kind in Norway with 150 employees engaged in research, teaching and popularising the science of biology and geology.

The advertised position seeks applicants experienced in the taxonomy of fungi. The position will entail responsibility for the collections of these and their use in modern research where competence in classical taxonomy as well as molecular methods is desired. Experience in attracting external financing to enhance the museums collection-based research profile is also desirable. The successful candidate will have responsibility for the fungal collection at NHM and its continued expansion (at present 6000 examples per year). National labour division within mycology implies a special responsibility at NHM for basiodiomycetes rather than the ascomycetes or other fungal groups.

In addition the successful applicant will be expected to supervise students at M.Sc. and Ph.D. levels, carry out administrative duties connected to the position and take part when necessary, in all aspects of the museums external activities and responsibilities to the general public.

Further details of the job description, responsibility and duties are to be found in a separate document available from the personnel officer tel.: +47 22 85 18 19; grethe.garfjeld@nhm.uio.no.

The application should contain documentation of qualifications, previous employment, scientific and museum experience, lecturing and administrative experience and ability to attract external research funding.

Assessment of applicants follows current regulations that place the main emphasis on the academic works submitted with the application. Account will also be taken of research management and participation in research projects if sufficient documentary evidence of this activity is provided. In addition weight will be placed on pedagogical qualifications, publicizing work and other activities. All aspects of the applicants background will be taken into consideration before appointment is made. NHM reserves the right to decide on the appointment of an Associate Professor or Full Professor, according to the applicants overall qualifications, including the right not to appoint.

Documentary evidence of pedagogical competence must be provided. Applicants who cannot produce documentary evidence of basic pedagogical competence may nevertheless be appointed, provided they acquire this competence within a period of two years after having been appointed.

As a general rule an interview will be used in the appointment process, and trial lectures may also be required.

The University of Oslo wants to have more women and also more people with an immigrant background in permanent academic posts. Women and people with an immigrant background are therefore encouraged to apply.

Applicants who are not competent in Norwegian, Swedish or Danish must acquire such competence within two years subsequent to their appointment (relevant courses are offered). Competence in English in the interim period is mandatory.

The University of Oslo has an agreement for all employees, aiming to secure rights to research results a.o.

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For further information, please contact: Head of Department, Professor Rune Halvorsen (tel: +47 22 85 16 29; r.h.okland@nhm.uio.no) or Research Manager, Fridtjof Mehlum (tel: +47 22 85 17 23; fridtjof.mehlum@nhm.uio. no).

Pay grade: Associate Professor: 57-66 (NOK 416,300 491,800 per annuum) Full Professor: 65-83 (NOK 483,100 733,000 per annuum)

Closing date: 6 May 2008

Ref.No.: 2008/1723

The application should be addressed to the University of Oslo. Four sets of the application, CV, copies of certificates and grades and documentation of other qualifications, complete reference list of all scientific publications list of publications as well as Scientific publications submitted for appraisal should be sent within deadline to: Natural History Museum, P.O.Box 1072 Blindern, N-0318 Oslo, Norway.

In addition applicants must submit a more detailed application form available from the NHM personnel officer grethe.garfjeld@nhm.uio.no or http://www.admin.uio.no/opa/ledige-stillinger havard.kauserud@bio.uio.no havard.kauserud@bio.uio.no

OregonStateU ResAssist SalmonEvolution

Oregon State University is accepting applications for a full-time, fixed term FACULTY RESEARCH ASSISTANT at the Hatfield Marine Science Center, Oregon State University, Newport, OR. Reappointments are at the discretion of the principal investigator. RESPONSIBILITIES: DNA extraction and microsatellite characterization of Oregon's coastal Chinook and Coho salmon stocks. Visit the Project CROOS website or contact Renee Bellinger at renee.bellinger@oregonstate.edu for more information.

REQUIREMENTS: BS in genetics, ecology or evolution with emphasis on statistics. At least one year of molecular genetics experience in PCR, DNA extraction. APPLICATION: To review the full position announcement or to apply refer to Posting 0002453, website http://oregonstate.edu/jobs . CLOSING DATE: May 5, 2008. OSU/AAEO

M. Renee Bellinger

Marine Fisheries Genetics Laboratory

Oregon State University

2030 Marine Science Drive

Newport, OR 97365

Phone: 541-867-0213

fax: 541-867-0345

"Bellinger, Renee" <renee.bellinger@oregonstate.edu>

RochesterU LabTech WolbachiaEvolutionaryGenetics

Research technician position in the laboratory of Professor John Werren, Department of Biology.

Wolbachia are among the most abundant parasitic bacteria on the planet. We are investigating their diversity, molecular evolution and effects on insects. Responsibilities include conducting PCR based molecular genotyping of bacteria and insects collected from around the world, analyzing DNA sequences using computer based genetic methods, assisting with quantitative PCR and RNAi knockdown of host genes involved in interactions with Wolbachia, and routine laboratory duties. Strong organizational skills are required for this position and some experience with PCR and sequence analysis is desired. This position is supervised by the PI and senior Lab Techs.

If interested, please contact Rachel Edwards (redwards@mail.rochester.edu) or John Werren (werr@mail.rochester.edu).

John Werren <jackwerren@yahoo.com>

RoyalSociety Editor

The Royal Society, the UK's premier scientific body, has published peer-reviewed scientific journals since 1665. The Society has a dynamic and growing journals publishing operation and, as part of our strategic development, we wish to appoint an Editorial Co-ordinator.

We are seeking an energetic and enthusiastic team player with excellent communication, organisational and interpersonal skills, a strong interest in all aspects of science and excellent scientific judgement.

You will play a key role in the scientific assessment of papers submitted for publication, selecting reviewers, taking decisions at key stages of the peer-review process and assisting with the development of our prestigious journals. This is an excellent opportunity for someone beginning a career in scientific publishing. You should have at least a first degree in science.

More information is available at http://-royalsociety.org/vacancy.asp?id=3D7633 Closing date 23rd May 2008.

This email is sent on behalf of The Royal Society, 6-9 Carlton House Terrace, London SW1Y 5AG, United Kingdom.

Claire.rawlinson@royalsociety.org

Simula Research Lab

Simula Research Laboratory conducts basic research in the fields of communication technology, software engineering and scientific computing. The research in the Scientific Computing (SC) department is focused on the development of numerical methods, algorithms and software, and large scale biomedical and systems biology oriented simulation studies applying these methods. In recent years, the main application area for computational research studies has been the simulation of the electrical and mechanical activity of the heart. Currently, we plan to extend our computational research to simulations of the evolutionary dynamics of genetic networks controlling the properties of organisms.

The aim of the research project is to study key evolutionary processes such as the adaptation of organisms to their environment, the splitting up of a species into multiple species and the development of multicellular organisms from a single fertilized cells. A key aspect of the research will be to study how the architecture and dynamics of genome organization and gene regulatory network structure influence the properties of organisms and hence how they influence the above mentioned evolutionary processes and how this contrasts with findings from more classical population genetics models.

Our understanding of genome organization and gene regulatory networks has changed dramatically over the last decade. A large part of DNA that was previously considered junk turns out the be functional after all, coding for RNAs that are however not translated into proteins. These RNAs in turn are often involved in regulating the expression of genes, which were previously thought to be exclusively regulated by proteins. Incorporating these new insights into our models is another key aspect of the research project.

Modeling formalisms used will typically be discrete, individual- based, event-based, and often spatially extended and will involve the explicit modeling of the evolution of genes, genomes and gene regulatory networks determining the properties of simulated agents. The project will be supervised by a new member of our research group, Dr. Kirsten ten Tusscher (http://www-binf.bio.uu.nl/khwjtuss/).

Simula offers excellent opportunities for doing high quality research, generous support for travels and equipment, and competitive salary (around 47.000,-Euro/69.000,- USD for a Ph.D. position)

We are looking for candidates who fulfill one or more of the following requirements: - a strong interest in evolutionary biological research - a University degree in computational biology, systems biology, biomedical engineering, artificial life, artificial intelligence, computer science, physics or applied mathematics - experience with computational modeling, simulation and analysis of complex (biological) systems.

The position requires excellent English writing skills and high marks from the BSc and MSc degree. Women are encouraged to apply. For more information contact Joakim Sundnes (sundnes@simula.no) or Kirsten ten Tusscher(tentussc@simula.no). To apply, email a short application letter, curriculum vitae, copies of transcripts and grades, and a publication list to jobs@simula.no. The subject of the email must contain 0830 Scientific Computing.

Application deadline: May 16, 2008

sundnes@simula.no sundnes@simula.no

UArizona LabManager DrosophilaEvolution

Lab manager UCSD at SRA II level. My laboratory is moving to EBE at UCSD July 1 and I am looking for a senior level technician to serve as the manager of the laboratory. We study Drosophila evolutionary biology using multiple experimental approaches. Qualifications include knowledge of Drosophila culture, routine molecular techniques, proficiency with sequence analysis software, equipment maintenance, laboratory safety protocols, record keeping and the ability to work independently and supervise undergraduates. For additional information please contact Therese Markow at tmarkow@arl.arizona.edu and visit the laboratory website at http://eebweb.arizona.edu/faculty/markow/index.htm Applications should be made through the University of California San Diego, job number HR 45862 at http://joblink.ucsd.edu/ by April 30.

Therese Ann Markow Regents' Professor Department of Ecology and Evolutionary Biology BSW 310 University of Arizona Tucson, AZ 85721

Office: 520 621 3323 Lab: 520 626 2772 FAX: 520 626 3522

tmarkow@arl.arizona.edu http://eebweb.arizona.edu/faculty/markow/index.htm tmarkow@public.arl.arizona.edu

UCaliforniaLosAngeles EvolutionInvasiveSpecies

Title: Summer research experience for undergraduates (REU) at UCLA

Location: Los Angeles, CA

Description: We are seeking 1 undergraduate applicant for summer research on a project examining the evolutionary impact of an invasive species. The REU student will be able to participate in field and laboratory research and there is opportunity to develop an independent project. The student will work under a faculty mentor and closely with graduate students and postdocs.

The REU student will assist on a project which aims to determine if Pacific tree frog (Pseudacris regilla) tadpoles are adapting to an invasive predator, the red swamp crayfish (Procambarus clarkii) in the Santa Monica Mountains near Los Angeles, CA. Anti-predator adaptations (morphological and behavioral) will be compared between tadpoles from streams with crayfish and tadpoles from streams without crayfish. Tadpoles will be collected from the wild and photographed for morphological analysis. The behavioral responses of tadpoles will then be tested to crayfish chemical cues and finally, a field predation experiment will be performed to determine the tadpoles' abilities to evade predation. In addition, the project will determine the population genetic structure of the Pacific tree frog throughout the Santa Monica Mountains with specific attention to the effects of urbanization and roads on P. regilla's genetic structure. This project would allow the REU student to learn molecular genetic techniques in the laboratory.

Qualifications: Applicants must be US citizens and currently enrolled as undergraduates (no graduating seniors). Must be available for approximately 10 weeks during the summer (June-September, start and end dates flexible). Enthusiasm for ecology and evolutionary biology and a positive attitude is a must. Students wishing to attend graduate school for a Master's or PhD are desired. Must be physically willing and able to hike in hot dry weather and get wet in the streams. Field sites contain hazards such as poison oak, rattlesnakes, and steep rocky terrain. Applications are encouraged from students from groups underrepresented in the biological sciences.

Salary: Stipend is available, to be determined, along with possible money for travel to Los Angeles but housing is not provided.

Contact info: If you are interested in the position, please email a letter of interest, CV/resume, and contact information of 3 references to: Katherine Pease at kpease@ucla.edu. Faculty mentor: Dr. Robert Wayne, UCLA, Dept. of Ecology and Evolutionary Biology

Deadline to apply: May 9, 2008

Katherine Pease, PhD student Department of Ecology and Evolutionary Biology University of California, Los Angeles 621 Charles E. Young Dr. S. Los Angeles, CA 90095-1606 310-825-5014 kpease@ucla.edu

UCaliforniaSantaCruz ResTech PlantEvolution

The Kay Lab in the Department of Ecology and Evolutionary Biology at the University of California, Santa Cruz invites applications for a research technician/lab manager.

The selected candidate will be responsible for helping to set up a new laboratory of plant evolutionary biology and assisting with research into flowering plant speciation, adaptation, and floral evolution. Duties include routine molecular biology procedures such as DNA/RNA extraction, PCR, DNA cloning, agarose gel electrophoresis, and DNA sequencing; assistance with carrying out large greenhouse experiments including the measurement of floral and vegetative plant traits and data entry; and occasional assistance with local fieldwork on California wildflowers. Laboratory organization/maintenance will include purchasing, setting up, and calibrating laboratory equipment, ordering supplies, keeping records of lab materials, maintaining records for lab safety, and training undergraduates and graduate students in basic lab and greenhouse procedures.

Desired qualifications include a Master's degree in Evolution and Ecology, Plant Biology, or related discipline; or a bachelor's degree with a minimum of one year working in an active biology research laboratory. Experience working with plants, quantitative and data management skills, familiarity with evolutionary genetics concepts and analyses. Good organizational, time management, and problem solving skills. The abilities to perform tasks in a clean, organized, methodical and analytical manner; learn and apply a variety of new techniques; work accurately with interruptions and to meet deadlines; work well independently and as part of a research team; interact effectively with a diverse group of faculty, staff and students; and demonstrate flexibility, initiative and good judgment.

The full job ad can be found at: http://apo.ucsc.edu/academic_employment/jobs/T08-55.pdf Also see the lab website at: http://bio.research.ucsc.edu/people/kay To apply please send a cover letter, cv, and contact info for three references to Kathleen Kay at kay@biology.ucsc.edu and reference position #T08-55. The job is open until filled and initial review of applications will begin May 15, 2008.

Kathleen Kay Assistant Professor Ecology and Evolutionary Biology Earth & Marine Sciences A308 UC Santa Cruz Santa Cruz, CA 95064 831-459-3446 http://bio.research.ucsc.edu/people/kay kay@biology.ucsc.edu kay@biology.ucsc.edu

UChicago LabTech DrosophilaTEs

Announcing a vacant full-time lab tech position available 1 May involving PCR screening of Drosophila for transposable elements in heat-shock genes, Drosophila maintenance and crosses, and phenotypic assays of development and thermotolerance. Ideal for a recent college graduate with some relevant experience wishing to spend a bridge year before graduate/medical studies. US citizenship or resident alien status required.

To apply: go to https://jobopportunities.uchicago.edu/ and search for requisition # 078977 The University of Chicago is an Affirmative Action / Equal Opportunity Employer.

Past lab research is described at the website below –

Dr. Martin E. Feder E-Mail: m-feder@uchicago.edu

Professor Department of Organismal Biology & Anatomy The University of Chicago 1027 East 57th Street Chicago, IL 60637 USA E-Mail: m-feder@uchicago.edu http://pondside.uchicago.edu/~feder/Martin_Feder.html m-feder@uchicago.edu m-feder@uchicago.edu

UCollegeLondon 2 EvolutionaryBiol

2 Academic Positions: Lecturer/Senior Lecturer

Research Department of Genetics, Environment & Evolution UCL Faculty of Life Sciences

The Research Department of Genetics, Environment & Evolution seeks two outstanding scientists to undertake research and teaching in evolution, ecology, environmental biology or related disciplines that will complement our existing strengths. One of the posts will be jointly held with the Department of Earth Sciences and will focus on Palaeobiology.

The appointments will be on the Lecturer or Senior Lecturer scales (Grade 8: £34,793 - £41,545 plus £2,649 London allowance or Grade 9: £45,397 - £49,606 plus £2,649 London allowance). Candidates should have a minimum of three years' post-doctoral experience. The successful candidates will establish independent, externally-funded research groups and contribute to teaching of our BSc degree programmes. The Departments of G.E.E. and Earth Sciences were rated highly (5) in the last National Research Assessment Exercise and 24/24 for the last Teaching Quality Assessment.

Application forms and further information can be obtained from Caroline Gougerty, (c.gougerty@ucl.ac.uk tel: +44 (0)20 7679 7011) or from: http://www.ucl.ac.uk/biology/academic-staff/vacancies/ Informal enquiries can be directed to the Head of Department, Prof Steve Jones (j.s.jones@ucl.ac.uk). Appointees are expected to be in post by October 2008. We particularly welcome female applicants and those from an ethnic minority, as they are under-represented within UCL at these levels. This is in line with section 48 of the Sex Discrimination Act and section 38 of the Race Relations Act. – Dr Max Telford Reader in Zoology Department of Biology, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel: +44 (0)20 7679 2554 Fax: +44 (0)20 7679 7096 http://www.ucl.ac.uk/biology/-academic-staff/telford/telford.html Perl scripts for downloading http://homepage.mac.com/maxtelford/-FileSharing9.html Mrimpatient: If you cant wait to see latest result of MrBayes analysis.

TranslatorX: Align nt sequence according to the aa translation.

Xstem and Ystem: Software for using secondary structure data in rRNA phylogenetic analyses.

Xenoturbella You Tube video http://uk.youtube.com/-watch?v=3DyJXNcoxL2Xs The Linnean Society of London http://www.linnean.org/ Zoonet: Marie Curie Research Training Network http://www.zoonet.eu.com m.telford@ucl.ac.uk

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UColorado ComparativeGenomics

Comparative Genomics Laboratory Technician Position U. Colorado School of Medicine

The Consortium for Comparative Genomics at the University of Colorado School of Medicine has an opening for a master laboratory technician in its high-throughput genomics laboratory. This is a full-time position funded by the Consortium for Comparative Genomics and the UC Cancer Center. The successful candidate will be expected to perform major and minor facets of molecular biology laboratory work required for running and maintaining the Roche-454 FLX ultra-high throughput genome sequencer operated by the Consortium. The position is an excellent opportunity for interested persons to become heavily involved with diverse cutting-edge comparative genomics research (medical and otherwise). The position will be supervised by David Pollock and Todd Castoe, and the postdoc would also be joining the evolutionary genomics research group led by David Pollock (HYPERLINK "http://www.evolutinoarygenomics.com" www.evolutinoarygenomics.com).

The position would be located at the new UC-Health Sciences Center Anschutz Medical Campus in Aurora, Colorado, on the outskirts of Denver. (http://-www.uchsc.edu/)

Specific Duties: The duties of the position holder will center around performing all technical laboratory aspects required to run diverse samples on a 454-FLX high-throughput automated genome sequencer housed in the School of Medicine. Specifically, the job involves assessing sample quality and quantity from users, communicating with users and other directors regarding sample diagnosis and project design, carrying out molecular biology laboratory work including PCR, oligo ligation, and other misc. steps within the 454-FLX sample preparation protocol, and maintaining an organized accounting of reagent use and costs. This position requires close interaction with various project directors as well as smooth integration with other laboratory work housed in the UC Cancer Center Core facility. There is also broad future potential, if desired, for the position to expand into intellectual design and implementation of experiments, and also into specific collaborative work with participating scientists.

Requirements: A master^{1}s degree in a relevant field or equivalent experience is preferred (e.g, bachelor^{1}s degree plus two or more years work experience). The candidate must be a highly motivated, self-organizing and independent worker with the ability to also collaborate in a team setting. Computer literacy is required, and additional computer experience with Unix, and/or programming experience is a plus. Any genomics, DNA sequencing, or statistical experience is also a strong plus, but not absolutely required. Deep understanding of molecular biology is preferred.

Salary: The salary range for this position is between $35,000 and $65,000 per annum, depending on qualifications.

To apply: Please forward a cover letter, CV/Resume and names of three references to Kathy R. Thomas, Administrative Coordinator, Computational BioScience Program, PO Box 6511, Mailstop 8303, Aurora, CO 80045-0511, or email to HYPERLINK "mailto:Kathy.R.Thomas@uchsc.edu" Kathy.R.Thomas@uchsc.edu

Review of applicants will begin immediately and continue until the position is filled. Multiple openings may be available.

The University of Colorado is committed to diversity and equality in education and employment.

Todd.Castoe@UCHSC.edu Todd.Castoe@UCHSC.edu

UGeneva HumanPopulations DeadlineMay9

THE DEADLINE FOR SENDING APPLICATIONS FOR THE FOLLOWING PROFESSOR POSITION IN THE UNIVERSITY OF GENEVA HAS BEEN POSTPONED TO MAY 9TH, 2008:

PROFESSOR POSITION:

The Faculty of Sciences of the University of Geneva (Switzerland) has an opening for a position as

Full or Associate professor (professeur ordinaire ou adjoint) in Biological Anthropology

Full-time appointment. Teaching will be in French. The successful candidate is expected to conduct a research group. Anthropological research in biometry, epidemiology or demography of present and / or past human populations will be considered with particular attention ; social anthropology is excluded. The position is also open for Assistant Professors (Tenure Track).

DEGREE REQUIREMENT : Ph.D or equivalent.

STARTING DATE : August 1st, 2008, or as agreed

Applicants with relevant experience in research and teaching should send their application before May 9th, 2008 to : Dean of The Faculty of Sciences, Quai E.-Ansermet 30, CH-1211 Genève 4, Switzerland, where further information concerning the job description and working conditions may be obtained.

Applications from women are particularly welcome.

For more information, please contact the Department of anthropology and ecology at +41 22 379 69 67.

– Prof. Alicia Sanchez-Mazas Laboratoire dAnthropologie, Génétique et Peuplements (AGP) Département dAnthropologie et dEcologie Université de Genève >>>>> Adresse physique: 12, rue Gustave-Revilliod 1227 Genève, Suisse Adresse postale: Case postale, 1211 Genève 4, Suisse Tel. +41 (0)22 379 69 84 (Ligne directe) Fax +41 (0)22 379 31 94 http://agp.unige.ch/fr/ Alicia.Sanchez-Mazas@anthro.unige.ch

UGuelph 3 Biodiversity

Biodiversity Institute of Ontario University of Guelph Associate Professor (1 position) Assistant Professor (2 positions)

Operating from a newly constructed facility, the Biodiversity Institute of Ontario (BIO) is committed to building multidisciplinary teams to probe issues ranging from molecular evolution to conservation. With a staff of 35 bioinformaticians, genomicists and biodiversity specialists, BIO is currently directing special effort towards the development of a DNA-based identification system for eukaryotic life. Together with colleagues in 25 other nations, the Institute is striving to activate the International Barcode of Life Project, a $150M research program that will gather DNA barcodes from 5M specimens representing 500K species. BIO now seeks to reinforce its scientific leadership by filling three tenure track positions:

Associate Professor, Molecular Biodiversity Assistant Professor, Molecular Ecology Assistant Professor, Molecular Biodiversity of Eukaryotes

These positions carry the expectation of a very strong commitment to research. Teaching responsibilities are anticipated to be primarily at the graduate level, while service activities will relate to the oversight of certain BIO research facilities or activities. BIO provides access to an outstanding research infrastructure including a state-of the-art sequencing facility (high-volume ABI capillary and 454FLX sequencers, robotic liquid handlers) and a strong informatics team. Each successful candidate will be appointed to the academic department appropriate to their expertise and research interests, and seconded to the BIO on an initial 5 year renewable appointment.

