EvolDir

January 1, 2005

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

Oslo WilliHennigSociety Jul25-29

Announcing the 24 meeting of the Willi Hennig Society, 25-29 July 2005 in Oslo, Norway.

This conference on phylogenetic biology (both theoretical and empirical) will be held at the Quality Fagernes Hotell (http://www.choicehotels.no/html/en-gb72665.jsp) in the beautiful mountains just north of Oslo, Norway. The start date of the meeting is meant to coincide with the tail end of the International Botanical Congress (http://www.ibc2005.ac.at/) being held in Vienna, Austria, from 17-23 August. As such, one hope is that a large contingent of botanists travelling to the IBC can also include Hennig XXVI in their schedules.

Single or double rooms with a full pension package will be available, as will cheaper options for youth hostel bookings with or without full pension at the nearby Quality Fagernes Hotell. Package rates have been negotiated to rather reasonable costs, and all sessions will be held on-site at the hotel.

Presentations are invited within pre-planned symposia, or as selected from contributions (e.g., from poster submissions) as time permits. All poster presentations are welcome. The Willi Hennig Society strongly encourages participation from students and postdocs on their devoping research, either theoretical or empirical. There are several cash student prizes that will be awarded.

CALL FOR SYMPOSIA PROPOSALS:

Please email Victor A. Albert (victor.albert@nhm.uio.no) with concrete plans for symposia, including a 1-2 paragraph description, and a list of proposed speakers and their topics. These symposia proposals will be assessed in light of other proposals registered.

Please check back on the Evoldir web site for additional information on registration prices and travel suggestions as they become available.

Victor A. Albert Professor and Head, Botanical Garden

The Natural History Museums and Botanical Garden University of Oslo P.O. Box 1172 Blindern NO-0318 Oslo, Norway

Visiting address: Sars' gate 1, NO-0562 Oslo

+47 22851698 tel +47 22851824 fax +47 48224268 mob
http://folk.uio.no/victoraa/index_files/slide0002.htm
Victor Albert <victor.albert@nhm.uio.no>

Oslo WilliHennigSociety Jul25-29 2

Announcing the 24th meeting of the Willi Hennig Society, 25-29 July 2005 in Oslo, Norway.

This conference on PHYLOGENETIC BIOLOGY (both theoretical and empirical) will be held at the Quality Fagernes Hotell (http://www.choicehotels.no/-html/en-gb72665.jsp) in the beautiful mountains just north of Oslo, Norway. The start date of the meeting is meant to coincide with the tail end of the International Botanical Congress (http://www.ibc2005.ac.at/) being held in Vienna, Austria, from 17-23 August. As such, one hope is that a large contingent of botanists travelling to the IBC can also include Hennig XXVI in their schedules. Of course, all other interested parties in the phylogenetic and phylogenomic community are also encouraged to attend.

Single or double rooms with a full pension package will be available, as will cheaper options for youth hostel bookings with or without full pension at the nearby Quality Fagernes Hotell. Package rates have been negotiated to rather reasonable costs, and all sessions will be held on-site at the hotel.

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CALL FOR SYMPOSIA PROPOSALS:

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Please check back on the Evoldir web site for additional information on registration prices and travel suggestions as they become available.

Victor Albert <victor.albert@nhm.uio.no>

Paris MathEvol Jun17-21

Mathematics of Evolution and Phylogeny Institut Henri Poincaré, Paris, June 17-18 and 20-21, 2005.

Web site ———–

http://www.lirmm.fr/MEP05/ Organizers ————–

Olivier Gascuel (CNRS, Montpellier) Mike Steel (Univ. Canterbury, Christchurch)

Theme ——–

This conference which follows a similar workshop that was held in June 2003. The subject is evolution, which is considered at different scales: sequences, genes, gene families, organelles, genomes, and species. The focus is on the mathematical and computational tools and concepts, which form an essential basis of evolutionary studies. Recent years have witnessed rapid progress in this area, with models and methods becoming more realistic, powerful, and complex. The goal of the conference is to provide pedagogical presentations of the main subjects in the field, from basic principles to the cutting edge, with time for discussion and debate. There will be presentations by some of the leading experts in the field. Each speaker will survey a broad range of methods, techniques and results. Young scientists will also be selected, to give short talks or present posters.

Expert Speakers ——————

Elizabeth Allman (Univ. Southern Maine) Laurent Excoffier (Univ. Bern) Joe Felsenstein (Univ. Washington) Dan Gusfield (Univ. Berkeley) Daniel Huson (Univ. Tuebingen) Bret Larget (Univ. Wiscousin) Arne Mooers (Univ. Simon Fraser) Pavel Pevzner (Univ. California) Allen Rodrigo (Univ. Auckland) Charles Semple (Univ. Canterbury, Christchurch) Mike Steel (Univ. Canterbury, Christchurch)

Call for Presentations of Young Scientists ——

Young scientists will be selected, to give short talks or present posters. Those wishing to do so should email Olivier Gascuel and Mike Steel with an extended abstract of the intended presentation, with links to published papers or manuscripts (gascuel@lirmm.fr, M.Steel@math.canterbury.ac.nz)

Deadline: February 28, 2005,

Location and registration ——

The conference will be held in the French mathematical Institut Henri Poincare, situated in the centre of Paris, close to the Luxembourg garden. The registration web site will be open soon (address is above). The registration fee is 100 Euros. Early registration are encouraged as in 2003 the meeting filled up and registration was closed (with a waiting list) sometime before the meeting.

LIRMM, 161 rue Ada, 34392 - Montpellier - FRANCE Tel. (33 or 0 from France) 4 67 41 85 47 Fax. (33 or 0 from France) 4 67 41 85 00 http://www.lirmm.fr/~w3ifa/MAAS/perso.html gascuel@lirmm.fr

gascuel@lirmm.fr

PennStateU NorthEastEcolEvol Mar18-20

Northeast Ecology and Evolution Conference 2005

March 18th-20th The Pennsylvania State University University Park, PA

Registration and abstract submission is now open for the Northeast Ecology and Evolution Conference (NEEC), March 18 - 20 at The Pennsylvania State University (University Park, PA). Web registration via our secure server will remain open until March 4, 2005. Abstracts will be accepted on-line until February 4, 2005.

To register now visit the conference website: www.ecology.psu.edu/neec NEEC is a professional meeting organized by graduate students and post-docs to provide a forum for advanced undergraduates, graduate students, and post-docs to present their research in the form of a poster or talk. Poster and Talk topics for NEEC 2005 include animal behavior, biodiversity, biogeochemistry, biogeography, biological invasions, chemical ecology, community ecology, conservation and management, disease ecology, ecophysiology, ecosystems ecology, effects of climate change, evolution of development, genome evolution, marine biology, microbial ecology, molecular ecology, molecular evolution, paleobiology, philosophy of biology, phylogenetics and systematics, plant and animal interactions, population ecology, population genetics, quantitative trait mapping, reproductive biology, soil ecology, spacial ecology and landscape ecology, speciation, symbiosis, and urban ecology.

The weekend will include a reception and panel discussion on “Setting Up a Research Program” on Friday night and a keynote banquet on Saturday night. The keynote speaker will be Dr. Peter Kareiva. Dr. Kareiva has a very distinguished career in ecological research and presently serves as Lead Scientist for the Nature Conservancy. The title of his talk is Conservation Struggles to Mature from “Reactive Teenager” to “Judicious Adult”: Salmon, Return on Investment, and Strategic Priorities

For further information visit the conference website at www.ecology.psu.edu/neec or contact us at neec2005@yahoo.com.

NEEC 2005 Organizing Committee

RothamstedUK MathMolBiol Mar21-22

MASAMB-2005 (Mathematical and Statistical Aspects of Molecular Biology)

The 15th Annual meeting of 'Mathematical and Statistical Aspects of Molecular Biology' will take place at Rothamsted Research, Harpenden on 21 and 22 March 2005.

The conference web site can be found at http://www.rothamsted.bbsrc.ac.uk/bab/masamb Bioinformatics and statistical genetics, twin themes of the long-running series of annual MASAMB meetings (see the archive at http://www.ebi.ac.uk/goldman-srv/masamb), have gained huge impetus from large-scale genome sequencing projects and development of high-throughput biological assay systems, including gene-expression microarrays. These immense data resources, and the underlying complexities of molecular and cell biology, provide exciting research opportunitities for numerate scientists.

With typically around 60-80 participants from mathematics, statistics, computer science, bioinformatics, biology and related fields, the MASAMB meetings provide an intimate setting for exchange of ideas in methodological and applied research. Research students and scientists newly entering the field of genomic research are particularly welcome.

TALKS on research relevant to the workshop are invited. The meeting will contain approximately 12 half-hour talks selected from participants' submissions. Abstracts must be submitted using the on-line system at the MASAMB-2005 web site (see above). Submitted abstracts will be reviewed by the organising committee and selected speakers will be informed by 27th January. Speakers will be asked to make their presentation available in electronic form for inclusion on this website after the meeting (pdf or Powerpoint format).

