EvolDir

August 1, 2007

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

AMNH NewYork ConservationGenetics Sep27-29

REGISTRATION IS OPEN – POSTER ABSTRACT SUBMISSION – LAST CALL FOR POSTERS

REGISTRATION FEE: STUDENTS (US$100), POSTDOCS, RESEARCHERS, PROFESSORS (US$250)

ConGen3: The 3rd biannual International Symposium on Conservation Genetics

sponsored by the American Genetic Association

Date: 27-29 September, 2007

Location: American Museum of Natural History, New York, NY, USA

Website: http://genomics.amnh.org/congen3 E-mail: congen3@gmail.com

ConGen3 will be held at the AMNH Sackler Institute for Comparative Genomics in New York City.

Session topics:

- Genetic research for biodiversity surveys, characterization of unique microbial communities, and barcoding initiatives. - Conservation Genetics in Time: conservation phylogenetics and tree reconstruction for identification of hidden biodiversity and examination of hybrid zones. - Ex Situ Conservation Genetics: intensive metapopulation management in theory and practice. - Conservation Genetics in Space: landscape conservation genetics including explicit spatial modeling. - Genetics of Invasive Species: patterns and control.

Interested participants can exchange information on New York City related travel and housing options on the online forum http://groups.google.com/group/congen3

On behalf of the organizers: George Amato (American Museum of Natural History) Gisella Caccone (Yale University) Rob DeSalle (American Museum of Natural History)

Sergios-Orestis Kolokotronis Sackler Institute for Comparative Genomics American Museum of Natural History Central Park West at 79th Street New York, NY 10024 -USA- tel +1 212 313 7648 koloko@amnh.org http://koloko.net koloko@amnh.org

Atlanta Bioinformatics Nov15-17

CALL FOR PAPERS

The 6th Georgia Tech - ORNL International Conference on Bioinformatics -

In silico Biology: Gene Discovery and Systems Genomics Atlanta, Georgia, November 15-17, 2007

10 year anniversary of the first conference in 1997 – Gene Discovery in silico

This year, Georgia Tech continues the tradition of organizing bi-annual International Conference on Bioinformatics, bringing together leading, world- renowned researchers in genomics and bioinformatics to present recent advances in the field and to discuss open problems.

In the ten years since the first such Georgia Tech Conference "Gene Discovery in silico" held in November 1997, astonishing progress has been made in genome related biological science and engineering. There is a strong evidence that these popular Georgia Tech meetings have served well the interests of the dynamic and highly productiive bioinformatics research community.

Important Dates Conference dates: November 15 - 17, 2007

Deadline for poster abstract subsmission: September 30, 2007 Notification of acceptance of abstracts: October 7, 2007

Registration begins: August 1, 2007 Deadline for early registration: October 19, 2007 Deadline for late registration: November 8, 2007

Conference Website http://www2.isye.gatech.edu/-binf2007/ CONFIRMED PLENARY SPEAKERS Joel Bader, John Hopkins University, Baltimore, MD, USA Jean-Michel Claverie, University of Mediterranee, Marseille, France James Galagan, Broad Institute, Cambridge, MA, USA Roderic Guigo, IMIM, Barcelona, Spain Artemis Hatzigeorgiou, University of Pennsylvania, Philadelphia, PA, USA Anders Krogh, University of Copenhagen, Copenhagen, Denmark Hanna Margalit, Hebrew University, Jerusalem, Israel Steven Salzberg, University of Maryland, College Park, MD, USA Alexander Souvorov, National Center for Biotechnology Information, NIH, Bethesda, MD, USA Mario Stanke, University of Gettingen, Gettingen, Germany Shamil Sunyaev, Harvard University, Cambridge, MA, USA Martin Tompa, University of Washington, Seattle, WA, USA Olga Troyanskaya, Princeton University, Princeton NJ, USA Martin Vingron, Max Planck Institute for Molecular Genetics, Berlin, Germany Zhiping Weng, Boston University, Boston, MA, USA Soojin Yi, Georgia Institute of Technology, Atlanta, GA, USA

CONFERENCE CHAIRS Mark Borodovsky, Georgia Tech and Emory University Eva K. Lee, Georgia Tech and Emory University

PROGRAM COMMITTEE Pierre Baldi, University of California in Irvine David Bader, Georgia Tech Andrey Gorin, Oak Ridge National Laboratory King Jordan, Georgia Tech Michael Krauthammer, Yale University Eberhard Voit, Georgia Tech and Emory University Igor Zhulin, Oak Ridge National Laboratory and University of Tennessee

ADMINISTRATION Harry Sharp, Georgia Tech

CONFERENCE LOCATION The Global Learning & Conference Center, located in Midtown Atlanta near the center of the 1996 Olympic development, close to the Fox Theatre and Margaret Mitchell house.

Georgia Tech Conference Announcement <conf@opal.biology.gatech.edu>

Banff CambrianExplosion Aug3-7

Dear Madam, Sir,

An International Conference on the Cambrian Explosion Banff, Alberta August 3 - 7 2009

We invite you to attend a special Conference on the Cambrian Explosion to commemorate the 100th anniversary of the discovery of the Burgess Shale by Charles Doolittle Walcott. We cordially extend this invitation to all geologists, paleontologists, geochemists and biologists interested in the profound organismal, ecological and environmental changes that occurred during the Precambrian-Cambrian transition. Moreover, we think that this meeting would be of great interest to historians of geology and anyone curious about the origins of animals.

Our conference web site provides some introductory information, including the reply form and the first circular for this meeting: http://www.geology.utoronto.ca/-facultycaron/Walcott2009.htm We would be very thankful if you could add this meeting announcement on your website.

Sincerely,

INTERNATIONAL SCIENTIFIC AND ORGANIZING COMMITTEE

Co-Chairs: Dr. Jean Bernard Caron (Royal Ontario Museum, Toronto), jcaron@rom.on.ca Dr. Doug Erwin (Smithsonian Institution, Washington), ERWIND@si.edu David Rudkin (Royal Ontario Museum, Toronto), davidru@rom.on.ca

Members: Matt Devereux (University of Western

Ontario, London), mdevereu@uwo.ca Dr. Stephen Dornbos (University of Wisconsin-Milwaukee), sdornbos@uwm.edu Dr. Sarah Gabbott (University of Leicester), sg21@le.ac.uk Dr. Robert Gaines (Pomona College), robert.gaines@pomona.edu Dr. Charles Henderson (University of Calgary), cmhender@ucalgary.ca Dr. Paul Johnston (Mount Royal College, Calgary), pajohnston@mtroyal.ca Kimberley Johnston (Palaeontographica Canadiana), kimberley@paleos.ca Dr. George Pemberton (University of Alberta), george.pemberton@ualberta.ca Dr. Jean Vannier (Universite' Claude Bernard Lyon 1), jean.vannier@univ-lyon1.fr Dr. Xingliang Zhang (Department of Geology, Northwest University, Xian), xlzhang@pub.xaonline.com Dr. Maoyan Zhu (Nanjing Institute of Geology and Palaeontology, Chinese Academy of Sciences), myzhu@nigpas.ac.cn

Dr. Jean-Bernard Caron Associate Curator of Invertebrate Paleontology Burgess Shale Collection Department of Natural History Royal Ontario Museum 100 Queen's Park Toronto, Ontario, M5S 2C6 CANADA Tel.: 416-586-5593 Fax: 416-586-5863 E-mail: jcaron@rom.on.ca

ICCE-Walcott-2009 : http://www.geology.utoronto.ca/facultycaron/Walcott2009.htm http://www.rom.on.ca/collections/research/jcburgess.php http://www.rom.on.ca/collections/curators/caron.php – Francesco Santini

Postdoctoral Fellow, Chang Lab Department of Ecology and Evolutionary Biology University of Toronto

25 Harbord Street Toronto, Ontario, M5S3G5 Canada Phone: (416) 946-7222 Fax: (416) 978-8532

I am forwarding this on behalf of Dr. Jean Bernard Caron (Royal Ontario Museum, Toronto), jcaron@rom.on.ca, to whom queries should be directed Ontario Museum, Toronto), jcaron@rom.on.ca, to whom queries should be directed

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BarHarbor SerpentineEvol Jun16-23

The Sixth International Conference on Serpentine Ecology - June 16 - 23, 2008

The conference will be held on the campus of the College of the Atlantic in Bar Harbor, located on Mount Desert Island on the rocky coast of Maine. The Conference provides an opportunity for the gathering of serpentinophiles from around the world, every 2-4 years, to share and discuss their findings relating to the broad and inter-disciplinary field of serpentine ecology. Participants include botanists, zoologists, ecologists, pedologists, geologists, microbiologists, evolutionary geneticists and conservation biologists studying aspects of plant-animal-soil relations of serpentine (ultramafic) outcrops. Many attendees work across disciplines to explore the fascinating relationships that exist between extreme habitats and life.

The link to the conference is www.coa.edu/serpentine

Cheers, Nishi

Nishanta Rajakaruna College of the Atlantic 105 Eden Street Bar Harbor, ME 04609, USA Phone 207 288 5015 ext 261 Fax 207 288 3780 http://home.coa.edu/faculty/webpages/nrajakaruna/ Nishanta Rajakaruna <nrajakaruna@coa.edu>

Edinburgh Phyloinformatics Oct22-24

This October 22-24 there is a phyloinformatics workshop at the e- Science Institute in Edinburgh, Scotland, hosted in conjunction with the Isaac Newton Institute for Mathematical Sciences's Phylogenetics Programme. For more details visit the web site: http://www.nesc.ac.uk/ esi/events/710/ .

Background

As phylogenetics scales up to grapple with the tree of life, new informatics challenges have emerged. Some are essentially algorithmic - the underlying problem of inferring phylogeny is computationally very hard. Large trees not only pose computational problems, but can be hard to visualise and navigate efficiently. Methodological issues abound, such as what is the most efficient way to mine large databases for phylogenetic analysis, and is the "tree of life" the appropriate metaphor given evidence for extensive lateral gene transfer and hybridisation between different branches of the tree. Phylogenies themselves are intrinsically interesting, but their real utility to biologists comes when they are integrated with other data from genomics, geography, stratigraphy, ecology, and development. This poses informatics challenges, ranging from the more general problem of integrating diverse sources of biological data, to how best to store and query phylogenies. Can we express phylogenetic queries using existing database langauges, or is it time for a phylogenetic query language? All these topics can be gathered together under the heading "phyloinformatics". This workshop brings together researchers with backgrounds in biology, computer science, databasing, and mathematics. The aim is to survey the state of the art, present new results, and explore more closely the connections between these topics. The 3 day workshop will consist of 10 talks from invited experts (45 minutes each), plus 3 group discussion sessions (45 mins - 1 hour each). A poster session will be held in the middle of the meeting for investigators who wish to present their results, and there be also be time set aside for additional discussion and interaction.

The invited speakers are: Prof. Mike Sanderson (USA) http://ginger.ucdavis.edu/sanderson.html Professor Mark Blaxter http://www.nematodes.org/ Professor Todd Vision http://www.bio.unc.edu/Faculty/Vision/ Dr. William Piel (USA) http://www.acsu.buffalo.edu/~wpiel/ Prof. David Hibbett (USA) http://mor.clarku.edu/ Dr. Alexis Stamatakis (CH) http://diwww.epfl.ch/~stamatak/ Prof. Olaf Bininda-Emonds (DE) http://www.personal.uni-jena.de/~b6biol2/ Prof. Rod Page (UK) http://taxonomy.zoology.gla.ac.uk/rod/rod.html Dr. Charles Semple (NZ) http://www.math.canterbury.ac.nz/~cas83/ Prof. Stephen Willson (USA) http://www.public.iastate.edu/~swillson/ Regards

Rod

Professor Roderic D. M. Page Editor, Systematic Biology DEEB, IBLS Graham Kerr Building University of Glasgow Glasgow G12 8QP United Kingdom

Phone: +44 141 330 4778 Fax: +44 141 330 2792 email: r.page@bio.gla.ac.uk web: http://taxonomy.zoology.gla.ac.uk/rod/rod.html iChat: aim://rodpage1962 reprints: http://taxonomy.zoology.gla.ac.uk/rod/pubs.html Get Systematic Biology through the Society of Systematic Biologists Website: http://systematicbiology.org Search for taxon names: http://darwin.zoology.gla.ac.uk/~rpage/portal/ Find out what we know about a species: http://ispecies.org Rod's rants on phyloinformatics: http://iphylo.blogspot.com Rod's rants on ants: http://semant.blogspot.com .Oct22-24

Edinburgh SpeciationSymposium Aug30

SPECIATION SYMPOSIUM; 30th August 2007; Edinburgh, UK

Speakers: Jim Mallet (UC London); Alfried Vogler (Imperial London); Nick Barton (Edinburgh); Christian Lexer (Kew); H Peter Comes (Salzburg); Mike Ritchie (St Andrews); Roger Butlin (Sheffield); John Willis (Duke); Salvatore Cozzolino (Naples); Simon Hiscock (Bristol); Chris Jiggins (Cambridge); Peter Linder (Zurich)

Speciation Symposium programme: www.systass.org/biennial2007/symposia.shtml#speciation

Hosted at the Systematics Association Biennial Conference

CLOSING DATE FOR REGISTRATION: 30 JUNE

Late registration fee applies after this date

Registration and further details: www.systass.org/biennial2007

Sponsors: Systematics Association, Linnean Society, Genetics Society, Molecular Ecology, Botanical Society of the British Isles.

Jess Barrett <JBarrett@rbge.ac.uk>

Marseilles 11thEvolBiolMeeting Sep19-21

Dear all, The list of up dated first accepted abstracts for the 11th Evolutionary Biology Meeting at Marseilles is avalable. Few spots for poster only are still avalable http://www.up.univ-mrs.fr/evol-cgr/ All the best, Axelle Pontarotti – Axelle Pontarotti Logistical Organisation Committee

EA 3781 Evolution Biologique Université d'Aix Marseille I - case 19 Centre St Charles 3 Place Victor Hugo 13331 Marseille Cedex 3 33491106489 http://www.up.univ-mrs.fr/evol We are organizing the 11th Evolutionary Biology Meeting at Marseilles - 19-21 September 2007

http://www.evolutionary-biology.org http://www.up.univ-mrs.fr/evol-cgr/ egee@up.univ-mrs.fr

Marseilles 11thEvolBiolMeeting Sep19-21 program

Dear All,

We are pleased to announce you that the program of the 11th E B M at Marseilles is now available on http://www.up.univ-mrs.fr/evol-cgr/ We also wanted to inform you that few spots for posters remain available.

Best regards,

Axelle P;

Axelle Pontarotti Logistical Organisation Committee

EA 3781 Evolution Biologique Universitï¿½ d'Aix Marseille I - case 19 Centre St Charles 3 Place Victor Hugo 13331 Marseille Cedex 3 33491106489 http://www.up.univ-mrs.fr/evol We are organizing the 11th Evolutionary Biology Meeting at Marseilles - 19-21 September 2007 http://www.evolutionary-biology.org http://www.up.univ-mrs.fr/evol-cgr/ egee@up.univ-mrs.fr

MoscowStateU CompPhylogenetics MolSyst Nov16-19

Dear colleagues,

The Faculty of Biology of Moscow State University (FB MSU), Belozersky Institute for Physicochemical Biology of MSU (BIPB MSU), Faculty of Bioengineering and Bioinformatics of MSU (FBB MSU) and Kharkevich Institute for Information Transmission Problems of the Russian Academy of Sciences (IITP RAS) organize the international conference ≪Computational Phylogenetics and Molecular Systematics≫ (16-19 November 2007, Moscow, Russia).

This conference commemorates the 50 years since the first experimental study on molecular systematics was published in Russia, which marked the onset of contemporary molecular phylogenetics and a number of related disciplines, including molecular biology, evolutionary biology, biochemistry, computer science, and bioinformatics. The conference is aimed at gathering leading scientists from Russia and abroad in computational biology, genomics, theory and application of comparative analysis of genetic blueprints. The conference mission is to provide a stimulating platform for exchange of ideas and experiences, cross-disciplinary interactions, and long-term national and international collaborations. Participation of postgraduate and postdoctoral fellows is encouraged to foster development of the next generation professional network.

The conference scope includes but is not limited to: * computational analysis of DNA, RNA and protein sequences; * methods and algorithms of phylogenetic analysis; * oriented software development; * parallel and distributed computing in genetic data analysis, datamining; * evolution of genome, regulatory elements and genetic control systems; * dating evolutionary divergences with molecular data; * phylogenetics in hot topics of organismal evolution and systematics, phylogenomics; * applied molecular phylogenetics (barcoding, molecular anthropology, molecular epidemiology, forensic science, etc.).

Further information on the conference is available from the announcement text attached. Your inquiries will be answered upon request at frontdesk@cps2007.bio.msu.ru or rusin@iitp.ru.

Kind regards, Organizing Committee CPMS 2007

PDF: http://www.smbe.org/downloads/CPMS_1007.pdf SMBE <frontdesk@cps2007.bio.msu.ru>

NHM London LERNAnnualConference Sep14

LERN Annual Conference Friday 14th September 2007 Flett Lecture Theatre, Natural History Museum, London

CALL FOR TALKS AND POSTERS If you are a post-graduate or post-doctoral student, working on any aspect of evolutionary research, you are welcome at our FREE one-day conference.

If you would like to present a talk or poster, please submit a title and abstract (100-150 words) by 31st July 2007. Talk slots are always overbooked, so early submission will increase chance of success. Prizes will be awarded for the best talk and poster!

Keynote speakers: Sandra Knapp (Botany, Natural

History Museum) and Armand Leroi (Evolution of Development, Imperial College)

Visit http://londonevolution.net/ for information on how to register and to submit abstracts.

– Laura Fortunato Department of Anthropology University College London 14 Taviton Street London WC1H OBW, UK

email: l.fortunato@ucl.ac.uk tel: +44 (0) 20 7679 5463

http://www.cecd.ucl.ac.uk http://www.ucl.ac.uk/heeg http://londonevolution.net l.fortunato@ucl.ac.uk

NewYork AMNH Conservation Genetics Sep27-29 posters

POSTER ABSTRACT SUBMISSION – LAST CALL FOR POSTERS

REGISTRATION FEE: STUDENTS (US$100), POSTDOCS, RESEARCHERS, PROFESSORS (US$250)

ConGen3: The 3rd biannual International Symposium on Conservation Genetics

sponsored by the American Genetic Association

Date: 27-29 September, 2007

Location: American Museum of Natural History, New York, NY, USA

Website: http://genomics.amnh.org/congen3 E-mail: congen3@gmail.com

ConGen3 will be held at the AMNH Sackler Institute for Comparative Genomics in New York City.

Session topics:

- Genetic research for biodiversity surveys, characterization of unique microbial communities, and barcoding initiatives. - Conservation Genetics in Time: conservation phylogenetics and tree reconstruction for identification of hidden biodiversity and examination of hybrid zones. - Ex Situ Conservation Genetics: intensive metapopulation management in theory and practice. - Genetics of Invasive Species: patterns and control.

Interested participants can exchange information on New York City related travel and housing options on the online forum http://groups.google.com/group/congen3

On behalf of the organizers: George Amato (American Museum of Natural History) Gisella Caccone (Yale University) Rob DeSalle (American Museum of Natural History)

— Sergios-Orestis Kolokotronis Sackler Institute for Comparative Genomics American Museum of Natural History Central Park West at 79th Street New York, NY 10024 -USA- tel +1 212 313 7648 koloko@amnh.org http://koloko.net koloko@amnh.org

PurdueU Genomics Sep10-12

Purdue University is hosting a major genomics conference from 10-12 September, 2007. Confirmed speakers include Ron Phillips, Steve O'Brien, Jim Womack, Robert Baker, John McDonald, Ed Buckler, Frank Collins, Michael Sanderson, Jeff Bennetzen, Hopi Hoekstra, and many others. Cash awards will be given for student posters in the categories of B.S., M.S., and Ph.D. This will be a small meeting (in terms of registrants) so we hope there will be ample opportunity to interact with all the speakers. The deadline for early registration is 31 July 2007. See http://www.entm.purdue.edu/conference/index.html for complete information and help with registration.

dewoody@purdue.edu

RoyalSocietyLondon Phylogenetics Apr28-29

Royal Society scientific discussion meeting: "Statistical and computational challenges in molecular phylogenetics and evolution"

28 & 29 April 2008, The Royal Society, 6-9 Carlton House Terrace, London SW1Y 5AG, UK

Organized by Professor Ziheng Yang FRS and Dr Nick Goldman

Synopsis

The rapid growth of genetic sequence data has provided much-needed power for resolving controversial species relationships and studying the evolutionary process, but has also posed many statistical and computational challenges to the field. This meeting will bring together scientists with a diverse range of backgrounds, and in particular researchers actively developing statistical methods and computational algorithms used in modern phylogenetics software. Statistical and computational challenges facing the field will be discussed in the meeting, for example, efficient tree search algorithms under likelihood, Markov chain Monte Carlo algorithms for Bayesian phylogenetics, estimation of species divergence dates by incorporating uncertainties in the fossil record and statistical tests of phylogenies.

Speakers

Invited speakers include Professor David Balding, Dr Nicolas Galtier, Professsor Olivier Gascuel, Dr Mark Holder, Professor John Huelsenbeck, Dr Ari Loytynoja, Professor Rasmus Nielsen, Professor Mark Pagel, Dr Tal Pupko, Professor Bruce Rannala, Professor Allen Rodrigo, Dr Alexandros Stamatakis, Dr Marc Suchard, Professor Jeff Thorne, Professor Arndt von Haeseler, and Dr Simon Whelan.

Registration

This meeting is free to attend but pre-registration is essential. The online registration form and programme information can be found at: http://www.royalsoc.ac.uk/event.asp?id=6067&month=4,2008. Lunch tickets cost 15 pounds a day if you want lunch.

z.yang@ucl.ac.uk

Seattle FishGenetics Sep17-18

Six decades of fishery genetics: A retrospective view and a vision for the future 17-18 September 2007 Seattle, WA Sponsored by: NOAAï¿½s Northwest Fisheries Science Center School of Aquatic and Fishery Sciences, University of Washington

Visit www.regonline.com/sixdecades or email robin.waples@noaa.gov for meeting information, registration and information on submitting to the poster session.

In the 1960s the advent of protein electrophoresis revolutionized the fields of genetics and evolutionary biology, and Dr. Fred Utter, with his team of scientists at the Montlake Laboratory (current headquarters of Northwest Fisheries Science Center), were among the first to adopt these methods for application to natural fish populations for conservation and management. Dr. Utter also developed a strong relationship with the University of Washington School of Fisheries (now the School of Aquatic and Fishery Sciences) that enabled many students to gain experience with and be trained in the use of genetics and evolutionary biology as applied to fisheries management issues. Many of these students are now prominent figures in the field. To build on that legacy, we are sponsoring a Symposium, dedicated to Fred Utter and his six decades of contributions to fishery genetics, that will be both retrospective (reviewing applications up to the present day) and prospective (looking ahead to new developments in the next decade).

Mike.Ford@noaa.gov

Tremont SEPEEG Sep21-23

subject: SEPEEG/SEEPAGE 2007

The 2007 SouthEastern Population Ecology & Evolutionary Genetics Conference (SEPEEG, also known as SEEPAGE) will be held at the Great Smoky Mountains Institute at Tremont on Sep 21-23.

Dan Simberloff will give this year's Keynote Address on 22 Sep.

This small, friendly meeting is an excellent opportunity for students and faculty in the Southeast to present their research and exchange ideas. The venue is in the heart of the Great Smoky Mountains and presents many opportunities to experience the natural history of the region.

For more information and registration, visit our website: http:// web.utk.edu/~bfitzpa1/seepage.html

The deadline for registration has been set as 1 Sep 2007. The cost for all participants is $130 - this includes two nights of lodging, seven meals, and various refreshments and snacks.

We look forward to seeing you at Tremont,

The Organizers (University of Tennessee, Knoxville) Jim Fordyce Ben Fitzpatrick Matt Niemiller Graham Reynolds

Ben Fitzpatrick <benfitz@utk.edu>

UMontpellier HumanEvolution Apr2-4 Call for papers

EHBE

European Human Behaviour and Evolution Conference

2-4 April 2008

University of Montpellier

First call for papers: We are pleased to announce our third annual conference. As last year our aim is to create a multidisciplinary European forum in which researchers applying evolutionary theory to the behavioural sciences can meet and exchange ideas. To this end we are now soliciting abstracts for paper presentations.

Submissions can be made through the website: <http://www.ehbes.com/>www.ehbes.com The deadline for submission is Friday 23 November 2007.

This is to be a pre-read conference. Those accepted to present will be expected to produce a full paper version of their presentation by the end of February 2008.

Information about how to register will be made available during summer 2007.

We look forward to hearing from you.

Conference organizers: Charlotte Faurie Michel Raymond

EHBE Steering Committee Rebecca Sear (London School of Economics) Tom Dickins (University of East London) David Lawson (University College London) Kevin Laland (St Andrews University)

Charlotte Faurie & Michel Raymond Conference organizers European Human Behaviour and Evolution Conference (EHBE 2008) <http://www.ehbes.com/->www.ehbes.com Institut des Sciences de l'Evolution (CNRS UMR 5554) Universitï¿½ Montpellier II - CC 065 Place Eugï¿½ne Bataillon F-34095 Montpellier cedex 05 TEL: +33 (0)467 144 632 FAX: +33 (0)467 143 622

ehbe08@univ-montp2.fr

GradStudentPositions

ColoradoStateU EvolInvasivePlants

The Department of Bioagricultural Sciences and Pest Management at Colorado State University announces the availability of four PhD assistantships in the evolutionary ecology and management of invasive plants. These positions provide stipend and research support for the pursuit of a PhD degree within the Department's graduate program or within the University's interdisciplinary Graduate Degree Program in Ecology.

The research topics for the positions are: - Resource-based variation in plant tolerance to herbivory and biological control efficacy (With advisor Andrew Norton (apnorton@lamar.colostate.edu)).

- Comparative invasion ecology and management of black henbane (Hyoscyamus niger) (With advisor Ruth Hufbauer (hufbauer@lamar.colostate.edu)).

- Precision mapping, modeling, monitoring, and integrated management of key invasive plants on riparian and upland sites in the Colorado front range (with advisors Phil Westra (pwestra@lamar.colostate.edu) and Tom Stohlgren (toms@NREL.colostate.edu))

- Adaptive management of secondary invasions following tamarisk removal (With advisor Scott Nisson (snissen@lamar.colostate.edu) and collaborators Phil Westra, Anna Sher, and Ken Lair).

Join the outstanding ecology, entomology and weed science programs at Colorado State University! See us at: http://www.colostate.edu/Depts/-bspm/ http://www.ecology.colostate.edu/ http://-www.NREL.colostate.edu/ For more information and application instructions, please email the contact person listed for each project. Successful applicants will be expected to begin their degree program in 2008. Deadlines for application materials are August 1, 2007 for Spring 2008 admission, Dec. 1 2007 for Summer 2008 admission, January 1, 2008 for Fall 2008 admission. If you are interested, contact the relevant person as soon as possible.

CSU is an EO/AA employer.

hufbauer@lamar.colostate.edu

ETH Zurich BombusHostParasite

ETH Zï¿$\frac{1}{2}$rich, Institute of Integrative Biology (IBZ)

The Experimental Ecology Group (Paul Schmid-Hempel) is seeking to fill a

Ph.D. Position (Diversity of parasites in natural systems)

to work on questions of host-parasite interactions using Bombus spp. and their parasites as the study system. In particular, the proposed framework for this study is to investigate the diversity of pathogens in natural populations of various Bombus species. Our questions ultimately relate to the co-evolutionary dynamics of the host interactions with protozoa, viral and bacterial parasites, the epidemic processes in natural populations, or the spread and effect of infectious parasites in ecological communities of host species. We work with molecular tools but the emphasis in this project would be on ecological studies in populations and communities. In particular, little is known about the occurrence, distribution and correlates of parasitism in the diverse sets of Bombus species. The project aims at gathering this knowledge, and use it to test some major concepts of ecological theory and host-parasite coevolution. Although the prime motivation are questions of basic importance, the project is embedded in a larger set of studies conducted at ETH addressing the significance of ecological and genetic variation in natural systems with respect to disease, climatic change and environmental degradation.

The ideal candidate likes to work with this system, an interest at the crossroads of ecology, genetics and evolution and a background in any of the relevant fields. Salary and other conditions in accordance with local regulations. The normal duration of a PhD at ETH is 3 years. Special conditions for acceptance into the PhD program of ETH may apply; a degree equivalent to a M.Sc. is normally required. Preferred starting date 1 October 2007 or thereafter. Please send applications, with CV, names of referees, and short statement of your interests in this position to Prof. Paul Schmid-Hempel, preferably by email (psh@env.ethz.ch). Screening of applications will start 15 August 2007 or until post is filled. For more information, you may check our web page (www.eco.ethz.ch).

Paul.Schmid-Hempel@env.ethz.ch

ImperialCollege SilwoodPark TaxonomicBias

A NERC funded PhD studentship is available at Imperial College's Silwood Park Campus, Ascot, UK to work on any of the following projects. Anyone interested should contact Donald Quicke as soon as possible at the address below including a brief CV, statement of why they are interested and in which project, contact details and names and contact details of 2 academic referees. Applicants should hold at least a 1st or Upper Second class degree in a relevant subject or equivalent. The grant provides living expenses and tuition fees for UK citizens.

Project 1 - An investigation into bias in taxonomy

Systematic bias in the way taxonomic research is carried out is a major stumbling block in understanding global diversity. Such bias can start in the field as collection bias: some methods favouring some taxa over others. Of the the specimens collected, only some will end up being prepared and mounted as museum specimens, and only some will end up being studied in detail and end up being assigned to existing species, or described as new species. It has been shown in several taxa that larger organisms tend to be described before smaller ones, probably because larger taxa are both easier to find and easier to study. In addition, bias exists amongst geographic regions with tropical areas tending to be less well studied than temperate areas.