Associate Professor, Molecular Biodiversity A background in molecular evolution and bioinformatics is critical; applications from individuals with interests in freshwater invertebrates are particularly encouraged. Candidates must have an established research program, past success in gaining external funding for biodiversity research, a demonstrated record of teaching excellence at all levels and a strong publication record. The successful candidate can expect appointment with tenure.

Assistant Professor, Molecular Ecology A strong background in molecular evolution and bioinformatics and experience in collaborative research are critical. We are particularly interested in candidates whose research has employed DNA barcoding for studies in co-evolution and/or conservation biology.

Assistant Professor, Molecular Biodiversity of Eukaryotes A strong background in molecular evolution and bioinformatics and experience in collaborative research are critical. We are particularly interested in candidates whose research has examined the application of DNA barcoding in both theoretical and empirical contexts across varied kingdoms of eukaryotic life.

Applicants should submit a copy of their curriculum vitae and the names of three references to: Dr. Paul Hebert, Biodiversity Institute of Ontario, University of Guelph, Guelph, ON, N1G 2W1 by May 15, 2008. Electronic submissions are welcomed and should be directed to smannhar@uoguelph.ca. The above positions are available effective July 1, 2008.

All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. The University of Guelph is committed to an employment equity program that includes special measures to achieve diversity among its faculty and staff. We therefore particularly encourage applications from qualified aboriginal Canadians, persons with disabilities, members of visible minorities and women. Ad08-29

Susan Mannhardt <smannhar@uoguelph.ca>

UIceland Reykjavik EvolutionaryEcol

I would like to draw your attention to a vacant position in ecology including evolutionary ecology at the University of Iceland in Reykjavik.

The following ad appeared on Nature Jobs http://www.nature.com/naturejobs/science/jobs/49256 April 7:

The University of Iceland invites applications for a tenure-track academic position in ecology at the Department of Biology. The appointment will initially be for four years. The successful applicant will be responsible for a basic course in ecology and is expected to develop an active research and academic programme, including teaching at both undergraduate and postgraduate levels.

Applicants should have a Ph.D. in ecology or comparable academic background and good collaborative and communication skills.

The initial appointment will be at the rank of assistant professor with subsequent promotion governed by university regulations. Application details and more information can be found at: http://www.hi.is/page/vacant_positions For further information contact Professor Olafur S. Andresson, chairman Department of Biology (osa@hi.is).

The equal opportunities policy of the University of Iceland applies to all appointments.

Einar Arnason einararn@hi.is

einararn@hi.is

UIdaho Aide BacteriophageEvolution

Scientific Aide

Mathematics/Biological Sciences

Open for Recruitment: April 11, 2008 - May 5, 2008 Announcement #: 17536074344 Pay Rate: $14.42/hour, $14,996.80.year + DOE Full or Part Time: Part Time Shift: 20 hours/week Location: Moscow This position is contingent upon the continuation of work and/or funding.

Materials Required: Online Application (www.hr.uidaho.edu) Job References Letter of Qualification Resume

MAJOR FUNCTION: The Scientific Aide will assist the principal investigator and laboratory personnel in performing original research primarily in the area of bacteriophage evolution and ecology. In addition he/she will also direct the day-to-day aspects of running the laboratory.

MINIMUM QUALIFICATIONS: Education/Experience: Bachelor's degree in Microbiology, Biology, or related field; OR equivalent combination of education and/or experience totaling approximately 4 years. Good knowledge of: Scientific principles, computer software programs. Demonstrated ability to: perform a variety of specialized tasks and laboratory techniques specific to the needs of the position; operate, maintain, calibrate, troubleshoot and resolve basic problems with instruments and equipment; keep records and compile written information for reports; follow good safety practices; possess good interpersonal and communication skills; may train and supervise other workers. Physical ability to: perform assigned duties; may be required to work with toxic, volatile and corrosive chemicals and/or carcinogenic substances; may be required to work in adverse environmental conditions and/or carry or lift heavy materials. Must: Applicants who are selected as final possible candidates must be able to pass a background check and show proof of eligibility to be employed in the United States.

ADDITIONAL DESIRABLE QUALIFICATIONS:

One or more years of experience in a molecular biology or microbiology research laboratory. Experience with techniques used in microbiology. Knowledge of DNA sequence analysis, including experience with sequence analysis software and with the use of sequence databases.

Human Resources

PO Box 444332 Moscow, Idaho 83844-4332

HR: (208) 885-3612 -or- (208) 885-3728

TDD: (208) 885-3617

FAX: (208) 885-3602

UNebraska FieldAssist ResistanceEvolution

SUMMER FIELD ASSISTANT POSITION IN LINCOLN, NEBRASKA

Field assistant needed to work on project examining the effects of assortative mating on resistance evolution at the University of Nebraska-Lincoln.

Duties include:

Counting flowers Assessing pollinator abundance Maintaining experimental plot Maintaining virus treatments Entering data Weeding

EARLY MORNINGS are required for this position. 20-40 hours per week (full time status preferred).

$8 / hour

Contact: Dr. Diana Pilson dpilson1@unl.edu

or

Holly Prendeville hrp@unlserve.unl.edu – 402-472-2347

408 Manter Hall Lincoln, NE 68588

– Holly R. Prendeville, PhD candidate University of Nebraska School of Biological Sciences 348 Manter Hall Lincoln, NE 68588-0118

402-472-2347 hrp@unlserve.unl.edu

http://www.unl.edu/dpilson/GOURDS.html Holly Prendeville <hrp@unlserve.unl.edu>

UNewBrunswick ProtistanDiversity

University of New Brunswick - Marine Protistan Diversity The Department of Biology, University of New Brunswick (Fredericton), seeks applicants for a tenure-track position at the Assistant-Associate Professor level in Marine Protistan Diversity. The successful candidate will develop a strong research program examining genomic diversity from evolutionary and environment perspectives, emphasizing comparative genomics and protistan diversity at the species to genomics level in marine heterotrophic and/or phototropic protists. Specific research areas include, but are not limited to: exploring species diversity through molecular biology; evolution of organelles and organismal attributes; genome structure and function; and diversity with regards to biochemical and cellular processes. The candidate will be expected to mentor undergraduate and graduate students, as well as postdoctoral fellows, and teach undergraduate and graduate courses appropriate to departmental need and the candidate's expertise. The successful candidate must have a track record in research that will be highly competitive in attracting external research funding and HQP. The position is associated with the Canadian Institute for Advanced Research (CIFAR) and its newly established Integrated Microbial Biodiversity (IMB) program. The successful applicant will join a network of international researchers as a Scholar in the CIFAR IMB Program (information on this program can be found at www.cifar.ca). The applicant will also contribute to the Marine Environmental Barcoding component of the international Barcode of Life, a project aimed at investigating protistan biodiversity in the ocean with molecular techniques. The successful candidate will join biology, comparative genomics, bioinformatics and biodiversity (CEMAR: www.unb.ca/cemar). Additional research strengths in the Department of Biology include aquatic ecology and fish biology, conservation biology, and evolutionary biology. Information about Biology at UNB is available at www.unb.ca/fredericton/science/biology.

A PhD and relevant postdoctoral experience is required.

The closing date for applications is August 4, 2008. To apply, send a letter describing your research and teaching interests, a curriculum vitae with names, addresses, and e-mail contacts for three referees, representative publications, and a statement of teaching philosophy to:

Gary W. Saunders, Chair Department of Biology University of New Brunswick P. O. Box 4400 Fredericton, NB E3B 5A3

All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. Applicants should indicate current citizenship status. This position is subject to budgetary approval.

Stephen Heard

sheard@unb.ca Professor and Associate Chair Dept. of Biology

506-452-6047 University of New Brunswick FAX 506-453-3583 Fredericton, NB E3B 6E1

Steve Heard <sheard@unb.ca>

UOsnabruck Germany MolEvolution

The Department of Biology at the University of OsnabrÃ$\frac{1}{4}$ck (Germany) invites applications for a Research Associate (Wissenschaftlicher Mitarbeiter/in) (E 13 TV-L) in the field of Molecular Evolutionary Ecology

The department is seeking highly motivated candidates with experience and research interests in the area of molecular evolutionary ecology. The candidate will be able to run a molecular lab and should be familiar with Quantitative Realtime PCR and RNAi. The applicant should have a strong background in evolutionary biology, preferentially working with social organisms (vertebrates, invertebrates or 'social microbes'). He/she should establish externally funded projects, supervise students, contribute to the teaching mission of the department (in English or German language), and will have the opportunity to obtain the 'Habilitation' (a German qualification supportive in applications for professorships).

The position is available starting June 2008 for a maximum of up to six years. Initial appointment is for three years. Review of applications will occur until the position is filled.

The University of OsnabrÃ$\frac{1}{4}$ck is committed to equal opportunity in employment and gender equality in its working environment. We strongly encourage applications from qualified women. Applications from appropriately qualified handicapped persons are also encouraged.

Applicants should electronically submit a complete CV, reprints (pdf-files) of three representative papers and a concise description of current and future research concepts. Applicants should also arrange for three letters of reference to be submitted on their behalf to the address below.

Applications for this position are required by May 2nd 2008 and should be sent to:

Dean of the Department of Biology/Chemistry, University of OsnabrÃ$\frac{1}{4}$ck, BarbarastraÃe 11, 49069 Germany

For further information please contact Prof. Dr. Judith Korb, Behavioral Biology, e-mail: Korb@biologie.uni-osnabrueck.de; http://www.biologie.uni-regensburg.de/Zoologie/Heinze/Staff/JudithKorb/index.html Prof. Dr. Judith Korb Behavioral Biology University of Osnabrueck Barbarastr.11 D-49076 Osnabrueck Germany Phone: ++(49) (0)541 9692830 Fax: ++(49) (0)541 9692862 email: judith.korb@biologie.uni-osnabrueck.de

"Korb, Judith" <Judith.Korb@Biologie.Uni-Osnabrueck.DE>

Vienna GroupLeader TheoPopGen

Postdoc - Research Associate / Group Leader Position in Theoretical Population Genetics / Genomics at the University of Vienna

The mathematics and biosciences group (MaBS) at the University of Vienna is looking for a strong and highly motivated candidate for a senior postdoc / research associate position in evolutionary modeling and/or statistical data analysis. The research focus is flexible and includes work in molecular population genetics, evolutionary genomics, and quantitative genetics. See the MaBS homepage (www.mabs.at) for further information on our research interests.

Depending on the experience of the candidate, the position can be offered on the level of a Postdoc (for two years initially) or a Research Associate / Junior Group Leader (for up to five years). Postdocs are encouraged V and Research Associates expected V to develop an independent research program in addition to projects in cooperation. The starting date is negotiable.

Vienna is not only one of the worlds most liveable cities, but also offers an excellent research environment and currently develops into one of the main centers in evolutionary research in Europe.

Formal requirement is a PhD and a strong background and interest in quantitative evolutionary research (analytical or computational modelling or data analysis). Postdoc experience is expected for hires at the Associate level. The working language in the group is English, German skills are not essential. The reviewing process will start at the end of April and will continue until the position is filled. Full applications should include a CV with publication list, a summary of past and future research interests, and the names and email addresses of three potential referees. Applications and informal inquiries should be sent (preferably as a single pdf) to Joachim Hermisson (joachim.hermisson@univie.ac.at).

joachim.hermisson@univie.ac.at

WilliamMaryCollege Visiting PopulationBiology

VISITING ASSISTANT PROFESSOR OF CONSERVATION BIOLOGY

College of William and Mary

The Department of Biology invites applications for a one-year visiting faculty position in Conservation Biology, beginning in August 2008. The successful candidate will teach one upper division lecture/seminar course in population or organismal biology in the fall of 2008 and one upper division conservation biology course with one or two laboratory sections in the spring of 2009. Candidates with a quantitative approach to conservation and population biology are strongly encouraged to apply. Applicants must have a Ph.D. in an appropriate field. Postdoctoral experience is preferred. Candidates should have a demonstrated commitment to excellence in teaching and are encouraged, but not required, to engage in collaborative research projects with our current faculty members (http://www.wm.edu/biology).

Please send a letter of application, curriculum vitae, statement of teaching interests and philosophy, description of research interests, and three letters of reference to: Dr. George W. Gilchrist, Dept. of Biology, College of William and Mary, PO Box 8795, Williamsburg, VA 23187. Review of application materials will begin on May 1st and will continue until the position is filled. The College of William and Mary is an EEO/AA Employer.

George W. Gilchrist Email: gwgilc@wm.edu Director of Graduate Studies Phone: (757) 221-7751 Department of Biology, Box 8795 Fax: (757) 221-6483 College of William & Mary Williamsburg, VA 23187-8795 http://gwgilc.people.wm.edu/ gwgilc@wm.edu gwgilc@wm.edu

Other

Accelrys petition followup

Hi all - re. http://www.petitiononline.com/gcg/ A huge THANKS to all of you that signed my petition! Within the first week online I got almost 150 signatures, and John Devereux himself most recently signed it. I sent Rob Brown of Accelrys an 'official' copy of the petition and the signatures at the end of last month. However, but not surprisingly, I have yet to receive one word back from Accelrys. I realize that we can't force them to do anything, but I at least thought that they would have the courtesy to respond to it somehow. The petition did result in a news story though. GenomeWeb News' bioinformatics newsletter, BioInform, published the story on April 4th. See my copy at:

http://bio.fsu.edu/~stevet/BioInformGCG.pdf Some may feel that the BioInform story suggests the petition was merely a means of influencing commercial negotiations with Accelrys regarding code release, and have nothing to do with public domain availability, but this was never my objective. It is and remains a plea not to kill the package, and in particular SeqLab, by whatever means possible, but preferably within some type of open source arrangement. Furthermore, Accelrys argues in the article that many more people have signed the petition than bought in to the package, and that this somehow invalidates the petition. This is completely irrelevant as the GCG license has always been to an institution, allowing as many people in that institution access as wanted, not to individual investigators. Here at FSU I have supported over 100 GCG users with one GCG license over the years. June should be interesting for us all. We'll have to see if Accelrys honors their commitment to those of us with "perpetual" licenses to provide non-node-locked, non- expiring versions of the license after June 30, 2008. Time will tell.

Cheers - Steve

Steven M. Thompson stevet@bio.fsu.edu http://bio.fsu.edu/~stevet/cv.html FSU SCS / BioInfo 4U

Florida State University School of Computational Science

1st floor DIRAC 150G Tallahassee, Florida 32306-4120 850-644-4490

2538 Winnwood Circle Valdosta, Georgia 31601-7953 229-249-9751

stevet@bio.fsu.edu

Accelrys petition followup 2

Hello all -

A brief note to let you know what's happened since my posting this last Wednesday:

Rob Brown of Accelrys did contact me, finally. He says, and I quote:

"The petition and the subsequent BioInform article produced a significant response and generated inquiries from a number of third party companies who now wish to discuss various possibilities relating to GCG with us.

We are now in the process of following up on all of those which is taking some time."

So, it looks like some good has come out of the process, although this doesn't look like the open source type of arrangement that many of us hoped for. Regardless, it may mean that the package will not be dying.

And, Accelrys sent me my new non-node-locked, non-expiring license key!

Cheers - Steve

Steven M. Thompson stevet@bio.fsu.edu http://bio.fsu.edu/~stevet/cv.html FSU SCS / BioInfo 4U

Florida State University School of Computational Science

1st floor DIRAC 150G Tallahassee, Florida 32306-4120 850-644-4490

2538 Winnwood Circle Valdosta, Georgia 31601-7953 229-249-9751

stevet@bio.fsu.edu stevet@bio.fsu.edu

Accelrys petition followup 3

Hi all -

I would like to offer my apology to Accelrys and its employees for suggesting that the company would not follow through on their commitment to supply non-node-locked, non-expiring license keys to all current GCG custyomers with "perpetual" licenses. As I mentioned in my last posting Accelrys is now involved in that process and I have received my new key. It was never my intent to discredit Accelrys, nor its employess. I merely had not been informed that the process was underway. I am sorry that I miswrote and hope that any hard feelings can be overcome. Thank you.

Cheers - Steve Steven M. Thompson stevet@bio.fsu.edu http://bio.fsu.edu/~stevet/cv.html FSU SCS / BioInfo 4U

Florida State University School of Computational Science

1st floor DIRAC 150G Tallahassee, Florida 32306-4120 850-644-4490

2538 Winnwood Circle Valdosta, Georgia 31601-7953 229-249-9751

stevet@bio.fsu.edu stevet@bio.fsu.edu

AFLP ABI answers

Dear all,

I would like to thank you for your quick and helpful replies concerning AFLPs. As many of you were interested in the answers, here comes a short summary of them:

Purification of selective PCR products: -most people do not do a sephadex purification because one might loose fragments -those who do a sephadex purification report that this leads to a reduction of primer-dimers and a better resolution and clarity in the range from 75-500 bp -one can also try a purification of PCR products following precipitation protocols for sequencing

Sample volume: -1-3 [cid:image001.png@01C898A1.8EAF7840] multiplexed PCR product in 10-15 [cid:image002.png@01C898A1.8EAF7840] l total volume (HiDi and Standard)

Injection time: -10-40 (or even 90) seconds

PCR protocol: -use of other/better Taqs or PCR kits (see also Trybush et al, Can. J. Bot. 84: 1347-1354 (2006)). -20-30x dilution of the multiplexed selective PCR product will lead to better/higher peaks

Again, many thanks to all of you who helped, and good luck with your AFLPs!

Simone Steffen

Institut für Spezielle Botanik und Botanischer Garten Bentzelweg 9a 55099 Mainz Germany

phone: +49 6131 3922624 fax: +49 6131 3923524 mail: ssteffen@uni-mainz.de<mailto:ssteffen@uni-mainz.de>

ssteffen@uni-mainz.de

AmerGeneticsAssoc Awards

The Council of the American Genetics Association invites applications from members of the Association for support of special events. The Association expects to make up to four awards of approximately $10,000-15,000 this year. Eligible events include specialized workshops open to Association members in areas of great current interest and short courses in some aspect of organismal genetics, but any event that would advance the purpose of the Association is eligible for support. We encourage members to think creatively about the types of events they could offer with support from the Association. All applications received will be carefully reviewed.

An application for a Special Event Award should include the following items of information:

1. The name(s) and title(s) of the individual(s) who will be responsible for organizing the event and overseeing the expenditure of any funds awarded.

2. The institution to which an award should be made, including the complete address of the relevant institutional department and the signature of an authorized institutional representative indicating the institution's willingness to administer the award if granted.

3. The title of the event for which an award is requested.

4. A rationale for the event explaining (a) why the event is timely or needed, (b) how the planned event will address the perceived need, and (c) how support from American Genetics Association will improve the event, e.g., by making it possible or by making it more affordable for graduate students and post-doctoral research associates. The rationale need not be longer than 1 page.

5. A description of the event including (if available): a list of primary participants (e.g., workshop leaders, course instructors), dates and location of the event, a preliminary schedule for the event, and a plan for how participants will be selected (if participation is limited). The description need not be longer than 2 pages.

6. A budget for the event showing how funds provided by an award from the Society would be used to support event activities. If funds are also being sought from other sources, the budget should show both how funds from the Association will be used and how funds from other sources will be used. (The sources of other funds need not be identified, but the application should indicate whether the funds are in hand.)

Applications for a Special Event Award should be emailed to Anjanette Baker at the AGA office (agajoh@oregonstate.edu). The Council will review all applications received before April 30, 2008, and make award decisions at its annual meeting in June 2008.

agajoh@oregonstate.edu agajoh@oregonstate.edu

Anther smut samples

We are performing a phylogeography study on the anther smut fungus parasitizing plants from the Caryophyllaceae family, and we would like ask Evoldir members who happen to see some infection during holidays, meetings or field trip if they would be so kind as sending us samples. The fungus Microbotryum violaceum produces its spores in the anthers of the infectes plants, that then become purple. We are most interested in spores from the plants Silene latifolia (=white campion, Silene alba), Silene dioica and Silene vulgaris. Samples from the US, the UK and South and Eastern Europe would be the most valuable. Infected flowers should be put in paper bags, and we would like ideally 5-15 samples per population. We can send more details and pictures. Many thanks in advance

–

Tatiana

Tatiana Giraud

Chargée de recherches Departement Genetique et Ecologie Evolutives Laboratoire Ecologie, Systématique et Evolution UMR 8079 CNRS-UPS-ENGREF Bâtiment 360 Université de Paris-Sud 91405 Orsay cedex France

phone: +33 1 69 15 56 69 + 33 6 34 64 45 14 fax: +33 1 69 15 46 97

http://www.ese.u-psud.fr/bases/upresa/pages/-giraud/index.html http://www.ese.u-psud.fr/ Tatiana Giraud <tatiana.giraud@u-psud.fr>

Chloroplast subst rates

Dear Evoldir members,

Is anyone aware of published evolutionary rates for specific chloroplast genes, as opposed to whole genome rates? I am particularly interested in the cpDNA protein-coding genes matK and ndhF, but I would also like to get a feel for the range of rates seen in other genes.

There's a nice table in Hewitt (2001, Mol. Ecol., 10, 537-549) that includes Li's (1997, Molecular Evolution. Sinauer Associates, Sunderland, MA) estimated rates of synonymous & non-synonymous in cpDNA, but I have been unable to find other relevant literature. Any suggestions would be greatly appreciated.