POSTERS (portrait format, maximum depth 120 cm) on research relevant to the workshop are invited for the poster sessions to be held on both days. To submit a poster, send an abstract using the MASAMB-2005 web based abstract submission. Accepted abstracts will be displayed on the web site. Following the meeting, posters may be published on this web site (pdf format required)

REGISTRATION costs £90 (before January 20th) which includes lunch on both days and the conference dinner. The cost for full-time students is £60. Late registrations, after 20th January (if places are available) will cost £110. Registration must be made using throough the MASAMB-2005 web system (see address above). The evening meal will take place at Rothamsted.

ACCOMMODATION may be requested through the workshop website at the designated conference hotel

(Hertfordshire Moat House, Markyate, offering swimming pool and gymnasium) at a preferential conference rate of £80. Hertfordshire Moat House bookings not made through the conference website (which generates the booking form when you register) will have to pay standard hotel rates. Hotels in the Harpenden area tend to get fully booked. Please ensure that you arrange accomodation at an early date.

Please post this information where others in your department will see it and tell anyone you think that may be interested in attending.

Nick Goldman Organising Committee, MASAMB-2005

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

UGeorgia SEEC Mar11-13

Please Distribute Widely **Apologies for Cross Postings**

FIRST CALL FOR ABSTRACTS

SEEC 2005 SOUTHEASTERN ECOLOGY AND EVOLUTION CONFERENCE THE UNIVERSITY OF GEORGIA ATHENS, GEORGIA 11-13 MARCH 2005 www.uga.edu/seec REGISTRATION DEADLINE: 4 FEBRUARY 2005

We invite all graduate, undergraduate, and postdoctoral researchers studying in the environmental and life sciences to submit abstracts for either oral or poster presentations at the 2nd annual Southeastern Ecology and Evolution Conference (SEEC) to be held March 11-13, 2005, at the The University of Georgia in Athens, Georgia. Talks will be delivered by Drs. Whit Gibbons, John Avise and Gary Barrett.

SEEC is a professional meeting intended for students in the environmental and life sciences to present their research to their colleagues in a comfortable, fun, and low stress environment. Such events are designed to encourage new friendships within our field and to share newly developed research ideas for feedback. While we expect most SEEC participants to be from the Southeast, we encourage and welcome all interested individuals to submit abstracts and/or attend.

To encourage attendance, registration is only $15 and covers meeting attendance, two continental breakfasts, snacks, coffee, a t-shirt, and $100 cash awards for the best oral and poster presentations. The early registration and abstract submission deadline is February 4, 2005, and may be completed at the following web site:

www.uga.edu/seec We look forward to seeing you at The University of Georgia in Athens for the 2nd Annual Southeastern Ecology and Evolution Conference this March!

For more information, go to www.uga.edu/seec

or email Tom Luhring at tluhring@uga.edu

Thomas Luhring <tluhring@uga.edu>

UOxford HapMap Mar15-18

Conference: Genomic Studies and the HapMap

University of Oxford, UK: March 15-18, 2005

By March 2005, Phase I of the HapMap (600,000 common SNPs typed in 270 individuals) will be complete and Phase II (an additional 2.25M SNPs in the same samples) will be well underway. But there remain many unresolved questions about how best to utilize this information in genetic research. This conference will be hosted by the Department of Statistics at the University of Oxford, and supported in part by the Wellcome Trust, and its primary focus will be the use of the HapMap resource in genomic studies: human disease studies, and other population genetic and evolutionary analyses.

"Genomic Studies and the HapMap" will provide an important opportunity for a diverse community of investigators-those involved directly in the International HapMap Project, those in the broader analysis community, and those whose focus is disease studies-to come together to define and discuss a range of issues related to the use of the HapMap resource. It will also provide up-to-date assessments of the progress and results from the project. Invited speakers from outside the HapMap project include Andy Clarke, David Clayton, David Cox, Mark McCarthy, Rasmus Nielsen, Jonathan Pritchard, Matthew Stephens, and Simon Tavaré. This conference follows a successful meeting held in the spring of 2004, which brought together well over 100 participants interested in methods and analysis related to the International Haplotype Map Project.

We invite participation and registration for this meeting and encourage the submission of abstracts for posters or short presentations.

The deadline for submitting an abstract is January 28, 2005.

The deadline for registration/lodging reservations is February 25, 2005.

Complete instructions for abstract submission and registration, and further details of the conference, can be found at the conference Web site, www.hapmap.org/oxford_conference/default.html <http://www.hapmap.org/oxford_conference/default.html> .

GradStudentPositions

Brussels EvolSex

PhD opportunities: Marie Curie Research training network (MRTN) SEXASEX - 4 positions available

Students and researchers interested in the paradox of sex in evolutionary biology are strongly encouraged to apply for a research position in the European Union Marie Curie Research Training Network SEXASEX, which is co- ordinated by Prof. Dr. Koen Martens, RBINSc, Brussels. Criteria of eligibility include: EU citizenship, less than 4 years of research experience for Young Researchers (YR), and a willingness to work in a European country other than the country of origin. We seek candidates who are enthusiastic about evolutionary biology, travelling and living abroad, learning in a multidisciplinary research environment and working in teams. All appointments will be for 3 years, YR are offered PhD positions. YR will be expected to obtain a PhD at the end of the project. The application of female candidates is especially encouraged; detailed information on child care facilities at the different institutions will be provided upon request. Aid can be sought if accompanying spouses also require employment abroad.

Project overview: Sex is the queen of evolutionary problems. It will be tackled by SEXASEX in a multidisciplinary approach, providing training and transfer of knowledge for a total of 360 person-months. 10 network researchers (6 young researchers (YR) and 4 experienced researchers (ER)) will receive training in 9 institutions across as many countries. A wide array of research tools will provide excellent training opportunities, for example through individual career development plans, individual tutoring and secondments, which will be supplemented by participation in courses and external workshops. Network-wide training will exploit the extensive experience of the partner institutions through five courses and summer schools for all network researchers. Complementary skills such as management and communication (verbal, written) will be developed, and gender awareness will be raised, in two network-wide meetings. The networks theoretical and empirical research will apply 13 major approaches, including novel genomic and karyological approaches, intraspecific phylogeography, ecology, behavioural studies, GIS analyses and theoretical modelling. With this multidisciplinary toolkit, SEXASEX will investigate why sex exists at all, given its evolutionary costs, using the model organism Eucypris virens, a non-marine ostracod species with both sexual and asexual reproduction. What determines its gender, what are the genomic consequences of long-term asexuality, what is the cohesiveness of a species with mixed reproduction, how do asexuals and sexuals compete and what is their historical zoogeography? The pluralistic approach of SEXASEX is unique and timely, using highly novel methodologies and dealing with cutting edge science based on European excellence and tradition. Please refer to http://www.naturalsciences.be/EVIRENS/ for more information.

Send full applications, comprising letter of interest, CV and coordinates of at least two potential referees before the 10th of January 2005 to

Dr Isa Schön, Royal Belgian Institute of Natural Sciences, Freshwater biology, Vautierstraat 29, B-1000 Brussels, Belgium E-mail (Isa.schoen@naturalsciences.be) Fax : +32 2 62 74 113.

Correspondence by email is preferred.

Applications for the following three positions, all starting beginning of May 2005, are now sought:

PhD POSITION 1: HISTORICAL BIOGEOGRAPHY OF SEXUAL AND ASEXUAL REPRODUCTION IN FRESHWATER OSTRACODS. Starting date: 1rst May 2005 Duration: 36 months Salary: country-specific plus tax-free mobility allowance Scientists in charge: Prof. Dr Koen Martens Dr Isa Schön Location: Brussels, Belgium Place of work: Royal Belgian Institute of Natural Sciences, Freshwater Biology Approach and methods to be applied: This project will test hypotheses attempting to explain the observed patterns of geographical parthenogenesis in E. virens in Europe. Special attention will be given to the post-glacial recolonisation hypothesis; pathways of recolonisation from glacia refugia will be reconstructed. Methodology: Estimates of morphological variability, DNA amplification and sequencing of mitochondrial genes, phylogenetic and phylogeographic reconstructions using both classical phylogenetic reconstructions and Nested Clade Analyses, GIS-based mapping of haplotypes, modelling Candidate profile: B. S., M.S. or equivalent (e.g. Diploma) in Biology, Zoology, Molecular Biology, Genetics, Geography or Evolutionary Biology. Some practical experience with the involved methods or ostracods is advantageous but not necessarily required. Only non-Belgian persons are eligible. Ph.D. degree may be either applied for at the Faculty of Biology at the University of Ghent (or another Belgian university) or at a local university

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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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DalhousieU MarinePopGenetics

Support for a graduate student (PhD or MSc) position is available to work in the area of population and conservation genetics of marine, anadromous or freshwater fish in the laboratory of Daniel Ruzzante Department of Biology at Dalhousie University, in Halifax, Nova Scotia, Canada. The student will have interests in one or more of the following areas: evolutionary biology, adaptive radiation, marine fisheries and the effects of exploitation on diversity, and in applying molecular genetic methods as well as phenotypic approaches to the examination of issues related to the interplay between natural selection and gene flow. Depending on the project, the work may have a significant fieldwork component. Ideally, the successful candidate will have some experience with molecular techniques and should have a strong interest and affinity to population genetics and statistics. Support is contingent upon acceptance to the Department of Biology graduate program. The Department of Biology has strengths in evolutionary/population and conservation genetics and the student will conduct the molecular aspects of his/her research in the Gene Probe Laboratory, a centralized molecular facility with ample opportunities for interaction with faculty, postdocs and students.