This project aims to detect, quantify and find methods to correct for such bias using data from existing databases, study of museum specimens and records, field studies carried out in various tropical and temperate localities. The research will focus on the large parasitic wasp superfamily Ichneumonoidea and will lead to a better understanding of the regional trends in life history strategy within the group.

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Project 2 - Molecular food-webs of tropical woo-borer parasitoids

Very few host records exist for parasitoids of tropical xylophagous insects compared with the diversity of potential hosts (mostly wood-borer beetle larvae) and their host trees. Consequently there is understanding of what features of hosts or host substrate are most important for structuring these food-webs. A major aspect of this lack of information is the difficulty of rearing parasitoids in the tropics and having confidence that they are actually attacking a given species of concealed host - rather than some other insect in the substrate. DNA sequencing can potentially overcome this enabling both parasitoid and host to be identified without the problem of rearing.

This project will comprise a mix of field sampling, and experimentation with lab-based DNA sequencing at Silwood.

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Project 3 - Identification of noise and hidden signals in phylogenetic data sets

All real phylogenetic data sets contain a mix of signals. It is the hope of most phylogenetic algorithms that the 'strongest' signal reflects the true phylogeny. However, in addition to nearly random noise (as might be expected from neutral mutations in DNA sequences) such secondary signals may reflect suites of characters being selected in response to, for example, ecological factors or life history features independent of the group's phylogeny. This project aims to develop methods whereby such 'hidden' secondary signals can be extracted from data sets, and will use these to explore existing and novel data sets, particularly involving parasitic wasps.

Dr Donald Quicke, Reader in Systematics, Division of Biology Imperial College London, Silwood Park Campus, Ascot Berkshire SL5 7PY, UK

NEW TELEPHONE AND FAX NUMBERS !!!!!!!! tel +44 (0)20 759 42238 fax +44 (0)20 759 42339

Visit my home page at: http://www.bio.ic.ac.uk/-research/dlq/dquicke.htm for more research group information, datasets, wasp pictures, publications, and links to other entomological and systematics web pages and details of short courses

d.quicke@imperial.ac.uk d.quicke@imperial.ac.uk

ImperialCollegeLondon SpeciesRangeDynamics

Species range dynamics and global change.

NERC Funded PhD studentship Division of Biology, Imperial College London.

Understanding how species respond to habitat loss driven by global change allows conservation planning to be forward-looking. Instead of focussing solely on current patterns of biodiversity, such an understanding would permit conservationists to identify which areas are likely to retain their importance and which areas may increase in importance, for example as a refuge from habitat loss. At present, models commonly use species' current environmental preferences to identify suitable areas under projected global change scenarios.

This project will use data on species' geographic ranges to investigate ways in which the current spatial patterns of diversity may help to inform the future movements of those species.

This studentship will be supervised by Dr. David Orme at the College's Silwood Park campus. The campus is home to the Ecology and Evolution section and to the NERC Centre for Population Biology. For further information on research in the section see http://www3.imperial.ac.uk/biology/research/ecologyandevolution/themes.

Initial enquiries should be made to David Orme (d.orme@imperial.ac.uk). Applicants should submit a CV and the names of 3 referees to Diana Anderson (d.anderson@imperial.ac.uk). There is no official deadline - applicants will be reviewed as they are received.

d.orme@imperial.ac.uk d.orme@imperial.ac.uk

LancasterU Darwinian influence

ESRC Collaborative (CASE) Studentship, Oct 2007-Sep 2010

Representing scientific creativity: the Darwin200 celebrations

Applications are invited for a fully funded, three-year ESRC Collaborative (CASE) PhD studentship. The studentship is available for a period of three years from October 2007, and will cover all tuition fees and provide an annual maintenance award. The successful applicant will undertake social scientific research of the UK celebrations of the life and work of Charles Darwin in 2009 in order to explore questions about the meaning and role of science and particularly of scientific creativity in contemporary society.

The student will be based in the Department of Sociology at Lancaster, but will interact closely with the CASE partner - the Natural History Museum - and with other members of the Darwin200 network of organisations. The project will be supervised by Dr Bronislaw Szerszynski and Professor Brian Wynne (Lancaster University) and Dr Johannes Vogel and Dr Bob Bloomfield (Natural History Museum).

Applications are welcome from candidates with an upper-second or first class undergraduate degree in a relevant discipline and a relevant Masters degree or equivalent professional experience.

For more information, go to: http://-csec.lancs.ac.uk/teaching/darwin200case.htm <http:/-/csec.lancs.ac.uk/teaching/darwin200case.htm> .

The closing date for applications is 6 July 2007. Enquiries about the research project may be addressed to Dr Bronislaw Szerszynski, tel: 01524 592659, email bron@lancaster.ac.uk.

g.to@nhm.ac.uk g.to@nhm.ac.uk

MaxPlanckSeewiesen BirdSong

The newly set up Independent Junior Research Group at the Max-Planck-Institute in Seewiesen (close to Munich/Starnberg, Germany) is offering a

PhD position in Animal Behaviour

We are looking for a PhD candidate to work on acoustic communication, sexual selection and vocal learning in songbirds. The project will combine laboratory and field work and will focus on the use and information content of song amplitude.

We are seeking a highly motivated candidate who is interested in exploring the mechanisms and functions of animal behaviour. Prior experience in bioacoustics would be an advantage; a ringing license would also be very helpful.

The successful candidate will join an independent junior research group at the Max Planck Institute for Ornithology. The group is headed by Dr. Henrik Brumm and offers excellent working conditions at an internationally renowned institute with facilities of the highest standards. The working language of the research group is German and English. The position is funded for a duration of three years, and is open until filled (preferred starting date: October 2007). Salary will be according to TvöD 13/2 (formerly BAT IIa/2).

The Max Planck Society is an equal opportunity employer. Disabled persons with comparable qualifications receive preferential status.

To apply, please send a cover letter describing your research interests, a complete CV and names of two referees by email to PHD.Birdsong@orn.mpg.de. For informal inquiries please contact. Dr. Henrik Brumm at brumm@orn.mpg.de.

Max Planck Institute for Ornithology Communication and Social Behaviour Group Eberhard-Gwinner-Str. Haus Nr. 11 D-82305 Starnberg (Seewiesen), Germany

Internet: www.orn.mpg.de Dr. Henrik Brumm Max Planck Institute for Ornithology Communication and Social Behaviour Group Post Box 1564 82305 Starnberg/Seewiesen Germany

Tel.: +49 (0)8157 932 355 Fax: +49 (0)8157 932 344

Henrik Brumm <brumm@mail.orn.mpg.de>

Milan Bioinformatics

PhD position in Bioinformatics and Evolutionary Genomics

1 PhD position (4 years) is available within the PhD Program in Molecular Medicine of the European School of Molecular Medicine.

The student will be a member of the research group "Bioinformatics and Evolutionary Genomics of Cancer" of the IFOM-IEO Campus (Milan, Italy) For details on the project, please visit http://www.ifom-ieo-campus.it/research/ciccarelli.php Applicants should hold a M.Sc. degree in mathematics, physics, biology, or related field.

To apply, please reach http://www.semm.it/-appli_mm.php Deadline: 25 September 2007

With best regards Veronica Viscardi

Secretary of SEMM IFOM-IEO Campus Via Adamello 16 20139 Milan Italy Tel.+39.02.574.303.262 Fax +39.02.94.37.59.91 http://www.semm.it Veronica Viscardi <veronica.viscardi@semm.it>

OhioStateU TranscriptionFactors via phylogenetics

Graduate Position: Ohio State University

We seek a graduate research associate who will perform research using existing or inferred phylogenetic information to identify clusters of orthologous and paralogous groups of transcription factor protein sequences. The student will benefit with a diverse training in comparative genomics and phylogenetic inference and experimental biology of transcription factors.

Please contact Daniel Janies <danjanies@hotmail.com>

danjanies@hotmail.com

Potsdam GlobalChangeAdaptation

3-Years GRANT for a Ph.D. student ECOLOGY Potsdam (Berlin) GERMANY

Within the Potsdam Graduate Initiative on "Modelling the response of populations, species and communities to global change" a grant for a Ph.D. student is available from now onwards to study

the

Propagation of variability patterns from individual populations to complex food webs based on an outstanding data set on long-term observations of plankton abundance with high taxonomical resolution and using advanced techniques for time-series analysis such as spectral and wavelet analysis. This Potsdam Graduate Initiative conducts interdisciplinary research and an education program which deals with different ecological and evolutionary aspects of the response of populations, species, and communities to global change and other anthropogenic impacts. The PhD projects combine recent developments in theoretical ecology as well as process-based and statistical ecological modelling to answer and is linked to our EU Programme FEMMES and other project on ecological modelling.

The project mentioned above is supervised by Prof. Dr. Ursula Gaedke (Ecology & Ecosystem Modelling, Institute for Biochemistry and Biology; http://www.bio.uni-potsdam.de/professuren/-oekosystemmodellierung), Prof. Dr. Jï¿½rgen Kurths (Nonlinear Dynamics, Institute for Physics; http://-www.agnld.uni-potsdam.de/) and Dr. David Vasseur, Calgary, Canada.

Variability patterns of natural populations and communities are of focal interest e.g. within the ongoing biodiversity-stability debate. Extending previous research (e.g. Vasseur et al. (2005, OIKOS), Huber & Gaedke (2006, OIKOS) and Vasseur & Gaedke (2007, Ecology), all papers are available upon request), we aim to study variability patterns at different temporal scales at the level of individual phyto- and zooplankton populations, how they are related to ecological characteristics of the species and trophic interactions within the food web, and how they propagate to the level of functional groups, communities and the entire food web.

The mechanistic understanding is enhanced by relating these variability patterns in biomass to those of production which indicate the turn-over rates within the system.

Applicants must have an above-average Master's degree or equivalent in Natural Sciences and a good background and interest in statistics and theoretical ecology. The willingness, both to do interdisciplinary research and to actively participate in the activities of the Potsdam Graduate School, is a prerequisite for the application.

Applications, preferably in electronic form, should be send as soon as possible and should include a CV, copies of degree certificates, and possibly a letter of recommendation to Prof. Dr. Ursula Gaedke (email: gaedke@uni-potsdam.de). For more specific information see also the web pages and the literature provided and/or contact us.

Duration: 3-Years-Grant Closing Date: Until the position is taken Country: Germany Location: University of Potsdam (near Berlin)

e-mail: Stefan.Saumweber@uni-potsdam.de

Stefan Saumweber Universitï¿½t Potsdam Maulbeerallee 2 D-14469 Potsdam Germany Fon +49 331 977-1922 Fax +49 331 977-1948 http://www.bio.uni-potsdam.de/professuren/oekosystemmodellierung saumwebe@uni-potsdam.de

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PurdueU HighwaysAsBarriers

PhD Assistantships in Wildlife Ecology and Genetics

Two PhD students are sought within the Department of Forestry and Natural Resources at Purdue University to collaborate on a project evaluating the role of Interstate Highways as barriers to dispersal, gene flow, and metapopulation stability for small and medium-sized mammals in the state of Indiana. The goals of this project are to: 1) utilize genetic data to assess the role of Interstate Highways as barriers to dispersal and gene flow in a suite of mammals which vary in size and dispersal ability, and 2) utilize high resolution telemetry data and spatially explicit individual based simulation models in conjunction with genetic data to understand the mechanisms underlying the isolating effects of interstate highways. Students will work cooperatively on extensive live trapping of study animals (eastern chipmunks, fox squirrels, gray squirrels, and raccoons) in order to collect tissue samples, mark and recapture subjects for density estimates, deploy radio collars for movement studies, etc One student will work with Dr. Gene Rhodes to explore the genetic consequences of interstate roads on the movement behavior and population structure of the focal species. The second student will work with Dr. Pat Zollner to utilize high temporal resolution telemetry data on movement patterns for development of spatially explicit individual based models for each species. Both students are expected to have excellent academic credentials including the completion of a relevant (wildlife, ecology, genetic, modeling, etc..) M.S. degree prior to arrival at Purdue. For the position in Dr. Rhodes' lab it is desirable for the student to have prior experience with the collection of microsatellite genotype data and the analysis of spatially explicit genetic data. For the position in Dr. Zollner's lab it is desirable for the student to have prior experience using individual based models and coding computer programs (preferentially in C#). Both students should have demonstrated an ability to work well in team settings because this project will require them to cooperate extensively with each other as well as with the project's PIs and other collaborators within Purdue and the Indiana Department of Natural Resources. PhD stipends in the Department of Forestry and Natural Resources at Purdue for January admissions are based on an annual figure of $19,140.00. Students interested in applying for either of these positions should submit a statement of interest, a C.V., GRE scores and their cumulative GPA along with the name and contact information of three references to Drs. Rhodes or Zollner for initial evaluations by July 30, 2007. Note that review of official applications for admission into the Department of Forestry and Natural Resources will begin September 15th 2007 and the selected candidates are expected to begin their program of study at Purdue in January of 2008. Questions about the genetic portion of the project can be addressed to Dr. Gene Rhodes (rhodeso@purdue.edu; 765- 494-3601). Questions about the simulation modeling portion of the study can be addressed to Dr. Pat Zollner (pzollner@purdue.edu; 765-496-9495).

Purdue University is an Equal Access/Equal Opportunity/Affirmative Action employer. Women and minorities are encouraged to apply.

Emily Latch latche@si.edu

TrinityCollege HybridAsh

Graduate position Trinity College Dublin (TCD) & Teagasc invites applications to undertake an MSc/PhD research project entitled:

Identifying the scale of suspected hybrid ash (F. excelsior x F. angustifolia) in Ireland'

Ash is an important hardwood species for farm forestry in Ireland. The Irish government introduced substantial planting grants around 1992 for farmers to plant trees with an extra premium for planting hardwood species including ash. Consequently plants and seeds of several species were imported to fill the needs (from various sources including France, Czech Rep, Poland and the Netherlands). Many of these plantings developed poor morphology and growth. It was clear that the problem was due to the source of the material and that the imported material was probably hybrid ash derived from F. excelsior and F. angustifolia. Today, there are at least 100 afforested sites in which suspected hybrid ash was planted. There is a lack of understanding of hybrid ash in general, its occurrence in Ireland, and potential of it to interbreed with native ash. This proposal therefore aims to carry out a set of morphological and molecular DNA tests to characterise material from suspected sites and to assess the potential of these plantations to interbreed with indigenous ash.

This project will be jointly supervised by Dr Trevor Hodkinson (TCD) and Dr Gerry Douglas (Teagasc Kinsealy) and collaborate with Nathalie Frascaria-Lacoste, Universite Paris-Sud XI, Orsay, France. The student will receive an annual tax free stipend of 21,000 Euro for maintenance and to cover university fees. Fees are approximately 5,000 Euro for EU students and 10,000 Euro for non-EU students. There will be opportunities for extra money from teaching and demonstrating on undergraduate courses and invigilating examinations. The Graduate student will initially register for an MSc at TCD under the terms of the Walsh Fellowship Scheme and the work will be undertaken at Teagasc, Kinsealy Research Centre, and the Department of Botany TCD.

Applicants must have a first or upper second class Bachelors, or Masters, degree in a biological science or relevant subject. To apply or to obtain further information, please send a CV including research interests and contact details of two referees and a letter of motivation to trevor.hodkinson@tcd.ie and gerry.douglas@teagasc.ie by Friday 13th July 2007

– Dr Trevor Hodkinson Department of Botany School of Natural Sciences University of Dublin, Trinity College D2, Ireland

Phone: 353-1-8961128 Fax: 353-1-8961147 Email: trevor.hodkinson@tcd.ie

hodkinst@tcd.ie

UArkansas EnvGenomics

Ph.D. Graduate Assistantships, Environmental Genomics at the University of Arkansas and University of Nevada, Las Vegas

Two NSF-funded graduate research assistantships are anticipated to support Ph.D. candidates interested in functional genomics of adaptation to stressful environments. The project involves laboratory and field experiments designed to discover patterns of gene expression in populations of cactophilic Drosophila mojavensis. Our general goals are to uncover whole-genome patterns of gene expression in populations exposed to natural abiotic and biotic stress. Ultimately, we wish to pinpoint clusters of functionally interacting genes expressed throughout the life cycle in different environments, and predict limits of phenotypic plasticity and adaptation, particularly in response to stressful environments and long-term global climate change. Laboratory experiments will involve DNA microarrays to study gene expression changes due to different host cacti and environmental stresses, as well as differences in epicuticular hydrocarbons. Field-related work will include monitoring of wild flies, demography of wild populations, and analysis of hydrocarbon and RNA profiles. The positions are part of a collaborative project involving the Univ. of Arkansas, Fayetteville, and the Univ. of Nevada, Las Vegas. One research assistantship will be available at each institution. Please note that these positions are contingent upon receiving final funding approval from NSF.

Applicants must gain admission to the Ph.D. program in the Department of Biological Sciences at the University of Arkansas or the School of Life Sciences at UNLV. Application information is available at http://biology.uark.edu/1251.htm and http://biology.uark.edu/1251.htm prospective.html. Stipends start at $22.8K/12 months; tuition and benefits are also covered. Supplemental funding is available on a competitive basis for applicants qualifying for Doctoral Fellowships at the Univ. of Arkansas (http://biology.uark.edu/1255.htm). These positions are expected to begin January 2008 (spring semester); admission for the fall semester, 2007 is also possible. The deadline for spring semester applications is November 15, 2007.

To apply, please contact us for information and assistance.

William J. Etges Allen G. Gibbs Department of Biological Sciences School of Life Sciences University of Arkansas University of Nevada Fayetteville, AR 72701 USA Las Vegas NV 89154 USA 479-575-6358 702-895-3203 wetges@uark.edu allen.gibbs@unlv.edu http://comp.uark.edu/˜wetges/wetges.html sols.unlv.edu/faculty/gibbs.html

UA-F and UNLV are equal opportunity/ affirmative action employers.

wetges@uark.edu wetges@uark.edu

UBern MigrationBirdFluVectors

PhD position, CMPG, University of Bern, Switzerland

Genetic analysis of migration in bird flu vectors

We are looking for a highly motivated PhD candidate to work on the genetic population structure of two potential vectors of avian influenza ï¿½ the tufted duck (/Aythya fuligula/) and the common pochard (/Aythya ferina/). The project aims at determining the levels of genetic differentiation among breeding populations throughout the range of the two species and inferring the origin of ducks on European and Asian wintering grounds. The first half of the project will include extensive fieldwork for sample collection and will involve travel in Europe and Asia. The second half of the project will be lab-based and involve sequencing and microsatellite genotyping.

We are seeking independent candidate with excellent organizational skills and the willingness to travel and carry out field work under potentially difficult conditions. Good knowledge of written and spoken English is essential, some knowledge of Russian (or related languages) would be a plus. The ideal candidate has a background in evolutionary biology, especially population genetics and phylogeography, and experience with molecular lab work and data analysis. A degree equivalent to a biology diploma or M.Sc. is required.

The student will be supervised by Gerald Heckel and Irene Keller. We offer a stimulating research environment in the in the Computational and Molecular Population Genetics lab (CMPG; head: Laurent Excoffier) with excellent facilities for laboratory work and computational analyses. The position is funded for three years, and the anticipated starting date is November 1 2007 or soon thereafter. For informal inquiries, please contact gerald.heckel@zoo.unibe.ch <mailto:gerald.heckel@zoo.unibe.ch>.

Information on the research group, the University of Bern, or life in Bern can be obtained from http://cmpg.unibe.ch/ <http://www.cmpg.unibe.ch/> and http://www.cmpg.unibe.ch/> Please send your application including CV, list of publications (if available), a letter outlining your past research and motivation for this position (max. 2 pages), and contact details of 2-3 referees in a single pdf file to gerald.heckel@zoo.unibe.ch <mailto:gerald.heckel@zoo.unibe.ch>. The deadline for applications is August 12 2007.

Dr. Gerald Heckel Computational and Molecular Population Genetics (CMPG) Zoologisches Institut Universitaet Bern Baltzerstr. 6 CH-3012 Bern Switzerland Tel.: +41 (0)31 631 30 29 Fax: +41 (0)31 631 31 88 Email: gerald.heckel@zoo.unibe.ch http://cmpg.unibe.ch/people/heckel.htm gerald.heckel@zoo.unibe.ch

UExeter MolProtistEvol

>From September/October 2007 is available a PhD-studentship in eukaryotic cell/genome evolution.

The exact project is dependent on the candidates background and research interests but falls within the broadly defined area of microbial eukaryotic evolution. The project can range from a lab intensive study to a computer intensive study or a combination of both. As such experience in molecular biology and/or bioinformatics would be an advantage. In addition, experience with protists (either free-living or parasitic) would be advantageous.

Exeter is an exiting new place to be starting your PhD as three new appointments (Drs Thomas Richards, Mark van der Giezen and Bryony Williams) are combining their resources and labs in order to set up a new research centre focused at understanding early eukaryotic evolution.

Our research spans various disciplines and includes molecular evolution, cell biology, biochemistry, bioinformatics, molecular ecology and genomics. To get an idea about our research interests, please have a look at: Richards T.A., and Cavalier-Smith T. (2005) Myosin domain evolution and the primary divergence of eukaryotes. Nature 436, 1113-1118. Richards, T.A., and van der Giezen, M. (2006) Evolution of the Isd11/IscS complex reveals a single alpha-proteobacterial endosymbiosis for all eukaryotes. Mol Biol Evol 23: 1341-1344. Tovar, J., Len-Avila, G., Snchez, L., Sutak, R., Tachezy, J., van der Giezen, M., Hernndez, M., M^{1}ller, M., and Lucocq, J.M. (2003) Mitochondrial remnant organelles of Giardia function in iron-sulphur protein maturation. Nature 426: 172-176. van der Giezen, M., and Tovar, J. (2005) Degenerate mitochondria. EMBO Rep 6: 525-530. Williams B.A., Slamovits C.H., Patron N.J., Fast N.M., and Keeling P.J. (2005) A high frequency of overlapping gene expression in compacted eukaryotic genomes. Proc Natl Acad Sci U S A. 102, 10936-10941. Williams B.A., Hirt R.P., Lucocq J.M., and Embley T.M. (2002) A mitochondrial remnant in the microsporidian Trachipleistophora hominis. Nature. 418, 865-869.

Exeter (Devon) is about 2.5 hrs west of London and is famous for its quality of life and beautiful beaches. Both the sea and Dartmoor National park can be seen from our institute.

For further information, please see www.vandergiezen.org or contact Mark van der Giezen at m.vandergiezen@exeter.ac.uk

PLEASE NOTE: Until August, I am working at Queen Mary, University of London (m.vandergiezen@qmul.ac.uk)

Dr. Mark van der Giezen Senior Lecturer in Evolutionary Biology Geoffrey Pope Building School of Biosciences, University of Exeter Stocker Road, Exeter EX4 4QD, UK Tel: +44 (0)1392 269171 Fax: +44 (0)1392 263434 e-mail: m.vandergiezen@exeter.ac.uk http://www.vandergiezen.org m.vandergiezen@exeter.ac.uk

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UIrelandMaynooth HoriGeneTransfer

Hi folks,

A position has become available unexpectedly in my lab for a graduate student to work with me on a project to investigate the role of horizontal gene transfer in prokaryotes.

The ideal student would either be a first-class graduate computer scientist with some knowledge of molecular biology or a molecular/evolutionary biologist with some knowledge and interest in computing.

The project is funded by Science Foundation Ireland to work at the National University of Ireland Maynooth. The students fees are paid if the student is from the European Union. Students from outside the EU might be required to top-up the fees from their own funds. Additionally, the student will be paid 17,000 Euro p.a., increasing by 3.125% annually.

More information on what we do in our lab can be found in our website: http://bioinf.nuim.ie/ Interested students should contact me directly.

Best,

James.

– Dr. James O. McInerney, Bioinformatics Laboratory, Department of Biology, National University of Ireland, Maynooth, Co. Kildare, Ireland. P: +353 1 708 3860 F: +353 1 708 3845 E: james.o.mcinerney@nuim.ie – Take a look at our website — http://bioinf.nuim.ie/ james.o.mcinerney@nuim.ie james.o.mcinerney@nuim.ie

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UKonstanz MolEvolBiol

A Ph.D. position in molecular evolutionary biology is available in the lab of Axel Meyer in the Department of Biology at the University of Konstanz in Germany. The evolutionary biology group is an international group of students and postdocs that also includes the labs of Gerrit Begemann on zebrafish developmental genetics and Shigehiro Kuraku on evolutionary developmental biology. The main language spoken in the lab is English.

We are looking for an energetic Ph.D. student who is interested in speciation, molecular evolution, bioinformatics/genomics, or evolutionary developmental biology. The specific research projects we are recruiting for involve (1) research on phylogenetics and population genetics of cichlid fishes (2) as well as the discovery and functional characterization of (e.g. coloration) genes underlying the diversification of cichlid fish in Africa and in Nicaragua.

The great lakes in East Africa house some of the world's most diverse freshwater ecosystems. Lakes Victoria, Malawi and Tanganyika are particularly well-known for their adaptive radiations of hundreds of endemic species of cichlid fishes. We are interested in understanding speciation, phylogeography, molecular evolution and molecular phylogenetics of these cichlid fish assemblages. Also, we wish to identify and characterize the function of genes that are involved in the phenotypic diversification and presumably speciation of cichlid fishes. Several molecular biological, "devo-evo" and genomic approaches, including candidate gene approaches, DNA-chip technology, characterization of ESTs, in situ hybridization in cichlids and transgenics in zebrafish are used to address these questions. We are also interested in evolutionary genomic questions and the evolution of novel gene functions after gene and genome duplications.

Some recent publications of the lab include: Verheyen et al. (2003). The origin of the superflock of cichlid fishes from Lake Victoria, East Africa. Science 300: 325-329. Salzburger et al. (2005). Out of Tanganyika: Genesis, explosive speciation, key-innovations and phylogeography of the haplochromine cichlid fishes. BMC Evolutionary Biology 5: 17. Barluenga et al. (2006). Sympatric speciation in Nicaraguan crater lake cichlid fish. Nature 439: 719-23 Braasch et al. (2006). Asymmetric evolution in two fish-specifically duplicated receptor tyrosine kinase paralogons involved in teleost coloration. Molecular Biology and Evolution 23:1192-1202.

Funding is available for at least 2 years. A Ph.D. thesis in Germany is supposed to be finished within about 3 years and is supposed to be written in English. Ph.D. salaries are approximately 20 to 25,000 Euros annually, (depending on marital status, age, etc.) before deductions for taxes, health insurance and retirement contributions.

The position is open immediately. The review of applicants will begin immediately until the position is filled. To apply, please email a curriculum vitae, including a list of publications, a statement of research interests, and the names and email addresses of two references to axel.meyer@uni-konstanz.de.

Prof. Axel Meyer, Ph.D. Department of Biology Konstanz University 78457 Konstanz, Germany Email: axel.meyer@uni-konstanz.de

For more information visit http://-www.evolutionsbiologie.uni-konstanz.de/-index.php?section – Prof. Axel Meyer, Ph.D. Lehrstuhl für Zoologie und Evolutionsbiologie Department of Biology Building M, Room M806 University of Konstanz 78457 Konstanz Germany

fon + 49 7531 88 4163 fax + 49 7531 88 3018

secretary: Ingrid.Bader@uni-konstanz.de tel. + 49 7531 88 3069

www.evolutionsbiologie.uni-konstanz.de Axel Meyer <axel.meyer@uni-konstanz.de>

ULausanne DrosophilaAdaptation

PhD position, University of Lausanne, Switzerland Evolutionary genetics of learning and other adaptive traits in Drosophila

A PhD position is available in Tad Kawecki's research group at the Department of Ecology and Evolution, University of Lausanne (we are moving there this summer). Most of the work in our lab concentrates on the evolutionary biology of learning and memory, and their relationships with aging, stress resistance and immunity. We use Drosophila as the study system (for more information see http://www.unifr.ch/biol/-ecology/kawecki). The PhD candidate will carry research within this broad framework, the PhD project will be developed depending on his/her interest and capacities. The daily language of the research group is English and no preexisting knowledge of French is required; however, learning some French would make living in Lausanne more pleasurable. The position is offered for three years with a possible extension for another year. The initial salary is CHF 34,200 per year and may be supplemented through a teaching assistantship. The starting date is negotiable.

The PhD student will enroll in the Doctoral School in Ecology and Evolution run by the Department. With over 20 research groups working in diverse areas of evolution and ecology, the Department of Ecology and Evolution at the University of Lausanne is a highly interactive, international research and study environment (see at www.unil.ch/dee). Located on the shore of Lake Geneva, Lausanne is an attractive city with a diverse cultural offer, while the proximity of the Alps and Jura mountains opens countless opportunities for outdoor activities.

To apply, send a CV, a short description of research experience and interest, and names and email addresses of two referees AS A SINGLE PDF FILE to tadeusz.kawecki@unil.ch, with “Learning PhD” on the subject line. We will begin to screen the application on September 3, 2007.

Tadeusz Kawecki Department of Biology University of Fribourg Chemin du Musee 10, CH-1700 Fribourg, Switzerland www.unifr.ch/biol/ecology/kawecki phone +41 26 300 88 71 fax +41 26 300 96 98 e-mail tadeusz.kawecki@unifr.ch New address from August 1, 2007 Department of Ecology and Evolution University of Lausanne Biophore CH 1015 Lausanne Switzerland email tadeusz.kawecki@unil.ch

tadeusz.kawecki@unifr.ch tadeusz.kawecki@unifr.ch

ULausanne FuncEvolGenomics

PHD POSITIONS IN FUNCTIONAL EVOLUTIONARY GENOMICS

Center for Integrative Genomics (CIG), University of Lausanne, Switzerland

Two PhD student position (duration ~3-4 years) are available in the evolutionary genomics group of Henrik Kaessmann. Starting dates of the positions are flexible.

POSITION 1 (evolutionary bioinformatics):

We are seeking talented and highly motivated applicants (preferably with some experience/background in molecular evolution), who have strong programming skills (or the willingness and drive to acquire them) and an interest in evolutionary bioinformatics (comparative genomics) analyses.