Cheers, Ryan (email:rcgarrick@vcu.edu)

Ryan Garrick Department of Biology Virginia Commonwealth University 1000 W. Cary Street Richmond, VA 23284-2012

http://dyerlab.bio.vcu.edu/ rcgarrick@vcu.edu rcgarrick@vcu.edu

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Duck samples

Dear all,

for my PhD project I am searching for people who are working on wild waterfowl, especially ducks in at least one of the following countries:

It mainly concearns eastern Europe and the Balkans:

- Belarus - Ukraine - Czech Republic - Slovakia - Hungary - Romania

- Croatia - Bosnia-Herzigovina - Serbia-Montenegro - Albania - Former Yugoslawian Republic/Mazedonia - Greece - Turkey - Bulgaria - Moldova

- Italy - Sicily - Sardinia - Malta - Ireland

If you are working, or know someone who is working there, please let me know. In the further contact I will explain more details. Contacts to hunters are useful for me, too. So, if you know hunters who are hunting ducks in the above mentioned countries, please connect with me.

Many thanks for any possible hint!

Cheers, Robert

Robert H. Kraus PhD student Wageningen University Resource Ecology Group Droevendaalsesteeg 3a 'Lumen' Building, Number 100 6708 PB Wageningen The Netherlands

Phone +31 317 483530 Fax +31 317 419000 Email robert.kraus@wur.nl http://www.reg.wur.nl/-UK/Staff/Kraus/ robert.kraus@wur.nl

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Estimating founder population size answers

Dear EvolDir Members

I had a few requests to post answers to my recent question about estimating founder population size. The original post and answers are at the bottom of this email. Many thanks to all that replied, most suggestions helpfully directed me to papers and software that have tackled similar problems.

I hope this helps!

Jacqui

ORIGINAL POSTING

Dear EvolDir members

I am attempting to estimate founder population size for a recently introduced population (c. seven years/max 10 generations) of Anolis using microsatellite data. Standard estimates of effective population size are likely to be inappropriate in this case since mutation rate cannot be accurately estimated due to the recent nature of the introduction.

I have come across a paper (Rasner et al 2004, Molecular Ecology) that attempts to answer the question using the number of alleles (n) within the most variable locus in the introduced population as an absolute minimum estimate of the founder population size. (Eight generations were assumed to have passed between founding and sampling). The paper then uses simulation to resample a specified number of 'founder individuals' from the native population 1000 times and calculates the proportion of times that at least this number (n) of alleles are captured in the samples. The smallest number of founders consistent with the data was taken to be the number that gave a probability > 0.05 of capturing n observed alleles (Rasner et al 2004).

My questions are

first, does anyone know of a method for estimating founder population size using microsatellite data in such a recently founded population?

second, is there a program in the public domain that can handle a simulation such as that described above? It is presumably relatively easy to write such a program, unfortunately it is not my expertise!

Many thanks for your anticipated help on this problem, Jacqui Eales Doctoral candidate, Bangor University, Wales, UK

ANSWERS:

"Andrew J. Bohonak" See the following papers (pdfs on my web site), in which I have simulated founding events similar to that you describe: Vandergast, A. G., A. J. Bohonak, D. B. Weissman and R. N. Fisher. 2007. Understanding the genetic effects of recent habitat fragmentation in the context of evolutionary history: phylogeography and landscape genetics of a southern California endemic Jerusalem cricket (Orthoptera: Stenopelmatidae: Stenopelmatus). Molecular Ecology 16: 977-992. Bohonak, A. J., N. Davies, F. X. Villablanca, and G. K. Roderick. 2001. Invasion genetics of New World medflies: testing alternative colonization scenarios. Biological Invasions 3: 103-111. Bohonak, A. J., and G. K. Roderick. 2001. Dispersal of invertebrates among temporary ponds: are genetic estimates accurate? Israel Journal of Zoology 47: 367-386. (Special Issue: Ecology of temporary pools) Hairston, N. G., Jr., L. J. Perry, A. J. Bohonak, M. Q. Fellows, C. M. Kearns and D. R. Engstrom. 1999. Population biology of a failed invasion: paleolimnology of Daphnia exilis in upstate New York. Limnology and Oceanography 44: 477-486.

Dear Jacqui Eales, have a look at Wang (2005) Estimation of effective population size from data on genetic markers. Phil Trans R Soc B 360:1395-1409. and at his software page: http://www.zoo.cam.ac.uk/ioz/software.htm Maybe this helps, cheers, Rodolfo Jaffé

Hi Jacqui, It may be worth looking at some of Mark Beaumont's programs: http://www.rubic.rdg.ac.uk/~mab/software.html There is a nice use of such approaches in Goossens et al. 2006 Plos Biol, 4(2) 0285-0291, looking at very recent bottlenecks in Orangutans. Good luck, Mark de Bruyn

Hi Jacqui, Check out E. C. Anderson and M. Slatkin, Estimation of the number of individuals founding colonized populations. 2007. Evolution 61: 927-983, and the corresponding software. Also see http://www.plosone.org/article/fetchArticle.action?articleURI=info:doi/10.1371/journal.pone.0000868 - an article of mine where I estimate founder population size for a North American invasive bee species (using forward simulations).

Cheers, Amro Amro Zayed, PhD NSERC Postdoctoral Fellow Department of Entomology University of Illinois at Urbana-Champaign

Hi Jacqui, Have you tried Rmetasim (Strand 2002)? We used this program to estimate the number of founders in non-native populations of bulllfrogs in Europe (Ficetola et al. 2008). We used mDNA data but it also works with microsatellites. I send you the two papers.I hope this helps. Aurélie Bonin, Grenoble

Hi Jacqui, I wanted to do something similar for a species that had been introduced for biological control. I used msVAR, which is freeware. I used it to estimate current population

— / —

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

Evolution2008Meeting Roommate

Hello,

I am a female postdoc researcher and looking for a roommate to share a $66 double dormitory room during the evolution 2008 meeting in Minneapolis, MN. I plan to stay between June 19th and 25th. Please email me (tyuri@ufl.edu) if you are interested.

Tamaki Yuri Dept. of Zoology University of Florida P.O. Box 118525 Gainesville, FL 32611-8525 Phone: (352) 870-7067 Fax: (352) 392-3704

Tyuri@ufl.edu Tyuri@ufl.edu

Genetic data simulation answers

Dear all

Many thanks to all that replied to my request for a simulation software for genetic data.

Many people asked to have a copy of the answers. Below there is my original question and all the replies.

Thank you again to all.

My question:

I'm looking for a simulation software for genetic data that allows:

- input genotpypic data - perform random mating simulation for several generations

Easypop doesn't allow to input data file. I'm greateful to all for any help.

REPLIES:

Hi Daniele,

You could try Nemo. A friend of mine built it and I have been using it extensively. There is functionality built into Nemo to read from an input file and to perform random mating simulations, but I am not sure how easy it is to construct an input file from scratch with your own data. I've copied Fred's email here, as he programmed it originally, so you might ask him.

Good luck! Sam

http://nemo2.sourceforge.net/ http://sourceforge.net/projects/nemo2/ Hi Daniele,

it sounds like BOTTLESIM could be what you are looking for. It does however not model migration or mutation, only drift: http://chkuo.name/software/BottleSim.html Cheers, Frank

Dear Daniele,

The software HybridLab from Nielsen can do this and uses a genepop input file. Although initially devloped for hybridisation simulations, when using twice the same population, it creates random mating within this population. It is however not automated to run for several generations, requiring a script or manual uploading of the result file as input for every generation.

If would be happy to get the other responses you get on this topic.

buona fortuna !

ciao

Greg

references:

http://www.dfu.min.dk/ffi/uk/populationgenetic/hybridlab/ http://www.blackwell-synergy.com/doi/pdf/10.1111/j.1471-8286.2006.01433.x?cookieSet=1 Hi,

Have you tried simuPOP (by Peng) or FPG. I have never used them, so Im not sure they can do what you ask.

Peng and Kimmel 2005. simuPOP: a forward-time population genetics simulation environment BIOINFORMATICS APPLICATIONS NOTE 21(18), pages 3686-3687

Good luck

Miguel NavascuÃ©s

FPG http://lifesci.rutgers.edu/ ˜ heylab/HeylabSoftware.htm#FPG Dear Daniele. Regarding your question at EvolDir: HYBRIDLAB might do the trick, except I'm not sure that it automatically can simulate over several generation. You may have to do a separate run for each generation and then use the output file from the previous simulated generation. Anyway, I've attached two references, so you can check them out Good luck Morten Allentoft

Finally, I add to the list ManagedPop (Written by Kenneth Birnbaum, Charles M. Peters, Philip N. Benfey, and Rob DeSalle). It is a drift simulation that projects loss of allelic diversity in populations with overlapping generations that receive an input of progeny from a small (in terms of genetic identity) second population.

Daniele.Porretta@uniroma1.it
Daniele.Porretta@uniroma1.it

Genetic data simulation answers2

Dear all

I received these other interesting suggestions about software for genetic data simulations:

1) Mendelâs Accountant: a biologically realistic forward-time population genetics program By J Sanford, J Baumgardner, W Brewer, Gibson P, and W Remine. Scalable Computiong: Practice and Experience 2007. Vol 8 (2) pp. 147-165 http://www.scpe.org It investigates the process of mutation and selection.

2) Hi Daniele,

You might want to check out rmetasim, especially if you are familiar with R. See linum.cofc.edu/software

cheers, Allan Strand <stranda@cofc.edu>

Daniele.Porretta@uniroma1.it
Daniele.Porretta@uniroma1.it

Haplotype inference software

Hello EvolDir - I am looking for softwares that will infer haplotypes from ambiguous genotypes using actual sequence data. Or, does anyone know of a way to easily convert sequence data into 0/1/2 as required for programs like PHASE? I feel if I do this manual, I can just as easily infer the haplotypes myself! Many Thanks!!!

–

Jaime Elizabeth Blair, PhD Postdoctoral Fellow Department of Biology Amherst College jblair@amherst.edu Phone: (413) 542-8333 http://www.amherst.edu/ ˜ jblair http://-jaime.e.blair.googlepages.com "Jaime E. Blair, PhD" <jblair@amherst.edu>

Hypervariable mitochondrial region

Dear Evoldir members, Some one can help me with my problem: I work with a limpet species (Gastropoda) and I have been trying some mitochondrial genes (16S, Cyt B, COI) for a phylogeographic study obtaining low number of variable sites and informative sites. I'm looking for a hypervariable mitochondrial region to amplify. Does anyone of you know any region of these characteristics in Gastropods or any Mollusca (and the primers to amplify it)? Thank you very much

Biol. MarÃa Carla de Aranzamendi GenÃ©tica de Poblaciones y EvoluciÃ³n Facultad de Ciencias Exactas, FÃsicas y Naturales Universidad Nacional de CÃ³rdoba Argentina Tel: +54-351-4332090 int. 34

juan_jmart@yahoo.com.ar

Hypervariable mitochondrial region answers

Dear Evoldir members, Sorry for the delay to post the answers I got for a hypervariable mitochondrial region to amplify in Gastropods or any Mollusca. Unfortunately I didnt receive good news, apparently gastropod mt genome doesn't have a HVR or even very many intergenic spaces. here are some of the main answers I received. Thank you all.

I'm afraid I've got some bad news for you. I've wished many times that my land snails had a hyper variable region so I could get some better resolution in the shallow regions of my phylogeny. Sadly it seems the gastropod mt genome doesn't have a HVR or even very many intergenic spaces, attached is a review that cites all the whole mt genome sequences published for molluscs if you want to check it out for yourself.

You may not find enough variation in the mitochondrial DNA. Many inverts have slower evolutionary rates for mtDNA nearly equal to their nuclear genome. This was the case in some California limpets that I helped a student with. You also may be looking at relatively recent divergence among the populations, as well.

In the group of the pulmonates I've looked for exactly the same as you: hypervariable loci on the mitochondrion. Alas, it did not work for me either. I've also checked CO1 and 16S. However, SNPs seem to be much more abundant on CO1 than on 16S, and enzymatic digestion may give lots of variation. In addition, in many groups there is this hypervariable region on the mitochondrion called the d-loop.

Carla

Biol. Mara Carla de Aranzamendi Gentica de Poblaciones y Evolucin Facultad de Ciencias Exactas, Fsicas y Naturales Universidad Nacional de Crdoba Argentina Tel: +54-351-4332090 int. 34

To: juan_jmart@yahoo.com.ar

ISSR PCR

I am using ISSR in an aromatic plant. I had have a lot of problem with the PCR, and I would like to know how I can improve my PCR and obtaine more ISSR bands. Actually I am using 1X of buffer, 4mM of Mg, 0.2 mM of each dNTP, 0.2 ul og taq and 0.5 uM of primer.

Adriana Suarez

Biology Student

CINBIN Centro de Innovacion en Biotecnologia Industrial y Biologia Molecular

UNIVERSIDAD INDUSTRIAL DE SANTANDER
Km. 2 via Refugio, Sede UIS Guatiguara, Piedecuesta,
Santander Zip Code 678, Bucaramanga, COLOMBIA
Phone: 57+7+6550803 Fax: 57+7+6540557

adrizua@yahoo.com

LI-COR software

FAB-Lab is trying to acquire extra USB software keys (aka dongles) for analysis of microsatellite genotyping gels using the LI-COR software package Gene ImagIR. They're no longer available from LI- COR, or from their former supplier Scanalytics, or from the company that bought out Scanalytics (and discontinued the product while keeping the license). We're trying Grizzly and similar hardware resellers. If any EvolDir members have such keys to sell, we would buy them at the "market rate" (whatever that is).

Thanks, Mike

Michael Hart Department of Biological Sciences.....office.778-782-4473.....(SSB 8104) Simon Fraser University.....lab.778-782-3538.....(SSB 6165) 8888 University Drive.....department.778-782-4475.....(Shrum B8255) Burnaby, BC V5A 1S6.....fax.778-782-3496 CANADA.....www.sfu.ca/-biology Michael Hart <mwhart@sfu.ca>

Meiosis and genetic repair

dear and reputable members of the evoldir,

i wanted to let you know about some remarkable evidence proving that meiosis delivers a unique form of genetic repair which rejuvenates drastically cells that have "aged" because of previous mitotic divisions. Your feedback is most welcome and ideas for collaborations very encouraged.

nobody knows for which purpose eukaryotic cells sometimes go through meiosis rather than mitosis. on the contrary, mutation biologists have known since the 1960s that meiosis in yeast and several other organisms is ~20-40x more mutagenic than mitosis, and recent work shows that hundreds of DSBs are generated during meiosis by the spo11 protein. meiosis therefore appears to be quite disadvantageous relative to mitosis (but assertions about meiosis entailing little or no cost appear regularly in the evolutionary-biology literature).

DNA repair has often been proposed as a main advantage of sexual reproduction, but all known types of DNA repair, including recombination repair, can occur without meiosis (e.g., during the extended G2 phase of "haploid yeast").

a couple of years ago, for a variety of reasons of no interest here, i came to the conclusion that meiosis must be highly adaptive and allow a form of DNA repair to take place that is unavailable to mitotically growing cells.

serendipitously, last fall I found spectacular confirmation for my ideas in laura hoopes' pomona college website where she describes how meiosis rejuvenated very markedly yeast "mother" cells which had accumulated genetic damage during previous budding events (and she states that spo11 is required!). the evidence is described in the 4th-last paragraph of

http://pages.pomona.edu/~llh04747/yeastage.html ; a pdf generated by me of this web page is available upon request.

similarly spectacular meiotic rejuvenation has also been documented for paramecium. please google "Macieira-Coelho meiosis transplantation Aufderheide" and follow the citations there.

remarkably, even paramecium's endogamy cycle delivers a strong rejuvenation: in absence of conjugation partners, an old paramecium exhausted by previous asexual divisions can rejuvenate itself by letting its micronucleus undergo meiosis and then using two of the resulting haploid nuclei to generate a new rejuvenated diploid micronucleus (with the other two being destroyed). this endomeiosis+synkary process does not involve any cell divisions or cell fusions and old paramecia die fully dysfunctional if both this process and conjugation are blocked experimentally.

furthermore, forestry people have known for ages that they cannot reproduce trees asexually forever and that at a certain point they have to use meiosis to reset the aging clock.

last but not least, even reduced-genome specialists like giardia and microsporidia have kept the spo11 gene !

meiotic rejuvenation appears therefore to be universal and i believe it's a safe bet to assume that this rejuvenation is meiosis' raison d'etre. this huge advantage of meiosis should "solve" the questions about the origin and maintenance of meiosis (but not of outcrossing) as well as the question of the "maintenance of males" whenever mitotic asexuality is the "asexual" alternative.

as you can imagine, dear and reputable members, confirming and expanding the above observations – especially at the molecular level by characterizing biochemically the damage– not only is biology of the deepest kind but is also likely to lead to preventive and therapeutic biomedicine of immense importance.

indeed, it is very likely that the special kind of disabling genetic damage that eukaryotic cells accumulate as they divide asexually –and that is repaired so effectively by meiosis-will turn out to be reversible by artificial means without the help of meiosis.

in principle, one should be able to subject young and old micronuclei and yeast nuclei to progressive preparative biochemical stripping, throw the extracts obtained after various steps of preparation at an HPLC and other automated analytico-chemical techniques, and then contrast the obtained compound spectra of young and old nuclei, etc.

unfortunately, my initial consultations indicate that enriching for the damage will not be easy, but perhaps one could engineer the enzymes likely to be directly involved in this unique form of repair (spo11, rev3; see below) so they become glued covalently to their substrates and the complexes can then be isolated with specific antibodies.

importantly, even if whole-body rejuvenation treatments will turn out to be toxic, one could still repair stem cells outside the body and then inject the cells back into appropriate organs, etc.

— / —

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

Molluskan DNA extraction answers

Dear all,

As some of you requested, here are the replies I received (even the ones written in portuguese). I did a copy-paste on the answers but in case you need any further information, feel free to contact me.

Once again, thank you for all the information and hope it helps for those (also) in need!

Best regards, Carla Pereira

Hi,

I just read your thread on Evoldir. I sometimes had problems amplifying any sort of marker from my DNA preps (nothing molluscan though), even when they contained ample amounts of DNA. I found that an RNA digest of the DNA extractions got rid of that problem. Somehow RNA fragments seemed to interfere with my PCRs. Not sure if you do an RNAse digest with your extractions anyway, but if not that might be worth a shot.

Cheers,

Basti

Bastian Bentlage Dept. of Ecology and Evolutionary Biology The University of Kansas Lawrence, KS USA

hello, you might've tried this already, but, i've extracted RNA from mussels and found that doing a lithium chloride re-precipitation (after you've extracted the DNA fully and resuspended do another precipitation). The protocol is in Molecular systematics (hillis, moritz, and mable) in the rna/dna extraction chapter. best of luck! Anne Dalziel University of British Columbia Vancouver, Canada

Hi,

We have been working on a few molluscan species in our lab - mostly squid and abalone. Generally we have fouund the Qiagen DNEasy kits to work pretty well for DNA extractions for these species. However, you did not mention how your tissue was preserved, or how old the specimens were. One thing we have found is that samples more than a couple of years old can be a bit hit and miss, especially if they've been stored in less than perfect condiditon. Basically, the fresher the sample, the better the chance of successful DNA extraction and PCR amplification. I think generally, from my experience, alcohol preservation works better than freezing for molluscs and other species that have high mucopolysaccharides.

You also havent mentioned what primers/approach you were using for the PCR. Again we have found that most "universal" primers are unreliable for molluscs and that it is pretty important to develop species-specific primers. If you have managed to get at least some individuals to PCR and sequence, then check how well your primers match, it may be that there has been a small change in the primer-binding site that is causing your problem and it might be a good idea to try to design new primers.

I hope this helps

Regards

Karen Miller

Dr Karen Miller Institute of Antarctic and Southern Ocean Studies University of Tasmania AND Australian Antarctic Division Private Bag 77 Hobart, 7000 Tasmania Australia

Hi,

I have recently worked with a number of marine organisms, including molluscs, crustaceans, fish and ascidians, and I generally find that the molluscs and fish are among the easiest to work with (I worked with snails of the genera Siphonaria and Nassarius, as well as the mussel Perna perna). You lack of success may be due to a number of other factors, e.g. the tissue you are targeting is not ideal (I usually cut off a very small piece from the foot of the snails), you are using too much tissue, the samples were not preserved well (frequent freezing and thawing degrades DNA, have you tried fresh tissue?) or the primers you are using are not working for all your species. I have found that if it's mtDNA you're after, Folmer's COI primers usually work well (Folmer et al. 1994), and Palumbi's (1991) 16Sar and 16Sbr combination is also reliable. But I have just found a Siphonaria species for which the COI primers do not work, and have used a different design for that. If you're suspecting that the primers are the problem, I suggest you get both of these and if one works and the other doesn't, you know where the problem is.

Hope this helps and best of luck, Peter

Dr Peter R. Teske Postdoctoral Researcher Molecular Ecology Lab Dept. of Biological Sciences, E8C Macquarie University Sydney, NSW 2109 Australia

Hi,

Try adding BSA (Bovine serum albumin) to your PCR to around 0.8 Âµg/ÂµL final concentration. It works well in removing inhibitors.

Good luck Jonas

Hello,

I would much appreciate if you could forward any answers you might get to me (or the list server), since we are facing similar problems and are quite interested to hear possible solutions.

Thanks a lot in advance,

Stefan

We always extract our Littorina samples with this protocoll:

Mitochondrial cytochrome b sequencing. DNA was extracted and purified using a modified CTAB protocol (Winnepenninckx et al. 1993): a small piece (1-2 mm 3)* *of foot tissue was homogenized in 300 Î¼l *[You can increase this up to 700]* CTAB buffer (100mM Tris-HCl pH 8.0, 1.4 M NaCl, 20mM EDTA, 2% hexadecyltrimethylammonium bromide [CTAB] and 0.2% Î^{2}-mercaptoethanol) and 10Î¼l of 10mg/ml proteinase K *[You can increase this to 20]* and kept a

— / —

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

MouseDir ListServ

Dear Colleagues,

The newly established Max Planck Institute for Evolutionary Biology in Ploen, Germany recently held a two-day symposium for Evolutionary Biologists work with Wild Mice (Mus musculus ssp.).

One of the results of this meeting was the establishment of a ListServ specifically serving the mouse Evolutionary Biology community. The list is meant to facilitate communication among our community in matters concerning resources, information, future meetings, job opportunities, etc.