For more information please contact: Daniel E Ruzzante, Associate Professor and Canada Research Chair in Marine Conservation Genetics, Department of Biology, Dalhousie University, Halifax, Nova Scotia, Canada, B3H 4J1.(e-mail: daniel.ruzzante@dal.ca, http://www.dal.ca/~ruzzante ; Canada Research Chairs http://www.chairs.gc.ca

Daniel.Ruzzante@Dal.Ca

LeidenU EvolAnimalBehaviour

Graduate position:

PhD position (AiO) in Animal Behaviour , Institute of Biology (IBL), Leiden University, the Netherlands

Applications are invited for a research project funded by the Institute of Biology Leiden (IBL), entitled: "Urban speciation: A study on habitat-dependent divergence in urban and forest populations of the European blackbird" to be conducted in the Behavioural Biology group.

The Behavioural Biology group at Leiden University investigates various aspects of animal communication. We are interested in proximate mechanisms underlying behaviour, but also in the evolution of signals and the impact of signals on evolution. One of our goals is to gain insight into the role of vocal divergence in the process of speciation, for which we study a variety of songbird species.

We are looking for a PhD-student to investigate the impact of urbanization on communication among male and female blackbirds (Turdus merula) and whether anthropogenic forces drive signal evolution in such a way that it could promote reproductive divergence. We offer facilities and relevant expertise to embark on this challenging project within our international group.

Profile: All candidates should have an MSc-degree (doctoraal) in Biology, preferably with a specialization in Animal Behaviour. We are especially looking for students that have experience with molecular techniques relevant to population genetics, bird netting in the field, or, to a lesser extent, bioacoustic methodologies.

The appointment is for a maximum of 4 years and is expected to lead to the completion of a PhD-thesis. The gross monthly salary is 1813 in the first year and increases progressively each year to 2283 in the fourth year. Salary and fringe benefits are conform the Collective Employment Agreement for Dutch Universities.

A full description of the project is available and can be obtained from:

Dr. Hans Slabbekoorn, e-mail: Slabbekoorn@RULSFB.LeidenUniv.NL website Behavioral Biology Group: http://wwwbio.leidenuniv.nl/~eew/g6/s5.html Those interested should apply not later than two weeks after publication of this advertisement. We need: curriculum vitae, a cover letter and names and addresses of three referees. Please send your application to: Leiden University, Faculty of Mathematics and Natural Sciences, Ms. M.J.C.A. van Leeuwen, Human Resource Adviser, P.O. Box 9504, 2300 RA Leiden, The Netherlands.

——————- Dr. Hans Slabbekoorn

Behavioural Biology (IBL) Leiden University

phone: 31 71 527 5049 fax: 31 71 527 4900 ——————- http://wwwbio.leidenuniv.nl/~eew/G6/staff/slabbekoorn.html slabbekoorn@rulsfb.leidenuniv.nl

MountAllisonU DiatomGeneticVariability

Graduate Opportunity in Harmful Microorganisms, Mount Allison University and Fisheries and Oceans Canada, Biological Station at St. Andrews, New Brunswick, Canada.

We invite applications for a Masters student in the biology of harmful diatoms. The student will contribute to an ongoing research program assessing the genetic variability of domoic acid producing Pseudo-nitzschia clones isolated from areas near salmon farming operations in Passamaquoddy Bay, New Brunswick. Thresholds of each of the clones at which mortalities or stresses in Atlantic salmon occur under controlled laboratory conditions will also be examined.

The ideal candidate will have experience with phytoplankton culture (preferably diatoms), be familiar with standard phytoplankton enumeration and cell-viability techniques as well as standard molecular methodology (DNA extraction, PCR, etc.).

To apply, please send a resume, transcript, abstract of Honours Thesis (if applicable) and the contact information of three references to Dr. Irena Kaczmarska, Department of Biology, Mount Allison University, 63B York Street, Sackville, N.B. E4L 1G7, Canada, e-mail address: iehrman@mta.ca. Review of applications will begin immediately and will continues until the position is filled. The initial appointment will be for one year, with continuation of support pending on satisfactory performance, with the possibility of further extension by collaborating on future research proposals, including international programs.

Alberto Amato PhD student Villa Comunale

80121 Napoli -Italy- e-mail: amato@szn.it alberto.amato3@tin.it Tel.: +39 081 5833-259 - 296 - 219 Fax: +39 081 7641355

www.szn.it Alberto Amato <amato@szn.it>

NHM London EvolBiol

New PhD projects in Evolutionary Biology available at the Natural History Museum London are detailed at the following site:

http://www.nhm.ac.uk/science/rco/postgrad/phd/-studentships_NHM_05.htm with an application deadline of 4th March 2005

Dr Mark Wilkinson Merit Researcher Department of Zoology, The Natural History Museum, Cromwell Road, London, SW7 5BD, UK

Tel: +44 (0)20 7942 5164, Fax: +44 (0)20 7942 5054 E-mail: M.Wilkinson@nhm.ac.uk or marw@nhm.ac.uk Homepage (follow links to download my phylogenetic software)

<http://www.nhm.ac.uk/zoology/home/-wilkinson.htm> See also

<http://www.bioinf.org/molsys/> m.Wilkinson@nhm.ac.uk

PurdueU PopBiol

Graduate Assistantships at Purdue University

Purdue University is soliciting applications for graduate assistantships (both M.S. and Ph.D.) in population biology. Research in our department spans the natural resource disciplines, but includes wildlife & fisheries management, conservation biology & genetics, population dynamics, and molecular ecology. Motivated and potentially competitive applicants should send a short letter of interest, including cumulative GPA, GRE scores, and contact information for three references to a potential faculty mentor at the Department of Forestry & Natural Resources, Purdue University, West Lafayette, IN 47907-1159. M.S. and Ph.D. assistantships are currently funded at roughly $16,000 and $18,000 per year, respectively (plus a substantial waiver of tuition & fees). The cost of living in West Lafayette is low, and we are only an hour from Indianapolis and two hours from Chicago. See http://www.agriculture.purdue.edu/-fnr/html/graduate.html for more information. COMPLETE applications must be received by January 5, 2005 to be considered. Women and minorities are encouraged to apply. Purdue University is an equal opportunity affirmative action employer.

J. Andrew DeWoody 1159 Forestry Building Purdue University West Lafayette, IN 47907 765-496-6109 dewoody@purdue.edu

UAlaskaAnchorageFairbanks EvolBiol

The University of Alaska (Anchorage-Fairbanks) invites applications for Graduate Study from students with interests in evolutionary biology, population genetics, systematics, or molecular ecology. Two-year fellowships, with annual stipends of $22,000, are available for incoming students (MS or PhD). Support in additional years is anticipated to be available from teaching and research assistantships. Additional information on these fellowships and application instructions can be found at: http://www.alaska.edu/epscor/funding/-epscorpgagrad.html The Department of Biology and Wildlife and the Institute of Arctic Biology at UAF provide a dynamic setting in which to pursue a graduate degree. Our program is highly collaborative, and offers a diverse array of graduate student course offerings in evolutionary biology. The 50 faculty and >100 graduate students offer a vibrant intellectual community with interests in biological systems. Facilities include a newly modernized DNA CORE lab with high throughput sequencing, SNP detection, microarray and proteomics capabilities an ancient DNA extraction facility, a state of the art greenhouse and animal growth quarters, an extensive collections of Alaskan plants, mammals and birds at the University of Alaska Museum of the North . Regional study areas include Toolik Field station and Bonanza Creek LTER.

The location of the University offers unparalleled opportunities for research in understudied natural communities (the storied 365 million acre classroom) and the climate offers a great opportunity to enjoy winter sports and long summer days. The campus is situated on a sunny hill, overlooking the town of Fairbanks, with a view of the Alaska Range. Fairbanks is an extremely welcoming community, with many opportunities for outdoor sports. Groomed cross country ski trails start just outside the building, downhill skiing less than 15 minutes from campus, and many places for hiking, bird watching and snow machining. Denali National Park is just 2 hours from campus. Your graduate-student life will be an unforgettable life-time experience in this beautiful subarctic region.

Applicants are encouraged to contact faculty with whom they would like to work, and to specify that faculty member in their graduate school application. Additional information on faculty research interests can be found at http://www.iab.uaf.edu/facstaff.html. All students applying for graduate work with the above faculty will be considered for these fellowships. Application instructions can be found http:/-/www.bw.uaf.edu/bw_graduate.html. Review of applications will begin 1 February 2005.