Available projects include the analysis of the functional evolution of new genes that emerged in primates and other mammalian lineages. However, other projects are possible, depending on the skills and interests of the applicant. Data available from genomic databases may be complemented with experimental data (large- and small-scale) in collaboration with the wet lab unit of the group.

POSITION 2 (molecular evolution, wet lab-based):

We are seeking highly talented and motivated applicants with a strong interest in molecular evolution, who have strong experimental lab skills (or the drive to acquire them) in molecular and/or cell biology.

Projects include the analysis of the functional evolution of new genes in primates and other mammalian lineages, but other projects are possible and can be developed together, depending on the skills and interests of the applicant. A strong bioinformatics unit in the group is available for larger-scale analyses and/or within group collaborations, for example to explore and identify new candidate genes.

A Master of Science degree or equivalent is required to be accepted for the PhD programme at the University of Lausanne.

The salaries for these positions are ~30,000 Euros per year in the beginning of the PhD.

For more information on the group and our institute more generally, see the website: http://www.unil.ch/-cig/page7858_en.html The language of the institute is English, and its members form an international group that is rapidly expanding. The institute is in Lausanne, a beautiful city at Lake Geneva amidst an impressive alpine scenery.

Informal inquiries may be addressed to: Henrik.Kaessmann@unil.ch

Please submit a CV, statement of research interest, and two letters of recommendation (and/or names of referees) to:

Henrik Kaessmann, Ph.D. Associate Professor Center for Integrative Genomics Genopode University of Lausanne CH-1015 Lausanne Switzerland E-mail: Henrik.Kaessmann@unil.ch Phone: +41-(0)21-692-3907 (administrative assistant, Annick Crevoisier: -3960) Fax: +41-(0)21-692-3965 http://www.unil.ch/-cig/page7858_en.html

Some recent publications from the lab:

Vinckenbosch, N., Dupanloup, I. & Kaessmann, H. (2006) Evolutionary fate of retroposed gene copies in the human genome. Proc. Natl. Acad. Sci. USA 103, 3220-3225.

Marques, A., Dupanloup, I., Vinckenbosch, N., Reymond, A. & Kaessmann, H. (2005) Emergence of young human genes after a burst of retroposition in primates. PLoS Biol. 3:e357.

Burki, F. & Kaessmann, H. (2004) Birth and adaptive evolution of a hominoid gene supporting high neurotransmitter flux. Nature Genet. 10, 1061-1063.

Emerson, J. J., Kaessmann, H., Betrán, E. & Long, M. (2004) Extensive gene traffic on the mammalian X chromosome. Science 303, 537-540

Henrik.Kaessmann@unil.ch Henrik.Kaessmann@unil.ch

ULeuven EvolBiol

4 YEAR PhD POSITION IN EVOLUTIONARY BIOLOGY Catholic University of Leuven, Leuven (B)

A 4 year PhD position for an evolutionary biologist is immediately vacant at the Laboratory of Aquatic Ecology (Catholic University of Leuven) in the research group of Prof. Filip Volckaert to study Strong selection pressures and micro-evolutionary responses in the three-spined stickleback.

Description: The project investigates the conceptual and methodological integration of ecology and evolutionary biology. The successful candidate will study the evolutionary response of the three-spined stickleback to strong selection pressures (predation and parasitism) in an ecological context. Patterns of phenotypic variation will be explored in natural populations and phenotypic adaptation tested experimentally. The stickleback is a prime model for evolutionary research with access to an impressive molecular toolbox, enabling the understanding of the link between phenotypic and genomic responses to environmental and anthropogenic factors. Evolution in sticklebacks has been studied in our team over the past five years (see Raeymaekers et al. 2005 and 2007, Molecular Ecology). The project starts on 1 October 2007 and is supervised by prof. Filip Volckaert and dr. Joost Raeymaekers.

The team: The Fish Genetics Team has a strong expertise in neutral and adaptive evolution, including field monitoring, experimental design, medium-throughput genotyping, the analysis of genetic, genomic, and phenotypic data with up-to-date statistical approaches, and modeling for heuristic and operational analyses. Topics addressed include phylogeny, barcoding, phylogeography, population genetics, local adaptation and rapid evolution (natural and fisheries induced), enhanced selection in aquaculture (aquaculture genomics), co-evolution between host and parasite, spatio-temporal dynamics of nursery grounds and the management of aquatic habitats. Our team comprises 6 PhD students, 4 postdocs, 2 technicians and a team leader. The historic KULeuven, founded in 1425, has a very stimulating research environment. The modern city of Leuven with its medieval roots offers a high quality of life.

Profile: High motivation, background in evolutionary biology, interest or experience in field based experimental research is strongly recommended. Research will be carried out in collaboration with a multidisciplinary team of ecologists, evolutionary biologists and population geneticists.

Financing: The successful candidates fellowship (approximately 1600 / month netto) is funded by a national project of excellence (GOA). The candidate is expected to apply for a national IWT fellowship.

Application deadline: Please send a letter of motivation, C.V., and two letters of reference to Filip Volckaert by 6 August 2007.

Contact:

Dr. Filip Volckaert Katholieke Universiteit Leuven Laboratory of Aquatic Ecology, [Research Group on Fish Genetics (room 01.01)] Postbox 02439 Ch. Deberiotstraat 32 B-3000 Leuven, BELGIUM Phone: +32 16 32 39 72 (office) or +32 16 32 39 66 (secretariat) Fax: +32 16 32 45 75 Mailto:filip.volckaert [at] bio.kuleuven.be URL: <http://www.kuleuven.ac.be/bio/eco>http://bio<http://www.kuleuven.ac.be/bio/eco>.kuleuven.be<http://www.kuleuven.ac.be/bio/eco>/eco

Filip Volckaert <Filip.Volckaert@bio.kuleuven.be>

ULiverpool EvolAnthro

New: MSC in Cognitive and Evolutionary Anthropology School of Anthropology, University of Oxford, England What makes us human? What makes culture possible? The University of Oxford's new Institute for Cognitive & Evolutionary Anthropology announces a new 12 month MSc in Cognitive & Evolutionary Anthropology to commence in October 2007. This program explores human thought, behaviour, and culture from the perspectives of the evolutionary and cognitive sciences. Candidates will take courses in primate behavioral ecology, human evolution (with a behavioral ecology emphasis), mind and culture, and quantitative methods in the human sciences; and complete a supervised 10,000 word dissertation. Program staff includes Professor Robin Dunbar, Professor Harvey Whitehouse, and Dr. Justin Barrett. Additional information about the course and how to apply is available at: <http://www.isca.ox.ac.uk/admissions/how_to_apply.shtml#msc>. Please note that applications for the 2007-2008 year will be accepted only until July 26, 2007.

Julia Lehmann, PhD School of Biological Sciences University of Liverpool Liverpool, L69 7ZB

"Lehmann, Julia" <J.Lehmann@liverpool.ac.uk>

UNottingham EvolBiol

The Institute of Genetics within the School of Biology at the University of Nottingham offers the following MRes courses in Evolution for start September 2007:

Evolutionary Biology: The MRes in Evolutionary Biology involves the study of adaptation of organisms to their environment, at the whole organism and molecular scales. Studies available include the evolutionary and behavioural ecology of insects and mammals and other species, genetic variation in wild populations of fungi, ecological genetics, and the interface between evolution and development. In addition, a number of researchers are interested in estimation of the deep phylogeny of major groups of organisms, such as pulmonate molluscs and protists. One of our staff members, Angus Davison, uses an evolutionary approach to attempt to understand the origin of the use of 'sex' darts during courtship in slugs and worms.

Molecular Evolution: The MRes in Molecular Evolution involves the study of the evolutionary relationships among organisms and gene families using molecular methods, with evolutionary trees (phylogenies) generated from the analysis of DNA and protein sequences. The programme involves both laboratory work (DNA extraction, PCR and sequencing) and bioinformatics (DNA sequence alignment and phylogeny reconstruction). Research areas within which projects are available include: studies on the evolutionary relationships in the molluscs (in particular the land snails) and the link between molluscan phylogenies and biogeography; studies on the molecular taxonomy of spiders and the link between rates of molecular and morphological diversification; studies on the evolution of spider silk gene families and the relationship between silk diversification and speciation; studies on the phylogeny of the foraminifera and the distribution of different genetic types across the oceans; and studies on genetic diversity and cryptic speciation in nematodes.

Population Genetics: The MRes in Population genetics involves the study of the genetic variation that exists in wild populations, and the forces, such as selection, mutation and genetic drift, that shape this variation. Particular interests in the School involve the molecular genetic variation of humans, and variation in wild populations of molluscs, foraminiferans and Drosophila. Projects may include studies on molecular evolution and phylogenetics using computer analysis of DNA and protein sequences; the genetic changes that are associated with speciation; evolution of transposable elements; and the population genetics of genome structure.

Comparative Genomics: With whole genome sequences being available for numerous organisms across all kingdoms of life, numerous questions concerning genome evolution to gene function, phylogenetic relationships to genetic and metabolic networks, genotype to phenotype of complex traits, can be addressed through comparative genomics. Bioinformatic analysis of related genomes leads to testable hypotheses. Research available covers all of these areas.

For further details of our MRes courses and the applications procedure please see http://-www.nottingham.ac.uk/biology/courses/taught-msc/-research.phtml For information on research within the Evolutionary Biology group at the University of Nottingham please see http://www.nottingham.ac.uk/-genetics/research/peg.php

Chris.Wade@nottingham.ac.uk
Chris.Wade@nottingham.ac.uk

UOttawa PlantEvol

University of Ottawa, Canada.

A Masters or PhD position is available in the laboratory of Anne-Gaelle Rolland-Lagan, starting September 2007 or January 2008.

Our laboratory uses a combination of experimental work (e.g. fluorescence microscopy), computational tools (e.g. image processing), and modeling to uncover mechanisms of morphogenesis (see link to lab web page below).

Available projects include quantitative analyses of vein pattern formation in leaves and quantitative analyses of single plant cell growth.

The candidate should have basic skills in (or be willing to learn some) computer programming, and satisfy the requirements of the universityï¿½s faculty of graduate and postdoctoral studies.

To apply, send a CV, contact details of two referees (academic), and a page describing your research interests to Dr. Rolland-Lagan (arolland@uottawa.ca). For more information, contact Dr. Rolland-Lagan (arolland@uottawa.ca).

Links : http://www.science.uottawa.ca/˜arolland (Dr. Rolland-Lagan) http://www.etudesup.uottawa.ca/Default.aspx?tabid=1868 (Faculty of graduate studies)

Dr. Anne-Gaï¿½lle Rolland-Lagan Biology Department, University of Ottawa, 30 Marie Curie Private, P.O. Box 450, Station A, Ottawa, Ontario, Canada, K1N 6N5 Phone: (613) 562 5800 ext 2942 Office: Gendron 279 Lab: Careg 224

ag_rolland824@hotmail.com

UQueensland EvolGenomicsSexualSel

PhD Scholarship, Evolutionary Genomics and Sexual Selection

A PhD Scholarship is available in Steve Chenoweth's lab at the University of Queensland, Australia. Broad areas of interest include, but are not limited to, intragenomic conflicts and the evolution of sexual dimorphism, the genetic basis of sexually-selected traits and mating preferences, and the evolution of reproductive character displacement. Our approach is largely empirical and uses a model Australian Drosophila system, D. serrata, to study sexual selection and its consequences. The range of genomic tools available for D. serrata, is expanding and presently includes QTL mapping lines, an EST library and custom microarray platform, with SNP panels and a BAC library under development.

Projects are free to involve any combination of field work, population genomic, quantitative genetic and experimental evolution approaches. Students with interests in statistical genetics are also encouraged to apply.

Available: immediately

Eligibility: All nationalities, with applicants who are not Australian or New Zealand citizens or residents required to apply for a fee-waiver from the University.

Contact: please send a CV including, two academic referee contacts and a brief summary of research interests to Dr Steve Chenoweth, School of Integrative Biology, University of Queensland, s.chenoweth@uq.edu.au, http://profiles.bacs.uq.edu.au/Steve.Chenoweth.html

Steve Chenoweth ARC Research Fellow / Senior Lecturer School of Integrative Biology University of Queensland Australia 4072

phone: +617-3365-2188 fax: +617-3365-1655 www.sib.uq.edu.au

Steve Chenoweth <s.chenoweth@uq.edu.au>

UZurich TheoBiol

Numerical Analyst, Computational Scientist or Applied Mathematician for Ph.D. position in theoretical biology at the University of Zurich

A candidate with previous exposure to numerical analysis or computer science is desired for a Ph.D.studentship in evolutionary biology. The population genetics group at the Institute of Zoology has formed a research team to study the evolution of biochemical and morphological adaptations in cyanobacteria. The physiology of the latter class of organisms exhibits two of the most important biochemical adaptations in the history of life: nitrogen fixation and photosynthesis. They have also evolved multicellularity. Our group, which is composed of both theoreticians and experimentalists, attempts to understand the evolution of these adaptations through a combination of empirical and theoretical approaches. As a theoretician, the candidate will be engaged in two classes of modelling approaches. The first is the development of model-based methodologies for phylogenetic estimation and measures of genetic relatedness. This would involve the construction of theoretical models based on population processes, and the subsequent development of methods for estimating phylogenetic and population genetic signals arising from the latter processes. The developed methodology would then be tested against real data. The second class of research project focuses on the development of models for the evolution of biochemical adaptations. Based on the candidate's tastes, this can range from evolution of ODE based models of biochemical processes, to more abstract theoretical models of parallel computation occuring in chemical media. The environment of the lab is multidisciplinary and we do our utmost to accommodate candidates from diverse academic backgrounds. Working language of the group is English, though knowledge of German may be a plus for easing administrative interactions within the University (not to mention improving the candidate's social existence). Programming skills in C, R, Python, Matlab/Maple/Mathematica/Octave would be a plus. In addition, knowledge of computer architecture, Fortran77, Assembly, Lisp or familiarity with the internal workings of numerical analysis or computational algebra packages would be venerated (though clearly not a must). Previous exposure to evolutionary biology and/or knowledge of any one of the following areas of mathematics would be a plus: probability theory, graph theory and differential equations. The opportunity exists to interact with experimentalists. The candidate should feel comfortable with interacting with biology students who may not have a quantitative background. Intellectual flexibility, combined with a genuine interest in biology are a must.

Ph.D. candidates at the University of Zurich should already possess a Masters degree (or alternatively, the equivalent of the Diplom in the German system) at the time of starting the program. The successful candidate would be supported by an annual stipend of roughly 38,000 Swiss Franks. Duration of study is usually 3-4yrs. Interested candidates should send electronic versions of a cover letter and their CV with reference lists to "evolzurich@gmail.com". Applicants should mention the earliest date at which they would be able to start and are also welcome to attach PDF versions of one or two of their previous publications if applicable (though prior publication is not a requirement). Applications will be accepted until August 15th. 2007. Due to potential high volume of electronic applications, applicants who have not received a response by August 20th. 2007 may assume that their application was not successful.

Contact address:

Homayoun Bagheri, Ph.D. Assistant Professor of Population Genetics Institute of Zoology, University of Zurich Winterthurerstr. 190, CH-8057 Zurich, Switzerland

Application Email. evolzurich@gmail.com http://-www.zool.uzh.ch/Research_en.html Tel. (41) 44 635 6623 Fax. (41) 44 635 6887

bagheri@zool.uzh.ch bagheri@zool.uzh.ch

Jobs

Australia Volunteer SongbirdEvol

Volunteers are needed for work on Brown songlarks in Australia, Sept-Nov 2007.

If you are interested in getting more field experience in a nice place like Australia, here is an excellent opportunity for you. We are looking for volunteers that have a genuine bird interest, and preferably have experience with bird watching or bird handling.

The project aim to investigate the effect of maternal yolk hormones on nestling growth and begging behaviour in the endemic Australian brown songlark. The brown songlark is one of the worldâs most sexually size dimorphic species, with males being 2.3 times larger than the female, which make the system very suitable for investigating sex-specific maternal effects and sibling competition.

The fieldwork is based in south-eastern Australia and includes: locating birds and nests, collecting eggs (for hormone analyses), capturing and ringing birds, hand rearing of chicks, and behavioral recordings. Volunteers are needed during three months (Sept, Oct, and Nov). We provide you with food and accommodation during your stay. If you have good experience and can stay during the whole period we can consider paying your travel expenses. Please send your CV if you want us to consider that option.

If you want more information about the project or if you are interested in working with us contact:

In the Netherlands: Prof. Jan Komdeur: J.Komdeur@rug.nl Rest of the world: Dr. Caroline Isaksson: caroline.isaksson@zool.gu.se

Dr. Caroline Isaksson GÃuniversity Departement of Zoology Medicinaregatan 18 S-413 90 GÃSWEDEN +46-31-786 3657 +46-706-797608(mobile)

caroline.isaksson@zool.gu.se

Bogota PopulationGenetics

DEPARTMENT OF BIOLOGY GENETIC UNIT (GROUP OF MOLECULAR POPULATION GENETICS-EVOLUTIONARY BIOLOGY).

http://www.javeriana.edu.co/ciencias/dep_bio/
PROFFESOR CONVOCATORY

The Department of Biology of the Faculty of Sciences from the Pontificia Universidad Javeriana at Bogota (Colombia) is demanding an associated proffesor with the following characteristics:

Proffesional Biologist

PhD in Population Genetics or in Evolutionary Molecular Biology or Molecular Phylogeny.

Recognized experience in docent and research tasks at universitary level. Proffesional experience: at least 3 years in population genetics and similars with experience in molecular procedures, sequencing, karyotypic analyses, DNA extraction from all type of tissues, including old and museum tissues and from feaces, data analysis and programs for coalesce and simulations and a strong biostatistic, mathematical analysis and programation profile.

Article production in the last 8 years.

Absolutelly fluent in Spanish and English.

Assigned functions:

Teaching: Theoretic and practical courses in General Biology, Genetics, Molecular Biology and Evolutinary Biology at Bsc and Msc and PhD levels

Research: Formulate and develop research projects focused in population genetics, molecular ecology, phylogeny-phylogeography with molecular procedures and mathematical models.

Selecciï¿½n procedures

Those interested in this position must present the following documents:

Complet Curriculum vitae

Copies of the obtained degrees

Copies of the published articles in the last 8 years

Additional documents could be demanded

Personal interview

The candidates with all the aforementioned requeriments, must show an academic presentation of one hour related with the research project focused within the population genetics-evolutionary biology field. For other requeriments, please, contact to

- Ingrid Schuler, PhD. Director, Departamento de Biologï¿½a. Pontificia Universidad Javeriana. Bulding 54, Officine. 201. ischuler@javeriana.edu.co.

- Manuel Ruiz-Garcia, PhD. Chief Molecular Population Genetics-Evolutionary Biology group. Departamento de Biologï¿½a. Pontificia Universidad Javeriana. Bulding 54. Laboratory 405 A. mruiz@javeriana.edu.co

There is time until July 20, 2007 to receive documentation. Prof. Manuel Ruiz Garcia.PhD Coordinador Unidad de Genï¿½tica Departamento de Biologï¿½a Facultad de Ciencias Pontificia Universidad Javeriana Cra 7 43-82 Bogotï¿½ D.C. Colombia

mruiz@javeriana.edu.co

Caracas Molecular Lab Manager

VERSION EN CASTELLANO ABAJO

LAB MANAGER POSITION IN MOLECULAR ECOLOGY

We seek a highly motivated research assistant to join a recently-created lab applying molecular genetic techniques to a wide variety of questions in ecology, evolution and conservation biology (http://www.ivic.ve/ecologia/ueg/). Responsibilities include: DNA extraction, sequencing and genotyping as well as data management and analysis, training students, and coordinating lab meetings, along with general lab maintenance including purchasing supplies and managing work orders.

Qualifications: 1. Bachelors degree or higher in molecular genetics, evolutionary biology, molecular ecology, or related field. 2. Extensive research experience with up-to-date techniques in molecular data collection, including DNA extraction from degraded tissues, PCR optimization, gel electrophoresis, sequencing and genotyping. 3. Familiarity with genetic analyses of sequence and/or microsatellite data and ability to learn computer analysis programs. 4. Demonstrated ability to produce high-quality results with minimal supervision, to work on a wide variety of systems, to train others, and to collaborate effectively and cheerfully in a research team. 5. Fluency in spoken and written Spanish (English a plus).

This is an appointment initially for one year from 01 August or when the position is filled, with core funds guaranteed to convert to a permanent position after that time, depending on performance. Salary commensurate with experience and scientific production, equiv. US$16-40,000/year. Benefits include full medical coverage (self + 3 family members), paid individual and collective vacations, retirement, and loan co-op membership, among others. The Instituto Venezolano de Investigaciones Cientificas is Venezuela's foremost research institution, with a campus in cloud-forested hills within commuting distance of the capital, Caracas.

Interested applicants should send the following by email to kmrc@ivic.ve before July 30:

1. Cover letter, detailing qualifications for and interest in the position. 2. Full CV, including published acknowledgements as well as publications, along with grades associated with the most recent degree obtained. 3. Names, postal addresses, and e-mail addresses of three references.

ALL QUALIFIED PERSONS OF ANY NATIONALITY, RACE, RELIGION, GENDER ETC. ARE ENCOURAGED TO APPLY

Kathryn M. Rodríguez-Clark, Ph.D. Unidad de Ecología Genética Centro de Ecología Instituto Venezolano de Investigaciones Científicas Apartado 21827 Caracas 1020 A Venezuela Tel: +58-212-504-1889 Fax: +58-212-504-1617 kmrc@ivic.ve or kmrodriguezclark@gmail.com

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POSICIÓN DE MANAGER DE LABORATORIO DE GENÉTICA MOLECULAR

Buscamos un asistente de investigación altamente motivado para trabajar en un laboratorio de reciente creación, en el que se desarrollan diversas técnicas de genética molecular aplicadas a una amplia gama de preguntas en ecología, evolución y biología de la conservación (http://www.ivic.ve/ecologia/ueg/). Las responsabilidades asociadas al cargo incluyen: extracción de ADN, secuenciación y genotipado; manejo y análisis de datos; entrenamiento de estudiantes y personal de investigación; coordinación de reuniones de laboratorio; y mantenimiento del funcionamiento general del laboratorio, incluyendo tareas administrativas como la compra de equipos y suministros y gestiones internas para la ejecución de órdenes de trabajo.

Requisitos: 1. Licenciatura o estudios de postgrado en biología (o áreas afines) con formación en genética molecular, biología evolutiva, y/o ecología molecular. 2. Extensa experiencia en investigación empleando las técnicas moleculares más recientes, incluyendo extracción de ADN a partir de tejidos degradados, optimización de PCR, electroforesis en geles de agarosa y poliacrilamida, secuenciación y genotipado. 3. Conocimiento de las técnicas de análisis genético de secuencias y/o marcadores microsatélites y habilidad en el manejo de paquetes estadísticos y de análisis genético. 4. Capacidad probada para producir resultados de alta calidad con mínima supervisión, para desenvolverse en una amplia variedad de sistemas, para entrenar a otros, y para trabajar en equipo. 5. Comunicación verbal y escrita perfecta de español. (El manejo fluido del inglés se considerará como una ventaja adicional.)

La contratación inicial es por un año, a partir del 1ro de agosto o cuando se ocupe el cargo. Hay fondos garantizados para posterior contratación como empleado fijo al finalizar el primer año, dependiendo de los resultados de la evaluación de desempeño laboral. Salario acorde a la experiencia demostrada y a la producción científica, equivalente a

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Eberhard-Karls-U Tuebingen Biosystematics

The Faculty of Biology of the Eberhard-Karls-University Tuebingen invites applications for the position (available starting 1.4.2008) of

Heisenberg-Professorship (W2) in Biosystematics

The appointment process is taking place within the frame of the Heisenberg program of the German Research Council (Deutsche Forschungsgemeinschaft, DFG).

The successful applicant will pursue an internationally high-ranking research agenda in the field of theory and development of phylogenetic methods in biosystematics with emphasis on mammals. Teaching obligations cover all aspects of zoology, in particular vertebrate evolution. Close collaborations with the interfacultary teaching and research platform Evolution and Ecology Forum EvE are expected. The position is linked with the supervision of the zoological collection and the zoological field station “Federsee”.

A formal requirement for appointment is the “Habilitation” or equivalent scientific and educational experience. The University of Tübingen is committed to strengthen the proportion of woman in research and teaching, and strongly encourages applications of qualified female scientists.

According to the rules of the DFG-program the position is designed as permanent following a first term of five years subject to a successful evaluation after three years. At the end of the first term, no new tenure procedure is required for the candidate’s permanent appointment.

Handicapped applicants with equal qualification will be given preferential treatment.

Please send your application including CV, certificates, list of publications and a summary of teaching experience by 23. 07. 2007 to: Dekanat für Biologie der Universität Tuebingen, Auf der Morgenstelle 28, 72076 Tuebingen, Germany

Nico K. Michiels (Prof.) Animal Evolutionary Ecology Zoological Institute, Faculty of Biology University Tuebingen Auf der Morgenstelle 28 E 72076 Tuebingen Germany

Tel. +49 7071 29 74649 Mobile +49 170 4758003 Fax +49 7071 29 5634

nico.michiels@uni-tuebingen.de http://www.uni-tuebingen.de/evoeco http://www.eve.uni-tuebingen.de

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

EdinburghCentreEcol 2 PlantEvol

The Centre for Ecology and Hydrology (CEH), part of the Natural Environment Research Council (NERC), is the UK’s Centre of Excellence for research in the terrestrial and freshwater environmental sciences. We are currently recruiting in a number of fields at a range of grades http://www.ceh.ac.uk/personnel/CurrentVacancies.htm . These include current open adverts for:

1. Senior Plant Ecologist. We are looking for a senior research scientist to help build and lead a team of plant ecologists at the Centre for Ecology and Hydrology, Edinburgh. Research in the team will focus on quantifying major threats to biodiversity, including invasive species, climate change and land use change. You will be a recognised leader in your field with a proven track record, the ability to attract funding and experience in supervising research staff and students. We expect you to develop your own research to meet the objectives of the CEH and NERC science strategies. To succeed in this role you will need to be an effective decision maker and have excellent interpersonal and communication (written and oral) skills. Being a team player

and having a proven knowledge of project management is essential. You will also have proven record in generating funding for research and publishing in leading international journals. Good data handling and statistical skills are d esirable. The right candidate should have a PhD or equivalent in ecological science and be able to adapt to change and learn new skills/techniques quickly. The salary is £34,650 progressing to £45,440. In addition NERC offer a pension scheme, 30 days' annual leave and $10\frac{1}{2}$ days' public and privilege holidays.

Closing date for receipt of applications 25 July 2007. Please see the website http://www.ceh.ac.uk/personnel/CurrentVacancies.htm for further details

2. Plant Population Ecologist. We are looking for a Plant Population Ecologist who is an experienced scientist with demonstrable skills in either demographic studies or manipulative experiments in plant ecology, a good publication record in a relevant field, statistical skills and income generating potential. You will be expected to develop your own research and communicate effectively with others in CEH. You will be expected to develop research on the drivers of biodiversity loss, such as invasive species, land use change and climate change. Future research opportunities will include research on ecosystem processes and animal-plant interactions. Your research should have relevance to the conservation of biodiversity. Outputs will therefore not only include high quality science publications but also reports for relevant stakeholders. As well as collaborating within CEH, you will be encouraged to collaborate with other organizations in the UK and else where in Europe. You will be able to communicate with mathematicians & ecologists and explain your work clearly to a non-specialist audience. You will possess good statistical skills and have the ability to work with spreadsheets and databases. You will be able to manage your time effectively in order to meet research planning requirements and reporting deadlines. The salary for this post is £22,220 progressing to £27,440 per annum. In addition NERC offer a pension scheme, 30 days' annual leave and $10\frac{1}{2}$ days' public and privilege holiday per annum.

Closing date for receipt of applications is 3 August 2007. Please see the website http://www.ceh.ac.uk/personnel/CurrentVacancies.htm for further details

3. Macroecologist. We are looking for a Senior Scientist with expertise in macroecology to further develop our research in this critically important discipline. The post holder will be analyzing large-scale, long term biological and environmental data sets to: describe and explain temporal and spatial patterns of biological abundance, diversity and distribution, link these to drivers of environmental change, including climate, land use change, and biological invasions, quantify and predict the implications of changing species distributions for population processes, ecosystem function and conservation biology, attract research funding and build collaborative links with UK and European research partners. The successful candidate will have an excellent track record in personal research in macroecology or a related area. You will have the ability to review critically large-scale spatial datasets to identify both their research potential and their limitations. You must have skill s in spatial and/or temporal modelling approaches in order to: describe and explain temporal and spatial patterns of biological abundance diversity and distribution, link these to drivers of environmental

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FalklandIslands VolunteerAssist

Wanted - Volunteer Field Assistant on Falkland Islands October 2007 - January 2008

We are looking for a field assistant to help with a project on the evolutionary ecology and conservation of shorebirds on the Falkland Islands.

The Project: We are investigating the breeding and behavioural ecology of two-banded plover (Charadrius falklandicus) and rufous-chested dotterel (Ch. modestus), and their interactions with predators including the striated caracara (Phalcoboenus australis). Work involves searching for and monitoring nests, juveniles and ringed adults, capturing birds for measurement, and behavioural assays.

The Place: The Falkland Islands are renowned for their magnificent bird life, as well as good numbers of other animals such as elephant seals and killer whales. The plover project is based on Sea Lion Island (http://www.sealionisland.com/index.php/uk/38/), the only site in the Falklands to be an Important Bird Area, an Important Plant Area, and a proposed National Nature Reserve. It is also a Ramsar designated Wetland of International Importance. As Darwin observed of the Falklands avifauna in 1833, the birds on Sea Lion Island are extraordinarily tame, and it is possible to study them at close quarters.

Accommodation on Sea Lion Island is in a Portakabin, with occasional hot water and heating. Conditions are basic, and the weather is harsh, with strong, cold winds and some rain and snow.

The Field Assistant: We are looking for someone with a degree in Biology, Zoology, Ecology or a related subject, preferably with some field experience.