If you have interest in joing the ListServ please send a message to: imailsrv@evolbio.mpg.de and in the body (not subject!) type the following command: subscribe mousedir <your name here>

Thank you,

Rick Scavetta

– Rick J Scavetta Max-Planck-Institut fuer Evolutionsbiologie Abteilung Evolutionsgenetik August-Thienemannstrasse 2 24306 Ploen (Germany) Tel.: 04522 763 279 scavetta@evolbio.mpg.de

rscavett@uni-koeln.de

M-ratio bottleneck test

i have a query to ask to the evoldir community concerning the use of the software M_p_val.exe which calculates the M-ratio of Garza & Williamson to detect recent population bottlenecks. I have tried using this program for some time without any success. Is any one out there familiar with this software, and if so could they possibly give some insight on how to use this software, as the authors do not provide much help to use this program.

Thanks in advance for your help!

Cheers,

Philippe

–

Philippe Henry PhD Student Ecological & Conser-

vation Genomics Laboratory (ECGL) Centre for Species at Risk and Habitat Studies (SARAHS) Unit of Biology and Physical Geography Irving K. Barber School of Arts and Sciences University of British Columbia Okanagan 3333 University Way, Kelowna, BC, Canada, V1V 1V7 http://people.ok.ubc.ca/mirussel/phenry/phenry.html
Philippe Henry <phenry@interchange.ubc.ca>

M-ratio bottleneck test answers

Dear evoldir members,

i recently asked for suggestions on how to use the M_P_val.exe software for calculating the Garza & Williamson M-Ratio for population bottleneck.

Here is a summary of the many replies i got:

- this software runs under Mac OS 9 or any classic compatible machine. (not the new intel processors!)

- the file format is described by the authors under this link: http://137.110.142.7/uploadedFiles/Divisions/FED/Staff_Pages/Carlos_Garza/ratioin.txt (i followed the example above and used Genealex to get the information to put together the input file. i used a .dat file extension as suggested by some.)

- i had my input file in the same folder as the M_P_val.exe file and the software ran smoothly!

Thanks to all those that helped out. I hope this will be helpful to others!

cheers philippe

–

Philippe Henry PhD Student Ecological & Conservation Genomics Laboratory (ECGL) Centre for Species at Risk and Habitat Studies (SARAHS) Unit of Biology and Physical Geography Irving K. Barber School of Arts and Sciences University of British Columbia Okanagan 3333 University Way, Kelowna, BC, Canada, V1V 1V7 http://people.ok.ubc.ca/mirussel/phenry/phenry.html phenry@interchange.ubc.ca

NESCent CallForProposals

Call for Proposals - NESCent Sabbatical Scholars, Working Groups and Catalysis Meetings

The National Evolutionary Synthesis Center (NESCent) is now accepting proposals for sabbatical scholars, working groups and catalysis meetings. Proposals for postdoctoral fellowships are accepted at the December 1 deadline only. Proposals for sabbatical scholars (one semester to a full year), working groups and catalysis meetings are accepted twice a year, with June 15 and December 1 deadlines. Proposals for short-term visitors (2 weeks to 3 months) are considered four times a year, with deadlines on January 1, April 1, July 1 and September 1. For more information, please see our website at https://www.nescent.org/science/proposals.php . khenry@nescent.org

NESCent EvolutionaryData

Dear colleagues,

Together with a consortium of journals and scientific societies in evolutionary biology and related disciplines, NESCent and the MRC are studying attitudes and practices in data sharing among evolutionary biologists. We are inviting all evoldir readers (including students, postdocs, educators and senior researchers) to help in this effort by completing a short survey: http://datadryad.org/survey/ . We estimate that the survey will take less than 20 minutes of your time. Your responses are critical for guiding the design of the next generation of supplemental data archives for evolutionary biology.

Responses must be received by April 16th, 2008

We thank you in advance for your participation, and look forward to seeing your responses. A summary will be posted to evoldir shortly afterwards.

Todd Vision Associate Director for Informatics, U.S. National Evolutionary Synthesis Center (NESCent) http://www.nescent.org Jane Greenberg Director, Metadata Research Center (MRC) School of Information and Library Science University of North Carolina at Chapel Hill http://www.ils.unc.edu/mrc/
tjv@bio.unc.edu tjv@bio.unc.edu

PCR Smears

Hi All,

I am a second year graduate student working on Phylogeny of Hemidactylus geckos of India.

This is about the PCRs.

For the past few months, I have been getting smears (without bands) in Cyt B primer set. The major issue here is that from the very beginning, the samples had been yielding good results with cyt B primers...I should say that they were behaving themselves. Since December 20th,2007, I have been getting this strange result of only smears without bands in the PCRs of cytB. The smears are showing up in negative as well.

We have run all the troubleshoots including ordering new primers twice. but alas...no progress. At least now we are not getting smears...but no bands as well. We even designed new set of primers for cytB but we are not getting any bands with them as well.

DNA of the samples is not a problem because it has been yielding bright and crisp bands with the other primers.

Can you suggets some solution to this problem.

Thanks and regards Rohini Bansal

– Regards

Er. Rohini Bansal Ph.D. student Dr. Praveen Karanth's Lab CES, IISc, Bangalore-560012 India

bansalrohini@gmail.com

Phylogeography funding

Dear collegues

I am writing in request for any pointers you may have in possible grant applications for funding my PhD. The topic is phylogeography/population genetics and focusses on Australian fauna. I have a few application in with Aussie agencies, but at the moment I am running thin on applications to U.K agencies. I would gladly like to hear about any such schemes which offer funding for lab or field work as I have a fair amount of money to raise to pay for research costs. I will be registered at a U.K University but will spend the most part at an Australian University.

I thank you in advance for any help you may give.

Cheers

Jack Lighten j.lighten@hotmail.co.uk

jack Lighten <j.lighten@hotmail.co.uk>

Phylogeography Funding answers

Hi Please find the few answers I recieved on sources for funding in Phylogeography and Australian fauna studies, in relation to PhD projects. Additional to below I made applications to the following agencies.

1#What is your project? I am also a ph d student doing phylogeography etc. I focus on freshwater crayfish. Have you tried the ABRS (Australian biological resources survey) or ARC (Australian Research Council)?Here's the link: http://www.environment.gov.au/biodiversity/-abrs/admin/grants/index.html 2#This organization may be useful to you: http://www.wcs.org/-international/tcbp/rfp Unfortunately, most of the grants I know about apply only to USstudents. Good luck with your search!

3#Join the Genetics Society now! They have grants available for fieldwork, to anyone who's been a member for at least a year:< http://www.genetics.org.uk/-heredity_fieldwork_grants > 4# I do gene migration stuff; how i would answer (muchmuchsweat)= read acknowledgementsof all key MSs.

jack Lighten <j.lighten@hotmail.co.uk>

Population structure sequence file formats

Dear colleagues,

I would like to know which are the most common file formats used with population structure studies for SEQUENCE data. GenePop can only be used with frequency based data. FASTA formats have no population structure information fields (although it could be "hacked" to include it). The only format that I know is ARLEQUIN.

Any comments would be appreciated. This is to decide which sequence formats will be initially supported in the Biopython Population Genetics module.

Many thanks, Tiago

– http://www.tiago.org tiagoantao@gmail.com

Population structure sequence file formats answers

Dear colleagues,

I would like to thank to the many who have answered. I have received more than 20 answers in more than 2 days. My big thanks. So that others can use the information sent to me and for future reference, here it is a summary of the answers.

The biggest suggestion seemed to fall to the Nexus file format.

PHYLIP and LAMARC formats were also referred quite a lot.

Also MIGRATE-N.

Other references were: IBDWS, BAPS, MDIV/IM, SITES (probably a couple were forgotten, I am sorry).

>From my (highly subjective) analysis Nexus and LAMARC formats will get further research. This will help extend the existing Bio.PopGen module of Biopython with a vital statistics submodule.

If you are interested in coalescent simulations and selection detection, biopython might already have content that interests you, please check http://biopython.org/-DIST/docs/tutorial/Tutorial.html#htoc101 Again, many thanks for all the fantastic feedback, Tiago

tiagoantao@gmail.com

Populus nigra samples

Hello!

I am trying to locate samples of Populus nigra (black poplar) from the central or eastern portion of its range (from Austria or Croatia eastwards) or the very southern portion of its range (North Africa) for my PhD project. The design of my project requires trees to be from a natural population (not genebank or plantation) of known location (latitude and longitude).

I would be thankful for any help in locating populations for collection of vegetative material. Of course, if you have DNA or cuttings you are willing to share, that would be wonderful as well!

Thanks for your time! Jenn

Jennifer DeWoody University of Southampton School of Biological Sciences Building 62, Room 6007, Boldrewood Campus Southampton SO16 7PX United Kingdom +44 (0)23 8059 4286 (voice)

j.dewoody@soton.ac.uk

SeqEdit software

Dear Evoldir-ers, I am looking for a free software for PC to edit sequences. I am looking for a software that will give me the option to view the sequence (ABI files), cut off (manually) the primer sequence and other "junk", edit single nucleotides (e.g., SNPs or heterozygotes), and export the edited sequence in FASTA format (or at least text file) for alignment in other software. I used the demo version of CodonCode Aligner, but it doesn't allow to export the edited sequence, and their prices are way above my (zero) budget. Any recommendations are welcomed. Thanks Yuval

– Yuval Sapir, PhD Researcher Institute of Evolution Haifa University Haifa, 31905, Israel e-mail: ysapir@bgu.ac.il Mobile:054-7203140; Lab: 08-6461997

ysapir@bgu.ac.il ysapir@bgu.ac.il

SeqEdit software answers

Dear EvolDir-ers, Thanks to all the 81 who responded my question and recommended FREE softwares for PC that allow to edit sequences and export FASTA files. If evolution was a democracy, I would have pick BioEdit:

50 respondents (~62%) mention it as the chosen one. However, thirteen other programs were also mentioned. Of them, Chroma and Mega got the highest score (15 and 10, respectively). Some people recommended more than one program, and few had also sent me the program itself. Bellow are the list of softwares (with the number of people recommended), the links for downloading sites and some comments, where applicable. Cheers! Yuval

1. BioEdit (50) http://www.mbio.ncsu.edu/BioEdit/BioEdit.html comments: “I am sure you must have received this suggestion a million times - make it 10E6+1 now :)... ”; “excellent”; “I have used it for 8 years, works perfectly well for what you need it for, although there are some small glitches (it is free after all), but nothing you can’t get used to”; “The only drawback is that it doesn’t allow you to compare several chromatograms in a single window as CodonCode does”; “you can view the chromatogram, take of the ends of the sequences and make many manual changes. It also does sequence alignment and contig formation.”;

2. Chromas (15) http://www.technelysium.com.au/chromas_lite.html comments: “Chromas Lite is freeware, veeeeeeeeery basic, but works well”.

3. Mega (10) http://www.megasoftware.net/ comments: “That’s easy: Use MEGA ;-) ”; “My favorite”; “The program MEGA is free, and the latest version has a sequence viewer, alignment editor, as well as building trees.”; “You can’t edit chromatograms of multiple sequences at once (like you can do in Sequencher), but you can do them individually ”

4. Vector NTI (6) https://commerce.invitrogen.com/index.cfm?fuseaction=userGroup.home >From Invitrogen - free for academics. Their site was down, so I didn’t check the validity of the link. comments: “a modular program within which the ContiExpress module would allow you to preform the tasks you describe.”; “As an academic researcher, you can get a free licence of Vector NTI owned by Invitrogen. I use it the same way as that you are looking for: view chromatograms, edit sequences, do the contigs etc.”; “gives a free one-year licence (details on their website), which can then be renewed after that for subsequent year-long periods (always free unless you are using it for commercial purposes)... I find it very similar to Sequencher (which is very user-friendly but expensive) and it didn’t take me much playing around to sort out all the functions. There are also many other programmes in the Vector NTI programme that you may find of use, for example, you can design primers and order them from Invitrogen from within the programme. You can import a variety of files including ABI, and can export in FASTA format from ContigExpress. ”

5. FinchTV (4) http://www.geospiza.com/finchtv/ comments: “you can use Finch TV (which is also free but only can show you one chromatogram at a time) which is a nice little program to edit chromatograms you can search for primer sequnces cut them off.... you can also easily make and see the reverse complement sequences... I use Finch TV first to check my chromatograms, make reverse complement sequences, cut off primers, correct some basees... then I save the files as FASTA and open them in Bioedit. In Bioedit you can make alignments.....”

6. Geneious (3) http://www.geneious.com comments: “The free version has a 2 week demonstration of the pro version. It does a lot more besides edit sequences.”

7. Staden (3) http://staden.sourceforge.net/ comments: “It has nice features such as showing the confidence of base calls and consensus sequences, it can show chromatograms when editing, it’s open source, and it’s completely free. It’s not as user friendly as some of the commercial packages, though.”; “It is great, free and for PCs. It should be able to do all the below tasks (you might have to read through the manual a few times though...)”

8. ProSeq (2) http://www.biology.ed.ac.uk/research/institutes/evolution/software/filatov/proseq.htm comments: “ProSeq is a fairly easy tool to use. I prefer v2.9, especially for editing and assembling contigs, but there is a more recent version available if you should chose.”

the following programs were suggested by one person each:

9. CLC

— / —

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Sequencing problems

Dear Colleagues,

Our sequencing has gone belly up and 3 months of extensive testing has not resolved the problem, maybe someone else in the evoldir community has had this particular problem before and might know the answer! Any help will be much appreciated!!!

THE PROBLEM: We are sequencing PCR products of Hepatitis B virus (HBV) extracted from plasma (Roche Viral DNA extraction kit). In the past (for several years) we got nice sequences, up to 1000 bases under extremely good conditions. Now we are getting barely 500 bases with a fluorescence signal that is incredibly high in the beginning and then abruptly drops after ˜ 150 bases to become very low. It is sometimes readable in Lasergene software and on Finch TV but really difficult to read in Sequence Navigator. The sequence is correct when compared to other HBV reference sequences.

We check the gel purified PCR products on a gel as well as by Nanodrop. On the gel the bands look fine but the Nanodrop suggest that we have significant contamination of our DNA, i.e. lower concentrations than expected from gel, bad ratios (high or low) and very dirty curves. I am starting to forget what a clean curve is support to look like!

We have TESTED the following PARAMETERS: operator (4 people) plasma sample (genotype, geographical region, even same sample but extracted at different times) amplified region (3200kb full genome or smaller fragments down to 300 bases) primer (we use about 15 primers through the whole genome) polymerase (Roche HiFi or ABi AmpliTaq) gel extraction kit (we used Qiagen, Omega and Macherey-Nagel) agarose water (we used HPLC purified water only as a test to compare to MilliPore) DNA concentration ABi sequencing kit lot sequencer (we have ABi 3100 in House and also send sample off to a large scale sequencing facility which have 3730xl; when we send samples off we only send purified PCR product and primer, they add the sequencing chemistry.) Organism (we also have a problem with a small batch of HIV samples that we tried to process)

As you would suggest, we have replaced all reagents - without success.

Here are a few more ODDITIES: All samples that have been gel extracted and purified before Dec 07 still work! Anything that has been PCR'ed since Dec 07 fails. We sequenced some old purified products after re-PCR and column purification with and without the gel extraction step and they also didn't sequence properly. Sequencing of old and fresh PCR products: old products give identical traces to original sequencing run and new products fail. Sequencing of HBV plasmids works as does ABi's control plasmid.

NB: We have had a pipette clinic in the lab in the first week of December after which the problems started - however, we use these pipettes to set up sequencing reactions with old product which still works. And we use brand new pipettes in the PCR room, so these have not been serviced in December.

FUTURE TESTS planned: Do the whole procedure in another lab. Give DNA and primers to someone else in another lab. Contact ABi again and find out if they have changed the chemistry without publicizing it. We have gone through their whole troubleshooting protocol but as many of you know, it is not easy to get high quality answers from ABi... Run some plasmid onto a gel, extract and sequence.

We believe that the problem lies somewhere in the gel extraction step but as we are using primers that amplify 8 genotypes we tend to have unspecific band and cannot avoid this step.

Any recommendation would be much appreciated and I will compile an answer email once I have had your responses. We are prepared to try anything - voodoo, rain dances, the PCR song...!

Many thanks,

Birgit

Birgit Meldal, PhD Division of Transfusion Medicine Department of Haematology University of Cambridge National Blood Service Center Long Road Cambridge CB2 2PT

Tel: +44 (0) 1223 548049 E-mail: bhmm2@cam.ac.uk

bhmm2@cam.ac.uk

Software BIMr

Dear Evoldir members,

We would like to inform you that we have released a new program for the estimation of recent migration rates. BIMr is a free software that makes inferences about recent proportions of immigrant genes in subdivided populations and that can identify the environmental factors that are responsible of observed gene flow patterns. BIMr is distributed under the terms of the GNU General Public Licence (GPL) and is available for all three major platorms from the following website: http://www-leca.ujf-grenoble.fr/logiciels.htm
The details of the method are described in :

Faubet P. and O.E. Gaggiotti, 2008. A new Bayesian method to identify the environmental factors that influence recent migration. Genetics 178: 1491-1504.

Best regards,

Pierre Faubet and Oscar Gaggiotti

oscar.gaggiotti@ujf-grenoble.fr oscar.gaggiotti@ujf-grenoble.fr

Software FastTree

We are pleased to announce the initial release of FastTree, a tool for inferring neighbor joining trees from large alignments. FastTree is capable of computing trees for tens to hundreds of thousands of protein or nucleotide sequences on most desktop computers.

FastTree uses: *profiles instead of a distance matrix to reduce memory usage *linear distances with a character dissimilarity matrix *a new "top hit" heuristic to achieve a sub N-squared run time *local support instead of bootstrap for node support values

FastTree is faster than computing a distance matrix, and up to 10,000 times faster than neighbor joining with bootstrap. FastTree is about as accurate as BIONJ with log corrected distances for well-supported nodes.

To download source code, binaries, or a preprint, please visit:

http://www.microbesonline.org/fasttree/ Abstract

Background: A fundamental goal of molecular evolution is to infer the evolutionary history the phylogeny of sequences from their alignment. Neighbor joining, which is a standard method for inferring large phylogenies, takes as its input the distances between all pairs of sequences. The distance matrix requires O(N^2 L) time to compute and O(N^2) memory to store, where N is the number of sequences and L is the width of the alignment. As some families already contain over 100,000 sequences, these time and space requirements are prohibitive.

Results: We show that neighbor-joining can be implemented in O(NLa) space, where 'a' is the size of the alphabet, by storing profiles of internal nodes in the tree instead of storing a distance matrix. Profile based neighbor joining allows weighted joins, as in BIONJ, but requires that distances be linear. With heuristic search, neighbor joining with profiles takes only O(N*SQRT(N) log(N)La) time. We estimate the confidence of each split (A,B) vs. (C,D) from the profiles of A, B, C, and D, without bootstrapping. Our implementation, FastTree, has similar accuracy as traditional neighbor joining. FastTree constructed trees, including support values, for biological alignments with 39,092 or 167,547 distinct sequences in less time than it takes to compute the distance matrix and in a fraction of the space. Traditional neighbor joining with 100 bootstraps would be 10,000 times slower.

Conclusions: Neighbor joining with profiles makes it possible to construct phylogenies for the largest sequence families and to estimate their reliability.

Morgan N. Price & Paramvir S. Dehal fasttree@microbesonline.org

Virtual Institute for Microbial Stress and Survival Arkin Lab Physical Biosciences Division Lawrence Berkeley National Lab

psdehal@gmail.com

Software multiGUI beta release

Dear EvolDir members

Myself, Federico Hoffmann and Juan Opazo are proud to release the first beta version of multiGUI. This program is our first attempt to make a graphical interface for multidivtime and its related programs. multiGUI simplify the procedure of running multidivtime, baseml, paml2modelinf and estbNew, by employing a user-friendly interface created with Python and wxPython. Although multiGUI is cross-platform, the current release is restricted to Windows XP and Vista. In the near future Linux and OS X versions will be also available.

At the moment we are intending to release multiGUI as a restricted beta for 20 users, to measure interest, define future strategies in the development, and track bugs that weren't caught previously. So for everyone interested in multiGUI, please send a message to

multigui@genedrift.org

with your name and the desired system, XP, Vista, Linux or OS X.

We will define a group of 20 (or more, or less, depending on interest) beta-users that will receive a link to download an installation package.

For more information please visit

http://www.genedrift.org/multigui.php Paulo, Federico and Juan nuin@genedrift.org

Software phyloXML version1 0

Hi:

phyloXML version 1.00 has just been released. See: http://www.phyloxml.org/ Thank you,

Christian Zmasek

czmasek@burnham.org

Software TREEFINDER

A new unpaid TREEFINDER version is online at:

www.treefinder.de TREEFINDER is a software to compute phylogenetic trees from molecular sequences.

New features are:

- computation of pairwise ML distances - construction of distance trees: NJ, BIONJ - least squares fitting of edge lengths - more DNA models: J1, J2, J3 (= TIM), TVM - more protein models: betHIV and witHIV - improved model proposer - more efficient TL

Distance trees can be built under topological constraints.

The models J1...J3 represent the 3 possibilities of joining two and two transversion parameters of the GTR. They have 3 free rate parameters and, together with the TVM, they fill the gap in complexity between the TN and the GTR. The model proposer proposes the new models if they are appropriate.

The TL interpreter is now three times faster and uses half the memory of the previous implementation.

Please note that I am still not being paid for my work and that I had no income for years. I wonder if somebody finds TREEFINDER worth offering me a compensation, a wage, a position, a perspective.

Gangolf Jobb

Gangolf Jobb <gangolf@treefinder.de>

Software VisCoSe

Dear Evoldir members,

VisCoSe : Visualization and Comparison of Consensus Sequences is available again after a server move: http://bio.math-inf.uni-greifswald.de/viscose/ The abstract (from 2004): We introduce visualization and comparison of consensus sequences (VisCoSe) as a WWW service and a stand-alone command line Perl script for visualizing and comparing consensus sequences of protein and nucleotide sequences. VisCoSe is the only interface available that simultaneously calculates consensus sequences of multiple data sets and automatically compares these consensus sequences. Furthermore, VisCoSe allows visualization of chemical properties of amino acids.