Matt Olson <matt.olson@uaf.edu>

UCopenhagen InsectCommunication

A 3-year PhD position will be available from July 2005 at Faculty of Sciences, University of Copenhagen, Denmark. The position is funded by the European Community via a Marie Curie Excellence Grant. The successful candidate will work in a new research group leaded by Dr. Patrizia D'Ettorre, which will be integrated in the laboratory of Prof. Koos Boomsma.

The research project will focus on Chemical Communication Code of Insect Societies, with a multidisciplinary approach (behavioural, chemical, electro- and neurophysiological analyses and genetics).

Applicants should have a Master degree in Biology or related disciplines, and are expected to have a background in Evolutionary Biology. Familiarity with general molecular evolutionary techniques, with chemical ecology techniques and neurophysiology is desirable but not compulsory.

Applications should include CV, list of publications, research interests and name and email address of one referee, and be sent by email to Patrizia D'Ettorre at patrizia.dettorre@biologie.uni-regensburg.de by January 31st 2005.

Dr. Patrizia D'Ettorre Dep. Biology I University of Regensburg D-93040 Regensburg phone +49 941 943 2996 fax +49 941 943 3304 http://www.biologie.uni-regensburg.de/Zoologie/Heinze/en/staff/dep/-dep_e.html patrizia dettorre <patrizia.dettorre@t-online.de>

UGoettingen MolecularPhylogenetics

Goettingen, Germany: Research Associate (PhD) position in molecular phylogenetics.

We invite applications for a research associate (PhD) position in a project funded by the German Research Foundation (DFG) The phylogeny of Calcarea“. The project is located in the Department of Geobiology (Working group of Jun.-Prof. Dr. Gert Woerheide) of the Geoscience Centre of the University of Goettingen (Germany). The Dept. of Geobiology is also part of the Goettingen Centre for Biodiversity and Ecology.

The project aims to reconstruct phylogenetic relationships among calcareous sponges (Porifera: Calcarea), primarily using a molecular multi-marker approach. Calcareous sponges are a small and phylogenetically unresolved group that plays a pivotal role for understanding early metazoan (diploblast) evolution. The successful applicant will amplify, clone and sequence multiple loci (rDNA, nuclear protein-coding and mitochondrial genes) and integrate data with detailed morphological investigations, data from lipid biomarkers (in collaboration with Prof. Thiel) and the fossil record (in collaboration with Prof. Reitner) for a global phylogenetic analysis aiming at a well-supported reconstruction of evolutionary relationships within and among calcareans.

We are seeking a highly motivated applicant with excellent molecular-phylogenetic skills, demonstrated by an above-average MSc (or equivalent, e.g. German Diplom”) thesis. Affinity to bioinformatics and willingness for overseas fieldwork should be given. SCUBA diving qualification and experience desirable but not essential.

The opportunity to enrol in the new PhD study course Biodiversity and Ecology“ will be given.

Requirements: Degree in Biology (MA, MSc, or equivalent degree); very good knowledge of molecular lab techniques and understanding of molecular evolution including methods to infer molecular phylogenies and state-of-the art computer programs for such analyses; excellent English language skills. Good working knowledge of UNIX/LINUX desirable.

Deadline for applications: 15 January 2005. The position is available for 2 Years and will be paid according to the German BATIIa salary scheme (part time).

Application: Send application including CV, PDF's of publications (if available), and details of 2 referees as PDF (only) by email or snail mail to Gert Woerheide (gert.woerheide@geo.uni-goettingen.de). Informal enquiries are also welcome to this address.

The Department of Geobiology of the Geoscience Centre of the University of Goettingen offers an excellent multidisciplinary research environment, its particular strength being due to the close interaction between Geosciences, the Goettingen Centre for Biodiversity and Ecology and the Biological Faculty including Bioinformatics.

More information, including a position description in German, can be found at www.geobiology.nu > vacancies or at www.geobiologie.uni-goettingen.de . The University of Goettingen is an equal opportunity employer. Women and members of minority groups including disabled persons are strongly encouraged to apply.

- Gert Wörheide Junior Professor for Geobiology Geoscience Centre Göttingen Dept. of Geobiology Goldschmidtstr.3 37077 Göttingen Germany

Centre for Biodiversity and Ecology University of Göttingen

phone: +49-(0)551 39 14 177 mobile: +49-(0)178 537 22 33 fax: +49-(0)551-39 79 18

gert.woerheide@geo.uni-goettingen.de

NEW WEBSITES, CHECK 'EM OUT!! www.geobiology.nu www.geobiologie.uni-goettingen.de www.gzg.uni-goettingen.de www.biodiversitaet.gwdg.de gert.woerheide@geo.uni-goettingen.de

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UGuelph Abalone Conservation Genetics

UGuelph.Abalone_Conservation_Genetics

I am looking to recruit a new graduate student to work in my lab at the University of Guelph to begin their studies in May 2005 to work on the conservation genetics of pinto abalone. The position is initially funded for two years. Your research will be part of a larger research project will develop a selective breeding program for cultured pinto abalone at the Bamfield Huu-Ay-Aht Community Abalone Project (BHCAP) in Bamfield, B.C., Canada. The project is lead by Dr. Elizabeth Boulding (Zoology, U. Guelph) in collaboration with Dr. Ian McMillian (CGIL & APS, U.Guelph) and Dr. Ussif Rashid Sumaila (Fisheries Centre, U.B.C.). This breeding program will apply modern animal breeding methodology to improve the cultured population for economically-important traits, while minimizing inbreeding accumulation. Such a breeding plan is essential because of the potential for rapid inbreeding accumulation resulting from the high fecundity of the abalone and limited rearing space in the hatchery. Your role on the team will genotype abalone tissue biopsies at 12 molecular markers (microsatellites) to monitor inbreeding, estimate genetic parameters, and to identify the parents of potential broodstock. Dr. Sumalias graduate student will help identify important traits to target for selection by predicting the relative economic value of these different traits in the global marketplace. Dr. McMillians postdoc will incorporate these economic weights into a multitrait selection index that will be used for genetic evaluation of potential broodstock. Pinto, or northern, abalone (_Haliotis kamtschatkana_) is a broadcast-spawning marine gastropod that occurs throughout coastal British Columbia, extending north into Alaska and south to California. In addition to its role as a member of a complex marine ecosystem, pinto abalone is valued as a food and cultural resource by coastal native peoples, and as a food resource by commercial fishermen and recreational divers. Historically, abalone populations were healthy enough to support a traditional fishery by native people and a commercial dive fishery until the late 1980s. In 1990, concern over reduced population levels instigated a closure to all harvesting of abalone, a closure that remains in place today. When populations not only failed to recover under 10 years of protection, but also declined further, the species was designated threatened by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC). It seems likely that captive breeding may be needed reintroduce abalone to areas were they have become so rare that they fail to find prospective mates. In order to apply, in the first instance you need to apply for admission to the graduate program in the Department of Zoology at the University of Guelph: http://www.uoguelph.ca/zoology/. Check the website for admission requirements, and note that you may have to write the TOEFL test if English is not your first language.

The Project TITLE: Conservation genetics of pinto abalone. OBJECTIVES: Assess the levels of inbreeding in captive populations of the pinto abalone. APPROACH: The project will use modern automated microsatellite analysis on a Beckman 3100 capillary machine approaches and statistical methodologies to estimate pedigrees and quantitative genetic parameters.

Duties The student will undertake a major part of the laboratory work, and may have some opportunity to travel to Bamfield Marine Sciences Centre on Vancouver Island, B.C.. Ideally, he/she will develop his/her own thesis research based on the project and expanding it. Part of his or her support may come from a teaching assistantship.

Minimum Qualifications Background suitable for enrollment in the graduate program in the Department of Zoology. The minimum requirement for admission is an undergraduate degree in Biology with at least a B (second class) average.

Desirable Qualifications Interest in population and quantitative genetics. Interest in the evolutionary biology, aquaculture and conservation genetics of mollusks. Previous experience in molecular genetics (DNA sequencing or microsatellite genotyping) helpful but not necessary.

Position Details The position is funded by AquaNet of NSERC Canada initially for a period of 2 years. The position will begin the summer semester of 2005 (probably 1 May 2005).

Salary Salary commensurate with qualifications and experience. Minimum salary CAN$16,000.00/year.

How to Apply As soon as possible, submit (via e-mail) a cv and a cover letter explaining your interest to: Dr. Elizabeth G. Boulding, Department of Zoology, University of Guelph, Guelph, ON N1G 2W1, Canada Telephone: (519) 824-4120 x 54961 FAX: (519) 767-1656, E-mail: boulding@uoguelph.ca Deadline: Continuous recruitment, applications will be reviewed beginning 15 January 2005 until the position is filled.

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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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UHawaiiManoa SnailEvol

To prospective graduate students.