Essential qualities: The successful applicant will be fit, hard-working and meticulous, and have sharp eyes. He or she will be capable of working independently and looking after him or herself, as much of the work will be unsupervised. Be aware that we will be working under lonely conditions over Christmas and the New Year. Most importantly, a positive attitude and sense of humour are essential!

Desirable qualities: Bird handling/ringing experience is a bonus, as is the ability drive 4 x 4 with manual gearshift.

Expenses in the Falklands (including food, accommodation and transport) will be covered, but the applicant must be prepared to pay their own way to the Falkland Islands.

IF YOU ARE INTERESTED, PLEASE MAIL OR EMAIL YOUR CV AND 2 LETTERS OF RECOMMENDATION. Applications will close on 10th September 2007.

Tamas Szekely, Professor of Biodiversity, University of Bath, UK James St Clair, PhD student

Contact: James St Clair 4 South, University of Bath, Claverton Down, Bath, BA2 7AY, UNITED KINGDOM Email: jjhsc20@bath.ac.uk

jjhsc20@bath.ac.uk jjhsc20@bath.ac.uk

GalapagosIslands DarwinFinches

FIELD ASSISTANT POSITION FOR RESEARCH PROJECT ON COGNITIVE EVOLUTION IN DARWIN'S FINCHES ON THE GALAPAGOS ISLANDS

A field assistant is needed for a research project on Darwin's Finches on the Galapagos islands from October 10, 2007 to March 10, 2008 (there is a possibility of retaining position for the next field season). We will be comparing the cognitive abilities of tool-using woodpecker finches (Cactospiza pallida) and non tool-using tree finches (Camarhynchus parvulus, Camarychus psittacula) in controlled experiments that will be conducted in aviaries on the Galapagos. The project field base will be at the Charles Darwin Research Station on Santa Cruz, an island of the Galapagos Archipelago (Ecuador).

Requirements: - enrollment at a German university, currently in Hauptstudium. It is necessary to have a completed Vordiplom but unfortunately, candidates who have already attained higher qualifications (i.e. Diplom) cannot be considered - good English language skills -good physical condition, as the work will involve long hours and sometimes strenuous physical activity - must be able to manage extreme temperatures (sometimes over 40ï¿½C during days) and be prepared to work 6 days per week - must work well with others, especially in groups - should not be afraid of handling live insects

Desirable qualities of the candidate: -interest in behavioural biology - field experience - experience conducting behavioural experiments - completion of at least one Hauptstudium course in behavioural biology - basic spanish language skills or the desire to learn the language - experience in handling and/or keeping birds

Responsibilities: conducting of behavioural experiments in aviaries, data entry, animal care, support during catching and handling of birds, insect collection

Costs: travel and living expenses will be covered by the project

Salary: 576 Euro/ month

Application: Interested students, please send a cover letter and resume via email to Sabine Tebbich (st50@st-andrews.ac.uk) and cc to Irmgard Teschke: irmgardteschke@googlemail.com

Application deadline: from now until position is filled.

irmgardteschke@googlemail.com

InnsbruckU ChairMolEvol

University of Innsbruck, Chair of Molecular Ecology

The Department of Ecology at the Innsbruck University School of Biological Sciences invites applications for the

Chair of Molecular Ecology

In case of a first-time appointment the contract will at first be limited to six years; given a positive evaluation the contract will then become unlimited. In all other cases the employment will be unlimited from the outset.

Duties include

- Representation of the subject of “Molecular Ecology” both in research and teaching with a main focus on “Animal Ecology”, - Active participation in the further implementation process of the Schools’ ecology programme and its research focus entitled “Ecology of Alpine Regions”, - The focus of research, ideally, should therefore be on the analysis of organisms and their functional relations in mountain ecosystems, - Establishment of innovative research especially in molecular ecology.

Employment requirements include

Expertise in molecular methods and concepts of animal ecology, a pertinent habilitation or equivalent qualification, publications in leading international refereed journals, involvement in international research, pertinent experience abroad, experience in the acquisition of research funds, superior teaching skills, leadership qualifications as well as the capacity for cooperation, teamwork and integration.

The University of Innsbruck is striving to increase the percentage of female employees, and therefore invites qualified women to apply. In the case of equivalent qualifications, women will be given preference.

Applications should be submitted no later than September 28, 2007 and should include the usual documentation (esp. curriculum vitae, publications list, list of courses taught, description of current and intended research, samples of the 5 most important works). All documents have to be submitted in digital format (CD-ROM, e-mail, etc.). Hardcopy (paper) is optional. Applicants are requested to provide important documents in English. Please send the requested material to: Universitï¿½t Innsbruck, Fakultï¿½ten-Servicestelle, Technikerstraï¿½e 17, A-6020 Innsbruck (fss-technik@uibk.ac.at).

The full (and only legally binding) text in German as well as additional information on the current status of the application process may be found at: http://www.uibk.ac.at/fakultaeten-servicestelle/-standorte/technikerstrasse/berufung/index.html For further informations about the Department of Ecology please visit our website: http://www.uibk.ac.at/-ecology/index.html.en Magdalena Stiftinger University of Innsbruck Institute of Ecology Sternwartestrasse 15, A-6020 Innsbruck Tel. +43 512 507 5971 magdalena.stiftinger@uibk.ac.at www.uibk.ac.at/ecology magdalena.stiftinger@uibk.ac.at

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MichiganStateU ResTech DrosophilaEvolGenet

Research Technician: Drosophila Evolutionary Genetics and Genomics

I am looking for an active and well-organized person with relevant research experience to work as a laboratory manager and research assistant in the laboratory of Ian Dworkin in the Department of Zoology at Michigan State University. My research involves using genetic and genomic approaches to study natural and mutational variation for wing shape and related phenotypes. The successful applicant will be helping establish a new laboratory and research program.

The precise details are:

Minimum Requirements: A bachelor’s degree in genetics, biology, or related field; minimum of six months of related work experience in basicmolecular biology protocols such as: PCR and RNA analysis; experience with basic insect husbandry, in particular with Drosophila melanogaster; experience with micro-dissections of tissues; experience in the use of spreadsheet software.

Desired Qualifications: Skilled with either Windows, OSX, or Linux operating systems; familiarity with Microsoft Excel; knowledge of high throughput molecular biology, in particular DNA sequencing, microarrays and quantitative PCR; experience with Drosophila genetics, in particular generating recombinant lines and crosses.

Job Summary: Performs general molecular biology and genetic techniques as applied to fly evolutionary genetics; prepares lab solutions; maintains Drosophila cultures and crosses; orders and sets up equipment and supplies; monitors and control hazardous and other materials used inthe laboratory; maintains lab records of supplies and orders; maintains database for oligos and strains.

Please apply by email with a letter expressing interest, your CV and names of three references to Ian Dworkin (idworkin at msu.edu) Applications should be received by August 10th, 2007. Start date is expected to be no later than September 1st, 2007.

Ian Dworkin <idworkin@msu.edu>

NHM London ResAssist SolanumEvol

PBI Solanum Research Assistant

A position as a Research Assistant at the Natural History Museum in London is available on an internationally collaborative project to produce a global monograph of the genus Solanum (Solanaceae). The project is a Planetary Biodiversity Inventory project funded by the United States National Science Foundation (NSF). Solanum includes approximately 1500 species and is one of the largest genera of angiosperms. The species level taxonomy, including images, keys and specimen data, is being made available over the Internet through our Solanaceae Source website (http://www.nhm.ac.uk/-research-curation/projects/solanaceaesource/).

Your responsibilities will include writing descriptions of selected species groups of solanums; specimen and image databasing and manipulation; field work for the collection of herbarium, seed and silica gel samples; some generation of molecular data for phylogeny reconstruction (mainly sequences of chloroplast and nuclear genes); maintenance and analysis of living greenhouse collections of Solanaceae; data analysis, presentation, and publication; the candidate will be involved in supervision of international visitors to the project and in the development and maintenance of the project database and website together with current project staff.

Candidates should have a higher degree in biology or a related subject and experience in plant systematics, field work and with working in a team; experience with Solanaceae is preferred but not required, as is experience with molecular systematics and a variety of methods of data analysis. The position is available for 18 months beginning in August 2007 (ending January 2009).

Salary (NHM Band 5) up to £ 24,000 (incl. NI and superannuation), depending upon experience and qualifications; 18 month short-term contract. Please apply via the NHM website (http://www.nhm.ac.uk/jobs) - search for jobs in Botany; you will need a supporting statement, a cv and two letters of reference. Letters of reference can either be attached or sent to Dr. Sandra Knapp at the e-mail address below, please be sure your referees put your name and PBI Solanum job in the subject line. For more information please contact Sandra Knapp (sk@nhm.ac.uk) Closing date for applications 3 August 2007

Lynn Bohs Department of Biology 257 South 1400 East University of Utah Salt Lake City, UT 84112 (801) 585-0380

Lynn Bohs <bohs@biology.utah.edu>

OhioStateU DatabaseProgrammer

Title: Job for database programmer Job Location: Ohio State University (bmi.osu.edu)

Ground-up design of phylogeographic service like that used in Genomic Analysis and Geographic Visualization of the Spread of Avian Influenza (H5N1)

http://www.informaworld.com/openurl?genre=-article&issn=1063-5157&issue=2&spage=-321&volumeV

The Database Programmer is responsible for extending and building new components of a PostGIS enabled PostgreSQL database architecture. In addition, the position is responsible for reviewing and designing efficient query approaches for both spatial and standard SQL statements. Will need to be able to create SQL queries for the non-SQL versed user, and reformat/manipulate results. The successful candidates will have demonstrated strength in analyzing and troubleshooting data and processing issues. Assists in the resolution of database capacity issues, replication, and other distributed data issues.

You must have a desire to learn and understand the data in order to work with the “big picture” in mind. Finally, you should be able to work independently and confidently make decisions.

Minimum 2 years PostgresSQL and PHP experience.

Salary commensurate with experience

Please send CV and links to relavent examples of previous work. Contact: Daniel Janies, (danjanies@hotmail.com) for more information.

danjanies@hotmail.com

PennStateU FruitFlyPopGenet

Pennsylvania State University

DEPARTMENT OF Entomology

Biological Research Technician

Phylogenetic and Population Genetics of fruit flies

A technician position is available in the department of Entomology at the Pennsylvania State University. The McPheron lab is performing phylogenetic analayses on tephritid pest species using mitochondrial and microsatellite DNAs. We seek an individual to participate in our project to perform various lab activities. The candidate should be motivated and organized with excellent oral and written communication skills. They should be able to work largely independently. Salary will range from $22,500 to $29,500 per annum depending on experience and will include benefits.

Minimum qualifications are a B.A.or B.S. in biology (or a related field), and demonstrable experience conducting research in a broadly-defined genetics or molecular biology lab. The applicant should be familiar with genetic analysis software such as MEGA, DNASP, Arlequin, and PAUP. Experience with troubleshooting and optimizing molecular biology protocols, and/or those who have previously worked with fruit flies or other small invertebrates is a plus but not required.

Job responsibilities will include performing basic molecular techniques (DNA extraction, PCR, sequencing, genotyping) as well as general lab management (including some supervision of undergraduate researchers). Opportunities for independent research projects will also likely exist.

Informal inquires about the position are welcome and can be directed to Raul Ruiz (rur132@psu.edu). To apply, send your resume or CV, and include a cover letter (describing your interest in the position and any relevant expertise).

Send your information/inquiries to:

Raul Ruiz Department of Entomology The Pennsylvania State University 501 ASI Bldg University Park, PA 16802 tel: 814-865-3345 fax: 814-865-3048 email: rur132@psu.edu web: http://www.ento.psu.edu/mcpheronlab/ rur132@psu.edu

Raul Ruiz <rur132@psu.edu>

RoyalBotanicGarden Kew HeadMolecularSyst

JOB TITLE: Head of Molecular Systematics, Royal Botanic Gardens, Kew

HOURS OF WORK: Full Time (41 Hours Gross)

JOB STATUS: Permanent

SALARY PER ANNUM: £40,000 to £45,000 per annum; 30 days holiday per year and a choice of defined benefit or stakeholder pension as well as a stunning and prestigious work environment.

DEPARTMENT AND LOCATION: Jodrell Laboratory, Molecular Systematics Section

JOB DETAILS:

It's not often you get the chance to do a job you love in stunning surroundings that's how we feel here at Kew. We have a reputation to be proud of, first class research facilities, unrivalled living collections and outstanding conservation programmes.

With responsibility for organising and motivating a team of Researchers, you will manage the Molecular Systematics Section (Jodrell Laboratory) for research on the evolution of plants and plant systematics/classification. Leading the research focus, you will identify problems and carry out well-defined scientific research. You will also have the chance to use your high profile within the 0100,0100,0100field of molecular systematics to raise funding externally to support the research work.

ESSENTIALS:

With a PhD plus extensive doctoral and postdoctoral research experience in plant molecular systematics, you will have undergone training in molecular biology techniques and plant systematics. You will have knowledge of relevant research methods including molecular biology and phylogenetic methodology along with knowledge of specialist background literature.

You will be a natural communicator, leader and manager who instils confidence in others. Your influencing and problem solving skills will be exceptional, as will your ability to make sound judgements and decisions. Good project and financial management skills are essential.

For a Job Description and Person Specification and further details please visit our website at "http://-www.kew.org"

Application is by CV and accompanying letter responding to the main points in the Job Description and Person Specification. Job Ref: 297

Please send your CV to the Human Resources Department, Administration Building, 47 Kew Green, Kew, Richmond, Surrey, TW9 3AB.

CLOSING DATE: 9.00am Monday 16 July 2007.

a.le.poer.trench@kew.org

Smithsonian Trop Res Inst OrnithologyAssistant

The Smithsonian Tropical Research Institute seeks a short-term field ornithologist to assist on several ongoing projects concerning the ecology and evolutionary biology of the birds of Panama. This position requires that the applicant be willing to collect (e.g. sacrifice) birds under existing permits from the Republic of Panama, and the applicant should have previous mistnetting experience; experience with firearms is a plus. This is a great opportunity to learn field techniques for museum ornithology in diverse and often remote habitats throughout Panama, and become familiar with patterns of avian diversity in the Neoptropics. The position is for six months starting in September. The assistant will receive 1000 USD per month, which is sufficient to cover all in-country expenses as well as to reimburse airfare to Panama. Applications are accepted until the position is filled. Please send a CV along with a statement of interest to Matthew Miller, millerma@si.edu.

harpy.toucan@gmail.com

SouthAfrica VolunteerFieldAssist

Volunteer needed as field assistants for the project:

Socio-Ecology of small Mammals in the Succulent Karoo of South Africa

August/September to November 2007

>From November 2007 onwards

We have one vacant position for a volunteer as field assistant at our project in South Africa. The volunteer could start immediately or August / September and should stay until the end of the year.

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. Whereas the research is mainly non-invasive, this is no job for extreme animal right persons (we take tissue and blood samples). 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 the masters' studies.

Costs: Students have to arrange their transport to the field site themselves. Per month, an amount of Rand 500 (around 70 Euro) must be paid for accommodation at the research station. Students must buy their own food etc in Springbok (costs of about R 1500 or 200 Euro/month). Including extras, you should expect to pay about 300 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 a volunteer for the period July/August to October/ November 2007, the breeding season. The next open positions will be December 2007 and January 2008.

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 and cc to stripedmouse@bluewin.ch.

More information under www.stripedmouse.com Contact via e-mail: carsten.schradin@zool.uzh.ch

Dr. Carsten Schradin Research Assistant, Zoological Institute, Department of Animal Behavior, University of Zurich, Winterthurerstrasse 190, 8057 Zurich, Switzerland. Tel: +41 - (0)44 635 5486

Honorary Researcher at the School of Animal, Plant and Environmental Sciences, University of the Witwatersrand, South Africa.

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>

UBath 2 EvolEcol

TWO POSITIONS AT THE UNIVERSITY OF BATH: EVOLUTION, ECOLOGY AND CONSERVATION

SEE FURTHER DETAILS http://www.bath.ac.uk/jobs/ Ref: 07H165A Title: Teaching Fellow in Evolutionary Ecology/Animal Behaviour Department: Department of Biology & Biochemistry Description: This full-time position for a fixed term of two years is in the broad field of ecology, animal behaviour and conservation biology. The successful candidate will contribute to undergraduate courses on population ecology, animal behaviour, field ecology, and will be involved in tutorials and other associated duties. Candidates should have a PhD in a relevant field that may include behavioural ecology, evolutionary ecology, conservation biology and zoology. This is a primarily a teaching position, and teaching experience is desirable, although candidates with research interests relevant to the Biodiversity Laboratory at the University of Bath, are encouraged to apply. In addition to the Application form and CV, please submit a concise statement of research interests (approximately 500 words). Selection will be based upon teaching excellence and promise, as underpinned by relevant research experience. Interviews are planned for August. The position is available from 1 September 2007. For further information please contact Tamas Szekely (T.Szekely@bath.ac.uk). Salary: Salary in the range ï¿½26,666-ï¿½31,840 (Grade 7) Contact: Application forms and further details may be obtained from the Human Resources Department, University of Bath, Claverton Down, Bath BA2 7AY, email jobs@bath.ac.uk quoting Ref No 07H165A. Alternatively, please phone the 24 hr answer-phone service on (01225) 386924, textphone (01225) 386039 quoting Ref No 07H165A. An online application form is accessible here Closing Date: 31st July 2007

Ref: 7H166A Title: Postdoctoral Research Officer in Evolutionary Ecology (Ref 07H166A) Department: Department of Biology and Biochemistry Description: Applications are invited for a postdoctoral position in the broad field of evolutionary ecology and behavioural ecology to investigate cooperation and conflict in avian societies. The successful candidate will use combination of approaches that may include, but not restricted to, field research, lab-based experiments, molecular ecology, genetics, neuroendocrinology and mathematical modelling. The postdoctoral researcher will be responsible for coordination of European Community projects on breeding systems and social behaviour of birds, and overseeing student projects related to these themes. Candidates should have a PhD in a relevant field that may include evolutionary biology, animal behaviour, molecular and/or quantitative genetics, mathematical modelling and zoology. In addition to the Application form and CV, please submit a Research Proposal (approximately 500 words). Selection will be based upon research excellence and promise, and relevance to current research themes of Biodiversity Lab at the University of Bath. This is a fixed term appointment for up to two years. Interviews are planned for August 2007. The position is available from 1 September 2007. For further information please contact Tamas Szekely (T.Szekely@bath.ac.uk). Salary: Salary in the range ï¿½26,666 - ï¿½31,840 per annum. Contact: Application forms and further details may be obtained from the Human Resources Department, University of Bath, Claverton Down, Bath BA2 7AY, email jobs@bath.ac.uk quoting Ref No 07H166A. Alternatively, please phone the 24 hr answer-phone service on (01225) 386924, textphone (01225) 386039 quoting Ref No 07H166A. An online application form is accessible here Closing Date: 31st July 2007

Dr Tamas Szekely Reader in Evolutionary Biology Dept of Biology and Biochemistry, University of Bath, Bath BA2 7AY, UK 01225 383676 (phone), 01225 386779 (fax), T.Szekely@bath.ac.uk (email) http://www.bath.ac.uk/bio-sci/biodiversity-lab/index.htm SEX, SIZE AND GENDER ROLES: evolutionary studies of sexual size dimorphism http://www.oup.com/uk/catalogue/?ci=3D9780199208784

bssts@bath.ac.uk

UGeorgia Speciation

To Whom It May Concern:

Please list on EvolDir the following Technician position:

A Research Assistant/technician position is available in the group of John Gittleman to work on macroecological and -evolutionary questions related to speciation, extinction and conservation.

The position will involve assisting in the organization of a new computer/informatics laboratory. Current projects include: global ecological patterns, phylogenetic systematics, correlated traits of differential speciation, rates of extinction among ecosystems, and transmission of global disease in mammals. Preference will be given to individuals with a strong background in biology, ecology and evolution. Applicants should have excellent analytical skills and a strong interest in the construction and analysis of large databases. Salary is in the range of $32,000 (plus benefits) per year. The new Odum School of Ecology will be growing with additional student, postdoc and faculty positions; this position will work for the Dean in assisting in the lab and expanding the computer informatics among faculty in the School.

The position is available immediately. Interested applicants should send a cover letter detailing their background and an updated CV, along with names of references and contact information of 3 references to:

Dr. John L. Gittleman, Dean Odum School of Ecology University of Georgia Athens, GA 30602 USA

e-mail: jlg@uga.edu phone: (706) 583-5537 fax: (706) 542-4819 web: http://blackbear.ecology.uga.edu/gittleman/index.html – Dr. John L. Gittleman, Dean Odum School of Ecology University of Georgia Athens, GA 30602 USA Phone: 706-542-2968 Fax: 706-542-4819

John Gittleman <jlg@uga.edu>

UKwaZuluNatal SA 2 PlantMolSyst

University of KwaZulu-Natal, South Africa

All appointments will be in terms of the prevailing University Employment Equity Policy and the Employment Equity Plan of the faculty/division (available at http://www.ukzn.ac.za/ESU). The University reserves the right not to make an appointment or to stop the process at any stage to headhunt or re-advertise the post to meet its equity goals. Candidates who do not meet the minimum criteria will not be considered.

SENIOR LECTURER/LECTURER IN PLANT MOLECULAR SYSTEMATICS (1xPOST) (REF NO.: SA29/2007)

LECTURER IN PLANT BIOLOGY/BOTANY (1xPOST) (REF NO.: SA33/2007)

SCHOOL OF BIOLOGICAL & CONSERVATION SCIENCES (PIETERMARITZBURG CAMPUS)

The School of Biological and Conservation Sciences is well established with a very active research profile and a substantial graduate school. It has excellent research facilities, including a comprehensive herbarium (NU) and botanical garden.

The successful applicant for the Plant Molecular Systematics post should have a strong background in this field and be familiar with modern molecular approaches to the study of biodiversity, evolution, conservation and/or related areas.

The successful applicant for the Plant Biology/Botany post should have research interests in ethnobotany, ecology (including eco-physiology), or evolutionary biology.

The appointees will be required to teach at undergraduate and postgraduate levels, to supervise research students and to establish strong research programmes. Assumption of responsibility for curation of the NU

Herbarium (assisted by dedicated technical staff) may be required.

POST in PLANT MOLECULAR SYSTEMATICS (REFSA29/2007):

SENIOR LECTURER: MINIMUM REQUIREMENTS: â A PhD in a relevant field; â Evidence of current research activity in plant molecular systematics with published papers in the international peer-reviewed scientific literature; â Experience in teaching at tertiary level.

ADVANTAGES: â Successful supervision of postgraduate students; â Experience in herbarium curation.

LECTURER: MINIMUM REQUIREMENTS: â An MSc by research in a relevant field; â Two years of post-MSc work experience/research in plant molecular systematics; â Evidence of recent publications in peer-reviewed scientific journals.

ADVANTAGES: â A PhD in a relevant field; â Experience in teaching at tertiary level; â Successful supervision/co-supervision of postgraduate students; â Experience in herbarium curation.

POST in PLANT BIOLOGY/BOTANY (REF:SA33/2007):

MINIMUM REQUIREMENTS: â An MSc by research in a relevant field; â Two years of post-MSc work experience/research in ethnobotany, plant ecology (including eco-physiology), or plant evolutionary biology; â Evidence of recent publications in peer-reviewed scientific journals.

ADVANTAGES: â A PhD in a relevant field; â Experience in teaching at tertiary level; â Successful supervision/co-supervision of postgraduate students; â Experience in herbarium curation.

For further information see the School website at http://www.ukzn.ac.za/biology or contact Prof. David Ward at ward@ukzn.ac.za

The remuneration package offered includes benefits and will be dependent on the qualifications and/or experience of the successful applicant. The selection process will commence on 23 JULY 2007 and will continue until a suitable candidate is appointed or a decision is taken not to fill the post.

Applicants are required to: â Stipulate which post and level they are applying for; â Submit a covering letter highlighting their experience in, and providing evidence for, each of the minimum requirements and advantages listed above, together with a detailed CV including the names, full addresses, fax numbers and e-mail addresses of three referees, to Mrs. C. Bhebhe, Human Resources Administration, University of KwaZulu-Natal, Private Bag X01, Scottsville, 3209, Ph. No. +27(0)33 260 5277 or e-mail bhebhec@ukzn.ac.za

UMichigan ResTech

Full Time Research Technician Position University of Michigan, Ann Arbor Contact: Chris Dick cwdick@umich.edu

Full time research technician needed to participate in plant molecular systematics and population genetics research in the labs of Paul Berry and Chris Dick at the University of Michigan.

Research and responsibilities include development of microsatellite DNA markers, DNA sequencing, data analyses, database organization, lab management, and training of students in lab techniques.

Available 15 August, 2007.

Please send CV and names of references to Chris Dick: cwdick@umich.edu

Christopher W. Dick, Ph.D. Ecology and Evolutionary Biology University of Michigan 830 North University Ave Ann Arbor, MI 48109-1048

Office phone 734-764-9408

http://www.lsa.umich.edu/eeb/people/cwdick/index.html -

cwdick@umich.edu cwdick@umich.edu

UMissouriColumbia Bioinformatics

Tenure Track Position in Bioinformatics and Computational Biology

The University of Missouri-Columbia invites applications for a tenure track faculty position in Bioinformatics and Computational Biology. The candidate will be hired into the Food for the 21st Century Animal Reproductive Biology Group. This is an established interdisciplinary reproductive biology group that is poised to make discoveries from genomic information gathered from agricultural species. This recruitment will build on a strong tradition of interaction between physical, biological and agricultural sciences on this campus. An ongoing campus initiative is coupled to community and state efforts to enhance research, education, and economic development in bioinformatics and computational biology. Of particular interest are the areas of:

* Systems biology (e.g. gene networks, modeling protein-protein interactions, and complex behavior at the sub-cellular and cellular levels) * Genome and sequence analysis including, comparative genomics, gene prediction and sequence annotation * EST analysis including predicting function from primary sequence * Database and browser applications

Recruitment will be at the Assistant, Associate or Full Professor level, depending on qualifications. Applicants must have a doctoral degree, postdoctoral experience, and evidence of outstanding research potential. It is expected that the successful candidate will participate in the core functions of the Reproductive Biology Cluster of the Food for the 21st Century program (http://cafnr.missouri.edu/arbg), and establish an internationally recognized research program via both independent and interdisciplinary collaborations, train graduate students, and contribute to the undergraduate or graduate instructional program. Successful candidates will be provided with excellent start-up funds, support, and a salary commensurate with experience. Columbia has the residential advantages of a medium-sized university city, excellent cultural opportunities, and easy access to St. Louis and Kansas City. Information about the Division of Animal Sciences can be found at the departmental link (http://www.asrc.agri.missouri.edu/). Questions and applications can be directed to: Dr. Jerry Taylor, Chair of the Search Committee at taylorjerr@missouri.edu. An application must include curriculum vitae with a complete list of publications and grant support, a concise summary of research interests and future plans, and the names of four individuals prepared to write letters of recommendation. To ensure full consideration, applications should be received by October 1, 2007. The University of Missouri is an Affirmative Action, Equal Opportunity employer.

Jeremy Taylor Professor and Wurdack Chair in Animal Genomics S135 ASRC University of Missouri 920 East Campus Drive Columbia, MO 65211-5300 Voice: (573) 884-4946 Fax: (573) 882-6827 E-mail: taylorjerr@missouri.edu <mailto:taylorjerr@missouri.edu> http://animalgenomics.missouri.edu <http://animalgenomics.missouri.edu

“Things are never so bad they can’t be made worse”

taylorjerr@missouri.edu

UNewBrunswick PopulationGenetics

The Department of Biology, University of New Brunswick (Fredericton), seeks applicants for a tenure-track position in Population Genetics. The successful candidate will develop a strong research program examining population genetics in any system. Teaching responsibilities will include a course in population genetics, involvement in core genetics or zoology teaching, and other teaching as negotiated. A PhD is required and post-doctoral experience is strongly preferred.

Existing research strengths in Biology include aquatic ecology and fish biology, conservation biology, and evolutionary biology. In addition, nearby regional and federal research groups in aquaculture, agriculture, and forestry offer opportunities for collaboration. Our faculty uses a full range of approaches including molecular biology, theoretical biology, and field organismal biology. Information about Biology at UNB is at www.unb.ca/fredericton/science/biology/ . Applications will begin to be reviewed on October 19, 2007, and will remain open until a suitable applicant is identified with an anticipated start in July 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 Dept. of Biology University of New Brunswick Bag Service 45111 Fredericton, N.B., Canada, E3B 6E1.

All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. Applicants should indicate current citizenship status. The University of New Brunswick is committed to the principle of employment equity.

– Steve Heard sheard@unb.ca Professor 506-452-6047 Dept. of Biology FAX 506-453-3583 University of New Brunswick

sheard@unb.ca

UOregon EvolBiol

As seen in the 20 July issue of Science:

The University of Oregon Center for Ecology and Evolutionary Biology (http://evolution.uoregon.edu/) and the Department of Biology invite applications for a tenure-track position (ASSISTANT PROFESSOR) in evolutionary biology. We are particularly interested in candidates studying the evolution of biological processes at the molecular level in order to address fundamental questions in evolutionary biology.

The successful candidate will have an outstanding research program and a commitment to excellence in teaching. Ph.D. required. Applicants should submit curriculum vitae, statement of research interests, statement of teaching philosophy, and three letters of recommendation to: Evolution Search Committee, Department of Biology, 1210 University of Oregon, Eugene, OR 97403-1210. To ensure full consideration, applications should be received by September 5, 2007.

The University of Oregon is an Equal Opportunity/Affirmative Action Institution committed to cultural diversity and compliance with the Americans with Disabilities Act. Women and minorities are encouraged to apply. We invite applications from qualified applicants who share our commitment to diversity.

CEEB offers a highly collegial and intellectually rich environment for research in evolutionary biology. We are nested within a unified Biology department of world-class quality and benefit greatly from direct interactions with colleagues in molecular biology, development, genomics, and neuroscience. Eugene is a progressive small city with high quality of life, abundant cultural amenities, and superb opportunities for outdoor recreation.