Application note: Spitzer M, Fuellen G, Cullen P, Lorkowski S. VisCoSe: visualization and comparison of consensus sequences. Bioinformatics. 2004 Feb 12;20(3):433-5.

=====Georg Fuellen alum.mit.edu/www/fuellen/

fuellen@uni-greifswald.de fuellen@uni-greifswald.de

SouthAfrica Volunteers SmallMammalEvolution

Volunteer needed as field assistants for the project:

Socio-Evolution of small Mammals in the Succulent Karoo of South Africa

Project: We study the reasons of group living, paternal care, communal nesting and social flexibility in the striped mouse. As this species is diurnal and the habitat is open, direct behavioral observations in the field are possible.

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

Work of field assistants: Trapping and marking of mice and rats; radio-tracking to determine home ranges and nest sites; direct behavioral observations in the field; experiments and observations with captive specimen under natural weather conditions; maintenance and cleaning of the research station.

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

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 750 (around 65 Euro) must be paid for accommodation at the research station. Students must buy their own food etc in Springbok (costs of about R 2000 or 170 Euro/month). Including extras, you should expect costs of about 250 Euros per month. Students get an invitation letter which they can use to apply for funding in their home country (eg. DAAD in Germany, SANW in Switzerland).

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

When and how long: Currently we are looking for two to three volunteers from May to December 2008. Especially for the period July to November help is needed. Field assistants are expected to stay at least 2 months, but longer periods of up to 6months are preferred.

How to apply? Send a short motivation letter stating why and for which period you are interested and your CV via email to carsten.schradin@zool.uzh.ch.

More information under www.stripedmouse.com Contact via e-mail: carsten.schradin@zool.uzh.ch

Dr. Carsten Schradin Research Associate, Zoological Institute, Department of Animal Behavior, University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland. Tel; +41 - (0)44 635 5486 Fax: +41 - (0)44 635 5490

(Tel. secretary: +41 - (0)44 635 5271)

Honorary Researcher at the School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, South Africa.

Succulent Karoo Research Station, Goegap Nature Reserve, Private Bag X1, 8240 Springbok, South Africa.

visit http://www.stripedmouse.com Carsten Schradin <carsten.schradin@zool.uzh.ch>

SSB New Logo Contest

Society of Systematic Biology LOGO CONTEST!

The Society of Systematic Biology needs a new and modern logo that represents our inclusive and international efforts to promote the systematic study of biodiversity. We solicit submissions of potential SSB logos from our membership (or potential members!). If you are a creative, artistic systematist, please consider submitting a logo for this competition.

Contest Details: 1) Prize: US$ 500 cash! Plus seeing your artwork on the cover of Syst Biol for years to come! 2) Submission Deadline: April 30, 2008. 3) Where to submit: please e-mail submissions to ssb_apps-mailbox@cornell.edu 4) Submission details: please submit LOW RESOLUTION (200 dpi max) versions of your artwork in JPEG format for initial consideration. If your logo is selected for judging we will request a higher resolution version from you.

The best logos are those that retain character even if shrunk, or in black and white. For some tips on the science of logo design, please follow these basic tips:

Logo Design Tips

Keep in mind that a powerful SSB logo:

* has graphic imagery that is appropriate to systematics;

* works well with our name, “The Society of Systematic Biologists”;

* is easy to read;

* communicates systematics clearly;

* has a strong, balanced image with no little extras that clutter its look;

* is distinctive and bold in design, making it easy to see at a glance;

* looks good in black and white, as well as in color.

Thanks for your support of SSB!

SSB Applications <ssb_apps@cornell.edu>

SYBR Safe DNA gel stain

Had anyone tried the Invitrogen SYBR Safe DNA gel stain as an ethidium bromide substitute? Could you please tell me if you found it satisfactory? Thanks.

PLEASE NOTE THE NEW PHONE NUMBER!

Alan W. Meerow, Ph.D., Research Geneticist and Systematist USDA-ARS-SHRS, National Germplasm Repository 13601 Old Cutler Road, Miami, FL 33158 USA voice: 786-573-7075; FAX: 786-573-7110 email: alan.meerow@ars.usda.gov

"Meerow, Alan" <Alan.Meerow@ARS.USDA.GOV>

SYBR Safe DNA gel stain answers

Sincere thanks to everyone who responded to my query. What a great resource we have in evoldir! I have compiled the responses to date below. Each paragraph is a unique response. The consensus in the community is that the vast majority of people who are using the SABR SAFE system have been very pleased with the results. Many recommend incorporation directly into the gel. All noted that it is more expensive than using ethidium bromide, plus a new camera filter needs to be purchased, but some savings are re-captured by the fact that the gels do not have to be disposed of as hazardous waste (but some labs do so anyway, just to be sure). Most noted the light sensitivity of this stain. One lab manager directed me to her blog which raises the issue of whether ethidium bromide is really all that hazardous (http://rrresearch.blogspot.com/2006/10/-heresy-about-ethidium-bromide.html). It does not work well or at all with RNA. Finally, a couple of labs are using GEL RED, another alternative, with good results.

Alan

———- Responses ————-

Yes, I made the transition in my old lab. I found it great in a number of ways - in particular I found it to be more sensitive - I could see bands that were not observable using EtBr. Indeed, bands that you cannot see by eye also became apparent once viewed through the special camera-lense filter required. Which brings me to the bad points - you need to first buy a new lense filter as recommended, which is not cheap. And overall its more expensive than EtBr. But if you have the money I would recommend it - I never regretted the switch.

We switched our laboratory over to Invitrogen's sybrsafe a year or two back. There are a couple of things probably worth noting. Firstly, it's a heap more light sensitive than EtBr so you can't pre-add the dye to agarose and store on the shelf for a while. This is not a big deal, it just means adding it fresh each time (or storing post stain solution away from light). I think the biggest thing is that it optimally fluoresces at a different wavelength from EtBr. We use a BioRad geldoc for visualisation and were originally using the same camera filter as for EtBr. This meant that the bands, although "see-able" were much fainter than with EtBr (and reasonably often, when bands on a gel were weak, we put it in EtBr for a while to get a decent view). Since then, we have purchased a different filter for Sybr and it's now a heap better, and I'd say every bit as good as EtBr. I'm totally happy with it, and even though it's a bit pricier than EtBr, I think it's worth it, and would totally recommend it (as long as you get a sybr filter for your camera). As an aside, Invitrogen market Sybr Safe as a totally "safe" alternative but I can't help but wonder if something that binds DNA can really be totally safe...

i have been using the SYBR Safe since i moved to UBC six months ago. We use it to test PCR amplifications generally with 1.5 - 2 % agarose gel. The results are totally satisfactory with the recommended dosage (e.g. 9ul for 90ml gel). I guess it depends on what application you want to make of it, i heard some people still used ETBR as they found it more sensitive for other applications.

we have been routinely using SYBR Safe for around 2 yrs now, and recommend it entirely... if you have 'very little' product though it may not be satisfactory, but in routine lab gels it should be an entirely useful replacement for ethidium bromide.

Yes. My experience with SYBR Safe is entirely positive. It is more sensitive to timing your lab work than EtBr, i.e. the gel with SYBR Safe cannot be prepared long in advance and subsequently should be covered to prevent light exposition, but I was satisfied with it.

We've been using SYBR Safe for a while now. We also bought Invitrogen's blue transilluminator to avoid using UV. Except of the price I think it is a good EtBr substitute. One thing though, it doesn't work with RNA, so we also kept the EtBr/UV facility.

We have indeed tried out this stain as an alternative to Ethidium bromide and it works reasonably well. One drawback is that it is sensitive to light and once the stain is made up it does not last that long (<1 week). We have found a much better alternative called Gel Red nucleic acid stain which we buy from Jomar Diagnostics (your distributor may be different). This stain can be added to the gel prior to pouring and will survive repeated microwaving and cooling cycles. It is also not light sensitive, can be stored at room temp and seems to last for many weeks without any loss of signal. I would recommend it over SYBR safe. Hope this info helps.

I'm currently working in a large genetics lab and we use SYBR DNA gel stain for all gels. Each aliquot of SYBR and TBE buffer can be re-used for up to 4 gels, and, on average, my gels look as good as they would with ethidium bromide.

— / —

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

UtrechtU Herbarium closure

Dear Friends,

Sorry for cross-posting, but I'd like to bring the following to your attention.

On 26th March 2008 the University Board of Utrecht University, The Netherlands, informed the employees of the Utrecht Herbarium that as of 1 June 2008 the Herbarium is to be closed and, with immediate effect, access to the collections, from national as well as international workers, is to cease. This must not be allowed!

*Closure of the Herbarium is a disaster for current national and international research!

*Closure of the Herbarium is a disaster for any future research!

*Closure of the Herbarium contradicts the Biodiversity Covenant signed by the Netherlands which ensures the accessibility of data relating to biodiversity (either under Dutch ownership or under Dutch guardianship)!

*Closure of the Herbarium is a disaster for all the botanical and ecological research taking place in South America, especially Suriname, Guyana, French Guyana and the Amazonian basin.

*Closure of the Herbarium is in effect a denial of the cultural- historical value of this Herbarium to The Netherlands and Suriname!

*Closure of the Herbarium is the start of scientific deterioration and wrecks the near-finalized plans for the creation of one Dutch Centre for Biodiversity [NCB].

What can you do?

Please sign the petition at www.SaveHerbariumU.nl and forward this email to others.

Thanks!,

Pieter

Dr. Pieter B. Pelser

Miami University - Botany Department 316 Pearson Hall Oxford, Ohio 45056 USA

Email: pelserpb@muohio.edu IChat: pelser@mac.com Tel. office: +15135294270 Tel. cell: +15133303952 Fax: +15135294243 http://pieterpelser.blogspot.com/ Pieter Pelser <pelserpb@muohio.edu>

WebSiteTools survey query

Dear Population Genetics/Genomics friends and colleagues,

We are polling the population genetics/genomics community for your interest in a suite of tools that would allow reasonably quick development of a web portal for dissemination of population genomics data sets. We are aware of several sites for different study species (e.g. maize, rice, arabidopsis) for dissemination of medium to large size data sets on molecular population genetic nucleotide sequence variation. These sites usually include some or all of the following items:1) DNA sequences for a panel of individual for hundreds to thousands of genes, 2) SNP genotypes for the same or a larger number of individuals, 3) geographical maps of the locations of samples individuals, 4) linkage maps of genes or SNPs, and other functionalities. Setting up a site such as this can require years of programmer time, however with simplified development tools the time required to set up such a site could be reduced to a few weeks. Moreover, a web portal development tool would allow the same template to be implemented for various different studies, thus users would not have to re-learn the environment with each new data set.

We have two main questions for you:

1) Do you know of any Population Genomics Web Portal Development Toolkit that is currently under construction?

If not, 2) Do you see a need for a Population Genomics Web Portal Development Toolkit? (if there is no other, we are considering development of one)

Thank you for your help and input.

Sincerely ,

Matt Olson Shawn Houston

University of Alaska Institute of Arctic Biology & Biotechnology Computing Research Group

Matt Olson <matt.olson@uaf.edu>

PostDocs

ArizonaStateU MalariaPopulationGenetics

Postdoctoral Research Associate in Population Genetics

A postdoctoral position is available for research in malaria parasite population/evolutionary genetics in Arizona State University. The position is funded for two years, with a possibility of extension. The successful applicant is expected to perform computational analysis of malaria parasite (Plasmodium falciparum and/or P. vivax) genomic data for inferring parasite demographic structure and evolutionary events involving antimalarial drug resistance. The project aims to elucidate whether or how rapidly the resistance to antimalarial drugs would emerge, become prevalent, or disappear under various parasite demographic structures and drug deployment policies. The successful applicant will collaborate closely with both Dr. Yuseob Kim (theoretical population genetics) and Dr. Ananias Escalante (evolutionary ecology of malaria parasites) of the School of Life Sciences in ASU. The applicant should have a solid background in population genetics theory and, preferably, experience in statistical data analysis for inferring the evolutionary history of population. Knowledge in malaria biology is not required. Candidates must have earned a Ph.D. or a related field at the time of appointment.

To apply send a CV, a personal statement and selected publication by email to yuseob.kim@asu.edu <mailto:yuseob.kim@asu.edu> or by mail: Yuseob Kim, Biodesign/EFG, Arizona State University, PO Box 875301, Tempe, AZ 85287-5301. Informal inquiry is encouraged. The initial deadline for receipt of applications is May 15, 2008, with applications reviewed weekly thereafter until the search is closed. Arizona State University is an affirmative action, equal opportunity employer committed to excellence through diversity.

Yuseob Kim <Yuseob.Kim@asu.edu>

AucklandNZ HumanPopulationGenetics

Postdoctoral Scientist, Molecular Poplution Genetics of Human Olfaction HortResearch, Auckland, New Zealand

Consumers our decisions to buy fruit are driven by our beliefs that the fruit will taste good and be good for us. However, foods do not taste the same to everyone. We aim to understand more about the variation in the perception of taste among consumers by studying differences in ability to detect aroma compounds and associated differences in genes encoding odorant receptors.

The research, which involves the use of sensory trials and genetic assays (SNP, odorant receptor gene sequencing), forms the basis of a three year fixed term postdoctoral position for a PhD graduate in molecular population genetics and an interest in sensory science. Familiarity with the design and analysis of association testing and molecular population genetic studies would be of benefit, as would experience in the high throughput collection and analysis of molecular variation data from SNPs to gene sequencing information.

www.hortresearch.co.nz .

For more information please visit our website, or contact Dr Richard Newcomb, HortResearch rnewcomb@hortresearch.co.nz

The successful candidate would also have the opportunity to interact with the Allan Wilson Centre http://-awcmee.massey.ac.nz/

To apply, send your application details, C.V. and a covering letter to Human Resources, Private Bag 92169 Auckland or vacancies@hortresearch.co.nz

Please quote the vacancy number 1059

Richard Newcomb (PhD) Science Leader: Molecular Olfaction HortResearch Mail: Private Bag 92169, Auckland 1142, New Zealand Courier: 120 Mt Albert Road, Mt Albert, Auckland phone +64 9 9257127 mobile +64 21 2268127 email rnewcomb@hortresearch.co.nz web www.hortresearch.co.nz < http://www.hortresearch.co.nz/ >

Richard Newcomb <RNewcomb@hortresearch.co.nz>

BeltsvilleMaryland HoneyBeePopulationGenetics

A Postdoctoral Research Associate position is available in Beltsville, Maryland, to study relationships between honey bees and their pathogens. The focus will be on genetic traits that affect pathogen virulence and the abilities of bees to mount an effective immune response. Two systems are under study: a larval bacterial disease (American foulbrood, caused by the gram-positive bacterium Paenibacillus larvae) and a disease of adult bees caused by the microsporidial parasite Nosema ceranae.

The project will combine population-genetic approaches, expression analyses, and controlled breeding experiments to answer evolutionary and applied questions related to variation across bee lineages in disease susceptibility, and the mechanisms by which pathogens invade bees. Draft genome sequences for bees and both of these organisms are available, and specific strategies in use here include genome annotation, gene-candidate validation using microarrays and qPCR, high-throughput sequencing/resequencing, and comparative genomics across insects. Depending on interests and expertise, alternate projects could focus on environmental factors important for disease, and the implications of social interactions on disease transmission.

Skill in computational biology, including genome annotation, would be extremely useful, as well as laboratory skills in gene expression and marker analysis. A background in studying social insects, host/pathogen interactions, or insect immune systems would be fantastic.

Available immediately, salary $US 58,206-$64,207/year plus benefits. If interested, please contact Jay Evans (jay.evans@ars.usda.gov) for more information.

Thanks,

Jay D. Evans

USDA-ARS Bee Research Lab

Beltsville, MD 20705 USA

PH 301-504-5143 FX 301-504-8736

More information on lab projects available at: http://www.ars.usda.gov/pandp/people/people.htm?personid=3D10065

Related past projects include:

Cox-Foster, D.L., Conlan, S., Holmes, E.C., Palacios, G., Evans, J.D., Moran, N.A., Quan, P., Briese, T., Hornig, M., Geiser, D.M., Martinson, V., vanEngelsdorp, D., Kalkstein, A.L., Drysdale, A., Hui, J., Zhai, J., Cui, L., Hutchison, S.K., Simons, J.F., Egholm, M., Pettis, J.S., Lipkin, W.I.(2007) A metagenomic survey of microbes in honey bee colony collapse disorder, Science, 318, 283-287.

Decanini, L.I., Collins, A.M., Evans, J.D. (2007) Variation and heritability in immune-gene expression by diseased honey bees. J. Heredity, 98, 195-201.

Qin, X, Evans, J.D., Aronstein, K.A., Murray, K.D, Weinstock, G.M. (2006) Genome sequences of the honey bee pathogens Paenibacillus larvae and Ascosphaera apis, Insect Molecular Biology, 15:715-718.

Evans, J.D., Aronstein, K.A., Chen, Y., Hetru, C., Imler, J-L., Jiang, H., Kanost, M., Thompson, G., Zou, Z., Hultmark, D. (2006) Immune pathways and defence mechanisms in honey bees Apis mellifera. Insect Molecular Biology, 15:645-656.

Evans, J.D. (2006) Beepath: An ordered quantitative-PCR array for exploring honey bee immunity and disease, J. Invert. Pathol 93, 135-139.

Evans, J.D., Pettis, J.S. (2005) Colony-level impacts of immune responsiveness in honey bees, Apis mellifera. Evolution,

59(10), 2270-2274.

Jay.Evans@ARS.USDA.GOV

CNRS Montpellier FungalPopGenetics

Dear Colleagues,

Please find here the description of a post-doctoral position available in my team, starting from next fall. This CNRS position is only open for non-French applicants, with a good scientific level. Thank you for sending this announcement to anyone interested !

Marc-André

15 MONTH RESEARCH POSITION IN MONTPELLIER (FRANCE)

Centre d'Ecologie Fonctionnelle et Evolutive - CNRS

Population genetics of ectomycorrhizal fungi

Fields of interest of our team: we focus on ectomycorrhizal fungi in temperate ecosystems. We are interested in plants that rely on the carbon provided by their mycorrhizal fungi (mixotrophy, mycoheterotrophy), impact of global change on ectomycorrhizal communities, and population genetics of ectomycorrhizal fungi. We are interested in the structure of these populations (gene flow, mating) and factors explaining their diversity, such as geographic distance, host species, and local soil conditions.

The present research position is funded by CNRS, and the European Evoltree program (http://www.evoltree.org/) will contribute to experimental expenses.

Working project in which the associated researcher would be involved: We have completed the genome sequencing of Laccaria bicolor, a model species for ectomycorrhizal symbiosis, and Tuber melanosporum, a prized edible species. The sequencing was performed under supervision of a joint team (Francis Martin, INRA Nancy) that is also involved in this project. The sequence data provide useful tools to design microsatellites and to identify genes under selection in ectomycorrhizal fungal populations. The applicant is free to choose his favourite model, and will be involved in the supervision of a PhD student on the other model.

For these two species, we aim at obtaining neutral markers (microsatellites) and describing population structure over Europe (+ America for L. bicolor). Here, the available genomes allow us to prepare an optimal marker set to analyse populations of fruiting body and ectomycorrhizae, their differentiation by distance (gene flow over Europe at least) and reproduction by allogamy versus autogamy (linkage disequilibrium). We will also search for fingerprints of species-level selection among candidate genes (involved in soil exploitation, symbiosis, or in sexuality), considering related species as outgroups. We will investigate balance of synonym versus non-synonym substitutions, and, at the population level, compare the geographic structure of polymorphism (if any) with that obtained for neutral markers.

Our team is part of larger a team focusing on co-evolution and population genetics in several models, including orchids, plants (especially domesticated), figs and their pollinators, ants and plants. We are part of the Centre d'Ecologie Fonctionnelle et Evolutive (ca 150 researchers on ecology and evolution). Montpellier is near the Mediterranean Sea, in a scientifically rich environment for plant and fungal sciences, evolutionary ecology and especially population genetics.

Our team contributes to the organization of a New Phytologist meeting in Montpellier, in December 2008 (http://www.newphytologist.org/ mycorrhizal/default.htm) on ecology of ectomycorrhizal fungi.

Requested experience: applicants should not have the French nationality. They should be experienced (as demonstrated by published papers) in at least three of the following areas:

1 - population genetics

2 - genomic sciences

3 - microsatellites & molecular ecology

4 - fungal ecology

5 - evolutionary genetics

Duration: 15 months, starting in Aug. / Sept. 2008. Salary ranges from 2 020 euro/month to 2 762 euro/month (level: associate researcher), depending on applicant's experience and diploma.

Contact: Marc-André SELOSSE (Professeur, Université Montpellier II), CEFE-CNRS, UMR 5175, Equipe co-évolution, 1919 Route de Mende, 34 293 Montpellier cédex 5, France - Tel. 33 (0) 4 67 61 32 31; Fax 33 (0) 4 67 41 21 38

Applications will be received until May 15th. In your first email/ letter, please list your fields of experiences using the numbers (1-5) listed above as well as the name and e-mail address of two referees.

Marc-André SELOSSE

Professeur, Université Montpellier II Centre d'Ecologie Fonctionnelle et Evolutive CNRS, UMR 5175, Equipe Interactions Biotiques 1919 Route de Mende, 34 293 Montpellier cedex 5, France Tel. 33(0)4 67 61 32 31; Fax 33(0)4 67 41 21 38 Tel. mobile 33(0)607 1234 18

Editeur du New Phytologist (http://www.newphytologist.org/) Editeur associé de Symbiosis (http://people.bu.edu/iss/ Symbiojournal.html).

Publications : www.cefe.cnrs.fr/coev/MA_Selosse.htm

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

DukeU ComplexTraitsYeast

NIH-funded postdoctoral positions are available at Duke University Medical Center (Durham, NC) to study quantitative (complex) traits in S. cerevisiae; for example, see Nature 416:326-330 (2002) and PLoS Genetics 2(2):e13 (2006).

http://www.duke.edu/web/microlabs/mccusker/ Applicants should have 0 to (at most) 2 years of postdoctoral experience and a strong background in at least one of three areas - yeast genetics, quantitative/population genetics and/or genomics/informatics - and a desire to expand into the other listed areas. While not a requirement, eligibility for NIH fellowships/training grants or other fellowship funding will be viewed positively. Start dates are flexible.