We are looking to recruit a new graduate student to work in my lab at the University of Hawaii on the systematics, phylogenetics and biogeography of Pacific island succineid land snails. The project is funded by the National Science Foundation. Dr. Marta deMaintenon is the co-PI.

In order to apply, in the first instance you need to apply for admission to the graduate program in the Department of Zoology at the University of Hawaii: http://www.hawaii.edu/zoology/. Check the website for admission requirements, and note especially the need to have not only the general GREs but also it is recommended that you have the Biology subject GRE. If you are interested, send me an e-mail with a cv and we can discuss it further.

The following is the formal announcement of the graduate assistantship that would support the new graduate student for the initial 2 years. Other funding will be available to support the student beyond this.

University of Hawaii at Manoa

Center for Conservation Research and Training Pacific Biomedical Research Center

Graduate Research Assistantship available

The Project TITLE: Revision and phylogeographic analysis of Pacific island succineid land snails OBJECTIVES: The project will undertake a systematic revision of the entire Pacific island succineid fauna (about 80 species). In addition, the project will investigate the evolutionary and geographic origins and diversification of the species and the routes via which, over evolutionary time, they have colonized these myriad islands. APPROACH: The project will use both traditional analysis of morphological variation as well as modern DNA sequencing approaches and analytical methodologies.

Duties The GA will undertake a major part of the laboratory work, and may have some opportunity to travel in the islands of the Pacific. Ideally, he/she will develop his/her own dissertation research based on the project and expanding it.

Minimum Qualifications Classified full-time graduate student admitted to and enrolled in the MS program in the Department of Zoology. Interest in the evolutionary biology and systematics of mollusks.

Desirable Qualifications Enrolled in the Ph.D. program in the Department of Zoology. Experience with phylogenetic analysis. Experience in molecular genetics (DNA sequencing) and/or anatomical dissection and characterization of mollusks.

Position Details The position is funded by NSF through the Center for Conservation Research and Training for a period of 1-2 years. The position is 0.50 FTE (i.e., 20 hours per week) and will begin the fall semester of 2005 (probably 1 August 2005).

Salary Salary commensurate with qualifications and experience. Minimum $1296.50/month.

How to Apply As soon as possible, submit (via e-mail) a cv and a cover letter explaining your interest to: Dr. Robert Cowie - cowie@hawaii.edu Phone: (808) 956-4909

Deadline Continuous recruitment, applications will be reviewed beginning 15 December 2004 until the position is filled.

Dr. Robert H. Cowie Center for Conservation Research and Training University of Hawaii 3050 Maile Way, Gilmore 408 Honolulu, Hawaii 96822 USA

Phone: (808) 956 4909 Fax: (808) 956 2647 http://www2.hawaii.edu/~cowie/

"Robert H. Cowie" <cowie@hawaii.edu>

ULouisianaMonroe SystematicBotany

We are looking to fill one masters student position for Spring 2005 in evolutionary and systematic botany at The University of Louisiana at Monroe. The position comes with a research assistantship to work in the herbarium (no teaching requirement). Herbarium NLU is one of the largest herbaria in the southeast with nearly 500,000 specimens. Interested students should contact either Kerry Heafner (heafner@ulm.edu) or myself.

Russ Minton, Ph.D. Molecular Genetics Lab Coordinator & Curator of Invertebrates Museum of Natural History Assistant Professor, Department of Biology University of Louisiana at Monroe Monroe, LA 71209-0520 ph: 318-342-1795 fax: 318-342-3312 http://www.ulm.edu/ ~ minton Russ Minton <minton@ulm.edu>

UMunich PlantPopulationGenetics

Graduate Student Position: Univ. of Munich PlantPopulationGenetics

A PhD position funded by the German Science Foundation (DFG) is available in the lab of Dr. Laura Rose at the University of Munich to study the molecular evolution of plant disease resistance in wild tomato species. This project will focus on elucidating the type and strength of natural selection operating on various genes in a disease resistance pathway within tomato species.

Applicants should have a master's degree or equivalent in biology or a related field. Previous laboratory experience and coursework in evolutionary biology and genetics are strongly recommended. The application should include a C.V., a 1-2 page statement of previous research experience, one letter of recommendation and addresses and telephone numbers of two additional referees. Applications should be submitted by email and will be reviewed beginning on January 24, 2005.

The University of Munich has a strong, interactive group in evolutionary biology, consisting of theoreticians and experimentalists including Wolfgang Stephan, John Parsch, Susanne Renner, Martin Parniske and Joachim Hermisson. We have a very international group and the everyday working language is English. The department is housed in a new, state-of-the-art BioCenter on the University of Munich High-Tech campus. More information is available on the web at: www.zi.biologie.uni-muenchen.de/institute/zi/abtlgn/evolutionsbiologie Applications and inquiries should be sent to:

Dr. Laura Rose Email: rose@zi.biologie.uni-muenchen.de

Department Biologie II Grosshadernerstr. 2 82152 Planegg-Martinsried Germany

Phone: +49 89 2180 74 150 Fax: +49 89 2180 74 104

The University of Munich is an Equal Opportunity/Affirmative Action Employer and has an affirmative action policy for the disabled.

rose@zi.biologie.uni-muenchen.de

UPotsdam PlantPathogens

PHD studentship on the role of plant pathogens in a large biodiversity-ecosystem functioning experiment

Applications are invited for a three-year PhD studentship in the Botany/Community Ecology lab of the

University of Potsdam, Germany, starting on February 1, 2005, or soon thereafter to work within a research group who is running a large biodiversity experiment to study effects of manipulated species diversity on ecosystem functioning and trophic interactions in Jena, Germany (see http://www2.uni-jena.de/biologie/ecology/-biodiv/index.html). The position is funded by the German Science Foundation DFG.

We are looking for a highly motivated student with a diploma or masters degree in biology, ecology, or plant pathology to work on the diversity and effect of plant pathogens in this experiment. The work will involve

- determination especially of fungal pathogens - monitoring of plants in the experiment for abundance and diversity of pathogenic fungi - growing and monitoring of further phytometer and common garden plants - with a second PhD student and a lab technician, to study the relationship between pathogen load, genetic plant variation, and plant fitness

The work requires high motivation to work with plant pathogens and in the framework of a large-scale experiment. Desirable qualifications are experience with population biology, experimental ecology, statistical treatment of ecological data, and team work, and a good knowledge of grassland plant species and other taxa of Central Europe.

Preferably by e-mail, applicants should send a motivation letter, a CV including teaching and research experience, and the names and e-mail addresses of two references to the address below (before 31 December).

Prof. Dr. Markus Fischer, Dr. Volker Kummer, Institut für Biochemie und Biologie, Universität Potsdam, Villa Liegnitz, Lennéstr. 7a, D-14471 Potsdam, Germany, Tel. ++49 331 977 4884, e-mail <mailto:fischerm@rz.uni-potsdam.de>fischerm@rz.uni-potsdam.de (http://-www.bio.uni-potsdam.de/spezbot/)

The Maulbeerallee site of the Institute of Biochemistry and Biology in Potsdam including the Botanical Garden is situated in the park of the castle of Sanssouci. Other research fields include Vegetation Ecology and Conservation (Florian Jeltsch), Animal Ecology (Dieter Wallschläger), Ecophysiology (Axel Gzik), Microbiology (Ingo Schneider), Evolutionary Biology (Ralph Tiedemann), and Freshwater Ecology (Ursula Gaedke, Alexander Wacker). Potsdam is located in close vicinity to Berlin. It offers a high quality of life, beautiful surroundings, and affordable accommodation and living (see http://www.potsdam.de).

Markus Fischer

Professor für <http://www.bio.uni-potsdam.de/-spezbot/index.htm>Biozönoseforschung/Spezielle Botanik Institut für Biochemie und Biologie Universität Potsdam Villa Liegnitz Lennéstr. 7a D-14471 Potsdam Germany Tel. ++49 331 977 4884 Fax ++49 331 977 4865 e-mail fischerm@rz.uni-potsdam.de http://www.bio.uni-potsdam.de/spezbot/ Markus Fischer <fischerm@rz.uni-potsdam.de>

URochester EvolBiol

I am writing to bring your attention to our Evolutionary Biology graduate program here at the University of Rochester. We have a strong, active and growing group of evolutionary biologists (see faculty list and research interests below). We are particularly strong in evolutionary genetics, and our department is noteworthy in being a “true” Biology Department, with interactions between evolutionary, molecular, cell, and developmental biologists, and a number of faculty that “bridge” between these disciplines. We have just hired two new junior faculty, Daven Presgraves and Justin Ramsey, and expect several new hires in the next few years. Financial support for graduate students is excellent. It includes a stipend (currently $22,000 U.S./year), health benefits, and tuition scholarships for all Ph.D. students in good standing. The support is particularly good because Rochester has a relatively low cost of living. Rochester is a medium-sized city on the south shore of Lake Ontario in western New York State; it features a lively cultural life, including the world-famous Eastman School of Music, a symphony orchestra, several museums, and a diversity of restaurants and nightspots. Outdoor attractions include the Finger Lakes region (which is renowned for sailing and wineries), excellent downhill and cross-country skiing, and a number of state and county parks for hiking.