Joe Thornton joet@uoregon.edu

UQuebecRimouski EcosystemEvol

The Universitï¿½ du Quï¿½bec ï¿½ Rimouski (UQAR) invites applications for a tenure-track position in Ecosystem Ecology. We seek top level scientists to hold a Level II, Canada Research Chair in Continental Ecosystem Structure and Function. We are interested in candidates with outstanding research experience in some of the following fields : ecosystem modelling, landscape ecology, biodiversity, and ecosystem restoration. Strong experience in northern temperate and/or subarctic/arctic ecosystems will be highly considered. This Chair will join the BIONORD research group of UQAR and the Centre d'ï¿½tudes Nordiques.

UQAR is actively developing a comprehensive research program in Northern Studies. Environmental problems that characterize ecosystems ranging from the Northern Deciduous Forest to the Arctic Tundra are key to this program. The Chair will complement the capacities of UQAR in various fields such as animal and plant ecology, forestry, systematics, evolutionary biology ,and biogeography. The Biology and Geography sections of UQAR include 300 undergraduate students and 100 M.Sc. and Ph. D. candidates, along with 17 faculties. The candidate will be encouraged to teach graduate and undergraduate courses and must show strong skills in student training at the master and doctorate levels.

The selected candidate will be asked to describe a research program in either of the above mentioned fields, and prepare an application to the Canada research Chair program. The position is conditional on the acceptance of the application by the board of the Canada research Chair program. The candidate will then become eligible for support by the Canada Foundation for Innovation. More information on deadline and required documents can be found at : http://www.uqar.qc.ca/directionServices/-ressourcesHumaines/FacultyProfResearch.asp .Information on Canada Research Chairs can be found at http://www.chairs.gc.ca/ The position must be filled by June 1st 2008

– France Dufresne, Ph.D. Dï¿½partement de biologie Universitï¿½ du Quï¿½bec ï¿½ Rimouski 300 allï¿½e des ursulines Rimouski, Quï¿½bec Canada G5L 3A1 Fax 418-724-1849 Tel 418-723-1986 (1223)

France_Dufresne@UQAR.QC.CA

UQueensland TelomereEvol

Queensland Government & the University of Queensland

Brisbane, Australia

Queensland Department of Primary Industries invests $100m pa in world-class basic and applied scientific research. Research in the Sustainable Fisheries Unit is focussed on providing new information about commercially exploited fisheries and by-catch species to improve the accuracy of mathematical models used to set catch limits. Within this brief, the Molecular Fisheries Laboratory (MFL) provides information such as genetic population structure, effective size and individual identification using the most recent advances in molecular and population genetics.

The laboratory is embarking on an ambitious new area of work to use telomeric DNA as a marker for individual age in a range of fisheries species. This will involve transferring scientific knowledge from the field of human cancer research, where telomeres are a significant research target, to non-model organisms such as lobsters, crabs and prawns. The ages of individuals of these species in the wild, and hence their growth, is poorly known. Individual growth is critically important in determining the optimal proportion of a resource that can be removed on a sustainable basis. Sustainable exploitation of fisheries resources is essential to ensure the future of the commercial and recreational fishing industry that is worth about $600 million pa to the Queensland economy.

MFL is searching for a molecular geneticist (full-time, initially for one year, $59,564 to 65,046 pa) and a postgraduate student (stipend $22,000 pa) to work on this project. Ideally you will have a background or interest in telomeric DNA and cell biology. The student will complete an MSc or PhD at the University of Queensland and be co-supervised by Dr Melissa Brown (School of Molecular and Microbial Sciences).

More information can be obtained from Jenny Ovenden (contact details below) or seek.com.au mycareer.com.au and careerone.com.au from 4th August. Closing date for geneticist position is 20th August 2007.

Jenny Ovenden Senior Research Scientist, Molecular Fisheries Laboratories Queensland Department of Primary Industries and Fisheries Floor 6, North Tower, Queensland Biosciences Precinct University of Queensland, St Lucia QLD 4072 Office +61 7 3346 2431 Fax +61 7 3346 2727 Mobile 0415 949 410 Email: Jennifer.Ovenden@dpi.qld.gov.au Website http://www2.dpi.qld.gov.au/fishweb/11629.html Call Centre 13 25 23

It's kind of fun to do the impossible - Walt Disney

Jennifer.Ovenden@dpi.qld.gov.au Jennifer.Ovenden@dpi.qld.gov.au

USheffield HouseSparrowEvol

Field assistants /volunteers to study evolution of group living in House Sparrows

For ca. 3.5 months - from the end of November 2007 until before Xmas and from January 2008 until mid March 2008.

I seek two highly motivated field assistants/volunteers to help me with fieldwork. The study site is located in the foothills of the Pyrenees in southern France. My project aims at investigating group living and group decisions in house sparrows. The project is in its start-up phase and requires extensive banding of birds. Banding experience and familiarity of handling birds are thus a merit. Field assistants are expected to be able to work independent and willing to take responsibility. The field work will comprise catching and banding birds, surveying movements of groups and assist with simple experiments in the field. Work will cover 5 days per week. Drivers licence at least for one of the assistants required. Basic knowledge of French or Basque language will facilitate work in the field since we will frequently interact with the locals to catch birds at roosts in gardens and around farm houses.

The study site is located close to the Pyrenees (ca. 15 km off St. Jean Pied du Port) in a small valley which is unaffected by tourism and is an excellent wildlife spot on one of the major European bird migration routes. The study site is within an hour's drive of the airports of Biarritz and Pau (both served by Ryanair).

Qualifications: 1) Bachelors degree in biology or similar qualification 2) Sociable personality and motivated 3) Willing to work outside 5 days per week. The climate at the study site during winter is mild and snow fall rarely. 4) Drivers licence (at least one of the assistants) 5) Used to handle animals, bird banding experience would be a plus.

The project will cover transport to and within study site, accommodation and food. Assistants with extensive bird banding or field work experience will be paid a salary of 500 per month.

If you are interested, send a short motivation letter stating why you are interested and your CV via email to:

michael.griesser@ebc.uu.se

Michael Griesser, PhD Population Biology, Department of Ecology and Evolution SE-75236 Uppsala, Sweden

until end of 2007: Department of Animal & Plant Sciences University of Sheffield S10 2TN, UK

Tel +44 (0)114 2220112 Fax +44 (0)114 2220002

m.griesser@shef.ac.uk http://www.popbiol.ebc.uu.se/-default.php?type=3Dpersonalpage&lang=3Den&id=-3D37

m.griesser@sheffield.ac.uk m.griesser@sheffield.ac.uk

UTexasAustin LabManager EvolAnalysis

RESEARCH SCIENTIST / LAB MANAGER

The position is to provide technical assistance in the evolutionary analysis of animals, plants, & microorganisms in the lab of Dr. Ulrich Mueller, Integrative Biology, University of Texas at Austin. Research integrates evolution, genetics, molecular ecology, microbiology, and animal behavior. Essential functions include research experiments on genetic and molecular-ecological analysis of animals, plants and microorganisms; training of new laboratory personnel on laboratory techniques and laboratory procedures; routine laboratory related functions.

Required qualifications: Bachelor's degree in biology. Preferred qualifications: Demonstrated knowledge of nucleic acid-research techniques and molecular-genetic techniques. Experience in acquiring and storing supplies, materials, and equipment in a biological laboratory. Experience with scientific equipment used in a genetics laboratory. Experience in DNA sequencing, sequencing analysis, and microsatallite DNA marker development (including genomic library preparation and cloning). Experience in high-throughput genotyping and a strong background in molecular biology. Preference will be given to candidates with the some of the following skills: DNA and RNA work; experience with robotics in extraction and PCR setup; DNA sequencing, RT-PCR. We also emphasize the ability to interact and work collaboratively with others, as the lab manager will work closely with post-docs, graduate students, and undergraduate researchers.

Contact information:

Ulrich G. Mueller W.M. Wheeler Lost-Pines Professor of Integrative Biology University of Texas at Austin Austin, TX 78712, USA

E-mail: umueller@mail.utexas.edu Phone: 512-232-5775

http://www.biosci.utexas.edu/IB/faculty/mueller.htm
Ulrich Mueller <umueller@mail.utexas.edu>

UToronto 2 FieldAssist

I am seeking 2 or 3 field assistants to work on a project measuring natural selection in the invasive plant, Lythrum salicaria (purple loosestrife). I am studying populations at three sites: (1) the city of Timmins in northern Ontario, Canada, (2) the Jokers Hill field station near Toronto, Ontario, and (3) Blandy Experimental Farm in Boyce, Virginia. Duties will involve taking simple measurements of size and timing of reproduction at one of these sites (~20-25 hours/week).

The ideal applicant will be reliable, self-motivated and comfortable working unsupervised at a field station in Ontario or Virginia. Preference will be given to students with previous field experience and/or an educational background in ecology and evolution. Beginning and ending dates of employment are flexible. Successful applicants will receive $250 per week plus accommodation costs.

If you are interested, please email your CV, and your preferred starting and ending dates, to: colautti@eeb.utoronto.ca

Info on the Barrett Lab: http://www.botany.utoronto.ca/ResearchLabs/barrettLab/index.html Rob Colautti, PhD Candidate Department of Ecology and Evolutionary Biology University of Toronto 25 Willcocks St. Toronto, ON M5S 3B2 Canada

Ph: 416-978-5603 Fax: 416-978-5878

colautti@botany.utoronto.ca colautti@botany.utoronto.ca

Valencia ComparativeGenomics

Bioinformatic position available at the Bioinformatics Department, CIPF, Valencia, Spain

BACKGROUND: A PhD position is available in the field of comparative genomics at the Bioinformatics Department (http://bioinfo.cipf.es), Centro de Investigacion Principe Felipe (CIPF), Valencia, Spain.

The position is funded by Education and Science Ministry (MEC) of Spain within the context of the project titled Comparative Genomics, Phylogenomics and Population Genetics of Human Disease Genes. The project is related to the search of positive selection signal in the human genome by comparison of mammalian sequences, the phylogenetic analysis of these genes and genotyping of SNP's variability in human populations. More information is available at http://bioinfo.cipf.es/-comparativegenomics. For references see:

J. Tarraga, I. Medina, L. Arbiza, J. Huerta-Cepas, T. GabaldÃ³n, J. Dopazo & H. Dopazo. Phylemon: a suite of web-tools for molecular evolution, phylogenetics and phylogenomics. Nucleic Acids Research 2007. Arbiza L., Dopazo J. and H. Dopazo. 2006. Positive selection, relaxation and acceleration in the evolution of human and chimp genome. PLoS Comp. Biol. 2 (4):e38. Arbiza L., Duchi S., Montaner D., Burguet J., Pantoja-Uceda D., Pineda-Lucena A., Dopazo J. and H. Dopazo. 2006. Selective pressures at a codon-level predict deleterious mutations in human disease genes. J. Mol. Biol. 358, 1390-1404.

RESPONSIBILITIES: The selected applicant will be working in a group consisting of 7 PhD. students, 3 postdocs, 5 staff scientists and three group leaders. The main responsibilities will include to conduct maximum likelihood analysis of positive selection, phylogenomic analysis, population genetic consulting, and analysis of gene expression data. Also, teaching occasionally short courses on comparative genomics and phylogenetics is among the responsibilities.

REQUIREMENTS: Candidates must have a masters degree in Biology, Bioinformatics, or related. Candidates must have experience the field of biomedicine as well as knowledge of programming languages such as R or C/C++. A Good oral and written English level is required. Background in population genetics is highly desirable.

TERMS: The appointment is for two years and is scheduled to start in september 2007. Salary, and terms of employment will be in accordance with the standards of the Spanish administration.

LOCALE: The Department of Bioinformatics (http:/-/bioinfo.cipf.es) at the CIPF hosts one of the largest groups of bioinformatics in Spain with a multidisciplinary focus on subjects such as functional genomics, comparative genomics and structural genomics. The CIPF is dedicated to international excellence in biomedical research and to translating new knowledge into improved medical practice. The successful candidate will join a new, rapidly expanding team with access to cutting edge technology in an environment of scientific excellence. The CIPF is located in the City of Arts and Science (http://www.cac.es/), one of the most modern districts in Valencia, near the sea and close to the city center.

HOW TO APPLY: PLEASE SEE: http://-www.cipf.es/pdfs/EmpleoUnidad/es/AUI11.2007.pdf DEADLINE: 13/07/2007

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HernÃn J. Dopazo, PhD Pharmacogenomics & Comparative Genomics Unit, Bioinformatics Department, Centro de InvestigaciÃ³n PrÃncipe Felipe c/ ep Avda. Autopista del Saler 16 (Junto al OceanogrÃfico), 46013, Valencia, EspaÃ±a. Tfn: (34) 96 328 96 80 ext: 1008 Fax: (34) 96 328 97 01 hdopazo@cipf.es http://-bioinfo.cipf.es/comparativegenomics/ hdopazo@cipf.es

Other

1957 publication

Can anyone identify for me this seminal publication from 1957? I can recall Nuttal from 100 years ago and Anfinsen 1959.

thanks Steve

At 02:34 AM 7/11/2007, you wrote: This conference commemorates the 50 years since the first experimental study on molecular systematics was published in Russia, which marked the onset of contemporary molecular phylogenetics and a number of related disciplines, including molecular biology, evolutionary biology, biochemistry, computer science, and bioinformatics.

Dr. Steven M. Carr Department of Biology Memorial University of Newfoundland St. John's NF A1B 3X9 CANADA (709) 737-4776 office / -4713 lab / -3018 FAX / -7498 dept e-mail: scarr@mun.ca webpage: http://www.mun.ca/biology/-scarr/Research.html "Dr. Steven M. Carr" <scarr@mun.ca>

AminoAcid coordinates

Hi everyone,

I was wondering how one would go about obtaining the 3D coordinates of amino acid residues in proteins from .pdb files? I've examined the FAQ file about the .pdb file format, but it isn't entirely clear (at least not to me) how to determine the 3D positions of each of the atoms. I think I understand how the data is stored, but I'm not sure.

Thanks, Brad Davis

davis@zoology.ubc.ca

AminoAcid coordinates answers

Hi everyone,

Thanks for the all the replies I got- they were very helpful and they confirmed my suspicions. Anyway, in order to pass on the information acquired:

Some book chapters were given as suggested readings: Chapter 11 of Beginning Perl for Bioinformatics By James Tisdall (I'll almost certainly be getting this).

It was also said that obtaining the desired data isn't easy, because the .pdb format was written in the days of FORTRAN. The .pdb file format specifies the contents of files by the contents of specific column numbers, rather than by field.

It was also suggested that depending on what I wanted to do, I might consider using another database such as MMDB or CATH/SCOP.

Here is an example of the relevant part of the .PDB file to my question:

ATOM 1 N SER 1 2.400 1.898 -4.584 1.00 0.00 N ATOM 2 CA SER 1 1.762 3.219 -4.845 1.00 0.00 C ATOM 3 C SER 1 0.295 3.018 -5.223 1.00 0.00 C

The 6th, 7th and 8th fields contain the x, y, and z coordinates of the atoms which make up the amino acid code.

Here is a link to an institution in Venezuela that work on obtaining the 3d coordinates of amino acids in proteins: http:// www.cecalc.ula.ve/BIOINFO/ Finally, the approach I used was as follows (a brief snippet of C code)

typedef struct { char amino_acid_code[3]; double x; double y; double z; } amino_acid_position;

char record_id[6], amino_acid_code[3]; char carbon_code[3]; int serial_number1;

do // keep reading entries until we get to the first atom entry { fscanf(in, “%s”, record_id); } while (strcmp(“ATOM”, record_id)!=0);

fscanf(in, “%*d %s %s %*s %d %lf %lf %lf %*f %*f %*s”, carbon_code, amino_acid_code, &serial_number1, &x, &y, &z);

do // get data on the location of each of the Carbon-Alpha atom for this amino acid residue { // store the serial number so we can use it as a comparison with the next read to determine when we’ve found a new amino acid

if (strcmp(“CA”, carbon_code)) { x_1=x; y_1=y; z_1=z; } fscanf(in, “%s %*d %s %s %*s %d %lf %lf %lf %*f %*f %*s”, record_id, carbon_code, amino_acid_code, &serial_number1, &x, &y, &z);

} while (serial_number1==serial_number2 && strcmp(“TER”, record_id)! =0);

Cheers, Brad Davis

davis@zoology.ubc.ca

Asian Cladoceran samples

Dear EvolDir Members:

I will be working on the phylogeography of two predatory cladocerans (Crustacea, Branchiopoda): Polyphemus pediculus and Leptodora kindii. We have got a lot of samples of these two species from North America and Europe, but we are still looking for samples from Asia. Therefore, we would greatly appreciate your help if you can provide us or help us look for samples of the two species from Asia.

If you can help or want to know more, please send me an email to exusen@gmail.com .

Thank you in advance!

Cheers, Sen Xu

exusen@gmail.com

Barton Evolution text

Evolution by Nicholas H. Barton (Edinburgh University), Derek E.G. Briggs (Yale University), Jonathan A. Eisen (University of California, Davis), David B. Goldstein (Duke University Medical Center), and Nipam H. Patel (University of California, Berkeley) Published by Cold Spring Harbor Laboratory Press, www.evolution-textbook.org. A new undergraduate textbook written by world-renowned researchers in population genetics, bacterial genomics, paleontology, human genetics, and developmental biology.

www.evolution-textbook.org www.evolution-textbook.org

EST library question

Dear EvolDir members,

I am looking for information about costs of developing expressed sequence tag (EST) libraries in the USA (California).

I would appreciate information on how much it would cost to: i) produce one or three-four libraries and ii) sequence 5000-10000 clones.

Have any of you had this work ordered from a company? What is the price for that? What kind of data would a company normally provide (libraries, sequences, or assemblies into unigenes)? Can you recommend any companies to do this?

Alternatively, how much time and money is required to do all the work yourself, with one human-power? Can you recommend any kits to use?

I appreciate any tips on whether you found it more efficient to produce one library and sequence more clones, or sequences fewer clones from several libraries produced from different tissues. Did you find the normalization step to be useful (worth the increased costs)?

I will post replies to EvolDir.

Thanks a lot Asta

*** Asta Audzijonyte Finnish Museum of Natural History

asta.audzijonyte@helsinki.fi

Freeze-drying lyophilizing PlantTissue

Hello I would appreciate advice on how to freeze-dry (lyophilize) plant tissue samples for maximum preservation of DNA quality when storing the freeze-dried samples at room temp. We currently use a Labconco Lyophilizer and freeze-dry the prefrozen (at -80C) leaf samples in batch mode in coin envelopes or plastic tubes at about -10C shelf temp and -40C collector temp. for 3 to 7 days and store them sealed with a desiccant at room temp. There are problems with DNA degradation especially in the tube-dried samples (desiccant is outside the small tubes). I recently read about the need for secondary drying at a temperature higher than ambient and a time 1/3 to 1/2 that required for primary drying. What in your estimation is a safe shelf temperature for secondary drying and a safe duration? Do you think that our primary freeze-drying conditions are optimal- or at least good enough? If you have a really good, tested freeze-drying (Lyophilizing) protocol for plant tissue samples or any other related helpful advise I'd much appreciate a note from you.

Sincerely

Heidi Schwaninger

Heidi R. Schwaninger, Ph. D. Molecular Geneticist New York State Agricultural Experiment Station USDA/ARS Plant Genetic Resources Unit 630 W. North Street Geneva, NY 14456-0462

Office: 315 787 2431 FAX: 315 787 2339 E-mail: Heidi.Schwaninger@ars.usda.gov

"Schwaninger, Heidi" <Heidi.Schwaninger@ARS.USDA.GOV>

Genesamp help

Hi all.

I've been having some problems running Genesamp. When I try to open the program, a black window opens and then closes itself automatically, along with an error sound. I tried to run it using the Run function in the Start menu (Windows XP) but the same thing ocurred. I tried to run it directly from MS-DOS but that didn't work either. I've changed computers (though not operating systems) and have still encountered the same problem. I was wondering if maybe some of you had faced a similar situation and/or had an idea how to solve the problem.

Thanks in advance.

Gisselle Perdomo Universidad Simon Bolivar Dpto. Estudios Ambientales Apdo. 89.000, Caracas 1080-A, Venezuela Phone: (58-212) 906 3043 Fax: (58-212) 906 3039 email: gisselle_p@yahoo.com Caracas - Venezuela

gisselle_p@yahoo.com

Gimlet Individual ID DataAnalysis

Dear All,

I am working on individual identification using microsatellite data. In my data set I have few samples with identical genotypes. I am analyzing the data using ï¿½Gimletï¿½ which does not recognize these genotypes as same rather shows the matching probabilities as same. In a large dataset it is creating confusions as some of the samples do not have complete genotype but they show similar matching probabilities. Is there any way we can differentiate between different genotypes with similar matching probabilities in a large data set? Also I would like to know that if any other program is available which will help me to make definite categorization of the genotypes while doing the analysis.

Any help in this regard will be highly appreciated.

Thanks in advance.

With regards,

Samrat Mondol Research Scholar Population & Evolutionary Genetics Group Dr. Uma Ramakrishnan's Lab (Lab-3) National Center for Biological Sciences Bangalore- 560065 Phone- 080-23666031/09886601554 Mail ID: samrat@ncbs.res.in

samrat@ncbs.res.in

GroupSize Parasitism Data

META-ANALYSIS SEEKING DATA ON GROUP SIZE AND PARASITISM

A National Evolutionary Synthesis Center (NESCent: www.nescent.org) working group is exploring ways to enhance meta-analyses and syntheses through broader requests for data. Here, we present one pilot request for data for a proposed synthetic work. Charles Nunn and Laszlo Garamszegi seek unpublished results and "pointers" to published results involving the association between group size and parasitism in vertebrates. The data will be used in a meta-analysis to investigate the links between sociality and parasitism. All published studies will be cited in resultant publications, and unpublished work may be given credit through consortium coauthorship for the person providing the data. For more information, please see:

http://www.biology.duke.edu/noorlab/Nunn.html If you have questions about the broader NESCent project of enhancing synthetic works, or have an idea for a synthetic work that you'd like to pursue that also would benefit from broader requests for data, please contact Mohamed Noor (Duke) or Maria Servedio (UNC-Chapel Hill), or see:

http://www.biology.duke.edu/noorlab/SEED.pdf Charles L. Nunn personal site: www.eva.mpg.de/primat/staff/charles_nunn/index.htm mammal parasites: www.mammalparasites.org phylogeny of sleep: www.bu.edu/phylogeny/index.html Max Planck Institute for Evolutionary Anthropology Deutscher Platz 6 04103 Leipzig, Germany email: nunn@eva.mpg.de tel.: ++49 (0) 341 3550 204 fax: ++49 (0) 341 3550 299

and

Department of Integrative Biology University of California Berkeley, CA USA tel.: ++1 510 643 2579

Charles Nunn <nunn@eva.mpg.de>

InsectPreservation DNAanalysis

Dear colleagues,

A recurrent query, I know, so my regrets to be resurrecting it again:

I am seeking convenient methods for storing insect samples (ants) for future DNA analysis (microsatellite DNA analysis - and if possible ideally also sequencing of a few MtDNA genes). Ethanol is fine except that one cannot take it along on plane journeys, and when sending back samples one has to send them as dangerous goods. A colleague sent me a guide from the Australian Museum on preservation methods, and I noticed that they suggested 15% trehalose. Would any of you have experience on using this for insects (what volumes?) and amplifying microsatellites from insects preserved in that manner? It seems one has to dry the samples after a 24hs bath in trehalose, which would be difficult to do in the field; also, trehalose may not penetrate well through an exo-skeleton.

Alternatively, do any of you have experience with using triple-distilled vodka (e.g. Balkan 176 which claims to be 88%; or the less strong ones of 40-50%) or other strong alcoholic beverages, which the Austr. Museum guide also suggests? Using such might still give problems when shipping the most flammable ones, but at least one could conveniently buy it in airports.

Other suggestions would equally be welcome.

Thank you much in advance for ideas and experiences. Please send replies directly to me at : Else.Fjerdingstad@qc.cuny.edu

Best regards,

Else Fjerdingstad

Else J. Fjerdingstad, Ph.D. Assistant Professor

Department of Biology Queens College, City University of New York 65-30 Kissena Boulevard Flushing, NY 11367, U.S.A.

Office: NSB E-118 Tel: +1 718 997 3421 Laboratory: NSB E-133/135D, Tel: +1 718 997 xxxx Fax: +1 718 997 3445 E-mail: Else.Fjerdingstad@qc.cuny.edu

http://qcpages.qc.cuny.edu/Biology/fac_stf/Fjerdingstad/fjerdingstad.html

else.fjerdingstad@qc.cuny.edu

Macaque micros

Hi All,

Anyone knows about a few Y STRs worked in macaques? I am working on paternity in bonnet macaques (Macaca radiata).

Thanks.

Deb

debapriyo@ncbs.res.in

Monomorium samples wanted

Monomorium samples wanted

Dear all,

I am looking for samples of pharaoh ants (Monomorium pharaonis) - dead or alive- from as many different localities around the world as possible, as part of my PhD. The species is introduced and found in and around houses in most countries. I am particularly interested in samples from India and Southeast Asia and any sample size will do; more than 1 individual would be good and 30+ workers in e.g. 96% alcohol would be great. I am also very interested in samples of other Monomorium species and live M. pharaonis colonies for laboratory experiments.

Thank you in advance,

Yours sincerely, Anna

Anna Mosegaard Schmidt Department of Population Biology Institute of Biology University of Copenhagen Universitetsparken 15 DK-2100 Copenhagen Denmark

E-mail: amschmidt@bi.ku.dk or anmschmidt@gmail.com

AMSchmidt@bi.ku.dk

Origin of gametologs

Gametologs? The August issue of Trends in Ecology and Evolution refers to the sex chromosomes as "gametologs:"

"We now know that the neognathous sex chromosomes follow the general pattern of sex chromosome evolution, with the initial cessation of recombination between the proto-sex chromosomes that is extended in a stepwise fashion along most of the length of the gametologs (the two different sex chromosomes), eventually leading to divergence into recognizable Z and W chromosomes."

Can anyone explain the origin, and rationale, of this term?

Donald Forsdyke, Department of Biochemistry, Queen's University, Kingston, Canada

forsdyke@post.queensu.ca

Reconstructing Evolution

Reconstructing Evolution: New Mathematical and Computational Advances Olivier Gascuel & Mike Steel (eds), Oxford University Press, July 2007 http://www.lirmm.fr/~gascuel/MAAS/NEWOUP-Book.html Since the pioneering work in phylogenetics in the 1960s, models have become increasingly sophisticated to account for the inherent complexity of evolution. They rely heavily on mathematics and aim at modelling and analyzing biological phenomena such as horizontal gene transfer, heterogeneity of mutation, and speciation and extinction processes. This book presents these recent models, their biological relevance, their mathematical basis, their properties, and the algorithms to infer them from data. A number of subfields from mathematics and computer science are involved: combinatorics, graph theory, stringology, probabilistic and Markov models, information theory, statistical inference, Monte Carlo methods, continuous and discrete algorithmics. This book arises from the Mathematics of Evolution & Phylogeneticsmeeting at the Mathematical Institute Henri Poincaré, Paris, in June 2005 and is based on the state-of-the-art reports presented by the keynote speakers. Ten chaptersbased around five themesprovide a detailed overview of key topics, from the underlying concepts to the latest results, some of which are at the forefront of current research.

Contents

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gascuel@lirmm.fr gascuel@lirmm.fr

Software GeoPhyloBuilder ARCGIS

GeoPhyloBuilder for ARCGIS is an extension for ERSIs ArcGIS that creates a spatial network, a geophylogeny, from a tree file and associated geographical data. Inferred nodes are positioned at the spatial centroid daughter nodes and tree depths assigned to z-values allowing rapid 3D visualization. Geophylogenies may be created as ArcGIS geodatabase feature datasets, set of shapefiles or in KML format for viewing in Google Earth. An ArcGIS license is required to run the software.

GeoPhyloBuilder can be downloaded from;

http://www.nescent.org/informatics/-download.php?software_id=1 Examples, help and GeoPhyloBuilder V The Movie are available from the GeoPhyloBuilder pages of the EvoViz Wiki;

https://www.nescent.org/wg_EvoViz/-GeoPhyloBuilder#Software_Information Reference: Kidd DM and Lui X (in press). GEOPHYLOBUILDER 1.0: an ArcGIS extension for creating 'geophylogenies'. /Molecular Ecology Notes/.

Best wishes

David Kidd

David Kidd <dk@nescent.org>

Software Migrate v2 3

Dear migrate-users,

I have updated migrate to version 2.3 and and also gave the website a face-lifting. The website changes are not completely finished yet: during the next couple of days it will be in some flux: but if you fail to download a specific file, let me know.

Most important changes since the 2.1 version - fixing a problem with the microsatellite mutation model (the Brownian approximation was not affected) - parallel runs on clusters improved - consolidation of the Bayesian framework - report of effective sample size in the Bayesian framework. - several memory leaks and inefficiencies fixed - no update of the manual yet, but I hope work on that soon.

you find migrate at http://popgen.scs.fsu.edu [In case you believe this is spam: your email address comes from my records of registered migrate users, this announcements are infrequent. If you want to be removed from the list let me know and I will adjust the registration database accordingly]

Peter

Peter Beerli, Computational Evolutionary Biology Group School of Computational Science (SCS) and Biological Sciences Department 150-T Dirac Science Library Florida State University Tallahassee, Florida 32306-4120 USA Webpage: http://www.csit.fsu.edu/-~beerli email: beerli@scs.fsu.edu

Peter Beerli <beerli@scs.fsu.edu>

Software ModelGenerator Online

Hi All, Just a quick note to let you know that the nucleotide and amino acid phylogenetic model selection program - ModelGenerator - is now available for online execution. Modelgenerator chooses from a set of 88 amino acid models and 56 nucleotide models and provides full best-fit model ranking information in the output. You can upload several alignments simultaneously and the results are emailed back to you.

ModelGenerator can be found at: http://-bioinf.nuim.ie/software/modelgenerator The online submission form can be found at: http://-distributed.cs.nuim.ie/multiphyl.php There is also a link from the ModelGenerator homepage to the online submission form.