Applicants should email their curriculum vitae and the names/email addresses of three references to John McCusker <mccus001@mc.duke.edu>.

John McCusker

John McCusker <mccus001@mc.duke.edu>

KansasStateU SunflowerGenomeEvolution

POST-DOCTORAL POSITION AVAILABLE TO STUDY GENOME EVOLUTION IN WILD SUNFLOWERS

A post-doctoral position is currently available in the laboratory of Mark Ungerer to work on a NSF funded project, "Hybrid speciation, transposable elements, and genome evolution in wild sunflowers". This project will investigate the possible causes and evolutionary consequences of massive retrotransposon proliferations that have occurred independently in the genomes of three hybrid sunflower species. Specific responsibilities of the post-doctoral researcher will include oversight of one or more major subprojects that examine the potential impact of retrotransposon proliferation on genome function and the environmental and genomic conditions under which retrotransposons can become transpositionally active. The position will require both laboratory and greenhouse work as well as seasonal excursions to the southwestern US to collect from natural populations and natural hybrid zones. Candidates must have strong molecular biology skills and training and/or interest in the fields of molecular and genome evolution.

To apply, send a cover letter describing your research interests/past research achievements, a C.V., and the names and contact information for three individuals willing to provide letters of recommendation. Materials should be sent to the address below. Review of applications will begin on April 25, 2008 and continue until the position has been filled. Ph.D. degree must be completed by start date. Kansas State University is an equal opportunity employer.

Dr. Mark Ungerer Division of Biology Kansas State University Manhattan KS 66506 Email: mcungere@ksu.edu

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MississippiStateU InvasiveSpeciesGenetics

Anticipated posting (May 2008): Post-doc in Landscape Evolution and Genetics (Invasive Species)

This will be a postdoctoral position to join an interdisciplinary team studying the evolution of invasive plants and insects in the southeastern United States. The successful candidate will be based in the plant evolution lab of Dr. Gary Ervin, but will have opportunities to collaborate with other faculty in the Mississippi State University Department of Biological Sciences. The current working group includes faculty with expertise in spatial evolution, quantitative ecology & evolutionary biology, population genetics, plant systematics, and plant evolution and field biology.

The ideal applicant will have expertise in at least two of the following areas, and a desire to engage in cross-disciplinary analyses of invasive species data: ecological modeling, landscape evolution, plant evolution, population genetics, or spatial statistics. Applicants also should be comfortable performing occasional field work under hot, humid conditions typical of the southeastern US. The objectives for this position will revolve around analyses of multiple invasive species datasets, especially data associated with research on the invasive herbivorous moth Cactoblastis cactorum. This research is funded by the USGS and USDA, and hosted by the Mississippi State University GeoResources Institute. Strong writing skills will be essential, including a demonstrated ability to publish in peer- reviewed journals.

This position will be immediately available (once posted), but screening of applicants will continue until a suitable candidate is identified. This will be a benefits-eligible position. Current funding provides for an 18-month term for this position, with additional years possible, contingent on continued funding and satisfactory performance of duties.

Interested individuals possessing a doctoral degree (or with degree imminent) from an accredited institution may make informal inquiries directly by e-mail to Dr. Ervin at: gervin@biology.msstate.edu

Such inquiries should include a CV, a brief statement of interest in and suitability for this position, and names and contact information of up to three references whom may be contacted directly. Formal application should be made through the MSU office of Human Resources Management (http://www.hrm.msstate.edu/-employment/postings.htm), once the position has been posted; anticipated posting date is May 1, 2008.

For further information, see:

Gary Ervin V http://www.msstate.edu/courses/-ge14/ MSU Department of Biological Sciences V http://www.msstate.edu/dept/biosciences/ MSU GeoResources Institute V http://www.gri.msstate.edu/-gri-lr.php Cactus Moth Monitoring and Detection Network V http://www.gri.msstate.edu/research/-cmdmn/ Invasive Plant Atlas of the Mid-South V http://www.gri.msstate.edu/ipams/ Mark E. Welch, Ph.D. Assistant Professor Dept. of Biological Sciences Mississippi State University P.O. Box GY Mississippi State, MS 39762

E-mail: mark.welch@msstate.edu Phone: 662.325.7564 Fax: 662.325.7939

Mark Welch <mark.welch@msstate.edu>

Moulis France DisperalEvolution

POSITION AS POST-DOCTORAL RESEARCH FELLOW for 2 YEARS in DISPERSAL EVOLUTION available at the Experimental Evolution Station of the CNRS in Moulis (Station dEcologie Expérimentale du CNRS à Moulis, France)

The position starts at the 1st of November 2008. The highly motivated candidate will study the role of condition-dependent dispersal in meta-population dynamics and evolution. He/She will conduct experiments in a vast system of semi-natural interconnected enclosures. The extent of the system and the equipment of each enclosure to record movements and environmental conditions are unique in Europe and offer excellent possibilities for dispersal research. As a model organism the Common Lizard is foreseen. Depending on the candidates skills and interests, the research could also incorporate a theoretical part about the role of information in dispersal evolution, metapopulation dynamics and invasion. This theoretical work can be developed in the context of species responses to climate change.

The Station dEcologie Experimentale in Moulis (SEEM) is a recently founded research and service unit of the Centre Nationale de la Recherche Scientifique (CNRS). SEEM, where the candidate will be working, is an interdisciplinary research group that combines the skills of population evolutionists, behavioural evolutionists, evolutionary biologists, and geneticists to study animal dispersal and any aspect of it. SEEM has a strong international flavour due its international staff and cooperation with institutes in the US and several European countries. SEEM is located in the foothills of the Pyrenean region Ariege (France). The station is currently undergoing extensive renovation and will soon host well equipped laboratories, comprising physiologic, genetic, and evolutionary lab facilities as well as experimental sites (Aviaries, a green house, metapopulation cage among others).

The successful candidate is required to hold a PhD or equivalent experience in a relevant area.

Applicants should submit a letter of application describing their scientific experience and interests with emphasis on how they expect to contribute to the project, curriculum vitae including a list of published work, copies of certificates, and copies of at most five publications. When evaluating the application, emphasis will be given to the applicants academic and personal prerequisites to carry out the project. Applicants may be called for an interview.

Interested candidates should either contact Jean Clobert (tel: +33 5 61 04 03 69; e- mail jean.clobert@ecoex-moulis.cnrs.fr) or Dirk S. Schmeller (tel: +33 5 61 04 03 73; e-mail dirk.schmeller@ecoex-moulis.cnrs.fr) for more detailed information concerning the position and the station. Applications should be sent to: Station dEcologie Experimentale du CNRS à Moulis, 09200 Saint Girons, France.

dirk.schmeller@EcoEx-Moulis.cnrs.fr
dirk.schmeller@EcoEx-Moulis.cnrs.fr

NHM London FishBiodiversity

THE NATURAL HISTORY MUSEUM

DEPARTMENT OF ZOOLOGY

Postdoctoral Researcher

?Evolutionary diversification in an endangered biodiversity hotspot: the Southeast Asian peat swamp forest fish fauna?

We seek a highly motivated and productive postdoctoral researcher to work on a 3-year NERC-funded research project on the evolutionary history of the peat swamp forest (PSF) ichthyofauna. The Southeast Asian peat swamp forests, found in the Sundaland biodiversity hotspot, are waterlogged forests that grow on a layer of dead plant material. PSF are characterized by a unique, vastly stenotopic freshwater fish community, which is adapted to highly acidic black waters and comprises several miniature taxa and narrow range endemics, many of which have only been discovered in recent years.

The successful candidate will use a multigene, molecular systematic approach to provide a robust phylogenetic framework of representative peat swamp forest fish clades, integrating relaxed molecular clock methodology and statistical phylogeography with geological and paleoclimatological data, in order to (1) reconstruct the time frame for the peat swamp forest fish diversification, (2) identify past demographic expansions and their taxonomic, geographic and temporal correlates, and (3) identify regions of elevated taxonomic and genetic diversity that contribute most to the evolutionary legacy of this unique ecosystem.

Applicants should have a PhD in molecular phylogenetics or related fields as well as a broad interest in systematics and evolution. They should be able to work on complex and demanding projects and enthusiastic about participating in extensive fieldwork in Southeast Asia.

The position requires experience in ichthyology, phylogenetic systematics, and population genetics. Excellent molecular (PCR, cloning, sequencing), and computational skills are essential, and knowledge of statistical phylogeography and GIS based approaches would be advantageous. The successful candidate will be supervised by Drs Lukas Rüber (PI), from whom additional information can be obtained (l.ruber@nhm.ac.uk), and Ralf Britz (Co-PI) both Department of Zoology, The Natural History Museum.

This NERC-funded position is available for 3 years. Salary is in the range of GBP 26,500 per annum. Closing date for applications 1 May 2008.

For further information, including a full job description, and to apply online please visit The Natural History Museum website at www.nhm.ac.uk/jobs under reference number NHM/AFS/ET.

Dr Lukas Ruber Department of Zoology The Natural History Museum Cromwell Road London SW7 5BD UK

Tel: +44 (0)20 7942 6208 Fax: +44 (0)20 7942 5054 e-mail: l.ruber@nhm.ac.uk

www.lukasruber.com www.nhm.ac.uk/zoology Forthcoming meeting: Southeast Asian Gateway Evolution (14-17 September 2009) http://sage2009.rhul.ac.uk/ Lukas Ruber <l.ruber@nhm.ac.uk>

Paris 1year PopulationModeling

Physiologically structured population models for viability analysis One Post-doctoral position 2008-2009 available at the Ecology-Evolution Laboratory (CNRS, UMR 7625) at the Ecole Normale Supérieure (CERES-ERTI) in Paris.

Applications are invited for a one-year postdoctoral position funded by R2DS (http://www.r2ds.centre-cired.fr/) to investigate the dynamics of small populations with plastic life histories using physiologically structured populations models.

Population persistence is notably conditioned by the degree of individual variation in reproductive success, which depends on variation in any part of the life cycle. Yet, the majority of studies that examined population extinction have tended to ignore life history variation and plasticity. Here, we wish to use life history models to inform the dynamics of small populations and ask how plasticity in life history traits influences extinction dynamics. Many aspects of life history can interact with population dynamics and the project concentrates on three of them, namely growth, maturation and survival.

The post-doc will explore this issue by developing models that account for variation in life history traits using the theory of physiologically structured populations (PSP). This theory takes into account that physiological development (e.g. growth, maturation) depends on the current state of the environment (e.g., temperature, food and predator densities). In turn, the influence of the population on the environment closes a feedback loop between environment, population and life history. The theory of PSP models is thus particularly well-suited to study the interaction between population dynamics and plastic life history. Small populations are subject to stochastic fluctuation in abundance. The project aims to study the feedback of this variability on life history and the consequences for extinction dynamics. The models will be parameterized with estimates from field and experimental studies undertaken with the common lizard, a species with strong thermal and food plasticity in life history traits.

The post-doc will be based at the Ecology-Evolution Laboratory (CNRS, UMR 7625) at the Ecole Normale Supérieure (CERES-ERTI) in Paris, where the applicant will work with David Claessen and Jean-François Le Galliard. This post-doc project is part of a research network on the dynamics of small populations funded by ANR from 2008 to 2012 and will therefore interact with a larger group of researchers. The post can start on September 1st or October 1st 2008 and will run for one year with a possible one year extension by applying to extended funding from the R2DS network in spring 2009. Gross salary will be 2500 per month. The starting date can be postponed in exceptional circumstances.

References: Claessen, D. (2005). Alternative life-history pathways and the elasticity of stochastic matrix models. American Naturalist 165: E27-E35. Le Galliard, J.-F., Fitze, P. S., Ferrière, R. and J. Clobert. 2005. Sex ratio bias, male aggression, and population collapse in lizards. Proceedings of the National Academy of Sciences USA 102(50):18231-18236. Claessen, D; Van Oss, C; de Roos, AM; Persson, L. 2002. The impact of size-dependent predation on population dynamics and individual life history. Ecology

83 (6): 1660-1675.

Candidate profile There are no nationality restrictions and the successful candidate will: (1) Possess a doctoral degree in ecology and/or mathematics, dating no more than 2 years before 1 October 2008, though the last condition may be negotiated in exceptional circumstances. (2) Not have worked in the hosting lab, nor have prepared his thesis within the hosting lab, except for a return after a period of absence of at least one year. (3) Have strong competence in modeling, with an interest in population dynamics, viability analyses and conservation biology and knowledge of C programming or closely related languages. (4) Have personal qualities needed for group work and inter-disciplinary study.

Contact Application: Chantal Cuisinier, tel.: +33 1 44 27 36 89, email: Chantal.Cuisinier@snv.jussieu.fr, postal address is CNRS UMR 7625, Université Paris 6, 7 Quai St Bernard, 75005 Paris Research project: David Claessen, tel.: +33 1 44 32 27 21, email: david.claessen@ens.fr

How to apply 1 Applicants have until April 30 2008 to send a completed application form available at http://jf.legalliard.free.fr/ to the Application contact point. 2 The lab director and a local jury will select one candidate from the application forms and contact the candidates from May 31 2008. 3 The regional office of the CNRS will be responsible for drawing up the contract.

galliard@biologie.ens.fr galliard@biologie.ens.fr

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References: Claessen, D. (2005). Alternative life-history pathways and the elasticity of stochastic matrix models. American Naturalist 165: E27-E35. Le Galliard, J.-F., Fitze, P. S., FerriÃre, R. and J. Clobert. 2005. Sex ratio bias, male aggression, and population collapse in lizards. Proceedings of the National Academy of Sciences USA 102(50):18231-18236. Claessen, D; Van Oss, C; de Roos, AM; Persson, L. 2002. The impact of size-dependent predation on population dynamics and individual life history. Ecology 83 (6): 1660-1675.

Candidate profile There are no nationality restrictions and the successful candidate will: (1) Possess a doctoral degree in ecology and/or mathematics, dating no more than 2 years before 1 October 2008, though the last condition may be negotiated in exceptional circumstances. (2) Not have worked in the hosting lab, nor have prepared his thesis within the hosting lab, except for a return after a period of absence of at least one year. (3) Have strong competence in modeling, with an interest in population dynamics, viability analyses and conservation biology and knowledge of C programming or closely related languages. (4) Have personal qualities needed for group work and inter-disciplinary study.

Contact Application: Chantal Cuisinier, tel.: +33 1 44 27 36 89, email: Chantal.Cuisinier@snv.jussieu.fr, postal address is CNRS UMR 7625, UniversitÃ© Paris 6, 7 Quai St Bernard, 75005 Paris Research project: David Claessen, tel.: +33 1 44 32 27 21, email: david.claessen@ens.fr

How to apply 1 Applicants have until April 30 2008 to send a completed application form available at http://jf.legalliard.free.fr/ to the Application contact point. 2 The lab director and a local jury will select one candidate from the application forms and contact the candidates from May 31 2008. 3 The regional office of the CNRS will be responsible for drawing up the contract.

galliard <galliard@biologie.ens.fr>

PennState MolecularEvolution AncientDNA

Post-Doctoral Associate: Ancient DNA and molecular evolution

A postdoctoral position in ancient DNA and molecular evolution is currently available in the laboratory of Beth Shapiro at the Pennsylvania State University.

Highly motivated individuals interested in the molecular evolution of serially sampled populations are encouraged to apply. The successful candidate will have the opportunity to focus on either experimental techniques for the extraction and characterization of ancient DNA, the development and/or implementation of computational techniques for the analysis of serially sampled sequence data, or a combination of these two approaches. Major research themes include understanding the response of populations of large mammal to climate change or other environmental upheaval, uncovering the genetic consequences of demographic changes and investigating molecular evolutionary changes in populations through time (see:http://www.bio.psu.edu/people/faculty/bshapiro/index.html) .

Applicants must hold a Ph.D. from an accredited college or university. The successful candidate will possess either a working familiarity with population genetics, evolutionary ecology and molecular biology (DNA extraction, PCR, cloning, sequencing, SNP identification), or be proficient in the use of software packages for phylogenetic and genealogic analysis. In addition, the successful candidate will be have the opportunity to interact with participating faculty, post-docs and students in the various interdisciplinary and interdepartmental programs at Penn State.

The initial appointment will be for two years with the possibility of renewal for a further year. Review of applications will begin immediately and will continue until the position is filled. Salary and benefits are competitive. Interested applicants should send a cover letter indicating their experience and interests, along with a CV and contact information for 3 references to Beth Shapiro (beth.shapiro@psu.edu).

beth.shapiro@gmail.com

RutgersU ShellfishEvolution

Dear EvolDir members,

Please feel free to distribute the following information about a postdoctoral position at our laboratory. Thanks,

Ximing Guo

Ximing Guo, Professor Haskin Shellfish Research Laboratory Institute of Marine and Coastal Sciences Rutgers University 6959 Miller Avenue, Port Norris, NJ 08349 Ph: 856-785-0074 x4324 FAX: 856-785-1544 Email: xguo@hsrl.rutgers.edu

==Postdoctoral Position In Shellfish Genetics

A postdoctoral associate position is available at the Haskin Shellfish Research Laboratory, Rutgers University. The position is funded by a grant from the USDA Northeastern Regional Aquaculture Consortium. Research will focus on the identification and mapping of genes and quantitative trait loci related to disease resistance in the eastern oyster, Crassostrea virginica. Applicants should have a Ph.D. and background in genetics and molecular biology. Prior experience in cloning, sequencing, genotyping and mapping studies is preferred. The appointment starts on July 1, 2008 or soon after, and is for one year with possible renewal. Search will continue until the position is filled. Interested individuals should submit a CV, a brief statement of interest, and three references to: Dr. Ximing Guo, Haskin Shellfish Research Laboratory, Institute of Marine and Coastal Sciences, Rutgers University, 6959 Miller Avenue, Port Norris, NJ 08349, USA. Phone: (856) 785-0074 x4324; Fax: (856) 785-1544; Email: xguo@hsrl.rutgers.edu. Web: http://-www.imcs.rutgers.edu . Affirmative Action/Equal Opportunity Employer.

xguo@hsrl.rutgers.edu

SaintJosephU Teaching

The Biology Department at Saint Joseph's University invites applications for a Teaching Postdoctoral Fellow at the rank of Visiting Assistant Professor to begin August 2008. This position is ideally suited for a person aspiring to an academic career where teaching and research are both valued. The postdoctoral fellow will work with a seasoned faculty mentor in the classroom and research laboratory, and will also co-mentor undergraduate and MS research students. Teaching duties will include introductory biology with the opportunity to develop a course in the applicant's area of expertise. Applicants must be able to demonstrate proficient teaching skills and contribute to one of the established research initiatives within the department. The fellowship includes funding for research supplies and travel. The position is for one year with potential for renewal for a second year. Applicants are strongly encouraged to visit our website and contact potential mentors prior to applying (http:// www.sju.edu/biology). Detailed application instructions are also at this website. Review of candidate files will begin April 30th , 2008. Applications will be accepted until the position is filled. Saint Joseph's University is a private, Catholic, and Jesuit institution and expects members of its community to be knowledgeable about its mission and make positive contributions to that mission. AA/EOE M/F/V/D.

cspringe@sju.edu cspringe@sju.edu

UCaliforniaIrvine EvolutionInfectiousDisease

One or more Postdoctoral Scholar positions are available to develop computational analyses and mathematical models of infectious diseases. The project will be jointly supervised by Robin Bush and Steven Frank, with opportunity to interact with a diverse group of evolutionary geneticists and infectious disease biologists at the University of California, Irvine (http://-ecoevo.bio.uci.edu). This position provides an opportunity to develop an independent line of research and to collaborate with our group on quantitative problems. Potential projects include computational analyses of molecular data, computational tools for inference, or dynamical models of epidemiology and evolution. Our research is funded by the NIH NIGMS MIDAS program (www.epimodels.org); the successful candidate will have opportunity to participate in MIDAS meetings and related activities.

This position requires a Ph.D. and a record of published research in areas related to molecular evolution, epidemiology, computational or mathematical biology. We require computational experience and quantitative skills, including competence in at least one commonly used programming language. Positions are initially for one year, with possibility of renewal. The positions are currently open, and the starting date is negotiable.

All qualified candidates, including women and minority candidates, are encouraged to apply. Applicants should submit a cover letter, a curriculum vitae, and the names, addresses and phone numbers of two references by email only to:

Dr. Robin Bush Department of Ecology and Evolutionary Biology 2644 Biological Sciences III University of California, Irvine Irvine, CA 92697-2525 rmbush@uci.edu

The University of California, Irvine has an active career partner program, is an equal opportunity employer committed to excellence through diversity, and has a National Science Foundation Advance Gender Equity Program.

Robin Bush <rmbush@uci.edu>

UCollegeCork ArabidopsisVariation

UniCollegeCork Arabidopsis Reproduction & Natural Variation

Our lab is seeking applications from highly motivated postdocs to work on genetics of reproduction in Arabidopsis thaliana polyploids. The successful applicant will work within a small team of researchers investigating sexual and asexual reproduction (apomixis). We seek enthusiastic and highly motivated candidates with excellent and proven skills in plant genetics, genetic mapping, molecular biology and reproduction (as demonstrated by their publication record). We particularly seek candidates with experience of association/QTL mapping, DIC/fluorescence microscopy, in situ hybridisation, cytogenetics and chromatin analysis in Arabidopsis thaliana. The project is funded for three years and collaborators include Dr Magnus Nordborg (Uni of Southern California), Dr Tom Juenger (Uni of Texas) and Dr Tim Sharbel (IPK Gatersleben). The successful applicant will work closely with two PhD students working within the same funded project.

Prospective applicants should send an e-mail outlining your research interest and motivations, including; (a) your C.V. (please list publications and experimental skills) & (b) contact details and e-mail addresses for 3 referees to: Dr. Charles Spillane, Genetics & Biotechnology Lab, Biochemistry Dept & Biosciences Institute, University College Cork, Cork, Ireland. E-mail: c.spillane@ucc.ie

Lab website: www.ucc.ie/spillane Deadline: 20th March 2008 UCC is an equal opportunities employer

“Spillane, Charles” <C.Spillane@ucc.ie>

UColorado ComparativeGenomics

Comparative Genomics Laboratory Postdoctoral Positions U. Colorado School of Medicine

The Consortium for Comparative Genomics at the University of Colorado School of Medicine has an opening for postdoctoral researchers in its high-throughput genomics laboratory. These are full-time position funded by the Consortium for Comparative Genomics and the UC Cancer Center. Successful candidates would be expected to perform major and minor facets of molecular biology laboratory work required for running and maintaining the Roche-454 FLX ultra-high throughput genome sequencer operated by the Consortium, and contribute intellectually to the comparative genomic research conducted through the consortium. Successful candidates would be expected to subdivide time-effort to maintain an independent genomics-based research program in addition to maintaining the effective sequencing throughput of the consortium. The position is an excellent opportunity for interested persons to become heavily involved with diverse cutting-edge comparative genomics research (medical and otherwise) in a highly collaborative setting. The position will be supervised by David Pollock and Todd Castoe, and the postdoc would also be joining the evolutionary genomics research group led by David Pollock (www.evolutinoarygenomics.com).