More information on the Department of Biology, faculty research interests, and application procedures may be found by visiting the graduate program web site at www.rochester.edu/College/BIO/-graduate/index.html . Sincerely yours,

James D. Fry Assistant Professor and co-chair, Graduate Admissions Committee

Faculty in Evolutionary Biology at the University of Rochester:

Thomas Eickbush – Molecular biology and evolution: integration of retrotransposable elements; origin and evolution of mobile elements; regulation of rRNA genes.

James Fry – Genetics of ecological adaptation in Drosophila; evolutionary effects of deleterious mutations; quantitative-genetic theory and methodology.

John Jaenike – Ecology and evolution of host-parasite interactions; sex chromosome meiotic drive; Wolbachia as male killers and causes of reproductive isolation in Drosophila; ecology of mycophagous Drosophila.

David Lambert – The evolution of developmental mechanisms; early patterning in molluscs and related groups; cytoskeletal basis of asymmetric cell divisions; evolution of novel phenotypes.

Allen Orr – Evolutionary genetics: genetics of speciation in Drosophila; genetics and theory of adaptation; population genetics.

Daven Presgraves – Evolutionary genetics: speciation genetics; molecular population genetics; genome evolution.

Justin Ramsey – Evolutionary ecology: mechanisms of adaptation and speciation in flowering plants; polyploidy and chromosome evolution.

John Werren – Evolutionary genetics: microbial-host interactions with emphasis on Wolbachia in arthropods, genetics of speciation and evolution of development; genetics, genetics and evolution of parasitic wasps (Nasonia); the role of "selfish" or "parasitic" DNA in evolution.

jfry@mail.rochester.edu

VanderbiltU EcolEvol

GRADUATE STUDIES IN ECOLOGY AND EVOLUTION AT VANDERBILT

Dear colleagues and prospective students,

The Department of Biological Sciences at Vanderbilt University seeks interested and highly motivated graduate students to join a group of laboratories with complementary research interests focusing on ecological and genetic mechanisms of evolutionary diversification. Ongoing research investigates all stages of evolutionary diversification (population structure, reproductive isolation, speciation, phylogenetic radiation) and several fundamental ecological processes (adaptation, ecological specialization, symbiosis, social interactions).

Online application to the graduate program is free.

Our group occupies a new (2002) building complete with our own DNA sequencing facility, abundant environmentally controlled rooms, and an adjoining state-of-the-art greenhouse. Vanderbilt researchers enjoy the participation of excellent undergraduates and the resources of a thriving medical center. Our beautiful campus is located in the heart of Nashville, a friendly and inexpensive city situated amidst the lush rolling hills of biologically diverse middle Tennessee. Graduate students receive generous stipends and are trained in a highly interactive inter-lab community.

Ecology & Evolution faculty, research interests include:

Patrick Abbot (abbot@uts.cc.texas.edu) social evolution, symbioses, molecular evolutionary genetics in insects and microbes

John Burke (john.m.burke@vanderbilt.edu) genetic basis of adaptation and speciation in plants

Dan Funk (daniel.j.funk@vanderbilt.edu) ecological specialization and speciation, phylogenetics, herbivorous insect biology

Manuel Leal (manuel.leal@vanderbilt.edu) animal communication and mate choice, predator-prey interactions, and sensory ecology in lizards

Dave McCauley (david.e.mccauley@vanderbilt.edu) population biology, population structure, local adaptation in plants and insects

For further information on research and graduate study at Vanderbilt, please consult our departmental web page at: http://sitemason.vanderbilt.edu/biosci. Specific questions can be directed to any of the above faculty.

Daniel Funk <daniel.j.funk@vanderbilt.edu>

Jobs

ArizonaStateU ComputationalBiol

Evolutionary Bioinformatics and Computational Biology

The School of Life Sciences and the Biodesign Institute at Arizona State University invite applications for a tenure-track assistant professor position in the area of bioinformatics relating to comparative and evolutionary genomics of humans and other animals. The candidate must have earned a doctoral level degree with a research emphasis in computational biology, population genetics, or molecular evolution. Preference will be given to candidates with research programs that emphasize theoretical and/or informatics-based analysis of genome sequence and polymorphism data. Applicant should show exceptional promise of establishing a vigorous, extramurally-funded research program, and will be expected to participate in undergraduate, graduate, and interdisciplinary training in the School of Life Sciences (http://sols.asu.edu). Senior assistant professors with vibrant research and teaching portfolios are also encouraged to apply. Selected individual will be housed in the Center for Evolutionary Functional Genomics (http://www.biodesign.org/efg) in the Biodesign Institute (http://www.biodesign.org), which contains state-of-the-art computing infrastructure for informatics research. Please send curriculum vitae, statements of research and teaching interests, and names and mailing addresses (e-mail and postal) of at least three references to Chair, Bioinformatics Search Committee, Arizona State University, P.O. Box 874501, Tempe, AZ 85287-4501. Inquiries, but not application materials, may be sent by email. E-mail: sols@asu.edu. The closing date for receipt of applications is December 27, 2004; if not filled, applications will be evaluated weekly thereafter until the search is closed. Anticipated start date is August 16, 2005.

Arizona State University is an Equal Opportunity/Affirmative Action Employer.

Brian C. Verrelli Center for Evolutionary Functional Genomics The Biodesign Institute Arizona State University (brian.verrelli@asu.edu)

Boston AntimicrobialUse

Applied Research Director for International Public Health

Opportunity for trained investigator to conduct studies concerning antimicrobial use and resistance.

Qualifications Ph.D. or M.D. with at least three years of post-doctoral experience in microbiology, epidemiology, population biology or related discipline; team management experience; a track record in peer reviewed publications and grant development. Mathematical modeling/risk analysis and infectious disease experience helpful.

Responsibilities Leads the organization's research activities. Serves as principal investigator on NIH projects and manager of scientific consortia and staff engaged in applied research and grant writing concerning infectious diseases.

§Oversees research coordination and consultant team §Designs scientific/clinical research objectives §Engages APUA's scientific advisory board §Analyses laboratory data on incidence and prevalence of infectious diseases §Develops and applies statistical methodologies for analyzing data §Takes the lead in large scientific meetings §Prepares and presents reports and articles for peer review §Prepares and oversees grant proposals §Represents organization at various national and international meetings §Develops global and organizational partnerships

The Alliance for the Prudent Use of Antibiotics (APUA) is a global organization dedicated to improving antimicrobial use through research and education. Founded in 1981 and located on the Tufts Medical School campus in Boston, APUA conducts its public health programs in coordination with affiliated chapters in over 50 countries and the leading national and international public health organizations.

Please forward resume and CV to: APUA Human Resources 75 Kneeland Street Boston, MA 02111-1901 apua-eaa@tufts.edu

Visit www.apua.org for more information about the Alliance for the Prudent Use of Antibiotics.

Revised: 12/29/04

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Jennifer Deerinwater Operations Department ALLIANCE FOR THE PRUDENT USE OF ANTIBIOTICS 75 Kneeland St Boston, MA 02145 Tel: (617)636-0966 Fax: (617)636-3999 www.apua.org med024 <med024@granite.tufts.edu>

BostonU MinoritySummerResearch

Dear Colleagues,

We are announcing the launch of The Diversity Project, a new research opportunity for under-represented minority undergraduate students, beginning in Summer 2005 at Boston University. Students will integrate hands-on field research on Indonesian coral reefs and cutting edge genetic research at the Marine Biological Laboratory, Woods Hole, Massachusetts. The project will explore the origins marine biodiversity in an effort to improve conservation of these remarkable ecosystems. Students are fully funded for both living and travel expenses. Visit http://people.bu.edu/pbarber/-Intro.htm for more information and on-line application. This research opportunity promises to be a remarkable personal and professional experience. Please encourage any students whom you believe would benefit from such an experience to apply. For further information, please contact Dr. Paul Barber (pbarber@bu.edu). We look forward to hearing from you.

Sincerely, Paul Barber

– Dr. Paul H. Barber Boston University Boston University Marine Program 7 MBL Street Woods Hole, MA 02543 (508)289-7685 phone (508)289-7950 FAX pbarber@bu.edu http://people.bu.edu/pbarber/ pbarber@bu.edu

CorvallisOR Tech AdaptationGenetics

GS-0404-07 Biological Technician (13-month term), PNW Research Station, Forestry Sciences Laboratory, Corvallis, OR

The Genetics Team of the PNW Research Station will soon be advertising for a Biological Technician as part of a research study on the genetics adaptation and evolution in bitterbrush, a key restoration shrub of the Intermountain West.

This 13-month research support position, funded via USDA-NRI competitive funds, will be located at the Forestry Sciences Laboratory in Corvallis, OR. The position will involve a range-wide survey of molecular genetic diversity in bitterbrush using plastid and nuclear DNA markers. The position will also include field work at common garden sites in Madras, OR and Powell Butte, OR, and will involve routine measurements of bitterbrush plants. Successful applicants will possess training in biology, botany, chemistry or molecular genetics, and will have demonstrated molecular and field experience.