Cheers, Thomas

THOMAS.M.KEANE@nuim.ie
THOMAS.M.KEANE@nuim.ie

Software Mol coanc

Dear Evoldir members,

Version 2.0 of the software MOL_COANC is ready to be downloaded from the site

<http://www.uvigo.es/webs/c03/webc03/XENETICA/XB2/Jesus/Fernandez.htm> http://www.uvigo.es/webs/c03/webc03/XENETICA/XB2/Jesus/Fernandez.htm This software allows for the estimation of coancestry coefficients between a group of individuals based on their molecular information, following the approach of Fernï¿½ndez & Toro (2006, Molecular Ecology). New features include the possibility of introducing a partially know genealogy, thus, the program will force the solution to fit with this predefined structure. For example: if we know that a group of individuals are FS, all of them will share both parents irrespective if the algorithm adds other members to the group. Another common situation is knowing at least the mother for all individuals in species where seeds or eggs are laid together.

Another improvement is the possibility of setting a ï¿½tolerance' parameter, defined as the number of loci where we allows for Mendelian incompatibilities when forming FS groups. This way we can cope with genotyping errors avoiding the inclusion of an individual in its correct FS group.

A bug has been also fixed. Previous version assumed that order of alleles in heterozygotes was always the same (i. e. always the ï¿½smaller' first). If not, errors in the FS compatibility checking could occur. Present version admits any order for the genotypes.

Sincerely

Jesï¿½s Fernï¿½ndez Martï¿½n Departamento de Mejora Genï¿½tica Animal 34-91 3471487 Instituto Nacional de Investigacïï¿½n y 34-91 3572293 (FAX) Tecnologï¿½a Agraria y Alimentaria (INIA) jmj@inia.es Crta. A Coruï¿½a Km. 7,5 28040 Madrid (SPAIN) http://www.uvigo.es/webs/c03/webc03/XENETICA/XB2/Jesus/Fernandez.htm

jmj@inia.es

Speciation in Birds text

Speciation in Birds by Trevor Price (University of Chicago) Published by Roberts and Company Publishers, www.roberts-publishers.com/price .“Speciation in Birds” will be a must readïnot only for ornithologists, but for evolutionary biologists of all stripesï“this is the most synthetic and innovative treatment of speciation ever published for any group of organisms.” Jonathan B. Losos, Monique and Philip Lehner Professor for the Study of Latin America, Harvard University

www.roberts-publishers.com/price www.roberts-publishers.com/price

StadenPackage question

Dear All,

I am interested to know your opinions about the free sequence editing programme STADEN. In particular I would like to know whether every set of forward and reverse sequence per sample, have to be treated extra in pregap and gap, or whether there is a way of applying the same settings in pregap to a whole lot of sequences and then edit the F and R contigs separately. I tried and it seemed less useful, e.g. in pregap you have to individually click to accept every single file, e.g. click 96 times for a whole seq plate.

Any comments, advice?

many thanks in advance, s

– Saskia Bode PhD student

Royal Belgian Institute of Natural Sciences, Freshwater Biology Rue Vautier 29, 1000 Brussels, Belgium

Tel : +32 (0)2 6274 326 http://www.evirens.group.shef.ac.uk/ saskia.bode@naturalsciences.be snsaskiab@gmail.com

saskia.bode@naturalsciences.be
saskia.bode@naturalsciences.be

StadenPackage question answer

Hi Saskia, in response to your query re Staden.

Depending on what you are doing, you might find programs like STARS (_http://neelix.molbiol.ox.ac.uk:8080/userweb/mchan/stars/_) or the recently developed PHINEUS (_http://www.phineus.org/_) useful. Both of these are designed with repetitive sequencing projects in mind, such as Multilocus sequence typing, or sequencing the same locus in many samples. STARS uses a STADEN environment, whereas PHINEUS stands alone, with the exception of needing Phred. Both do what you ask, which is to apply the same pregap (or equivalent) settings to a large number of datafiles. This includes clipping to the start and end points of a predefined allele. They then identify the F and R reads, match them up and produce a consensus. This may then be used to interrogate online databases.

Hope this helps

Best

Bill

Dr. W. P. Hanage, Imperial College Faculty of Medicine, Department of Infectious Disease Epidemiology, St Mary's Hospital, Norfolk Place. London. W2 1PG http://www1.imperial.ac.uk/medicine/people/w.hanage.html Tel. +44 (0)20 7594 3622 Fax. +44 (0)20 7594 3693 Mobile 07905 681291

Dear All,

I am interested to know your opinions about the free sequence editing programme STADEN. In particular I would like to know whether every set of forward and reverse sequence per sample, have to be treated extra in pregap and gap, or whether there is a way of applying the same settings in pregap to a whole lot of sequences and then edit the F and R contigs separately. I tried and it seemed less useful, e.g. in pregap you have to individually click to accept every single file, e.g. click 96 times for a whole seq plate.

Any comments, advice?

many thanks in advance, s

– Saskia Bode PhD student

Royal Belgian Institute of Natural Sciences, Freshwater Biology Rue Vautier 29, 1000 Brussels, Belgium Tel : +32 (0)2 6274 326 http://www.evirens.group.shef.ac.uk/ saskia.bode@naturalsciences.be snsaskiab@gmail.com

StatPackAnalysisMixtures sofware question

Hello,

I am working with databases to analyse a mixed-stock fishery, so I'm trying to use StatPackAnalysisMixtures software for the analysis. I use 13 microsatellites of between 14 and 56 alleles. To date, I have prepared a control file for a simulation, but when using all 13 microsatellites, there is always that error message ?All mixture genotypes are impossible. Reduce genotype tolerance parameter? even if I set the GPA at 100, and the other two tolerance criteria at 0. When I conserve only the 6 less polymorphic loci, the simulation runs. I tried to use more loci and it works until 9 loci, but the estimates are getting worse with more loci. I know it is supposed to work with more loci since a lot of papers used StatPackAnalysisMixtures in similar conditions as me. If you have any suggestions to help me, I would appreciate it !

Thanks

Marika Gauthier Pavillon Marchand Universitï¿½ Laval Quï¿½bec, Canada, G1K 7P4 marika.gauthier-ouellet.1@ulaval.ca

TansyRagwort samples

Dear all,

For my PhD I am studying Tansy Ragwort (Senecio jacobaea), from introduced and native origins. I would like to estimate the amount of genetic variation in introduced and native populations and determine the source populations of the invasive plants. To execute this, I am asking your help for the acquisition of seeds from Europe and Eurasia and the invasive areas Australia, New Zealand and North America. Ideally the seeds are sampled from 10-15 plants in a population and are bagged separately per plant (e.g. 5 capitula per plant). If no such seeds are available I am also interested in bulk samples of seeds as well.

Please note, if possible: - Exact location of the population - A brief description of the habitat (for example pasture, sand dunes, road margin, etc.) - Approximate size of the population - Feeding signs (and if possible what kind of damage) - Presence/ absence of the Cinnabar Moth (Tyria jacobaeae) For pictures and a description of Tansy ragwort and the Cinnabar Moth see: http://www.biology.leidenuniv.nl/ibl/S9/edu.shtml#Seneciojacobaea In exchange for your effort and time you will receive a typically Dutch present.

If you can help me or know someone who might be able to, please contact me via email at l.j.doorduin@biology.leidenuniv.nl.

I would be very thankful if you can help me out,

Yours Sincerley, Leonie Doorduin Section Plant Ecology Institute of Biology Leiden University The Netherlands

l.j.doorduin@biology.leidenuniv.nl

USheffield Sabbatical

An outstanding opportunity for a sabbatical visit has arisen in the Department of Animal & Plant Sciences, University of Sheffield. We (Jon Slate, Terry Burke and Roger Butlin) are seeking somebody with expertise in molecular evolution, population genetics or statistical genetics who can act as a mentor to 3 postdoctoral scientists undertaking evolutionary genetics data mining in ecologically relevant organisms. In particular they will be attempting to identify loci responsible for adaptively important variation in populations of littorinid winkles, passerine birds and Soay sheep.

In addition to assisting these researchers, the successful applicant will have an opportunity to investigate a large population genetic dataset of Arabidopsis lyrata and considerable scope to pursue/continue their own research interests.

The Department of Animal and Plant Sciences (http://www.shef.ac.uk/aps/index.html) is one of the largest whole organism biology departments in the UK and was ranked 5* (the highest possible grade) in the last Research Assessment Exercise. The Evolution and Behaviour Group is one of five groups within the department and has considerable strengths in evolutionary genetics, behavioural ecology, evolutionary entomology, and social evolution. The department is widely regarded as a dynamic and exciting work place. Furthermore, Sheffield is an excellent place to live as it is affordable, culturally stimulating and located on the edge of the Peak District National Park.

The post is available for 2 years, although we would consider applicants wishing to make shorter visits. Ideally the successful applicant would be in post by December 2006. The position is extremely generously salaried (~ £48,000 per annum). Initial enquiries to Jon Slate (j.slate@shef.ac.uk), Roger Butlin (r.k.butlin@shef.ac.uk) or Terry Burke (t.a.burke@shef.ac.uk). Unfortunately UK nationals are not eligible unless they have spent at least 4 of the last 5 years working overseas.

Dr Jon Slate Dept. Animal & Plant Sciences University of Sheffield Tel: 0114 2220048 Fax: 0114 2220002 Web: http://www.jon-slate.staff.shef.ac.uk/

j.slate@sheffield.ac.uk j.slate@sheffield.ac.uk

Undergrad genetics software

Hello-

We're currently working to update our undergraduate genetics computer lab. We currently use two programs Dos Genetics (Schmidel, 1995) and Virtual Genetics (Day, U of Western Ontario) in our labs. We're looking for computer-based (preferably Mac, though we can also use PC programs) genetics labs that cover basic Medelian genetics and patterns of inheritance (dihybrid crosses, sex-linked genes, etc.) as well as some molecular genetics topics (such as lac operon problems, and deletion mapping). I'm curious what software other schools are using and what they recommend. Any suggestions would be greatly appreciated.

Thank you, Jennifer Kovacs Georgia Institute of Technology Cherry Emerson 310 Ferst St. Atlanta, GA gtg647u@mail.gatech.edu

PostDocs

DukeU 6 FungalEvol

Six Postdoctoral Positions V Fungal Evolution

Assembling the Fungal Tree of Life (www.aftol.org)

We seek six Ph.D. level scientists to participate in a multi- investigator project to resolve the origins of major fungal lineages using genomic and morphological data (for a description of the the Fungal Tree of Life project see www.aftol.org). Four positions are available in the area of fungal phylogenomics. We seek candidates with experience in molecular evolutionary genetics, including DNA sequencing methods, comparative genomics and phylogenetic analysis of fungal genome data. One position, with focus on basal fungal lineages, is located in the Botany Department, University of British Columbia, Vancouver, Canada (contact M. Berbee, <berbee@interchange.ubc.ca>). Two positions are in the Biology Department, Duke University, Durham, NC (contact R. Vilgalys, focus on basal lineages <fungi@duke.edu> or F. Lutzoni, focus on lichenized ascomycetes <flutzoni@duke.edu>). One position, focusing on basal Basidiomycota (rusts and smuts), is located at Louisiana State University AgCenter (contact Cathie Aime, maime@agcenter.lsu.edu). The other two positions in fungal comparative biology/structural evolution are located in the Department of Plant Biology, University of Minnesota, St. Paul (contact D. McLaughlin, <davem@umn.edu>) and Department of Biological Sciences, Louisiana State University (contact M. Blackwell, <mblackwell@lsu.edu>). These postdocs will work closely with other labs to expand the AFTOL structural database (http://aftol.umn.edu), and should have interests in comparative biology/structural evolution and phylogenetic analysis. Previous experience working with a diversity of fungal organisms is desirable for all positions. All positions offer competitive postdoc salaries with health benefits, with an appointment period of 2 years plus possibility of renewal. If interested, please send a cover letter, vita and names of references to any or all of the contact persons listed above. Applications will be considered until October 1, 2007.

Dr. Rytas Vilgalys Biology Dept., Box 90338 Duke University Durham, NC 27708

Rytas Vilgalys <fungi@duke.edu>

INRA France EvolEcol

Dear colleague, please post this vacancy on your site. Regards, Jean-Francois Soussana

A 15 months post-doctoral position is available at the INRA Clermont-Ferrand research center. We are looking for a biologist, specialized in functional or community ecology, with first experience in modelling ecosystems. The aim is to model the role of plant functional traits for ecosystem processes. The project will be developed in collaboration with the Max Planck Institut in Jena and with several groups in France (INRA and CNRS) within the framework of the DISCOVER project. The overall aim of the project is to understand the role of biological diversity for key processes in grassland ecosystems (see www2.clermont.inra.fr/discover).

The monthly gross salary is of ca. 2160 Euros.

Applicants should send a letter of application, resume, and list of publications to: soussana@clermont.inra.fr (Dr. JF Soussana, UR 874 Agronomie, Grassland Ecosystem Research, +33 473 62 44 23)

Closing date for the application is September 10, 2007.

Dr. Jean-Francois Soussana Equipe Fonctionnement et Gestion de l'Ecosystï¿½me Prairial (Grassland Ecosystem Research) Directeur de l'Unitï¿½ d'Agronomie (URAC) INRA, UR874, 234, Av. du Brï¿½zet, Clermont-Ferrand, F-63100, France. Tel. +33 (0) 473 62 44 23, Fax. +33 (0) 473 62 44 57 www2.clermont.inra.fr/agronomie www2.clermont.inra.fr/discover

jean-francois.soussana@clermont.inra.fr

INRA GrignonFrance PlantPathogenEvol

An 18 months post-doctoral position is available at the INRA BIOGER research center, Grignon, France (30 mn from Paris). We are looking for a mathematician with a keen interest in biological systems, or an experienced programmer with interest in modelling population/epidemic systems (preferably with stochastic components).

The project will be developed in collaboration with Frank Van den Bosch, Rothamsted Research (UK) and is linked to ongoing research projects between both groups. This project forms a key component of the INRA-BBSRC funded project “Epidemiological and evolutionary models for invasion and persistence of disease”. The overall aim of the project is to devise and test modeling and experimental protocols to analyze and predict the effects of genetic control on the evolution, invasion and persistence of plant pathogens and the consequences of these for the design and durability of resistant varieties.

Closing date for the application is 31 august 2007.

For further information, see : http://www.international.inra.fr/join_us/positions/post_doctoral_positions/current_offers or : http://www.inra.fr/les_hommes_et_les_femmes/rejoignez_nous/completer_sa_formation/le_recrutement_de_post_doctorants/les_offres_en_cours Applicants should send a letter of application, resume, list of publications and two reference letters to Christian.Lannou@grignon.inra.fr Dr. C. Lannou Laboratoire de Pathologie Vegetale INRA BP 01 F-78850 Thiverval-Grignon, France

project description :

Invasion of a virulent mutant in a background of a resident strain. [keywords : Epidemiology ; Crop resistance management ; Stochastic model ; Spatial structure] Resistance to pathogens in cultivated plants is largely determined by monogenic resistance factors. In most situations, these resistance factors are overcome by the pathogen within a few years. Large research efforts are currently developed to extend the durability of plant resistance to diseases, either by introducing original combinations of resistance factors in new varieties or by developing crop management strategies to preserve the efficacy of the newly deployed resistance genes. Prediction of resistance durability is largely based on mutation rates (mutation from avirulent to virulent) and fitness costs (detrimental effect of this mutation to the pathogen fitness). However, a rapid examination of published data on mutation rates and population sizes suggest that any new resistance gene should be overcome instantly after its introduction in a crop. Yet durability of resistance is reported to be in the order of years to decades. The objective of the post-doc project will be to test a sequence of hypotheses that might explain why durability is not well predicted by the basic information on mutation rate and virulence cost. Particularly, the effect of the local spatial structure of the system will be examined, as well as the consequences of demographic stochasticity.

To test these hypotheses, a stochastic model for the invasion of a mutant in a background of a resident strain will be developed and analyzed.

The project will be largely based on data sets collected and analyzed by the Epidemiology group of BIOGER and describing wheat leaf rust (Puccinia triticina, a fungal pathogen of wheat) epidemiology : spore production (Rime D. et al. 2005. Plant Pathology 54:287-298 ; Robert C. et al. 2004. Phytopathology 94:712-721) local spore dispersal (Soubeyrand S. et al. 2006. Journal of Data Science 5:67-83 ; Soubeyrand S. et al. 2006. Statistical Methodology 3:464-482), leaf colonization and autoinfection (unpublished), population structures (Goyeau H. et al. 2006. Phytopathology 96:264-273 ; Goyeau H. et al. 2007. Fungal Genetics and Biology 44:474-483).

The Epidemiology group, BIOGER, INRA Grignon, develops research on fungal disease epidemiology and host resistance management. Re-introducing functional biodiversity in crops for resistance characters provides an ecological approach to disease control and could contribute to the sustainability of crop production. The project will be developed in collaboration with Frank Van den Bosch, Rothamsted Research (UK), leader of the Population dynamics and evolutionary ecology group. The central theme of this group is the development and application of parsimonious, generic models to study the population dynamics and evolutionary ecology of plants and their pathogens.

This postdoc will be part of a INRA-BBSRC project, involving INRA BIOGER (Grignon, France), INRA Bio3P (Rennes, France), Rothamsted Research (UK) and Cambridge University (UK). The post-doc might be expected to have

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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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INRA Toulouse France Sunflower StressAdaptation

STRESS RESPONSE AND ADAPTATION TO DROUGHT IN HELIANTHUS

An INRA funded post-doctoral position is available for three years at the Laboratory of Plant Microbe Interactions (Toulouse, France).

We are seeking a highly motivated candidate to take part in a starting group on sunflower adaptation to drought. The project will take advantage of new transcriptomic tools to identify genes that are differentially expressed at different developmental stages and in different organs. In addition, candidate genes will be chosen among the large number of gene families that has been identified in other species. Variants in Helianthus of selected genes will be characterized and described functionally by association genetics and functional genomics.

The successful candidate will have expertise in genetics, transcriptomics and/or functional genetics and will be interested to interact with agronomists and physiologists. He/she must have a PhD, a non-French citizenship and should start by January 1st, 2008.

The laboratory of Plant Microbe Interactions is part of the Institute of AgroBiosciences, Interactions and Biodiversity, which is member of the Toulouse Genopole, a leading area in biological sciences. Toulouse is one of the most attractive and dynamic cities in France and is only 1h30 from the mountain and the Mediterranean sea. Salary will be based on EU standards for post doctoral positions in France

Candidates should send a CV, and names and emails of three referees to Patrick Vincourt Patrick.vincourt@toulouse.inra.fr and Nicolas Langlade n.langlade@laposte.net

Nicolas Langlade, PhD Laboratoire Interactions Plantes Microorganismes UMR 441-2594 (INRA-CNRS) BP 52627 Chemin de Borde Rouge - Auzeville 31326 Castanet Tolosan FRANCE http://www.toulouse.inra.fr/centre/lipm/index_eng.htm nicolas.langlade@ens-lyon.fr nicolas.langlade@ens-lyon.fr

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ImperialCollege Macroevolution

Postdoctoral position developing a synthetic overview of macroevolution in planktonic foraminifera over the last 65 million years

Division of Biology, Silwood Park campus, Imperial College London Fixed term contract for up 3 to years Salary: £23,850 - £26,520 per annum

A postdoctoral research associate is sought for a 3-year NERC-funded post to develop a synthetic overview of macroevolution in planktonic foraminifera over the last 65 million years. Planktonic foraminifera have an unparalleled fossil record, providing the clearest available view of species dynamics over a long time scale, enabling us to produce the most comprehensive picture available of the large-scale evolutionary history of any group over a prolonged period. The job involves applying a range of statistical approaches (e.g., survival analysis, phylogenetically independent contrasts, time series analysis) to the fossil history of the group, developing necessary software in the statistical computing language R, and writing papers.

Job location and start date You will join Andy Purvis' group in the Ecology & Evolution section of the Division of Biology (see http://www3.imperial.ac.uk/-biology/research/ecologyandevolution), working at the Silwood Park campus of Imperial College London, but will also sometimes travel to Cardiff University. The position is available from 1st October 2007 but the successful candidate can start any time up to January 2008.

Further information An application form, job description and person specification can be obtained from the following link: http://www3.imperial.ac.uk/-employment/research/ns2007124cw Please send completed application forms, along with a cover letter, C.V., and names and contact details of two referees to Prof Andy Purvis, Division of Biology, Imperial College, Silwood Park campus, Ascot, SL5 7PY, U.K. E-mail: a.purvis@imperial.ac.uk Closing date: 5th August 2007

“Valuing diversity and committed to equality of opportunity”

a.purvis@imperial.ac.uk

ImperialCollege PopulationDynamics

Post-doctoral position investigating individual differences and the dynamics of animal populations

Applications are invited for a 3-year, post-doctoral position funded by the Natural Environment Research Council. The post holder will investigate the feedback between the dynamics of phenotypic traits and populations using long-term observational data from Soay sheep, silvereyes and meerkats, and experimental data from manipulations of soil mite populations.

A key step in understanding evolutionary change in stochastic environments is to understand links between changes in the distribution of heritable phenotypic traits and changes in the dynamics of populations caused by fluctuations in birth and death rates. In our recent research we have demonstrated how evolutionary change can influence the dynamics of populations, and how ecological variation can influence the strength and direction of selection, as well as the demographic rate via which selection operates most strongly. The post-doc will extend this research and will conduct statistical analyses of existing data, the construction of population models and the development of new theory. The ideal applicant will have, or will be about to complete, a Ph.D., as well as a strong quantitative background and an interest in ecological and evolutionary processes.

The post-doc will be based at Imperial College's Silwood Park Campus in Tim Coulson's group, but the project will involve close collaboration with Tim Benton in Leeds, Tim Clutton-Brock in Cambridge, Shripad Tuljapurkar in Stanford, and Ian Owens also at Imperial College London.

The post will start on October 1st 2007 and will run for three years. The salary will be in the range £23850 - £34750. Applicants should send a cover letter, application form and an up-to-date copy of their CV to Tim Coulson (t.coulson@imperial.ac.uk) by July 31st 2007.

Further details and an application form can be downloaded from http://www.bio.ic.ac.uk/research/-coulson/index.htm . t.coulson@imperial.ac.uk

IndianaU ReproductiveDiversity

An NIH T32 training grant to Indiana University has an open line for a post-doctoral fellow and invites applications. The training grant is supported by NIH-CHHD and is entitled, 'Common Themes in Reproductive Diversity.' It offers broadly integrative training in the areas of sexual reproduction and development with a focus on behavior, largely but not exclusively of animals. Research conducted by the participants addresses key questions in the development and expression of sex differences, as well as maternal and paternal effects on morphological, sexual, and social development. Indiana University's excellent support for research and its globally recognized strengths in animal behavior, endocrinology, human sexual health, and evolution of development ensure high quality training. Fellowships include a competitive salary based on current NIH pay scale commensurate with experience and funds to support research and travel. The successful applicant will help foster collaborations among faculty and serve as a professional model for pre-doctoral trainees. Ph.D in biology, psychology, neuroscience, chemistry, gender studies or related field required. Candidates are invited to make initial contacts with training faculty. To apply, please visit the following website to find instructions and forms to download: http://www.indiana.edu/~reprodiv/apply/ Please e-mail your completed application to Dee Verostko at dverostk@indiana.edu or send to 1001 East Third Street, Bloomington, IN 47405. The email subject line should read: Postdoc-Ketterson. For full consideration, applications should arrive by 15 August 2007 but later applications will be considered. Please note that the traineeship must begin in April 2008. Trainees must be citizens, non-citizen nationals, or permanent residents of the US. The search will continue until the position is filled. Indiana University is an Equal Opportunity / Affirmative Action Employer.

"Summers, Linda Rae" <lisummer@indiana.edu>

KansasStateU NematodeGenomics

Postdoc: Nematode Ecological Genomics

Postdoctoral Position: Nematode Ecological Genomics An NSF-funded postdoctoral position is available beginning Fall 2007 in the Herman lab (http://www.k-state.edu/hermanlab) in the Division of Biology at Kansas State University. We are studying the genomic responses of soil nematodes to environmental change. We are combining field-based approaches with laboratory approaches using a genetic model nematode (Jones et al. 2006, Mol. Ecol., 15, 2601; Ungerer et al., 2007, Heredity; Kammenga et al., 2007, TREE, 22, 273). Specifically, laboratory tests using C. elegans and native soil nematodes are used to determine which genes affect fitness in a changed environment. Ultimately we aim to determine which genes are expressed by nematodes as they respond to environmental cues in the field. Our studies are part of the Kansas State University Ecological Genomics Institute (http://www.k-state.edu/ecogen). The successful applicant will join an interdisciplinary group in an interdisciplinary research environment. The position is available for one year, with two additional one-year terms possible subject to performance and funding.

Kansas State University is located in Manhattan, KS, a pleasant college town nestled in the Flint Hills of Kansas, two hours west of Kansas City.

Preference will be given to applicants with expertise in Ecological Genomics, Molecular Ecology and Functional Genomics. C. elegans experience is also a plus, but not required. Applicants should have the interest and willingness to cross disciplines. Review of applications begins August 15, 2007 and will continue until the position is filled. To apply, send a brief cover letter, C.V. and a list of three references by email to:

Michael Herman Co-Director KSU Ecological Genomics Institute Division of Biology Kansas State University 266 Chalmers Hall Manhattan, KS 66506 Office: (785) 532-6741 Lab: (785) 532-6773 FAX (785) 532-6653 Email : mherman@ksu.edu http://www.ksu.edu/hermanlab Kansas State University is an equal opportunity employer and actively seeks diversity among its employees

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MaxPlanckSeewiesen BirdSong

The newly set up Independent Junior Research Group at the Max-Planck-Institute in Seewiesen (close to Munich/Starnberg, Germany) is offering a

Position as Research Scientist in Animal Behaviour

We are looking for a behavioural scientist for an investigation of sexual signalling in birds. The project will focus on the use, information content and costs of song amplitude. The aim is to bridge proximate mechanisms and the behavioural ecology of sexual signals by relating song production to endocrine mechanisms and metabolic costs, as well as to individual fitness.

The project will combine field and laboratory work. It will be based at the Max Planck Institute for Ornithology, but also will require field work in the French Alps.

We are seeking a highly motivated scientist with a strong background in animal behaviour. A PhD and and very good experimental and analytical skills in bioacoustics are required; a ringing license would be helpful.

The successful candidate will join an independent junior research group headed by Dr. Henrik Brumm. The

Max Planck Institute offers excellent working conditions and facilities of the highest standards. The working language of the research group is German and English. The position is funded for a duration of three years, and is aimed to start as soon as possible. Salary will be according to TvöD 13 (formerly BAT IIa).

The Max Planck Society is an equal opportunity employer. Disabled persons with comparable qualifications receive preferential status.

To apply, please send a cover letter describing your research interests, a complete CV, publication list and names of two referees by email to Postdoc.Birdsong@orn.mpg.de. Closing date: 6 Aug 2007. For informal inquiries please contact. Dr. Henrik Brumm at brumm@orn.mpg.de.

Max Planck Institute for Ornithology Communication and Social Behaviour Group Eberhard-Gwinner-Str. Haus Nr. 11 D-82305 Starnberg (Seewiesen), Germany

Internet: www.orn.mpg.de Dr. Henrik Brumm Max Planck Institute for Ornithology Communication and Social Behaviour Group Post Box 1564 82305 Starnberg/Seewiesen Germany

Tel.: +49 (0)8157 932 355 Fax: +49 (0)8157 932 344

Henrik Brumm <brumm@mail.orn.mpg.de>

MissouriBotGarden RosaEvol

Applications are invited for a postdoc position to study the evolution of Rosa (Rosaceae) in the context of molecular phylogeny using material of wild Rosa species. This study is led by Dr. Libing Zhang (Missouri Botanical Garden) with collaboration from Dr. Xinfen Gao (Chengdu Institute of Biology, Chinese Academy of Sciences).

The postdoc will be responsible for generating DNA sequences, training graduate students in the lab, analyzing data, and co-authoring manuscripts. Applicants should have a strong molecular systematics experience, preferably also including cloning skills. The postdoc is welcome to work on his/her own projects in addition to the study of Rosa. The position is for one year with possible extension of up to three years.

The postdoc will be based at the Chengdu Institute of Biology, Chinese Academy of Sciences (http://www.cib.ac.cn/blue_cib/index.html). The city, Chengdu, over 2,500 years old, is rich in culture and well-known for the food (Sichuan cuisine) and is close to the mountains where many wild Rosa species naturally occur. The salary is comparable with that of an assistant professor in Chengdu. The flight to Chengdu will be paid and possibly also the flight back from Chengdu after the position ends. Economic housing is provided. The start date is flexible but preferably by September 2007. Applicants should email a short cover letter, cv, and names and contact information of three references to Dr. Libing Zhang (Libing.Zhang@mobot.org) by 6 August 2007.

Li-Bing Zhang <gonggashan@gmail.com>

NIH Bethesda LINE1evol

POSITION:

Post-doctoral fellowship in the Section on Genomic Structure & Function, Laboratory of Molecular & Cell Biology, NIDDK, National Institutes of Health, Bethesda MD 20892 USA

AVAILABILITY: Autumn, 2007

TOPIC:

Experimental analysis of evolutionary inferences: the interaction between the mammalian L1 (LINE-1) retrotransposon and its host.

SUMMARY:

L1 elements have been replicating and evolving in mammals since 70 million years ago. During this time novel L1 families repeatedly arose, only to go extinct coincident with the emergence of another novel L1 family. This process has persisted to the present and generally resulted in a single evolutionary lineage of L1 families. The repeated emergence of successful L1 families has occurred despite the fact that they are deleterious to their host.

The pattern of mammalian L1 evolution resembles that of the influenza virus HA antigen in humans. The latter is explained by the successive emergence of viral variants that bypass existing host defenses (immunity) followed by the reestablishment of host immunity. We suggest that an analogous adversarial interaction between L1 and its host explains the pattern of L1 evolution.