The position would be located at the new UC-Health Sciences Center Anschutz Medical Campus in Aurora, Colorado, on the outskirts of Denver. (http://www.uchsc.edu/)

Specific Duties: The duties of the position holder will center around performing and managing technical laboratory aspects required to run experiments on a 454-FLX high-throughput automated genome sequencer housed in the School of Medicine, as well as data analysis. Specifically, this will involve assessing sample quality and quantity from users, communicating with users and other directors regarding sample diagnosis and project design, and carrying out molecular biology laboratory work including PCR, oligo ligation, quality control, and other steps within the 454-FLX sample preparation protocol. This position requires close intellectual interaction with various project directors as well as smooth integration with other laboratory work housed in the UC Cancer Center Core facility. There is excellent potential, if desired, for the position to expand into experimental design and grant-writing related to the postdocs own interests, as well as collaborative work with participating scientists. The successful candidate will be expected to maintain an academic research career as part of their efforts with the Consortium.

Requirements: A Ph.D. degree in a relevant field is required, and further research experience is preferred. The candidate must be a highly motivated, self-organizing and independent worker with the ability to also collaborate in a team setting. Computer literacy is required, and additional computer experience with Unix, and/or programming experience is a plus. Any genomics, DNA sequencing, molecular evolution, or statistical experience is also a strong plus. A deep and broad understanding of molecular biology is essential.

Salary: The salary range for this position is between $35,000 and $65,000 per annum, depending on qualifications.

To apply: Please forward a cover letter, CV/Resume and names of three references to Kathy R. Thomas, Administrative Coordinator, Computational BioScience Program, PO Box 6511, Mailstop 8303, Aurora, CO 80045-0511, or email to HYPERLINK "mailto:Kathy.R.Thomas@uchsc.edu" Kathy.R.Thomas@uchsc.edu

Review of applicants will begin immediately and continue until the position is filled. Multiple openings may be available.

The University of Colorado is committed to diversity and equality in education and employment.

Todd.Castoe@UCHSC.edu Todd.Castoe@UCHSC.edu

UEastAnglia Computational Systems Biology

Dear Colleagues,

I'd be grateful if you could circulate / advertise this as appropriate.

Best regards & thanks in advance, Jan

+- Jan T. Kim | email: jtk@cmp.uea.ac.uk | | WWW: http://www.cmp.uea.ac.uk/people/jtk | *—–=< hierarchical systems are for files, not for humans >=—–*

University of East Anglia, UK School of Computing Sciences

POST-DOCTORAL RESEARCH ASSOCIATE (Ref: RA477)

http://www.uea.ac.uk/hr/jobs/ra/ra477.htm GBP 28,290 - 32,795 per annum (w.e.f. 01/05/08)

A postdoctoral position is available for a computational systems biologist, to work on computational models of biological networks. The project is to develop a platform for scoring network models based on their consistency with gene expression data, and to apply this platform to investigate the networks that organise wounding responses in plants. The project team will be comprised of members from the School of Computing Sciences and the School of Biological Sciences. This post offers a unique opportunity to work on a computational systems biology project within a truly interdisciplinary environment.

You must have or be able to demonstrate:

* A doctoral degree in biosciences or computing (or equivalent experience) * An interest in computational models of biological networks, * The ability to work with and develop models and modelling software in a Linux / Unix environment, including the ability to understand and work with large biological data sets and statistics.

More information about the School of Computing Sciences can be found at http://www.cmp.uea.ac.uk/ Closing date: 25 April 2008.

jtk@cmp.uea.ac.uk

UGeorgia PlantEvolutionaryGenetics

UNIVERSITY OF GEORGIA DEPARTMENT OF GENETICS

POSTDOCTORAL POSITION IN PLANT EVOLUTIONARY GENETICS

A postdoctoral position is available in my lab. Although I am particularly interested in an individual with skills in QTL mapping, specifically genetic marker development in non-model species, I would also consider an individual more broadly interested in the evolutionary genetics of adaptation in plants or in the evoltutionary genetics of invasive species (see http://www.genetics.uga.edu/mauriciolab/ and http://www.genetics.uga.edu/pire/ for more details).

I am interested in hiring someone with some background in evolutionary or ecological genetics and with excellent bench skills. The ideal candidate will be organized, pay close attention to detail, and be able to work both independently and in collaboration with others. Independent side projects on the part of the postdoc are encouraged and will be supported intellectually and financially if feasible. A Ph.D. is required and this post-doc is only available to U.S. citizens or permanent residents.

There is also an opportunity for this postdoc to gain independent teaching experience (for extra pay) by teaching a small, 1-credit, discussion section for our undergraduate evolutionary biology course each semester.

The start date is late summer/early fall 2008. The initial appointment is for one year, with an additional two years' funding available conditional on satisfactory performance. The annual salary for this position will be commensurate with experience, and includes benefits. The University of Georgia is an Equal Opportunity Employer and I encourage applications from candidates from groups underrepresented in the life sciences.

Please send me an e-mail (mauricio@uga.edu) with the following information: a statement detailing your interest and qualifications for the position, a CV, a statement of your research interests, and the names and contact information for 3 people who could write on your behalf.

The Mauricio lab is a part of the diverse and interactive UGA Department of Genetics, for which more information can be found at http://www.genetics.uga.edu/ . Rodney Mauricio Department of Genetics Davison Life Sciences Building University of Georgia Athens, GA 30602-7223 mauricio@uga.edu http://www.genetics.uga.edu/mauriciolab mauricio@uga.edu mauricio@uga.edu

UMinnesota EvolutionaryGenetics

POST-DOCTORAL POSITION in Evolutionary Genetics

A post-doctoral position is available in my lab at the University of Minnesota to study evolutionary genetics and adaptation along a latitudinal cline and to conduct association genetic analyses in Poplar (Populus balsamifera). The research will involve analyses of a 500 + locus sample of nucleotide diversity from a rangewide sample (these loci were selected on the basis of genomic locations), collection and analyses of sequence data for 40 + genes that are candidates underlying variation in bud set, and analyses of SNP data from 25 sub-population samples (˜ 400 individuals). For more information go to http://www.popgen.uaf.edu/ This is a collaboration with Matt Olson at the Univ. of Alaska Fairbanks and is funded by a grant from the NSF.

The basic requirements are a Ph.D. in evolutionary biology or related discipline and an interest in evolutionary and ecological genetics. Experience in population genetic analyses, handling large data sets, and some program skills are desirable but not necessary. A late-summer start data is preferred but this is very flexible.

If interested please apply by June 1st. Applicants should send a CV, a short statement of research interests (˜ 1 page), and names and contact information of three references.

If you have questions contact me (ptiffin@umn.edu).

Peter Tiffin Dept. of Plant Biology University of Minnesota ptiffin@umn.edu

The University of Minnesota/Plant Biology is an equal opportunity educator and employer.

ptiffin@umn.edu

UMinnesota PrairieFlowerEvolution

A postdoctoral position is available on a project examining evolutionary consequences of population fragmentation of Echinacea angustifolia (purple coneflower) in North American prairie. This study, now in its 12th year and funded by NSF's LTREB initiative, joins demography of remnant populations with quantitative genetic experiments in the field and with modeling efforts to shed light on the feedbacks between numerical dynamics and genetic dynamics of Echinacea, and on its interactions with insects. The postdoc will collaborate with Stuart Wagenius (Chicago Botanic Garden) and Ruth Shaw (University of Minnesota) on quantitative genetic and demographic studies of the fragmented population and will have the opportunity to participate in developing evolutionary models that incorporate our accumulating understanding of genetic and demographic processes within the study system. There is considerable potential for the postdoc to develop additional research projects pertinent to the overall goals of this study.

See: Geyer, C., S. Wagenius, and R.G. Shaw. 2007. Aster models for life history analysis. Biometrika 94: 415-426. Wagenius, S., E. Lonsdorf, and C. Neuhauser. 2007. Patch aging and the S-Allee effect: breeding system effects on the demographic response of plants to habitat fragmentation. American Naturalist 169:383-397. Wagenius, S. 2006. Scale dependence of reproductive failure in fragmented Echinacea populations. Ecology 87:931-941. Wagenius, S. 2004. Style persistence, pollen limitation, and seed set in the common prairie plant Echinacea angustifolia (Asteraceae). International Journal of Plant Sciences 165:595-603. Lopez, S., F. Rousset, F.H. Shaw, R.G. Shaw and O. Ronce. 2008. Migration load in plants: role of pollen and seed dispersal in heterogeneous landscapes. J. Evol. Biol. 21: 294-309.

More information on the project, including links to papers, is available at http://echinacea.umn.edu/ The position, which could begin this summer, is available for two years, with possibility for renewal. The postdoc will be based in the Department of Ecology, Evolution and Behavior at the University of Minnesota, a stimulating and interactive community. Interested individuals may email Ruth Shaw (rshaw@superb.ecology.umn.edu) or Stuart Wagenius (swagenius@chicagobotanic.org) to learn more about the project. We will both be at Evolution 2008 in Minneapolis, June 20-24 and would be glad to meet with interested individuals then. Apply online at http://employment.umn.edu/-applicants/Central?quickFind=3D71903 (Requisition Number 155009) with a letter of interest describing research interests and experience, CV, and names and contact information of three individuals willing to send letters of reference. Review of applications will continue until the position has been filled.

The University of Minnesota is an equal opportunity/affirmative action employer.

SWagenius@chicagobotanic.org

UOslo CodGenomics

POSITION AS POST-DOCTORAL RESEARCH FELLOW/alt. RESEARCHER in GENOMICS

available at the Center for Ecological and Evolutionary Synthesis (CEES), Department of Biology, Faculty of Mathematics and Natural Sciences, University of Oslo.

The position is available for a period of 3-years.

A position as postdoctoral research fellow/researcher positions to work on the functional genomics and sequencing of the cod genome is now available. The position is financed by the Norwegian Research Council through the FUGE program and is a part of the GenoFisk marine platform where we are aiming at sequencing the full genome of several individuals of Atlantic cod. The results will be used to characterize genetic variability within major stocks and populations of Atlantic cod, and other related species for comparisons. We have access to facilities for experimental studies (breeding/rearing) of cod and are equipped to do gene expression analysis through our 454 sequencer.

The CEES, where the candidate will be working, is an interdisciplinary research group within the Department of Biology that combines the skills of population ecologists, evolutionary biologists, geneticists, and statisticians. It has a strong international flavour, and currently employs 17 faculty, 34 postdocs/researchers, 27 PhD students, 25 master students and 33 official international collaborators. The CEES has been awarded status as centre of excellence by the Norwegian Research Council, and is well funded. Information about the centre can be found at: http://www.cees.uio.no For further information please contact: Professor Nils Christian Stenseth, phone: +47 22854584, e-mail: n.c.stenseth@bio.uio.no. Professor Kjetill S Jakobsen, phone: +47-22854602, e-mail: k.s.jakobsen@bio.uio.no.

Deadline for application: 2 May 2008 REF. NR.: 2008/5167

Please read the full announcement, including instructions on how to apply, at: http://-www.cees.uio.no/about/vacancies/postdoc-genomics-020508 tore.wallem@bio.uio.no

UOxford SexChromosome PopulationGenetics

Postdoctoral position, University of Oxford UK

Post-Doctoral Research Associate: Grade 7: 26,666 - 32,796 UK pounds per annum (Currently 1UKpound is about 2 USD)

Applications are invited for a Research Associate to work on a 12 month project funded by John Fell Fund. The project will use latest high throughput pirosequencing technology for genetic and population genetic analysis. The project is mainly focused (but not necessarily restricted to) the analysis of population genetics of sex chromosome evolution and speciation in dioecious species of plant genus Silene. The successful candidate will ideally have a strong interest in evolutionary genetics and experience in analysis of large amounts of DNA sequence data generated by 454 genomic sequencers. Programming skills are essential. Molecular genetic experience is not essential, but will be an advantage. For informal enquiries about the project, please contact Dmitry Filatov on Dmitry.Filatov@plants.ox.ac.uk.

The deadline for applications is Friday 11th April 2008.

The position is available immediately to start as soon as possible.

Dmitry A. Filatov, PhD Department of Plant Sciences, University of Oxford, South Parks Road, Oxford, OX1 3RB, United Kingdom

Dmitry Filatov <Dmitry.Filatov@plants.ox.ac.uk>

UZurich MolEvolution

Postdoctoral fellowship in molecular evolution

A two-year postdoctoral fellowship in molecular evolution is available in the laboratory of Andreas Wagner at the University of Zurich. Applications will be considered from candidates with theoretical, computational, or experimental background. The Wagner lab at the University of Zurich studies biological evolution on all levels of organization, from genes, genomes, and genetic networks to whole organisms. Ongoing projects range from laboratory evolution experiments in yeast to human population genomics. A sample of our research can be found at http://www.bioc.uzh.ch/wagner/. Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and /or fundamental organizational principles of life. **

We are looking for an individual who has received his or her PhD within the last five years, who is highly self-motivated and can work independently. A successful candidate for an experimental project will have substantial research experience with molecular biological techniques, acquired in research projects with an evolutionary orientation. A successful candidate for a computational project will have a strong background in bioinformatics and computational biology. Applications without a demonstrated interest and research history in evolutionary biology will not be considered further.

The working language in the laboratory is English. German skills, although helpful, are not essential.

Zurich is a highly attractive city in beautiful surroundings, with a multinational population, and many educational and recreational opportunities.

To be considered, please send a single (!) PDF file merged from the following parts to jobs_aw@bioc.uzh.ch <mailto:jobs_aw@bioc.uzh.ch>: CV including publication list, a statement of research interests not exceeding three pages, as well as three academic references. Please include the word ?MOLEVOL? in the subject line. The application deadline is April 28, 2008. The position is available immediately.

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Christiane Gujan Administrative Assistant of Prof. A. Caflisch and Prof. A. Wagner Zurich University Institute of Biochemistry Winterthurerstrasse 190 CH-8057 Zurich Switzerland

Tel. 0041 (0)44 635 55 49 Fax 0041 (0)44 635 68 62

Christiane Gujan <gujan@bioc.uzh.ch>

UZurich YeastSystemsBiology

Postdoctoral fellowship in Quantitative Systems Modeling of Yeast

A postdoctoral fellowship in Systems Biology is available in the laboratory of Andreas Wagner at the University of Zurich. The project goal is to improve our understanding of the signaling, regulatory, and metabolic networks involved in the yeast response to the nutrients nitrogen and glucose. The successful candidate will develop and improve mathematical models of yeast nutrient signaling. He or she will use multiple criteria, such as robustness of network variants to noise and mutations, and the evolvability of network topologies, to establish models for further experimental testing. The position is funded through an interdisciplinary grant by the Swiss Systems Biology Initiative, to a consortium of experimental and computational laboratories. Pertinent consortium publications include Ciliberti et al. PNAS 104, 13591-13596, 2007 and Kuepfer et al. Nat. Biotech *25*, 1001-2006, 2007. The successful candidate will be embedded in an interdisciplinary group of experimentalists and theorists from several universities.

The Wagner lab at the University of Zurich studies biological systems on all levels of organization, from genes, genomes, and genetic networks to whole organisms. Ongoing projects range from laboratory evolution experiments in yeast to human population genomics. A sample of our research can be found at http://www.bioc.uzh.ch/wagner/. Lab members are a group with very diverse backgrounds and research projects, unified by their interests in evolution and /or fundamental organizational principles of life. **

We are looking for an individual who has received his or her PhD within the last five years, who is highly self-motivated and can work independently. The successful candidate will have a strong background in mathematical and computational biology. He or she will have a publication record in the mathematical modeling of cellular systems. An interest in evolutionary questions, and experience with bioinformatic data analysis will be a plus.

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

To be considered, please send a single (!) PDF file merged from the following parts to jobs_aw@bioc.uzh.ch <mailto:jobs_aw@bioc.uzh.ch>: CV including publication list, a statement of research interests not exceeding three pages, as well as three academic references. Please include the word $B!H(BYEAST$B!I(B in the subject line. The application deadline is May 1, 2008. The position is available as of August 1, 2008. It is available for one year initially, renewable up to three years.

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Christiane Gujan Administrative Assistant of Prof. A. Caflisch and Prof. A. Wagner Zurich University Institute of Biochemistry Winterthurerstrasse 190 CH-8057 Zurich Switzerland

Tel. 0041 (0)44 635 55 49 Fax 0041 (0)44 635 68 62

Christiane Gujan <gujan@bioc.uzh.ch>

Vienna EvolutionaryGenetics

POST-DOCTORAL POSITION: Molecular Ecology/ Evolutionary Genetics Konrad Lorenz Institute for Ethology, Vienna, Austria

We seek a highly motivated scientist who can work independently and is also interested in collaborating with scientists at our institute (headed by Dr. Dustin Penn). A strong background in behavioral biology (or evolutionary biology), molecular genetics, population genetics, statistical analyses (bioinformatics) is required. Research projects at the institute currently address a variety of topics, including the evolution of MHC polymorphisms, sexual selection, mating systems, and host-pathogen interactions.

We have a well-equipped molecular genetics laboratory, several technicians, and very good animal facilities, especially for fish and birds (see http://www.oeaw.ac.at/-klivv/). Our institute is located in the Vienna Woods, next to the Research Institute for Wildlife Ecology, Veterinary University of Vienna (http://www.fiwi.at/), only 30 min from the city center by public transport. Vienna is ranked in the top 2-5 cities in the world to live, it has a large international community, and English is commonly spoken (http://www.wien.gv.at/english/-). German is not necessary, but it is useful (the institute operates bilingually).

The position is initially for three years, with renewal possible, and the salary depends upon experience. Review of applications begins immediately and will continue until an applicant is chosen. Starting date is negotiable. To apply, please send (preferably via email) (1) a CV, (2) 2-3 publications, (3) a brief statement of research interests, (4) names of 3 scientists who can be contacted for letters of reference to the address below.

Alexandra Katzer Konrad Lorenz Institute for Ethology Austrian Academy of Sciences Savoyenstrasse 1a A-1160 Vienna, Austria Tel: +43 51581 2700 Fax: +43 51581 2800 office@klivv.oeaw.ac.at

A.Katzer@klivv.oeaw.ac.at A.Katzer@klivv.oeaw.ac.at

Vienna TheoPopGen

Postdoc - Research Associate / Group Leader Position in Theoretical Population Genetics / Genomics at the University of Vienna

The mathematics and biosciences group (MaBS) at the University of Vienna is looking for a strong and highly motivated candidate for a senior postdoc / research associate position in evolutionary modeling and/or statistical data analysis. The research focus is flexible and includes work in molecular population genetics, evolutionary genomics, and quantitative genetics. See the MaBS homepage (www.mabs.at) for further information on our research interests.

Depending on the experience of the candidate, the position can be offered on the level of a Postdoc (for two years initially) or a Research Associate / Junior Group Leader (for up to five years). Postdocs are encouraged V and Research Associates expected V to develop an independent research program in addition to projects in cooperation. The starting date is negotiable.

Vienna is not only one of the worlds most liveable cities, but also offers an excellent research environment and currently develops into one of the main centers in evolutionary research in Europe.

Formal requirement is a PhD and a strong background and interest in quantitative evolutionary research (analytical or computational modelling or data analysis). Postdoc experience is expected for hires at the Associate level. The working language in the group is English, German skills are not essential. The reviewing process will start at the end of April and will continue until the position is filled. Full applications should include a CV with publication list, a summary of past and future research interests, and the names and email addresses of three potential referees. Applications and informal inquiries should be sent (preferably as a single pdf) to Joachim Hermisson (joachim.hermisson@univie.ac.at).

joachim.hermisson@univie.ac.at

VirginiaCommonwealthU Bioinformatics

A postdoctoral position is available in this summer with flexibile time to join in the Bioinformatics Laboratory at Virginia Institute for Psychiatric and Behavioral Genetics, Department of Psychiatry, Virginia Commonwealth University School of Medicine. The successful candidate is expected to apply comparative genomics and systems biology approaches to studying genes involved in complex diseases. The current projects include data integration, gene ranking, network/pathway analysis of candidate genes for schizophrenia and alcohol dependence, and cross-species analysis of gene features. The position is for at least two years with possible extension. The candidate will have the opportunity to involve the expanding research program in the Center for the Study of Biological Complexity < http://www.vcu.edu/csbc/ >. The candidate will work in a dry lab environment. VCU was recently ranked No. 1 in high impact papers in Psychiatry < http://www.in-cites.com/research/2003/december_15_2003-2.html >.

The university is located in Richmond, the state capital of Virginia, within 90 minutes from the mountains, the beach, and Washington, D.C. More information can be found at the website http://bioinfo.vipbg.vcu.edu/. Virginia Commonwealth University is an equal opportunity/affirmative action institution.

The qualified candidates should be highly motivated in research and have a Ph.D. in molecuar biology, computational biology, or related when the job starts. Some experience in one programming language (Perl, Java, or C/C++) is desirable. Applicants should send a CV, *brief* statement of research interests, and reference to: Zhongming Zhao (zzhao_at_vcu.edu).

– Zhongming Zhao, Ph.D. Asst. Professor of Bioinformatics Depts. Psychiatry and Human Genetics and Center for the Study of Biological Complexity Virginia Commonwealth University PO Box 980126, Richmond VA 23298-0126 Phone: (804) 828-8129 Fax: (804) 828-1471

zzhao@vcu.edu zzhao@vcu.edu

WorkshopsCourses

China EvolutionaryGenetics

Please distribute to any undergraduates who might be interested:

Unique Opportunity for Ten Undergraduates 2009 Evolutionary Genetics Field Study Abroad in China

With funding from NSF's Partnerships for International Research and Education (PIRE) program, we are offering 10 undergraduates (U.S. citizens or permanent residents only) the opportunity to participate in a unique study abroad opportunity in China during the summer of 2009 (mid-May through mid-July).