The Forestry Sciences Laboratory is located in Corvallis, OR, and is about 90 minutes south of the Portland Metro area in the center of the Willamette Valley. Proximity to the Cascades, the spectacular Oregon coast, Oregon State University, and an excellent quality of life combine to make Corvallis a one-a-kind community. For more information on the community, you can contact the Chamber of Commerce (541-757-1505), look at our local newspaper (www.gtconnect.com/), or visit the City of Corvallis website at www.ci.corvallis.or.us/ . Anyone interested in further information or in receiving a copy of the vacancy announcement when it opens should contact Dr. Richard Cronn (541-750-7291; rcronn@fs.fed.us) before 12/31/2004. Announcements for this and other USDA Forest Service positions are posted on USA Jobs (http://www.usajobs.opm.gov/).

Note: The purpose of this Outreach Notice is to determine the potential applicant pool for the position, and to establish the appropriate recruitment method and area of consideration for the advertisement. Responses received from this outreach notice will be relied upon to make this determination

rcronn@fs.fed.us

EastTennesseeStateU EvolInvertZool

Assistant Professor, Invertebrate Zoologist. Department of Biological Sciences, East Tennessee State University. Tenure track, 9-month, assistant professor beginning August 15, 2005. Responsibilities include teaching introductory biology, invertebrate zoology, and upper level/graduate courses in area of specialization. Qualifications: Ph.D. required by start date; expectations include development of extramurally funded research involving B.S. and M.S. students; preference given to applicants with post-doctoral experience, expertise in community ecology and potential for research in Appalachia. The new faculty member will join a department with a diverse group of 13 faculty members whose interests range from molecular through population biology. The department serves over 200 majors and about 20 M.S. students. Each year, over 800 students enroll in our general education sequences, including separate courses with labs for biology majors and non-majors. The department has full research capabilities in molecular biology and an interdisciplinary Institute of Quantitative Biology in cooperation with the Department of Mathematics. Specialized facilities include an open computer lab, multimedia classrooms, internet access in every lab/classroom, two greenhouses, a dedicated undergraduate research facility, herbarium, and animal care facilities. Opportunities also exist for collaboration with departments of chemistry, health sciences, environmental health and various departments in the Quillen College of Medicine. Deliberations will begin on February 1, 2005 and continue until the position is filled. Women and other underrepresented groups are encouraged to apply. More information available at http://www.etsu.edu/biology. Send a letter of application, complete curriculum vitae, statements of teaching philosophy and research interests, copies of transcripts, and three letters of reference to Dr. Rebecca Pyles, Invertebrate Zoology Search Committee, at pylesr@etsu.edu.

–

Lev Yampolsky

Department of Biological Sciences East Tennessee State University Johnson City TN 37614-1710 Phone 423-439-4359 Fax 423-439-5958

Lev Yampolsky <yampolsk@etsu.edu>

HarvardU EvoDevo

EVOLUTIONARY DEVELOPMENTAL BIOLOGY

Harvard University Department of Organismic and Evolutionary Biology

The Department of Organismic and Evolutionary Biology (OEB) at Harvard University invites applications for one or more faculty positions in the field of evolutionary developmental biology. Candidates will be considered for appointment at either junior or senior levels. We seek outstanding scientists who will establish an empirical research program dealing with plants or animals (vertebrates or invertebrates) and who will teach both undergraduate and graduate students. We are especially interested in individuals who conduct rigorous, experimental tests of general problems in evolutionary developmental biology, and who employ molecular, genetic, morphological, functional, and/or phylogenetic approaches. Applications from or information about women and minority candidates are encouraged.

This search is part of a broader initiative to develop a large and comprehensive research program in evolutionary developmental biology at Harvard University, which will involve several departments in both the Faculty of Arts and Sciences and Harvard Medical School. Applicants should submit a curriculum vitae, statements of research and teaching interests, representative publications, and the names and addresses of three references to James Hanken, Director, Museum of Comparative Zoology, 26 Oxford Street, Cambridge, MA 02138, USA. Letters of nomination from third parties are also welcome. Review of applications and nominations will begin December 15, 2004.

Further information about OEB is available at its website: <http://www.oeb.harvard.edu>. Send e-mail inquiries to <aschellhammer@oeb.harvard.edu>.

Harvard University is an Affirmative Action/Equal Opportunity Employer.

sedwards@fas.harvard.edu

HarvardU Neuroethology

NEUROETHOLOGY Harvard University Department of Organismic and Evolutionary Biology

The Department of Organismic and Evolutionary Biology at Harvard University invites applications for one or more appointments at either a senior or junior rank in the field of neuroethology. We seek an outstanding scientist who will establish an empirical research program and teach both undergraduate and graduate students. The candidate would also be a member of the newly formed Center for Brain Science at Harvard with the opportunity to interact with faculty from other departments in the Faculty for Arts and Sciences and Harvard Medical School. We are especially interested in individuals who conduct rigorous, field and/or laboratory-based tests of general problems in neuroethology, and who employ genomic, neurobiological, endocrinological and/or behavioral approaches. We encourage applications from or information about women and minority candidates.

Applicants should submit a curriculum vitae, statements of research and teaching interests and representative publications, and should arrange for three letters of reference to be sent to Naomi E. Pierce, Chair, Neuroethology Search, Department of Organismic and Evolutionary Biology, 26 Oxford Street, Cambridge, MA 02138, USA. Nominations from third parties are also welcome. Review of applications and nominations will begin December 20, 2004.

Further information about the Department is available at its website: <http://www.oeb.harvard.edu> .Harvard University is an Affirmative Action/Equal Opportunity Employer.

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Naomi E. Pierce Hessel Professor of Biology Museum of Comparative Zoology Labs 26 Oxford Street Cambridge, Massachusetts 02138-2902 USA TEL: (617) 495-2576 (office) (617) 495 4012 (lab) FAX: (617) 495-5667 npierce@oeb.harvard.edu

Naomi Pierce <npierce@oeb.harvard.edu>

IRD France InsectPopDynamics

Dear Colleagues,

A full position for an ecologist specialized in insect population dynamics is open at IRD (Institut de Recherche pour le Développement), France. We are looking for an ecologist having a good knowledge in insect population dynamics and modelling and willing to work overseas on tropical models of economic importance. The recruited ecologist will work in a team of the IRD 072 Research Unit with population geneticists and specialists of biological control. He will first study a community of tropical phytophagous insects including invasive species in the Andean area of South America. A good knowledge about invasive species ecology will be appreciated. Application forms are available at IRD web site : http://www.ird.fr (English version then Recruitment and training)(concours CR1 n13). A knowledge of French language will be useful. In the French system a “Chargé de recherche de 1ère classe” is a researcher having between 5 and 10 years of professionnal experience after his PhD. For more detailed informations about this position, please contact J.F. Silvain, Head of the IRD Research Unit 072 “Biodiversity and evolution of plant - phytophagous insects - antagonists complexes” (silvain@pge.cnrs-gif.fr). Please, do not hesitate to spread this announcement.

Sincerely,

J.-F. SILVAIN

– Jean-Franois SILVAIN

Directeur de l’unité de recherche IRD “Biodiversité et évolution des complexes plantes-insectes ravageurs-antagonistes” (R072) c/o CNRS, Lab. Populations, Génétique et Evolution Bat. 13, BP1, 91198 Gif-sur-Yvette cedex Tél : 33 (0)1 69 82 37 38 Fax : 33 (0)1 69 07 04 21 Courriel : silvain@pge.cnrs-gif.fr

IndianaU ResearchAssoc

The Rieseberg Lab at Indiana University is seeking a temporary Research Associate to assist in greenhouse and molecular biology research from January through August of 2005 (with the possibility of an extension after this time, depending on lab funding).

Duties will primarily consist of carrying out greenhouse experiments with sunflowers (pollination crosses, seed germinations, and plant maintenance) as well as routine molecular biology techniques (including, but not limited to, DNA extraction, PCR, and microsatellite genotyping). Assistance with field experiments (seed germination, planting, phenotyping plants) and general lab maintenance will also be expected.

Preference will be given to candidates with relevant experience and who have demonstrated interest in pursuing scientific research.

Minimum skills: -Bachelor's degree in Biology, Molecular and Cellular Biology, Genetics or related field -Basic computer skills including word processing (Microsoft Word) and spread sheets (Microsoft Excel) -Ability to work independently, to assist graduate students and post-docs, and to work on multiple projects simultaneously

Pay dependent upon education and experience.

Position open until filled.

The Rieseberg lab uses a combination of genetic and ecological approaches to address questions in the areas of speciation, domestication, and conservation biology. For more information on the lab, please see http://www.bio.indiana.edu/-facultyresearch/faculty/Rieseberg.html For more information on this position, please contact either Amanda Posto (aposto@indiana.edu) or Eric Baack (ebaack@indiana.edu) by E-mail or phone (855-9018).