Projects that examine the interaction of L1 and its host:

- Analysis of the host factors that interact with regions of L1 that have been either highly conserved or undergone adaptive evolution.

- Analysis of the structural and functional consequences of adaptive changes undergone by L1 encoded proteins.

Also ongoing are projects that use L1 DNA “fossils” generated by now extinct L1 families to examine the history and architecture of the mammalian genome.

Additional information and references can be found at <http://www.niddk.nih.gov/intram/people/-afurano.htm> QUALIFICATIONS & APPLICATION:

Applicants must have received a doctoral degree within the last 5 years.

Thorough knowledge of molecular biology and proficiency in both the theory and practice of standard molecular biological and biochemical techniques is essential. Experience with molecular evolution and genetics would be beneficial but not required.

Interested applicants should send a CV & Bibliography, a short description of research interests, and have three letters of reference sent (all by email) to Anthony V. Furano: avf@helix.nih.gov.

– Anthony V. Furano

Building 8, Room 203 National Institutes of Health 8 CENTER DR MSC 0830 BETHESDA MD 20892-0830

avf@helix.nih.gov

Phones: Voice 301-496-6180 FAX 301-402-0053

<http://www.niddk.nih.gov/intram/people/-afurano.htm>

avf@helix.nih.gov avf@helix.nih.gov

NatlTaiwanU EvolGenet

Postdoctoral Position, Evolutionary Genetics Department of Life Science, National Taiwan University

We are seeking one enthusiastic researcher to join our group for a collaborative study supported by an NSC project. Positions are for two years, with possible extension, and can begin as early as August 1, 2007. We recently focus on expression differences between closely related species/races in Drosophila. Several candidate genes have been identified from genetic and microarray analyses. With the powerful genetic tools and genomics resources available in D. melanogaster, we will 1). validate the expression difference between species and their hybrids, 2). study the functional differences by molecular genetic approaches and 3) analyze the evolutionary process of genes evolving in species differentiation. Our work addresses a fundamental question in evolutionary biology and will provide an opportunity for the candidate to build a career in this area. Preference will be given to applicants with demonstrated experience in some or all of the following: basic molecular approaches, Drosophila genetics, and population/quantitative genetics.

To apply Applicants should send CV, 2-3 page statement of research accomplishments and interests, names and contact information for two references, and up to three reprints or preprints, by email to [3]ctting at ntu.edu.tw.[2]

Chau-Ti Ting Department of Life Science Institute of Ecology and Evolution Institute of Zoology National Taiwan University

Shun-Chern Tsaur <sctsaur@sinica.edu.tw>

OhioStateU MicrobialPhylogenetics

Postdoctoral Researcher in Microbial Phylogenetics and Community Analysis

Job Location: Ohio State University College of Medicine, Dept of Biomedical Informatics (bmi.osu.edu) and OSU College of Dentistry, Section of Oral Biology.

We seek a postdoctoral researcher to work with large multilocus sequence datasets in a collaborative project between bioinformaticists and oral microbiologists.

The research will involve phylogenetic, epidemiological, population and community analyses of mixed-species oral bacteria data.

Position is for 2 years with opportunities for renewal. Salary commensurate with experience.

Please contact Dan Janies <danjanies@hotmail.com>

danjanies@hotmail.com

Portugal 6 EvolEpidemiology

Six Postdocs in Evolutionary Epidemiology

The Theoretical Epidemiology and Evolutionary Biology groups at Instituto Gulbenkian de Ciência announce a collaborative programme at the interface between the two research areas.

The present call is for 6 Postdoctoral Fellows for an initial period of one year to develop theoretical models of molecular evolution and population dynamics as a motor for hypothesis-driven epidemiological research. Diseases of interest include influenza, bacterial meningitis, tuberculosis, malaria and cancer. The positions are funded by a Marie Curie Excellence Grant.

Applicants should hold a PhD in mathematical or biological sciences, in a broad sense, experience in molecular evolution, population dynamics, statistical epidemiology or bioinformatics. Familiarity with high-level computer languages is required. For further details visit www.igc.gulbenkian.pt . Applications, including research interests, CV, and three letters of reference should be sent to ggomes@igc.gulbenkian.pt.

Deadline for applications: September 7, 2007, or until the positions are filled.

Gabriela Gomes <ggomes@igc.gulbenkian.pt>

QueenMaryULondon BeeEvol

"Postdoctoral Research Assistant: Application of the Bumblebee Foraging Pheromone for Commercial Greenhouse Pollination

Ref: 07269/KR

Salary: £30,066 - £33,513 per annum

This full-time, 12 month fixed term post is funded through a NERC grant awarded to Professor Lars Chittka, Dr Nigel Raine (Queen Mary, University of London) and Dr Juliet Osborne (Rothamsted Research). The aim of the project is to find the optimum blend of foraging recruitment pheromones to encourage and maintain high levels of foraging behaviour in bumblebee colonies, and to test its efficacy at increasing crop yield of a commercially important crop (tomatoes) in greenhouse conditions.

The post holder will carry out behavioural experiments to assess the efficacy of different combinations and dosages regimes of artificial foraging recruitment pheromone components on the foraging activity of bumblebee (Bombus terrestris) colonies in the laboratory at Queen Mary, University of London. The potential effect of the optimum pheromone blend on pollination levels and crop yield of tomatoes will be tested in greenhouses at Rothamsted Research in an experiment lasting several months. During the project the post holder will need to work flexibly at both institutions as necessary. Having established the artificial foraging recruitment pheromone effectively mimics the natural bumblebee system to communicate the presence of food outside the nest, the post holder will develop a cost-effective automatic system to dispense pheromone. To increase general applicability of this innovative technology, the post holder will be involved in determining the recruitment pheromone components of a second bumblebee species.

Applicants should possess a PhD ideally in the area of invertebrate behavioural ecology, physiology or evolutionary biology. Working knowledge of pollination ecology and/ or pheromone chemistry would be desirable.

Informal enquiries may be made to Prof. Lars Chittka, e-mail address: l.chittka@qmul.ac.uk or Dr Nigel Raine, e-mail address: n.e.raine@qmul.ac.uk

Further details and a BLUE application form can be obtained from the School's website: http://www.sbcs.qmul.ac.uk/vacancies/index.shtml Alternatively, please visit the Human Resources website on: http://www.hr.qmul.ac.uk/vacancies/ Completed application forms together with a copy of your CV, quoting reference no. 07269/KR, should be returned to Ms Sunita Devi-Paul, School of Biological & Chemical Sciences, Queen Mary, University of London, Mile End Road, London E1 4NS, or by e-mail: sbcs-vacancies@qmul.ac.uk The closing date for applications is the 23 July 2007 at 5pm. Interviews will be held on the 2 August 2007. Applicants who are not contacted by the end of August 2007 should assume that they were not successful.

Working towards equal opportunities."

Dr Nigel Raine, School of Biological and Chemical Sciences, Queen Mary, University of London, 327 Mile End Road, London, E1 4NS.

Tel: 020 7882 3293

web: http://www.biology.qmul.ac.uk/research/staff/chittka/chittkalab/Team/Nigel.html

Nigel Raine <n.e.raine@qmul.ac.uk>

RutgersU PopGenetics

Postdoctoral Position in Population Genetics at Rutgers University

A postdoctoral position in the area of population genetics is available in the lab of Jody Hey, at Rutgers University. The research will involve adapting coalescent models to problems in population divergence, as well as developing statistical methods for fitting divergence models to data sets. These methods will be used to study problems in the divergence of human populations, as well as in other systems including Malawi cichlids and Chimpanzees.

This position is NIH funded for several years. The research will be in collaboration with Dr. Rasmus Nielsen of the University of Copenhagen.

Ideally a candidate should have experience in coalescent models and/or probabilty theory, and experience in programming using C/C++ or a similar low-level language.

The start date is flexible.

Applications should email Jody Hey (please include a CV) hey@biology.rutgers.edu http://-lifesci.rutgers.edu/ ˜ heylab/ The Hey lab is on the Busch Campus of Rutgers University. This is in central New Jersey, just outside of the city of New Brunswick - a small cosmopolitan city within commuting distance (by train) of Manhattan.

Jody Hey Professor, Department of Genetics Rutgers University Nelson Biological Labs (rm B326) 604 Allison Rd. Piscataway, NJ 08854-8082 732-445-5272 fax 732-445-5870 hey@biology.rutgers.edu http://-lifesci.rutgers.edu/˜heylab/ Hey@Biology.Rutgers.Edu

UArizona InsectResistance

POSTDOCTORAL RESEARCH ASSOCIATE Available September 1, 2007

Run large-scale greenhouse experiments and laboratory bioassays to investigate tritrophic interactions and insect resistance to Bacillus thuringiensis (see Gassmann et al. 2006. J. Econ. Entomol. 99: 920). Ability to work independently and publish in refereed journals required. Experience with bioassays and genetics preferred.

Send CV, 2 reprints, and names and contact information for 3 references to Bruce Tabashnik (brucet@ag.arizona.edu) or Aaron Gassmann (gassmann@ag.arizona.edu), Dept. Entomology, U. Arizona, Tucson AZ 85721.

Review of applications will begin immediately and continue until the position is filled.

University of Arizona is an Equal Opportunity Employer. For additional information, contact Aaron Gassmann (gassmann@ag.arizona.edu).

gassmann@Ag.arizona.edu gassmann@Ag.arizona.edu

UArizona PlantEvol

Travis Huxman, Larry Venable and I have postdoc funding for an individual who can work with us on linking ecological and evolutionary processes in a community of Sonoran Desert winter annuals. The goal of the project is to investigate whether the key tradeoff between growth and stress tolerance that structures the community presents a deeper constraint on plant phenotypes that operates within each species. The ideal candidate will have a background in quantitative genetics, community ecology, and plant physiological ecology. We are looking for someone to begin in the fall (start date flexible) and we have funding for three years, should the individual develop a satisfactory program. There will be opportunities to work at the University of Arizona and Colorado State University, where the facilities and communities are first rate. This is a nice opportunity for someone interested in linking subdisciplines in ecology and evolution in an experimental setting.

To apply, please send a brief letter of research interests, CV and the names of three references by email to Amy Angert (angert@email.arizona.edu). For more information, please contact us at Amy Angert (angert@email.arizona.edu), Larry Venable (venable@email.arizona.edu) or Travis Huxman (huxman@email.arizona.edu).

Amy Angert Department of Ecology and Evolution University of Arizona Tucson, AZ 85721

angert@email.arizona.edu angert@email.arizona.edu

UBasel 2 HostParasite

Universitat Basel, Switzerland Zoologisches Institut, Evolutionary Biology

2 Postdoc positions in host-parasite evolution

are available in the division of Evolutionary Biology, Institute of Zoology at Basel University. I am looking for 2 highly motivated post-docs with interest in the evolutionary biology of host-parasite interactions. These positions are funded to work on the evolutionary genetics of Daphnia and its microparasites (bacteria and microsporidians). A good background in evolutionary genetics, including knowledge of molecular methods is essential. For one of the two positions emphasize is in statistical genetics (QTL analysis) and population genetics. For the second position, experience with microorganisms and microbiological techniques is desired. Previous experience with Daphnia is not essential. Excellent written, verbal, and interpersonal skills, a superb work ethic, and the ability to think creatively and critically are desired. Starting dates are flexible, from November 2007 onwards. The positions are initially for 2 years, but may be extended.

The post-docs will be part of Dieter Ebert's group working on the evolution of host-parasite interactions, focusing on the Daphnia system. Details about the group can be found under: http://evolution.unibas.ch/ Please send application by E-mail to Dieter Ebert (dieter.ebert@unibas.ch). Applications (1 pdf file, please) should include a CV, a list of publications and a 1 page description of your research interests and motivation. Please give names and email addresses of two persons who are willing to write a letter of recommendation. Applications received before 30. August 2007 will be given full consideration. Interviews will be held in the second half of September or early October.

Contact information: Prof. Dr. Dieter Ebert, Universitaet Basel, Zoologisches Institut, Vesalgasse 1, 4051 Basel, Switzerland. http://evolution.unibas.ch Email: dieter.ebert@unibas.ch Tel. +41-(0)61-267 03 60 Fax +41-(0)61-267 03 62.

dieter.ebert@unibas.ch dieter.ebert@unibas.ch

UCRiverside PopGen

Postdoctoral position in fungal population genetics, University of California, Riverside

A full-time postdoctoral position is available in the laboratories of Greg W. Douhan and Frank P. Wong in the Department of Plant Pathology and Microbiology at the University of California, Riverside. The focus of the research is to investigate the population biology of Pyricularia grisea, causal agent of gray leaf spot of turf and rice blast. This work is currently in progress, therefore, a qualified candidate would have the opportunity to immediately begin collecting genotypic data using AFLP and/or microsatellite markers from sampled populations. DNA has been extracted from a large collection of isolates and mating type data has already been collected. This could prove to be a fruitful position for an ambitious candidate since there could be many additional research opportunities to work on other projects within the two labs.

Candidates should have a Ph.D. degree in plant pathology, genetics/genomics, bioinformatics/computational biology, or related disciplines. Proven ability to publish is highly desirable. Good analytical skills within population genetics and/or systematics are expected. Interest and/or experience working with fungi is not essential but is desirable.

The start date is flexible but the position can be immediately filled. The position has guaranteed funding for one year with a high likelihood of multi-year extension of funding. Salary is commensurate with experience and qualifications, with a minimum of $32,000/year. Postdoctoral researchers receive full University of California benefits.

Interested individuals should send a curriculum vitae, contact information for three references, electronic copies of at least two publications or manuscripts in progress that demonstrate the candidateâs skills, and a cover letter describing their interest in the position to gdouhan@ucr.edu.

Greg W. Douhan Department of Plant Pathology and Microbiology University of California Riverside, Ca 92521 Office: (951)-827-4130

gdouhan@ucr.edu gdouhan@ucr.edu

UCentralFlorida MatingSystemEvol

6/30/2007

A postdoctoral position examining the evolution of mating systems is available in the laboratory of Dr. Ken Fedorka, Department of Biology, University of Central Florida.

Project title: Sex-specific fitness consequences of the female immune response to insemination in Drosophila melanogaster.

Project summary: In many systems, females exhibit a strong, localized immune response to the male ejaculate that has been noted to kill sperm. Under conditions of sperm competition, males may evolve the capacity to interfere with the female immune response in order to increase sperm viability, and hence fertilization success. To address this possibility, the project will manipulate genes that code for female immune proteins and male ejaculate proteins in order to elucidate their potential effect on mating behavior, sperm viability and sperm competition. For more information regarding the project, my lab or the University of Central Florida, please contact me (fedorka@mail.ucf.edu) or visit

http://biology.ucf.edu/˜fedorka/lab The postdoctoral position can be filled immediately (8/1/2007) and will remain open until a suitable candidate is found. The position will be funded for two years ($36,000 /year), with a possible third year contingent upon financial support and favorable performance. Experience with Drosophila, real-time rt-PCR and RNAi preferred, but not required. Knowledge and/or a strong desire to study evolutionary behavior and ecological immunology would be highly beneficial.

If interested, please send a CV and a brief statement of research interests to:

Ken Fedorka Department of Biology University of Central Florida Orlando, FL 32816 Tel: + 1 407 8236685 fedorka@mail.ucf.edu

UColorado ComputationalBioscience

Colorado Computational Bioscience Program Postdoctoral Fellowship

Please note the very tight target date.

The Computational Bioscience Program at the University of Colorado School of Medicine and Boulder is requesting applications for postdoctoral fellowships funded in part by our new NLM training grant. The research performed may be in any area of computational biology, including molecular evolution and evolutionary genomics, and the intended training period is for two years, with a non-competitive renewal after one year. Interested applicants should submit a two-page research plan to work with one or more of our core faculty (Larry Hunter, David Pollock, David Osguthorpe, Dennis Lezotte, Rob Knight, Katerina Kechris, or Debra Goldberg). A current CV should also be included, along with a list of three references. See www.uchsc.edu/-compbio for more information about the program. We strongly encourage applicants to discuss their research interests with faculty members before applying. Electronic submissions are preferred. Please send to the Acting Director, David.Pollock@uchsc.edu. For this year, only US citizens are eligible for these fellowships. Applications should be submitted by July 15, 2007 to receive full consideration, but applications will be reviewed until the positions are filled.

David Pollock Acting Director, Program in Computational Bioscience Associate Professor, Department of Biochemistry and Molecular Genetics University of Colorado Health Sciences Center 303-724-3234, David.Pollock@uchsc.edu, WWW.EvolutionaryGenomics.com

DavidDPollock@yahoo.com

UDurham DeepSeaFishPopGenet

Population genetics and phylogenetics at the mid-Atlantic Ridge.

A three-year post-doctoral position is available in the Molecular Ecology Group at the University of Durham, Durham, UK. Funding is from NERC and in affiliation with the ECOMAR consortium and MARECO (part of the census of marine life). The project will involve population genetic comparisons for several deep-sea fish species across possible boundaries to gene flow at the ridge and sub-polar front, and phylogenetic investigations of invertebrate species (Holothuroidea and

Galatheidae) at the ridge. The work is facilitated by a full-time technician. The proposed start date is 1 October, 2007. The successful applicant will have a PhD and extensive experience with population genetic and phylogenetic lab and computer analyses. Initial applications should be sent to a.r.hoelzel@dur.ac.uk and include a copy of your c.v., contact details for three referees, and a cover letter. Applications will be reviewed until the position is filled. Further details will be requested of a subset of the initial applicants.

a.r.hoelzel@durham.ac.uk

UEastAnglia GeneticConflicts

SCHOOL OF BIOLOGICAL SCIENCES - UEA NORWICH UK

POST-DOCTORAL RESEARCH ASSOCIATE Genetic conflicts and the development of cancer (Ref: RA406)

£26,666 to £31,840 per annum £27,466 to £32,796 per annum (wef 01/08/2007)

A full time postdoctoral position, funded by the BigC Local Cancer Care (http://www.thebigcappeal.co.uk/-), is available for 12 months in the laboratory of Dr Tracey Chapman and Professor Dylan Edwards (see http://www1.uea.ac.uk/cm/home/schools/-sci/bio/people/Faculty) in the School of Biological Sciences and Biomedical Research Centre at UEA. An immediate start date is available and the position must be filled as soon as possible.

Recent insights from evolutionary biology into the study of cancer reveal much about genes that increase cancer risk. For example, evolutionary biology can explain why cancer is so prevalent and why endogenous and clinical anti-cancer mechanisms are often inefficient. Many genes that increase cancer risk are positively selected and there is evidence that much of this rapid evolution is fuelled by genetic conflicts of interest. Such conflicts arise when interacting parties have different interests and they can be potent drivers of evolutionary change. In this research project we will test for significant associations between cancer-predisposing genes, positive selection and genetic conflicts. The project will use surveys of published data, bioinformatic and meta-analyses, and will extend into the powerful, experimental domain by using gene expression microarray experiments in Drosophila fruitflies. Informal enquiries are welcomed, to Tracey Chapman, e-mail: tracey.chapman@uea.ac.uk

Closing date: 26 July 2007. Interview date: 8 and 9 August 2007

APPLICATION FORM and Further Particulars for the post:

http://www.uea.ac.uk/hr/jobs/ra/ra406.htm or by email from hr@uea.ac.uk

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

UGeorgia ApicomplexaEvol

POSTDOCTORAL POSITIONS AVAILABLE

Genome Evolution, Innovation and Adaptation in the Apicomplexa. NIH-funded postdoctoral associate positions are available in the Kissinger Research Group to study the evolution of the apicomplexan genome. The Apicomplexa are a phylum of unicellular eukaryotic parasitic organisms that are responsible for some of the world's worst diseases, like malaria. >15 genome sequences are available and more are in progress. Evolution of these genomes is dominated by differential gene loss and also gene acquisition via intracellular and lateral gene transfer. Research experience in molecular evolution, genomics, or bioinformatics is required. An ability to work in some flavor of UNIX and program in PERL or JAVA is preferred but not required. Experience with protists is a plus, but not required. Our group offers an interactive environment for research training. We are a highly interdisciplinary research group with interests ranging from wet lab studies of gene expression and non-coding RNAs to the development of tools for the efficient integration of diverse genomic and functional genomic data types. The University of Georgia has an Institute of Bioinformatics and a centralized Research Computing Center with several powerful computer clusters. For more information about our research group, please visit: http://mango.ctegd.uga.edu/jkissingLab/ Interested applicants should send a curriculum vitae and three letters of reference to: Dr. Jessica Kissinger, Dept. of Genetics & CTEGD, Coverdell Center, University of Georgia, Athens, GA 30602 or email to jkissing@uga.edu The positions are available immediately.

Selected Publications Mullapudi, N., Lancto, C., Abrahamsen, M., Kissinger, J.C. (2007) Identification of putative cis-regulatory elements in Cryptosporidium parvum by de novo pattern finding. BMC Genomics 2007, 8:13

Aurrecoechea, C., Heiges, M., Wang, H., Wang, Z., Fischer, S., Rhodes, P., Miller, J., Kraemer E., Stoeckert, C.J., Roos, D.S. and Kissinger, J.C. (2007) ApiDB: Integrated Resources for the Apicomplexan Bioinformatics Resource Center. Nucleic Acids Research 35:D427-430

Wang, H., Su, Y., Mackey, A., Kraemer, E., and Kissinger, J.C. (2006) SynView: A GBrowse-compatible Approach to Visualizing Comparative Genome Data.

Huang, J., N. Mullapudi, C.A. Lancto, M. Scott, M.S. Abrahamsen and Kissinger J.C. (2004) Cryptosporidium parvum: Phylogenomic evidence for organelle loss, intracellular and horizontal gene transfer. Genome Biology 5(11):R88

Striepen,B., A.J.P. Pruijssers, J. Huang, C. Li, M.J. Gubbels, N.N. Umejiego, L. Hedstrom and J.C. Kissinger. (2004) Multiple gene transfers in the evolution of parasite nucleotide biosynthesis. Proc. Natl. Acad. Sci., USA 101(9):3154-3159.

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Jessica Kissinger University of Georgia Center for Tropical & Emerging Global Diseases & Department of Genetics Paul D. Coverdell Center, Rm 335 500 D. W. Brooks Drive Athens, GA 30602-7394

TEL: +1 (706) 542-6562/6632 FAX: +1 (706) 542-3582 e-mail jkissing@uga.edu http://mango.ctegd.uga.edu/-jkissingLab/ http://www.ctegd.uga.edu/ PGP-Key: http://www.arches.uga.edu/ ˜ jkissing/public_key.html

Jessica Kissinger <jkissing@uga.edu>

UGeorgia Speciation

To Whom It May Concern:

Please post on EvolDir for postdoc position:

A postdoc position is available in the group of John Gittleman to work on macro-ecological and -evolutionary questions related to speciation, extinction and conservation, and in particular how spatial patterns of phylogenetic diversity relate to the effectiveness of global conservation strategies.

Preference will be given to individuals with a broad background in ecology and evolution. Applicants should have excellent analytical skills and a strong interest in the construction and analysis of large databases. Salary is in the range of $40,000 (plus benefits) per year. The new Odum School of Ecology will be growing with additional student, postdoc and faculty positions; this position will work for the Dean in assisting in the lab and expanding the computer informatics among faculty in the School.

The position is available immediately. Interested applicants should send a cover letter detailing their background and an updated CV, along with names of references and contact information of 3 references to:

Dr. John L. Gittleman, Dean Odum School of Ecology University of Georgia Athens, GA 30602 USA

e-mail: jlg@uga.edu phone: (706) 583-5537 fax: (706) 542-4819 web: http://blackbear.ecology.uga.edu/-gittleman/index.html – Dr. John L. Gittleman, Dean Odum School of Ecology University of Georgia Athens, GA 30602 USA Phone: 706-542-2968 Fax: 706-542-4819

John Gittleman <jlg@uga.edu>

UKonstanz MolEvol

A postdoc position in molecular evolutionary biology is available in the lab of Axel Meyer in the Department of Biology at the University of Konstanz in Germany. The evolutionary biology group is an international group of students and postdocs that also includes the labs of Gerrit Begemann on zebrafish developmental genetics and Shigehiro Kuraku on evolutionary developmental biology. The main language spoken in the lab is English.

We are looking for an energetic postdoc who is interested in speciation, molecular evolution, bioinformatics/genomics, or evolutionary developmental biology. The specific research projects we are recruiting for involve (1) research on phylogenetics and population genetics of cichlid fishes (2) as well as the discovery and functional characterization of (e.g. coloration) genes underlying the diversification of cichlid fish in Africa and in Nicaragua.

The great lakes in East Africa house some of the world's most diverse freshwater ecosystems. Lakes Victoria, Malawi and Tanganyika are particularly well-known for their adaptive radiations of hundreds of endemic species of cichlid fishes. We are interested in understanding speciation, phylogeography, molecular evolution and molecular phylogenetics of these cichlid fish assemblages. Also, we wish to identify and characterize the function of genes that are involved in the phenotypic diversification and presumably speciation of cichlid fishes. Several molecular biological, "devo-evo" and genomic approaches, including candidate gene approaches, DNA-chip technology, characterization of ESTs, in situ hybridization in cichlids and transgenics in zebrafish are used to address these questions. We are also interested in evolutionary genomic questions and the evolution of novel gene functions after gene and genome duplications.

Some recent publications of the lab include: Verheyen et al. (2003). The origin of the superflock of cichlid fishes from Lake Victoria, East Africa. Science 300: 325-329. Salzburger et al. (2005). Out of Tanganyika: Genesis, explosive speciation, key-innovations and phylogeography of the haplochromine cichlid fishes. BMC Evolutionary Biology 5: 17. Barluenga et al. (2006). Sympatric speciation in Nicaraguan crater lake cichlid fish. Nature 439: 719-23 Braasch et al. (2006). Asymmetric evolution in two fish-specifically duplicated receptor tyrosine kinase paralogons involved in teleost coloration. Molecular Biology and Evolution 23:1192-1202.

Postdoc salaries are approximately 45-50,000 Euros annually, (depending on marital status, age, etc.) before deductions for taxes, health insurance and retirement contributions.

The position is open immediately. The review of applicants will begin immediately until the position is filled. To apply, please email a curriculum vitae, including a list of publications, a statement of research interests, and the names and email addresses of two references to axel.meyer@uni-konstanz.de.

Prof. Axel Meyer, Ph.D. Department of Biology Konstanz University 78457 Konstanz, Germany Email: axel.meyer@uni-konstanz.de

For more information visit http://-www.evolutionsbiologie.uni-konstanz.de/-index.php?section=3D10

– Prof. Axel Meyer, Ph.D. Lehrstuhl für Zoologie und Evolutionsbiologie Department of Biology Building M, Room M806 University of Konstanz 78457 Konstanz Germany

fon + 49 7531 88 4163 fax + 49 7531 88 3018

secretary: Ingrid.Bader@uni-konstanz.de tel. + 49 7531 88 3069

www.evolutionsbiologie.uni-konstanz.de
axel.meyer@uni-konstanz.de axel.meyer@uni-konstanz.de

ULausanne DrosophilaAdaptation

Postdoc position, University of Lausanne, Switzerland Evolutionary genetics of learning and other adaptive traits in Drosophila

(I apologize for cross-posting) A postdoc position is available in Tad Kawecki's research group at the Department of Ecology and Evolution, University of Lausanne (we are moving there this summer). Most of the work in our lab concentrates on the evolutionary genetics of learning and memory, and their relationships with aging, stress resistance and immunity. We use Drosophila as the study system (for more information see http://www.unifr.ch/biol/ecology/kawecki). We are looking for a highly motivated and independent researcher who would develop his/her own project within this broad framework.

With over 20 research groups working in diverse areas of evolution and ecology, the Department of Ecology and Evolution at the University of Lausanne is a highly interactive, international research and study environment (see at www.unil.ch/dee). The daily language of the research group and the department is English and no preexisting knowledge of French is required; however, learning some French would make living in Lausanne more pleasurable. Located on the shore of Lake Geneva, Lausanne is an attractive city with a diverse cultural offer, while the proximity of the Alps and Jura mountains opens countless opportunities for outdoor activities. The position is initially offered until July 2009, extension is foreseen pending funding approval. The salary is about CHF 65,000-80,000 per year depending on experience. The starting date is negotiable.

To apply, send a CV, a short description of research experience and interest, and names and email addresses of two referees AS A SINGLE PDF FILE to tadeusz.kawecki@unil.ch, with "Learning postdoc" on the subject line. We will begin to screen the application on September 3, 2007.

Tadeusz Kawecki Department of Biology University of Fribourg Chemin du Musee 10, CH-1700 Fribourg, Switzerland www.unifr.ch/biol/ecology/kawecki phone

+41 26 300 88 71 fax +41 26 300 96 98 e-mail tadeusz.kawecki@unifr.ch New address from August 1, 2007 Department of Ecology and Evolution University of Lausanne Biophore CH 1015 Lausanne Switzerland email tadeusz.kawecki@unil.ch

tadeusz.kawecki@unifr.ch tadeusz.kawecki@unifr.ch

ULausanne FuncEvolGenomics

POSTDOCTORAL POSITION IN FUNCTIONAL EVOLUTIONARY GENOMICS

Center for Integrative Genomics (CIG), University of Lausanne, Switzerland

A research associate/postdoctoral position (2 years with possible extensions up to 5 years) is available in the evolutionary genomics group of Henrik Kaessmann. The starting date of the position is flexible (the position is available immediately but will remain open until suitable candidates have been identified).

We are seeking highly qualified and motivated applicants - preferably with a background in molecular evolution - who have strong skills in computational biology (bioinformatics, preferably with experience in data mining and comparative genome analysis). Statisticians and/or population geneticists with strong programming skills and an interest in evolutionary genomics are also encouraged to apply.

Available projects include the analysis of the functional evolution of new genes that emerged in primates and other mammalian lineages. However, other projects are possible, depending on the skills and interest of the applicant. Data available from genomic databases may be complemented with experimental data (large- and small-scale) in collaboration with the wet lab unit of the group.

The salary is in the order of 45,000 Euros per year.