The research focus of our PIRE grant is a forensic biogeographic study of species that are native to China and invasive in the southeastern U.S. as well as a growing number of species native to the southeastern U.S. and invasive in China. Each summer, we will run an 8 week OTS-style field course where we will visit biological communities throughout China. After the field course, students can elect to continue in short-term research internships in our partner labs in China.

Students will need to be prepared to take full advantage of this experience. Each spring semester, students will enroll at the University of Georgia (UGA) and take 3 courses; two in intensive elementary Mandarin Chinese and a laboratory course in genetics. No prior experience with Chinese language is required, although students should have had at least a course in introductory biology and preferably courses in ecology and evolutionary biology.

The cost to the student of the summer program is minimal: the grant covers travel to and within China, lodging and most meals. The student is responsible for insurance, visa costs and personal expenses. Students are also responsible for the costs of enrolling at the University of Georgia for all required courses (all students are charged at the in-state tuition rate of ~$200 per credit hour).

Applications for the 2009 program will be available online late this summer and the deadline for application is in the early fall. We encourage any interested students to contact us. For more information, please see the program web site: "http://www.genetics.uga.edu/pire/pirehome.html" or e-mail us at "pire@uga.edu"

Rodney Mauricio Program Director, UGA-China PIRE Department of Genetics University of Georgia

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Rodney Mauricio, Ph.D. Department of Genetics Phone: (706) 542-1417 University of Georgia FAX: (706) 542-3910 Athens, GA 30602-7223 e-mail: mauricio@uga.edu

Lab Web Page: http://www.genetics.uga.edu/mauriciolab PIRE Grant Web Page: http://www.genetics.uga.edu/pire Evolution at UGA: http://www.genetics.uga.edu/evolution mauricio@uga.edu mauricio@uga.edu

Highlands NorthCarolina SummerFieldCourses

Highlands Biological Station P.O. Box 580 Highlands, North Carolina 28741

Summer Field Courses in Organismal Biology in Highlands, North Carolina

The Highlands Biological Station, in Highlands, North Carolina, is offering its 2008 series of summer courses and workshops emphasizing the systematics, evolution, ecology, and conservation of various diverse taxonomic groups in the southern mountain region. HBS is an inter-institutional research center of the University of North Carolina. Highlands, North Carolina, is located in the southern Blue Ridge Mountains, at an average elevation about 3,800 feet, and situated near the Nantahala National Forest, Great Smoky Mountains National Park, Cherokee Indian Reservation, Appalachian Trail, Blue Ridge Parkway, and numerous other national reserves. Courses are geared toward advanced undergraduates/graduate students or professionals can be taken for academic credit. Financial assistance is available.

This year's course offerings (and professors) are:

- Biology of Plethodontid Salamanders (Steve Tilley-Smith College) 19-31 May - Mammals of the Southern Appalachians (Wayne Van Devender-Appalachian State Univ) 2-14 June - Biodiversity and Conservation of Birds (Rob Bierregaard-UNC-Charlotte) 16-28 June - Microbial Ecology (Sean O'Connell-Western Carolina Univ) 30 June-12 July - Fleshy Fungi of the Highlands Plateau (Andy Methven-Eastern Illinois Univ) 14-26 July - Spiders of the Southern Appalachians (Kefyn Catley-Western Carolina Univ) 28 July-9 Aug

This year's workshops are: - Graminoids (Grasses, Sedges, and Rushes) of the Southern Appalachians (Dwayne Estes-Austin Peay Univ) 12-17 May - Scientific Illustration (Nancy Lowe-Atlanta Botanical Garden) 7-12 July

Course descriptions and applications can be found at http://www.wcu.edu/hbs/-Education.htm#summercourses . Courses cost $400 per two-week course, plus $80 if taken for credit (four hours) and $50-$100 per week for housing.

For more information please call or email: 828.526.2602 or ahinkle@email.wcu.edu

Anya Hinkle <ahinkle@email.wcu.edu>

NESCent Computational Phyloinformatics Jul24-Aug4 DeadlineExt

Deadline Extension for Computational Phyloinformatics: April 22

http://www.nescent.org/courses/2008/comphy/ 24 July - 4 August 2008

In response to requests from our applicants, we are extending the application deadline for our course on Computational Phyloinformatics to Tuesday of next week, April 22. Computational Phyloinformatics is a 10-day summer course sponsored by and held at the National Evolutionary Synthesis Center (NESCent) in Durham, North Carolina (USA) that aims to give students practical knowledge and hands-on skills in phyloinformatics.

This course trains students, post-docs, faculty, and researchers in phylogenetic computational thinking: instead of being locked in to using point-and-click off-the-shelf software, we show you how to write your own scripts and programs to customize calculations, implement new statistical analyses, or devise pipelines for high-throughput phylogenetics.

Writing and distributing your own Mesquite module, pipelining data through BioPhylo, refining evolutionary models in HyPhy, archiving and querying your lab's productivity in a database, and designing comparative statistical analyses in R: these are not difficult tasks, but there are no textbooks to get you started – yet the explosion of phyloinformatic data means that the cutting-edge researcher has to be comfortable with computational tools. That's where we come in. This hands-on course gets you over the learning curve: we help you with the installations, show you what libraries to use, and get you comfortable with writing your own programs.

The course is divided into three parts:

- Part I: A tutorial review of either Perl, Java, or R (while optional, this part is strongly recommended).

- Part II: Students have the choice of pursuing (1) a Perl track, with focus on BioPerl and Bio::Phylo; (2) a Java track, with focus on how to write a Mesquite module and program workflows that utilize Mesquite modules; or (3) an R track, with a focus on comparative phylogenetic analysis using the libraries Ape, Ouch, and Phylobase.

- Part III: Students choose between (1) a database track (with focus on SQL, BioSQL and database queries of phylogenetic trees); (2) a HyPhy track (with focus on scripting molecular evolution hypothesis tests in a phylogenetic framework); or (3) an advanced R track (with focus on automating analyses using vectorized calculations, advanced plotting and animations, and the R-LaTex document system using Sweave).

Students in all tracks will learn how to write basic phylogenetic or comparative analysis scripts, parse NEXUS files, traverse and compute over trees, and make practical use of phylogenetic software libraries. These skills will be learned in a biological context, touching on a diverse array of topics (depending on the track) such as alignment of large numbers of sequences, ancestral state reconstruction, testing for positive selection, etc.

INSTRUCTORS James Balhoff, Marguerite Butler, R. Todd Jobe, Hilmar Lapp, Darin London, David Maddison, Spencer Muse, Jeff Oliver, Brian O'Meara, William Piel, Sergei L. Kosakovsky Pond, Ryan Scherle, Todd Vision, Rutger Vos

PREREQUISITES Biology: A solid understanding of phylogenetics - for example, having already taken the Workshop on Molecular Evolution (http://www.molecularevolution.org/) or equivalent coursework or experience. Computing: Prior experience with Perl, Java, or R; or careful study of the suggested reading materials (see web site). Students should have experience with basic Unix shell commands. All students are expected to bring their own Mac OSX computer (a limited number of loaners are available upon request).

FEES Tuition is $600.00. Accommodation is $50/night for a single occupancy apartment, $26/night for double occupancy apartment in housing provided at Duke University (students are also free to make their own housing arrangements). Travel awards of up to $450 each are available to subsidize travel expenses for applicants from underrepresented groups.

HOW TO APPLY Apply through the course website (http://www.nescent.org/courses/2008/comphy).

You will be asked to provide a resume, two references, a brief description of your computational and phylogenetic background, and your reasons for taking the course.

Course Director: William Piel (piel@treebase.org) Course Administrator: Jory Weintraub (jory@nescent.org) Organizing Committee: Hilmar Lapp, William Piel, Todd Vision, Jory Weintraub

william.piel@yale.edu william.piel@yale.edu

NESCent GMOD Jul11-13 ApplicationDeadlineApr15

Hello,

This is a reminder that we will start reviewing applications for the GMOD Summer School one week from today, on Wednesday, April 15.

See below, or these pages for more information. http://gmod.org/GMOD_Summer_School and http://gmod.org/GMOD_Summer_School_Statement_of_Interest Please let me know if you have any questions.

Thanks,

Dave Clements GMOD Help Desk

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GMOD Summer School July 11-13, 2008 National Evolutionary Synthesis Center (NESCent) Durham, North Carolina, USA

The first GMOD Summer School (http://gmod.org/GMOD_Summer_School) will be held July 11-13, 2008 at the National Evolutionary Synthesis Center (NESCent), in Durham, North Carolina, USA. GMOD is a collection of interoperable open source software components for managing genomic data. GMOD components are used in diverse contexts, with both emerging and established model organisms.

The course will provide an overview of GMOD and cover these popular components in detail: * Chado - a modular and extensible database schema * Apollo - genome annotation editor * GBrowse - genome viewer * CMap - comparative map viewer * Community Annotation System - GMOD's most popular components in a single system

This is a 2 1/2 day hands-on workshop aimed at teaching new GMOD users how to get up and running with popular GMOD components. There will also be a concurrent 1 day session aimed at principal investigators that will give decision makers an overview of what GMOD can do, how the project operates, and what level of resources are needed to use GMOD.

The National Evolutionary Synthesis Center (NESCent, http://nescent.org) has joined the GMOD project with the goal of lowering the barrier to entry for research communities focused on emerging model organisms. The GMOD Summer School is a part of this effort. NESCent is also extending GMOD components, particularly Chado, to better support comparative and evolutionary data.

If you are interested in attending the GMOD Summer School please submit a Statement of Interest by April 15, 2008. The course is free but enrollment is limited. For application information and a tentative program see:

http://gmod.org/GMOD_Summer_School —— NESCent offers various courses and workshops, as well as funding post-doctoral and sabbatical positions, working groups and other meetings. For more information about research and training opportunities at NESCent, visit http://nescent.org. Sign up for our quarterly electronic newsletter at http://www.nescent.org/about/contact.php to automatically receive information about events at NESCent.

clementsnescent@gmail.com

Porto Portugal GeneticDataAnalysis Sep9-15

3rd Conservation Genetics Data Analysis Course Recent Approaches for Estimation of Population Size, Structure, Gene flow, Landscape Genetics, Selection Detection & Bioinformatics

9 - 15 September, 2008, Porto, Portugal

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 20 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 15 June, 2008

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.

Instructors: Fred Allendorf, University of Montana, USA Mark Beaumont, University of Reading, England Oscar Gaggiotti, University Joseph Fourier in Grenoble, France Gordon Luikart, CIBIO, Portugal & University of Montana Albano Beja-Pereira, CIBIO, Portugal Mike Schwartz, US Forest Service, Missoula, USA David Tallmon, University of Alaska, Juneau, USA Robin Waples, Northwest Fisheries Science Center of the National Marine Fisheries Service, USA Miguel Angel Toro, Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria (INIA), Spain Gilles GUILLOT, Department of Applied Mathematics INRA, France.

Location: *The course will be held in the facilities at CIBIO (Center for Investigation of Biodiversity and Genetic Resources; http://cibio.up.pt/) on the Campus for Agricultural Sciences in the rural village of Vairão, just north of Porto, and a few kilometres from the Atlantic coast and the airport. Vairão is an ancient village whose origins can be traced back to the Roman Period (the Roman village Valeriani).

Application and cost: *For detailed information see http://popgen.eu/congen2008/. Accommodations and meals are included in the registration fee. Cost: 1,000 euros per person will cover all meals, lodging, transportation to and from the airport. Up to two reduced-cost scholarships could be available for candidates with no funding.

congen@popgen.eu

conservation genetics course <congen@mail.icav.up.pt>

Portugal MolecularMarkers and PopulationGenetics Jun23-27

Applications for the Bioinformatics Training Course

Molecular Markers and Population Genetics - MMPG08

June 23rd - 27th are now OPEN. The deadline is May 15th 2008.

More details at the course webpage: http://gtpb.igc.gulbenkian.pt/bicourses/MMPG08/index.html Please visit our website at

http://gtpb.igc.gulbenkian.pt for other courses available

Thank you for your continued interest in our activities

– Pedro Fernandes Centro Português de Bioinformática Instituto Gulbenkian de Ciência Apartado 14 2781 OEIRAS PORTUGAL

Pedro Fernandes <pfern@igc.gulbenkian.pt>

Sweden EMBO MolEvolution Jun30-Jul12

EMB/ZOONET Course on Molecular approaches to Evolution and Development

30 June - 12 July 2008 Fiskebäckskil, Sweden

Please visit the course web site for details:

http://cwp.embo.org/pc08-22/ Register Now! Registration Deadline: 30 April 2008

http://cwp.embo.org/pc08-22/application.html Please circulate this announcement to relevant groups within your institute. We look forward to welcoming you in Kristineberg.

– Dr Max Telford Reader in Zoology Department of Biology, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel: +44

(0)20 7679 2554 Fax: +44 (0)20 7679 7096 http://www.ucl.ac.uk/biology/academic-staff/telford/telford.html Perl scripts for downloading http://homepage.mac.com/maxtelford/FileSharing9.html Mrimpatient: If you cant wait to see latest result of MrBayes analysis.

TranslatorX: Align nt sequence according to the aa translation.

Xstem and Ystem: Software for using secondary structure data in rRNA phylogenetic analyses.

Xenoturbella You Tube video http://uk.youtube.com/watch?v=3DyJXNcoxL2Xs The Linnean Society of London http://www.linnean.org/ Zoonet: Marie Curie Research Training Network http://www.zoonet.eu.com m.telford@ucl.ac.uk

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Trento Italy TreeComparativeGenomics Aug3-5

We announce that the INTERNATIONAL WORKSHOP Population, Quantitative and Comparative Genomics of Adaptation in Forest Trees' will be held at the Centro di Ecologia Alpina (CEA; http: www.cealp.it), Fondazione Edmund Mach, on Monte Bondone, near Trento, Italy, August 3-5, 2008. This workshop will be hosted by CEA, in collaboration with the University of California, Davis (Department of Plant Sciences).

The aim of the workshop is to provide up-to-date knowledge about process of adaptation in forest trees, in light of recent developments offered by genomic approaches. The workshop is organised in different lectures, held by the instructors, plus general seminars by invited speakers. This is the outline of lectures and topics: Lecture Topic 1 Introduction, Population genetics

2 Introduction, Quantitative genetics

3 Genetic markers

4 Population structure, demography

5 STRUCTURE, software demo

6 Introduction, QTL mapping

7 Expresso and Cartographer software demo

8 Introduction, Association mapping

9 SNP analysis, PineSAP demo

10 SNP genotyping

11 Neutrality tests, DnaSAM demo

12 Association testing, Tassel demo

The workshop is primarily intended for young researchers, at doctoral and post-doctoral stage, but is also dedicated to people working outside academic institutions willing to acquire basic knowledge useful for implementing practical management and conservation plans.

Organizers: David Neale (Dept. of Plant Sciences, UC Davis) Cristiano Vernesi (Centro di Ecologia Alpina, Fondazione Edmund Mach) Claudio Varotto (IASMA, Fondazione Edmund Mach)

Course Instructors: David Neale (UCDavis) , Jill Wegrzyn (UCDavis), Andrew Eckert (UCDavis) and Santiago Gonzalez-Martinez (INIA, Spain). Invited speakers: Beppe Vendramin (CNR, IGV, Florence, Italy), Michele Morgante (University of Udine, Italy), Par Ingvarsson (Unversity of Umea, Sweden).

Local committee: Cristiano Vernesi, Elena Pecchioli and Annalisa Losa (secretary), Centro di Ecologia Alpina, Fondazione Edmund Mach.

Dates: August 3-5, 2008. Place: Centro di Ecologia Alpina, Viote del Monte Bondone, 38040 Trento, Italy. Registration: Due to the intensive activity scheduled, we decided to limit the number of participants to about 15 people. Potential participants are kindly requested to submit an e-mail (losa@cealp.it) along with a one-page cv and motivation for attending the workshop. Deadline for registration is May 10, 2008. If demand exceeds capacity, participants will be selected based on the relevance of cv and motivation. Applicants will be advised of acceptance by May 24, 2008. Fee: 200 which includes lunches,dinners (from August 3 to 5) and abstract book. Contacts: Annalisa Losa (CEA): losa@cealp.it, phone: +390461939543, fax +390461948190

Cristiano Vernesi Centro di Ecologia Alpina Fondazione Edmund Mach Viote del Monte Bondone - 38040 Trento - Italy tel +390461939529 - fax +390461948190 skypename: cvernesi

vernesi@cealp.it vernesi@cealp.it

UppsalaU SexualSelection Oct3

Dear all,

Welcome to a one-day workshop for PhD students and researchers in sexual selection (3rd Oct. 2008) at the Evolutionary Biology Centre in Uppsala, Sweden.

Gender perspectives on the development of sexual selection theory A GenNa workshop

Friday 3rd Oct. 2008 At the Evolutionary Biology Centre, Uppsala, Sweden

We welcome Ph.D. students and researchers in the field of sexual selection, working with sexual selection processes (competition for mating partners, competition to be chosen as a partner, competition for breeding opportunities, sexual conflicts, dynamics in sexual selection, sexually selected pre- and postmating processes etc.) in animals, plants and theory. We will reflect over and analyse what processes are predominantly studied in which sex and why. The aim is to increase our awareness and by discussing gender perspectives contribute to the development of a more gender-neutral evolutionary biology theory.

Invited lecturer: Distinguished Prof. Patricia Adair Gowaty, UCLA, USA

The programme in short: 8.30 Get together 9-10 A historical perspective on the development of sexual selection theory. Prof. P. Gowaty 10-12 Group discussions 12-13 Lunch 13-14 Future perspectives in sexual selection. Lecture P. Gowaty. 14-17 Discussions on a gender-neutral theory. 18- Dinner with continued discussions

Coordinators: Malin Ah-King, GenNa, Uppsala University (Malin.Ah-King@gender.uu.se) Ingrid Ahnesjö, Animal Ecology, EBC, Uppsala University (Ingrid.Ahnesjo@ebc.uu.se)

Do you want to participate? Send an email with a short motivation of your interest to the coordinators, 1st of June the latest. The workshop is limited to 30 participants. The workshop will require some preparatory work: reading articles and writing an abstract reflecting over gender-perspectives in your research.

Most welcome!

For information on GenNa see http://-www.genna.gender.uu.se/ Best wishes

Malin Ah-King. – Malin Ah-King Centre for Gender Research Uppsala University Box 634, SE-751 26 Uppsala Thunbergsv 3 H Phone: +46 18-471 22 77 Mobile: +46 70-255 67 66 Fax: +46 18 - 471 35 70 www.gender.uu.se/en/node133 E-mail: Malin.Ah-King@gender.uu.se

malin.ah-king@gender.uu.se malin.ah-king@gender.uu.se

UWashington StatisticalGenetics

Seattle Statistical Genetics Summer Institute

Some of the modules in the 2008 Summer Institute in Statistical Genetics are nearly full. Details and registration procedures are online at http://www.biostat.washington.edu Bruce Weir bsweir@u.washington.edu

– Bruce S. Weir Professor and Chair, Department of Biostatistics University of Washington Seattle, WA 98195-7232 Phone (206) 221-7947. Fax (206) 543-3286.

Bruce Weir <bsweir@u.washington.edu>

WellcomeTrust HumanGenomics Aug17-22

Dear all,

This school is an opportunity for current leaders in human genomics to interact with future stars in the field, and for students to learn and be inspired by those that have shaped human genomics in the last decade. We are organising the 1st School of Human Genomics at the Wellcome Trust Genome Campus from 17-22 August 2008. The School of Human Genomics is a 5-day meeting that brings together prominent human geneticists and senior PhD students.

The schedule of this course is designed to be highly interactive with integrated presentations by the tutors and students, discussions about current topics in human genetics, and one-to-one meetings between tutors and students. We expect that all tutors will stay for the duration of the meeting. Additional events will likely be scheduled in conjunction with the Human Genetics Department at the Wellcome Trust Sanger Institute.

The closing date for applications is 15th May 2008.

Course link: http://-firstcontact.hinxton.wellcome.ac.uk/-display_info.asp?id=3D106

Organisers:

Leena Peltonen, Wellcome Trust Sanger Institute, UK

Manolis Dermitzakis, Wellcome Trust Sanger Institute, UK

Tutors include:

Stylianos Antonarakis, University of Geneva, Switzerland

Dorret Boomsma, VU University Amsterdam

Aravinda Chakravarti, Johns Hopkins University, USA

Andrew Clark, Cornell University, USA

Nancy Cox, University of Chicago, USA

Nicholas Katsanis, Johns Hopkins University, USA

Kerstin Lindblad-Toh, Uppsala University, Sweden and Broad Institute of Harvard & MIT Boston, USA

James R Lupski, Baylor College of Medicine, USA

Mark McCarthy, University of Oxford, UK

Thomas Meitinger, Helmholtz Zentrum München, Germany

Gert van Ommen, Leiden University, The Netherlands

Simon Tavaré, University of Southern California, USA

Ken Weiss, Pennsylvania State University, USA

Registration Fees

The registration fee has not yet been finalised as it is subject to sponsorship of the course. Please note that a considerable amount of sponsorship has been obtained and so the registration fee will now be a maximum of £600.

The application form is available at the link below

http://www.wtconference.org/-WTSchoolofHumanGenomics.pdf < http://www.wtconference.org/-WTSchoolofHumanGenomics.pdf >

To obtain the form as a Word document email p.garland@wtconference.org.uk

The closing date for applications is 15th May 2008.

Leena Peltonen

Manolis Dermitzakis

Emmanouil (Manolis) Dermitzakis, PhD Investigator Population and Comparative Genomics The Wellcome Trust Sanger Institute Wellcome Trust Genome Campus Hinxton, Cambridge CB10 1SA UK e-mail: md4@sanger.ac.uk Tel: +44 (0)1223 494866 Fax: +44 (0)1223 494919 URL: http://www.sanger.ac.uk/Teams/Team16/ < http://www.sanger.ac.uk/Teams/Team16/ >

md4@sanger.ac.uk

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. ...plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterward

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.