For more information on the group and our institute more generally, see the website: http://www.unil.ch/-cig/page7858_en.html

The language of the institute is English, and its members form an international group that is rapidly expanding. The institute is in Lausanne, a beautiful city at Lake Geneva amidst an impressive alpine scenery.

Informal inquiries may be addressed to: Henrik.Kaessmann@unil.ch

Please submit a CV, statement of research interest, and two letters of recommendation (and/or names of referees) to:

Henrik Kaessmann, Ph.D. Associate Professor Center for Integrative Genomics Genopode University of Lausanne CH-1015 Lausanne Switzerland E-mail: Henrik.Kaessmann@unil.ch Phone: +41-(0)21-692-3907 (administrative assistant, Annick Crevoisier: -3960) Fax: +41-(0)21-692-3965 http://www.unil.ch/-cig/page7858_en.html

Some recent publications from the lab:

Vinckenbosch, N., Dupanloup, I. & Kaessmann, H. (2006) Evolutionary fate of retroposed gene copies in the human genome. Proc. Natl. Acad. Sci. USA 103, 3220-3225.

Marques, A., Dupanloup, I., Vinckenbosch, N., Reymond, A. & Kaessmann, H. (2005) Emergence of young human genes after a burst of retroposition in primates. PLoS Biol. 3:e357.

Burki, F. & Kaessmann, H. (2004) Birth and adaptive evolution of a hominoid gene supporting high neurotransmitter flux. Nature Genet. 10, 1061-1063.

Emerson, J. J., Kaessmann, H., Betrán, E. & Long, M. (2004) Extensive gene traffic on the mammalian X chromosome. Science 303, 537-540

Henrik.Kaessmann@unil.ch Henrik.Kaessmann@unil.ch

ULiverpool MicrobeSocialEvol

Postdoctoral position on the ecology of social evolution in microbes

School of Biological Sciences, University of Liverpool Fixed-term contract for up to 3 years Salary: £28645pa

A postdoctoral research assistant is sought for a 3-year Leverhulme Trust funded post that seeks to understand the interaction between ecology and social evolution using an experimental evolution approach. Explaining the widespread existence of social traits in microbes remains a challenge for evolutionary biology, yet the role of ecology has traditionally been overlooked. Recent work by our lab suggests that ecology is likely to play a crucial role by mediating both relatedness and the costs / benefits of cooperation (see Brockhurst, Buckling & Gardner 2007 Current Biology 17: 761-765). The successful candidate will design and carry out bacterial experimental evolution studies to test the role of ecology in social evolution; carry out statistical analyses; prepare manuscripts and help with the supervision of undergraduate students and laboratory management.

The appointed individual will hold a PhD in a relevant biological discipline. A background in evolutionary ecology and experience of experimental design and statistical analysis is required. Experience in experimental evolution, microbiological techniques and mathematical modelling would be advantageous. The postholder will be based in the School of Biological Sciences, University of Liverpool with Dr. M. A. Brockhurst as part of the Population & Evolutionary Biology Research Division.

The post is available for 3 years from the 1st of October 2007. Informal enquiries should be made to Dr. Michael Brockhurst (michael.brockhurst@liv.ac.uk; 0151 795 4557).

Closing date: 24th August 2007

For full details, or to request an application pack, visit: www.liv.ac.uk/working/job_vacancies/ or e-mail jobs@liv.ac.uk Tel 0151 794 2210 (24 hr answerphone)

Mike Brockhurst <michael.brockhurst@liverpool.ac.uk>

UOttawa SexualSelection

Postdoctoral Fellowship is available in the laboratory of Howard Rundle, University of Ottawa, Canada.

Funding is available for a 2 year postdoctoral fellowship investigating sexual selection and mate choice in Drosophila serrata. Our laboratory (http://www.science.uottawa.ca/~hrund050) uses experimental evolution and quantitative genetics to investigate the evolution of mate preferences within populations and their divergence among populations during the process of speciation. The postdoctoral fellow will take the lead role in the development of a large panel of inbred lines in D. serrata, and then use these lines to investigate questions surrounding individual variation in mate preferences, interlocus sexual conflict, good-genes, and other aspects of sexual selection.

Fellowships are open to Canadian and international candidates. The position is for two years and commences as soon as possible. The salary is CDN $40,000 per annum.

Applications should include a cover letter, a curriculum vitae, a short (1 page) description of proposed research, and the names and contact information (including e-mail) of three referees. All application materials should be submitted via email (preferably in pdf format) to Howard Rundle (hrundle@uottawa.ca), to whom queries may also be addressed. Evaluation of applications will begin immediately and continue until the position is filled.

Located at the confluence of English and French Canada, Ottawa is a rich and vibrant national capital of approximately 1 million inhabitants (http://www.ottawatourism.ca). The city offers a wide range of cultural activities in the visual and performing arts, as well as easy access to green spaces and wilderness. The University of Ottawa is located next to the historic Rideau Canal, steps from Parliament and within easy access to a wide range of research facilities of interest to evolutionary biologists including the Canadian Museum of Nature, the National Wildlife Research Center, Health Canada, and Environment Canada.

Note: this position is separate from the recently advertised Vision 2010 postdoctoral fellowship in Evolution Biology at uOttawa.

Howard D. Rundle Assistant Professor - Professeur adjoint Canada Research Chair - Chaire de recherche du Canada Department of Biology - Département de biologie University of Ottawa - Université d'Ottawa 30 Marie-Curie (277 Gendron) Ottawa, Ontario, K1N 6N5, CANADA

Office: +1 613-562-5800 x2835; Fax: +1 613-562-5486; Lab: +1 613-562-5800 ×6837 Email: hrundle@uottawa.ca; Skype: howarddrundle http://www.science.uottawa.ca/ ~ hrund050/ hrundle@uottawa.ca hrundle@uottawa.ca

UOxford GenomePedigrees

University of Oxford Mathematics, Physical and Life Sciences Division

DEPARTMENT OF STATISTICS

Postdoctoral Research Assistant Fixed term appointment of: 2 years Academic-related Research Staff Grade 7: Salary £26,666 to £32,796 (bar) per annum (as at 1 August 2007) The Research Project: From Population Genomes to Global Pedigrees.

The Appointment

Applications for the fixed term 2 years[1] duration post of Postdoctoral Research Assistant funded by EPSRC are invited from researchers interested in working on this high-impact project the inference of global pedigrees from genomes. Candidates should have relevant background and research experience in computer science and statistical modelling and mathematics.

Genomics and Bioinformatics are currently a particularly exciting area of modern science. There is an acute shortage of researchers trained on the analytical side of the subject, so that future job prospects for those moving into the field are very good, in both the academic and the private sectors.

The post thus offers the opportunity of a substantial impact on one of the major international projects in human genetics, within the context of very strong academic groups. The project involves a collaboration between Prof. Mike Steel (Christchurch, New Zealand) and Prof. Jotun Hein (Oxford, UK). The applicant will spent most time in Oxford, but will have 2 longer stays in New Zealand. The key goal of this project is: To investigate the possibility of pedigree inference from genomes under idealized models

To investigate combinatorial properties of pedigrees.

Selection Criteria

Knowledge of broad range of topics which come under the heading of computational biology and bioinformatics. High quality research skills in the field of mathematics, computer science or statistics. Strong background in computational biology, computer science, mathematics or statistics, preferably in more than one of these areas

A PhD, or equivalent research experience, will be required.

Further Information Informal enquiries should be directed to hein@stats.ox.ac.uk <mailto:hein@stats.ox.ac.uk> . A more detailed description of the project is available at http://mathgen.stats.ox.ac.uk/bioinformatics/grants/ where the funded grant proposal can be downloaded. The Department of Statistics in Oxford is one of the strongest in the UK. More general information about the research and teaching in the department is available from www.stats.ox.ac.uk <http://www.stats.ox.ac.uk/> . Terms and Conditions of Employment[RB1] <#_msocom_1> General conditions The current salary scale for the post is given above. The age of retirement for university appointments is 65. Staff are eligible to join the Universities Superannuation Scheme, a contributory scheme to which members pay 6.35 per cent of annual salary. Subject to the Statement of Pensions Policy which will be issued to the successful candidate, the appointee will be deemed to be in membership of the above pension scheme until such time as he or she gives notice in writing to exercise the right not to be a member of the scheme. The appointee will be entitled to 38 days of annual leave (this figure includes 8 public holidays and departmental closures over Christmas and Easter). The actual distribution of annual holidays, excluding the public holidays, is subject to the agreement of the Department. The University has a generous maternity leave scheme, which goes well beyond the statutory provisions; and operates two childcare nurseries and a holiday programme for school age children. Holders of research assistant positions are required to help with support teaching, for an average of three hours per week over the three 8 week academic terms, for which no additional remuneration is provided. This teaching would typically take the form of supervising or running practical or exercise classes, or occasional lecturing, and every attempt is made to match the teaching to the postholder's interests. This fixed term appointment will be subject to (i) the return of a completed medical questionnaire which is acceptable to the University, (ii) the provision of original documentation which indicates your right to work in the UK, and (iii) the completion of an initial probationary period of six month Application Procedure Applications should comprise a curriculum vitae and a list of publications together with the names, addresses, telephone, fax and e-mail details of three referees.

Applications (7 copies, one copy for candidates outside the UK) should be submitted to Personnel Administration, Department of Statistics, 1 South Parks Road, Oxford, OX1 3TG. Applications faxed to +44 1865 272595 or e-mailed to jobs@stats.ox.ac.uk are acceptable as long as they are followed by hard copy.

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UOxford HumanMalariaCoevol

UNIVERSITY OF OXFORD

DEPARTMENT OF STATISTICS

POSTDOCTORAL RESEARCH ASSISTANT

Fixed term appointment of 18 months - 2 years' duration Academic-related Research Staff Grade 7: Salary £26,666 to £32,796 (bar) per annum (as at 1 August 2007)

Detecting human-malaria co-evolution from genetic variation data

A fixed-term research position of 18 months to 2 years, funded by the Human Frontier Research Program (HFSP), is available to work with the research group of Professor Gil McVean on statistical issues concerning the joint analysis of genetic variation from humans and malarial (or other) pathogens. The start date for the post is negotiable but would ideally be as soon as possible. Well-qualified successful applicants are likely to be appointed at or near the top of the salary scale given above.

The post relates to the development, study, and application of novel statistical methods for analysing large-scale data sets on both host and pathogen variation. Specifically, the aim is to identify loci involved in co-evolutionary processes through collection and analysis of multi-population data. The research is part of a larger project involving the collaboration of the groups of Sarah Tishkoff (Maryland), Philip Awadalla (NC State) and Anna Tramontano (Rome).

Candidates should have a strong background in population genetics. Knowledge of modern statistics and its application in genetics would be an advantage, but candidates wishing to move into the genetics field are also welcome to apply. Good computational skills are essential and candidates should be able to program in a low level language such as C or C++. Candidates should have, or expect soon to have, a doctorate. The Department of Statistics in Oxford is one of the largest and strongest in the UK and a world leader in statistical genetics.

Informal enquiries should be directed to mcvean@stats.ox.ac.uk. Further particulars are available from http://www.stats.ox.ac.uk, or the address below.

Applications should comprise a curriculum vitae and a list of publications together with the names, addresses, telephone, fax and e-mail details of three referees and should be submitted (single hard copy) to Personnel Administration, Department of Statistics, 1 South Parks Road, Oxford, OX1 3TG. Applications faxed to +44 1865 272595 or e-mailed to jobs@stats.ox.ac.uk are acceptable as long as they are followed by hard copy.

Please always quote reference number: AM-07-006.

The closing date for applications is Friday, 31 August 2007.

Gilean McVean Professor of Statistical Genetics Department of Statistics 1 South Parks Road Oxford OX1 3TG UK

Tel: +44 1865 281881 Fax: +44 1865 281333 web: http://www.stats.ox.ac.uk/ ˜ mcvean mcvean@stats.ox.ac.uk mcvean@stats.ox.ac.uk

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UOxford PlantPopGenet

A postdoctoral position will be available to work on a project in plant population genetics/molecular evolution at the University of Oxford Plant Sciences department (UK). The direction of the project is flexible and the details will be discussed individually with the candidates.

The position is for eight months in the first instance. The candidate will be strongly encouraged to apply for EU FP7 Marie Curie (MC) fellowship for further funding of up to 24 months. Thus, we seek a highly motivated person with strong interest and track record of research in plant population genetics/molecular evolution, who will have a high enough chance to be successful with the application for the MC fellowship. Further information can be obtained from Dmitry Filatov: d.filatov@bham.ac.uk

Dmitry Filatov <d.filatov@bham.ac.uk>

UParisSud TreeEvol

Modelling the evolution of genetic diversity for complex traits in scenarios of environmental changes in tree species

We propose a one-year postdoctoral position on the modelling of the evolution of genetic diversity for complex traits and the genes underlying these traits in scenarios of environmental changes. This position is funded through the European Network of Excellence EVOLTREE (http://www.evoltree.org/). This postdoctoral position is opened for one year. It should start around October 1st. It is part of a joint collaboration between the following people:

- Frédéric Austerlitz, Laboratoire Ecologie, Systématique et Evolution, U.M.R. C.N.R.S./U.P.S./E.N.G.R.E.F. 8079, Université Paris-Sud, Bâtiment 360, F-91405 Orsay cedex, email: frederic.austerlitz@u-psud.fr webpage: http://www.ese.u-psud.fr/bases/upresa/pages/austerlitz/index_eng.html - Pauline Garnier-Géré, Frédéric Raspail, Antoine Kremer, UMR BIOGECO 1202, INRA-Bordeaux, Forest Genetics Group, 69 route d'Arcachon, 33612 CESTAS Cédex, FRANCE

- Sylvie Oddou-Muratorio, Christian Pichot, Unite de Recherches Forestieres Mediterraneennes, Domaine Saint Paul, Site Agroparc, 84914 Avignon Cedex 9

The postdoctoral fellow will be mainly located in the first laboratory (in Orsay, near Paris), but will be in strong interaction with the people from the two other laboratories in Avignon and Bordeaux. The position requires solid experience in computer science (in particular C programming), as well as in population and quantitative genetics. All candidates should then a motivation letter, a CV and the name and email of three references by email to Frederic Austerlitz before August 15th. Do not hesitate also to contact him in case more details are needed.

The aim of the postdoctoral work would be to develop models that account for changes in environmental conditions through time. To this extent, populations or metapopulations of individuals will be simulated. The individuals will be characterized by their phenotype for several adaptive traits, these traits being coded by several loci. The model will consider different possibilities for the relation between genotypes and phenotypes, including the possibility of pleitropy (involvement of a given gene in several traits). Different scenarios of climatic changes will be considered by allowing different model parameters to vary for one or several of the adaptive traits (e.g. variation of the optimal phenotype across time, for different intensities and time steps) or the quality of the environment. The impact of the different scenarios of climatic changes retained will be assessed on both phenotypic and genetic responses of populations.

The study will focus both on a local scale using the spatially-explicit individual-based software CAPSIS (Dreyfus et al., 2005) and a larger scale using the software METAPOP (Le Corre et al., 1997 ; Le Corre et Kremer, 2003) that considers panmictic populations connected by gene flow. Regarding the global scale, while the basic simulation framework is already implemented in METAPOP, the postdoctoral fellow will have to modify the source code in order to deal specifically with the questions addressed here, namely the implementation of scenarios of changes across time and the possibility to model several traits simultaneously. He/she will then be able to compare the results of METAPOP with the results of simulations performed at the local scale with CAPSIS, in which the expression of a phenotypic trait, and thus the relation between phenotype and fitness depends explicitly on spatial position of individuals through a demographic model. This demographic model describes explicitly how an individual with a given genotype in a given environment will survive, reproduce or disperse. The postdoctoral fellow will not be directly involved in the modification of the source code of CAPSIS but he/she will participate in the methodological choices of how introducing directional variation of the environment quality, and in the analyses of the simulations performed with this software.

The parameters of the simulations (e.g. seed and pollen dispersal curves, number of loci involved in the traits, quality of the environment) will be calibrated with data from the intensive study sites (ISS) of EVOLTREE and from the literature.

References

Dreyfus P., Pichot C., de Coligny F., Gourlet-Fleury S., Cornu G. et al. (2005) Couplage de modèles de flux de gènes et de modèles de dynamique forestière. Les Actes du BRG 5: 231-250. Le Corre V. et Kremer A. (2003) Comparative dynamics of genetic variability of an adaptive trait and its underlying genes in a subdivided population. Genetics 164: 12051219. Le Corre V., Machon N., Petit R. J. et Kremer A. (1997) Colonization

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UPittsburgh PhenotypicPlasticity

POSTDOCTORAL POSITION

PHENOTYPIC PLASTICITY IN AMPHIBIANS: A PHYLOGENETIC APPROACH

Applications are invited for a post-doctoral researcher to study the phenotypic plasticity of 50 species of amphibians from across the United States. Pending final approval of funds by NSF, this is a 3- year project that will examine predator-induced plasticity of amphibian embryos as well as predator- and competitor-induced plasticity of tadpoles.

This study is led by Dr. Rick Relyea (Univ. of Pittsburgh) in collaboration with Drs. Andy Blaustein (Oregon State Univ.), Jim Collins (Arizona State Univ.), John Fauth (Univ. of Central Florida), Whit Gibbons (Univ. of Georgia), Ray Semlitsch (Univ. of Missouri), Andy Sih (UC-Davis), and Patrick Stephens (NCEAS).

The postdoctoral researcher will be responsible for organizing the collaborating laboratories, supervising and executing a large number of experiments, analyzing the considerable amount of data that will be produced, coauthoring manuscripts, and participating in associated outreach activities. Applicants should have a strong experimental and analytical background, superb organizational skills, and interest in both ecological and evolutionary questions.

The postdoc will be based at the University of Pittsburgh. The starting salary is $33,000 plus benefits. The start date is flexible but applicants should be able to start by Fall 2007. Applicants should send a cover letter, cv, a brief statement of research interests (2 pages), and a list of references (all in pdf form) to Dr. Rick Relyea (relyea@pitt.edu) by 15 August 2007. Dr. Relyea will be attending the ESA Annual Meeting in San Jose, CA from 6 to 9 August and would be happy to meet with interested applicants.

Rick Relyea <relyea@pitt.edu>

UTennessee EvolutionaryTheory

Postdoc in Evolutionary Theory University of Tennessee, Knoxville

I am looking for a postdoctoral researcher interested in using mathematical models for studying one or more of the following topics: speciation, adaptive radiation, emergence in biological and social systems, biological networks, social, and cultural evolution. An ideal candidate will be using a combination of simple analytical models and intensive numerical simulations and will be motivated by biological questions and data. The position is for one year with a possibility of extension. More information about the ongoing work in the lab and the department is available from http://-www.tiem.utk.edu/˜gavrila . To apply email a curriculum vitae, a description of research interests and experience, relevant reprints, and the names, addresses, phone numbers, and e-mail of three references.

Sergey Gavrilets Department of Ecology and Evolutionary Biology Department of Mathematics University of Tennessee, Knoxville TN 37996 phone: (865) 974-3065 e-mail: gavrila@tiem.utk.edu web: www.tiem.utk.edu/ ˜ gavrila Sergey Gavrilets <gavrila@tiem.utk.edu>

UWyoming ExtinctElephantGenomes

Postdoctoral Researcher on Computational Analysis of Extinct Elephantid Genomes

Well preserved samples from several mammoths and mastodons have made possible not only the whole genome sequencing of these extinct organisms, but also addressing questions in elephantid comparative genomics and even mammoth population genetics. With multiple samples available from different geographic locations over a range of time points, innovative approaches to analyzing drift and selection from a comparative perspective can be developed. A position is currently available for a postdoctoral researcher in bioinformatics/genome annotation/applied molecular evolution/computational comparative genomics on this joint project between the Poinar (McMaster University), Webb (Penn State University), and Liberles (University of Wyoming) Research Groups. The position will be split between Laramie, WY (8-9 months per year) and Hamilton, ON, Canada (3-4 months per year). Applicants should have a Ph.D., good programming skills and familiarity with linux, be familiar with statistics, and have an interest in molecular evolution and/or population genetics. To apply, please send a CV, contact information for three references, and 2 .pdf copies of your favorite (significant) papers you have published together with a cover letter to liberles@uwyo.edu.

David Liberles <liberles@uwyo.edu>

Yunnan Bioinformatics

Inviting applications for a bioinformatics postdoc position

The Ecological Evolution Lab at Xishuangbanna Tropical Botanic Garden is inviting applications for a bioinformatics postdoc position. The responsibilities of the position will be data-mining genomic databases, assisting in the analysis of DNA sequence data generated from next-gen platforms and the development of a novel genomic signature technology (http://nar.oxfordjournals.org/cgi/content/abstract/gkl478v1). Currently, we are sequencing several species of tropical rainforest tree using the Solexa system and will be also exploring the use of 454 sequencing of chloroplast genomes. Applicants should have a PhD degree, with a focus on bioinformatics and strong cross-platform skills, including data management and analytical programming. Good command of English is necessary and publication in leading International journals expected.

Xishuangbanna Tropical Botanical Garden (XTBG), Yunnan, Chinese Academy of Sciences, is a comprehensive research institution focused on biodiversity conservation and sustainable uses of plant resources, with emphases on forest ecosystem ecology, conservation biology and resource plant development. The Ecological Evolution lab at XTBG is newly established at XTBG and is assembling an international team of researchers at various levels. This position will be based at either the Kunming branch or in the gardens, depending on the best working conditions.

Interested individuals should submit (1) a letter of application, (2) curriculum vitae including list of publications, electronically as PDF files to kuacs@xtbg.ac.cn, cc to chuck@xtbg.ac.cn

chuck@xtbg.ac.cn

WorkshopsCourses

Kunming BotanicalNomenclature Aug10-15

A Botanical Nomenclature Workshop, co-supported by Missouri Botanical Garden, Kunming Institute of Botany, Flora of China project, and Dr. Dan Nicolson, will be held at Kunming Institute of Botany, Chinese Academy of Sciences, Heilongtan, Yunnan 650204, China from August 10 to 15, 2007. Speakers will include four senior editors of the International Code of Botanical Nomenclature (Vienna Code): Fred Barrie, John McNeill, Dan Nicolson, and Nick Turland and the Chinese translator of the Vienna Code, Li-Bing Zhang. The lectures will be given in English with Chinese translation.

Primary Contact (Organizer): Professor Hua Peng: hpeng@mail.kib.ac.cn *Secondary Contact*: Mr. Nick Turland: nicholas.turland@mobot.org ** *Main workshop program:*

Friday, August 10, 2007 2:00 - 5:00 pm* Registration* 7:00 pm* Social Mixer at Kunming Botanical Garden* * *

Saturday, August 11, 2007 8:30 am *Welcome remarks by Director, Prof. Li De-Zhu* 8:45 am *Remarks by the organizer, Prof. Peng Hua* 9:00 am *Introduction and a brief history of the Code - John McNeill* 11:00 am Discussions 12:00 noon Break 2:00 pm *Terminology in botanical nomenclature** - Nick Turland* 4:00 pm Discussions

Sunday, August 12, 2007 8:00 am *S**tandard reference works and online resources in botanical nomenclature** - Dan Nicolson* 9:30 am Discussions 10:00 am *Publication of botanical names - John McNeill* 11:30 am Discussions 12:00 noon Break 2:00 pm *Typification - Fred Barrie* 4:00 pm Discussions

Monday, August 13, 2007 8:00 am S*tatus and priority of names and citation of authors - Fred Barrie*** 10:00 am Discussions 11:00 am Break 2:00 pm *Names of taxa above the rank of species - Nick Turland* 4:00 pm Discussions

Tuesday, August 14, 2007 8:00 am *Names of species and infraspecific taxa - Fred Barrie* 10:00 am Discussions 10:30 am *Names of fungi, fossils, hybrids, and cultivated plants - Nick Turland* 11:30 am Discussions 12:00 noon Break 2:00 pm *Orthography and gender of names - Nick Turland* 4:00 pm Discussions

*Wednesday, **August **15, 2007* 8:00 am *Rejection and conservation of names - Dan Nicolson* 10:00 am Discussions 10:30 am *Governance and future of the Code - John McNeill* 11:30 am Discussions 12:00 noon Break 2:00 pm *Main c**hanges in the Vienna Code - Li-Bing Zhang* 3:30 pm Discussions

Presenters:

Fred Barrie [fbarrie@fieldmuseum.org] Member, Editorial Committee, ICBN John G. Searle Herbarium Field Museum of Natural History Roosevelt Road at Lake Shore Drive Chicago, IL 60605-2496 U.S.A.

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Best wishes,

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LausanneU Phylogeny Sept3-7

Course of Phylogeny and Evolution using Bioinformatics

http://www.ch.embnet.org/CoursEMBnet/PagesPHYL07/Introduction.html September 03 - 07, 2007, Lausanne, Switzerland

This course is organized for PhD students from Switzerland and abroad.

The goal of this course is to learn to build and interpret phylogenetic trees from sequence data, whether to study species evolution or to study gene and genome evolution. This includes proper use of the main software, reading trees to infer relevant conclusions, and downstream analysis of evolutionary patterns. During the course, the students will be encouraged to analyse their own data.

The course is held in a one-week session, and requires full-time attendance. Students will be credited 2 ECTS if needed for their PhD program. Lodgings and meals are organized for students unable to commute from their places of residence. A registration fee of CHF 100.- is asked to all participants before the beginning of the course.

We will use EMBnet funds to give limited support to participants from outside Western Switzerland.

Speakers: * Nicolas Galtier, Institut des sciences de l'evolution de Montpellier, CNRS, France * Marc Robinson-Rechavi, Department of Ecology and Evolution, University of Lausanne & Swiss Institute of Bioinformatics * Nicolas Salamin, Department of Ecology and Evolution, University of Lausanne

Further details here: http://www.ch.embnet.org/CoursEMBnet/PagesPHYL07/Introduction.html
Marc Robinson-Rechavi http://www.unil.ch/dee/

page22707.html Department of Ecology and Evolution Biophore, University of Lausanne, 1015 Lausanne, Switzerland. tel: +41 21 692 4220 fax: +41 21 692 4165

Swiss Institute of Bioinformatics http://www.isb-sib.ch/ La liberte ne s'use que quand on ne s'en sert pas

Marc.Robinson-Rechavi@unil.ch

Lisbon ExtendingDarwinianFramework Sep10

Call for abstracts/participation:

EXTENDING THE DARWINIAN FRAMEWORK, LISBON, SEPTEMBER 10, 2007

http://www.uea.ac.uk/ ˜ e197/darwinWorkshop.html Associated with ECAL 2007.

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UPDATE: 3rd July 2007

* Paper Submission Closed * Call for Abstracts/Participation *

Submission of papers and oral presentations is now closed. However, we will continue to accept abstracts for poster presentations. We expect to announce additional invited speakers in the very near future, and hope to encourage researchers interested in all areas of evolutionary theory to attend this exciting workshop.

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This workshop will explore the formation of new levels of selection and inheritance, the origin of the first evolutionary units and novel modes of natural selection. Recent work in a variety of fields has presented a challenge to standard gene-centric evolutionary theory. Higher-level and non-genetic sources of heredity have been discovered. Artificial selection experiments have demonstrated a response to selection of whole microbial ecosystems, with concomitant implications for the formation of new evolutionary units. These results bear important relation to long-standing questions regarding the formation of new levels of biological organisation. The debate over levels of selection has an extended history. However, given recent empirical results and outstanding unresolved issues, it again seems pertinent to ask: What can selection act on? What sources of heritable variation exist? How can selection bring about new units of selection? And how can artificial life models help to answer such questions?

Areas of interest:

Major transitions in evolution, formation of new units of selection and/or levels of inheritance, non-genetic heredity/epigenetics, evolution of co-operation, ecosystem selection, multi-level selection theory, niche construction and extended heredity, origins of life, homeostasis and heredity/levels of homeostasis, self-organisation and formation of new levels of selection and heredity, development and selection, disambiguating co-evolution and higher-level selection, co-evolutionary transitions in life and the environment,...

More information at the workshop website:

http://www.uea.ac.uk/ ˜ e197/darwinWorkshop.html Please contact Hywel Williams (h.williams@uea.ac.uk) if you have any enquiries. Hope to see you in Lisbon!

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Apologies for cross-posting. Please circulate to interested parties.

h.williams@uea.ac.uk h.williams@uea.ac.uk

UVirginia ComputationalGenomics

Course announcement - Application deadline, July 15, 2007

Cold Spring Harbor COMPUTATIONAL & COMPARATIVE GENOMICS November 7 - 13, 200 Application Deadline: July 15, 2007

INSTRUCTORS:

Pearson, William, Ph.D., University of Virginia, Charlottesville, VA Smith, Randall, Ph.D., SmithKline Beecham Pharmaceuticals, King of Prussia, PA

Beyond BLAST and FASTA - Alignment: from proteins to genomes - This course presents a comprehensive overview of the theory and practice of computational methods for extracting the maximum amount of information from protein and DNA sequence similarity through sequence database searches, statistical analysis, and multiple sequence alignment, and genome scale alignment. Additional topics include gene finding, dentifying signals in unaligned sequences, integration of genetic and sequence information in biological databases.

The course combines lectures with hands-on exercises; students are encouraged to pose challenging sequence analysis problems using their own data. The course makes extensive use of local WWW pages to present problem sets and the computing tools to solve them. Students use Windows and Mac workstations attached to a UNIX server.

The course is designed for biologists seeking advanced training in biological sequence analysis, computational biology core resource directors and staff, and for scientists in other disciplines, such as computer science, who wish to survey current research problems in biological sequence analysis and comparative genomics.

The primary focus of the Computational and Comparative Genomics Course is the theory and practice of algorithms used in computational biology, with the goal of using current methods more effectively and developing new algorithms. Cold Spring Harbor also offers a "Programming for Biology" course, which focuses more on software development.

For additional information and the lecture schedule and problem sets for the 2006 course, see:

http://fasta.bioch.virginia.edu/cshl06 To apply to the course, fill out and send in the form at:

http://meetings.cshl.edu/courses/-courseapplication.asp Bill Pearson

wrp@virginia.edu wrp@virginia.edu

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

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.