Eric Baack 325 Jordan Hall, Dept. of Biology, Indiana University 1001 E 3rd St Bloomington, IN 47405 ph: (812) 855-9018 fax: (812) 855-6705

IndianaUSouthBend Bioinformatics

Indiana University South Bend seeks a tenure-track Assistant Professor of Bioinformatics starting August 2005. We seek a candidate who uses modern experimental and computational tools in genomics and/or proteomics to address basic biological questions. A Ph.D. in bioinformatics or related field is required. Postdoctoral experience is preferred. Teaching responsibilities will include undergraduate courses in bioinformatics, introductory biology and others related to the individual's area of expertise. The successful candidate will have the potential for excellence in undergraduate teaching and for developing an externally funded research program that will involve undergraduate and Master's students. Send curriculum vitae, statements of research interests and teaching philosophy, and three letters of recommendation to: Chair of Search Committee, Department of Biological Sciences, Indiana University South Bend, 1700 Mishawaka Avenue, South Bend IN 46615. Applicant review begins December 15, 2004, until position is filled. IUSB is an Affirmative Action/Equal Opportunity Employer and encourages applications from all qualified candidates.

dmarr@iusb.edu dmarr@iusb.edu

Madrid VolunteerFieldAssist

BIRD RESEARCH IN SPAIN: VOLUNTEER FIELD ASSISTANTS NEEDED

Our group (4 people) is studying several questions about the evolutionary biology of a population of Spotless Starlings nesting in nest boxes in an oak wood 50 km. from Madrid. We are looking for field assistants with preferably some field experience in bird ringing and observation. Work will involve capturing, measuring an ringing adult birds and nestlings, setting video cameras in nest-boxes and scoring behaviour from tapes and direct observation. Our fieldwork extends from late March to early July. We are willing to accept people that could stay for periods of at least two months within that time. We can offer free accommodation in our nearby field station as well as a weekly contribution towards food expenses.

If interested please contact Diego Gil (dgil@mncn.csic.es)

Diego Gil Departamento de Ecología Evolutiva Museo Nacional de Ciencias Naturales (CSIC) José Gutiérrez Abascal, 2 28006 Madrid Spain

------- Diego Gil Departamento de Ecología Evolutiva Museo Nacional de Ciencias Naturales (CSIC) José Gutiérrez Abascal, 2 28006 Madrid Spain

Tel: 00 34 91 411 13 28, ext. 1111 Fax: 00 34 91 564 50 78 email: dgil@mncn.csic.es

Oslo FieldAssist

BIRD RESEARCH IN NORWAY: FIELD ASSISTANTS NEEDED

We are looking for two field assistants in a study on the singing and spatial behaviour of great tits (Parus major) in Norway. The project is run in the surroundings of Oslo, under the supervision of Prof. Dr. Tore Slagsvold, between approximately 10 of April and end of May 2005.

Applicants are expected to sleep in their own tents at the field site, so a robust tolerance for cold weather and some enthusiasm for outdoor experiences is needed. Usually, however, most blizzards have already passed by at the time of field work.

We will observe our subjects throughout the breeding season, each day from before sunrise until after sunset. The assistants will

- monitor singing activity and territorial behaviour - help to catch birds - use radio telemetry to track the birds.

As a contribution towards expenses, we pay 800 euro for the field season.

Please send applications per e-mail, including CV, cover letter, and two addresses of references to

Dr. Valentin Amrhein

e-mail: anax.pca@wanadoo.fr

Research Station Petite Camargue Alsacienne University of Basel (Switzerland) Rue de la Pisciculture 68300 Saint-Louis France

UAlaskaAnchorage EvolutionaryMolPhysiologist

Endocrinologist or Molecular Physiologist University of Alaska Anchorage PCN: 304065

The University of Alaska-Anchorage invites applications for a tenure-track, tripartite faculty position at the assistant professor level in the Department of Biological Sciences The Department of Biological Sciences offers undergraduate (BS, BA) and graduate (MS) degrees in Biological Sciences, and collaborates with the University of Alaska Fairbanks to confer a PhD degree. The Department is the academic home to 17 tenure-track faculty, 2 part-time faculty, and 5 tenured faculty of the Biomedical Program (WWAMI). Academic and research focus areas within the Department include cell and molecular biology, ecology/evolutionary biology, and environmental physiology. The Department is strongly devoted to teaching excellence, strong science, and collaborative integration in teaching and research. Additional details regarding the Department's faculty and research interests can be found at biology.uaa.alaska.edu.

Responsibilities: The incumbent develops a strong research program in the area of endocrinology or molecular physiology, obtains extramural funding, and contributes to the development of the integrative physiology research group within Alaska Experimental Programs to Stimulate Competitive Research. The assistant professor teaches two courses and one graduate seminar per year. The standard 5-parts workload consists of 3-parts research, 1-part teaching, and 1-part university and/or public service.

Qualifications: APh.D. in biology or relevant scientific field is required. Candidate must have prior postdoctoral research experience; first authored a publication in a refereed journal; and previous teaching/research experience in a relevant area. Applicant must have demonstrated ability to obtain extramural funding and establish an independent research program.

Review Date: Review of applications will begin on January 27, 2005, and will continue until position is successfully filled.

Application Process: We do not accept application materials via e-mail. Please carefully follow the specific instructions given on each vacancy announcement. Please direct inquiries to Dr. Ian van Tets, Department of Biological Sciences, via email (afivt@uaa.alaska.edu) or by telephone (907.786.4705). The application packet for this position must include: * A University of Alaska Applicant Form - mandatory when applying for any UA position (available on our website at www.uaa.alaska.edu/uaahrs); * A cover letter (please note the PCN304065 on your cover letter); * A detailed professional vita containing educational preparation, work experience, research and publications; * Copies of teaching/student evaluations; * The names, email addresses,and telephone numbers of three (3) professional references; and * Copy of college transcripts verifying terminal degree (official transcripts will be required prior to hiring).

Please submit the application packet to: Human Resource Services University of Alaska Anchorage Administration Building, Rm 125 (Physical Address) 3211 Providence Drive(Mailing Address) Anchorage, AK 99508-4614

The complete vacancy announcement is available on the UAA/HRS website at www.finsys.uaa.alaska.edu/uaahrs or in UAA's Human Resource Services office located in the Administration Building on Alumni Drive, Anchorage, Alaska. Telephone: (907) 786-4608; Hearing Impaired TTY Phone: (907) 786-1420.

UAA is an AA/EO employer & educational institution. Applications for employment are subject to public disclosure under the Alaska Public Records Act.

UArizona EvolCurriculum

Coordinator of Advising and Curriculum Development

The Department of Ecology and Evolutionary Biology at the University of Arizona is seeking candidates for a full time position to coordinate advising and curriculum development for our department. This is a year-to-year appointed position. The person will be expected to have an extensive background in ecology, evolution and general biology and will interface regularly with faculty regarding advising and curriculum development. Duties include regularly advising and counseling students on academic, curricular, career and personal issues, and developing recruitment, advising and orientation programs and materials. This person will have a strategic role, along with academic faculty, in improving and expanding our undergraduate program in all aspects, including curriculum-related issues. Additionally, this person will supervise the undergraduate and graduate advising staff and coordinate interactions with College of Science advising personnel. Interested applicants must submit their materials at www.uacareertrack.com <http://www.uacareertrack.com/> (Job #31735).

Duties and Responsibilities:

* Hire, train and supervise advising staff. * Educate advising staff on advising practices and principles as necessary. * Advise and council undergraduate students on a day to day basis. * Maintain current and accurate records on students' advising and progress. * Conduct recruitment and orientation functions. * Create and distribute curriculum and advising documents. * Design and implement new approaches to advising and recruitment. * Track placement of EEB graduates. * Network at a professional level with faculty regarding advising and curriculum development. * Help develop a strategic curriculum plan for the three EEB majors.

Minimum Qualifications:

* Masters degree in Ecology and Evolutionary Biology or related field. * Experience in program coordination. * Excellent communication and teamwork skills.

Preferred Qualifications:

* Ph.D. in Ecology and Evolutionary Biology or related field. * Knowledge of University policies and procedures regarding undergraduate and graduate student admissions and academic progression. * Familiarity with College of Science curriculum content and requirements. * Experience in advising at the undergraduate level. * Good understanding of teaching and learning skills.

Amanda Burke <ajburke@email.arizona.edu>

UCaliforniaRiverside MolEvol

Faculty Position: Molecular Evolution

The Institute for Integrative Genome Biology at the University of California, Riverside (UCR) invites outstanding applications for an open-level position (assistant, associate or full professor) in molecular evolution or other areas of molecular genetics and genomics. The candidate will join a growing, interdisciplinary Institute with broad interests in genomics and post-genomics biology, and will be appointed as a faculty member in the UCR department of his/her discipline. The Institute is a major campus initiative that brings together researchers from various biological disciplines, as well as computational, physical and social sciences (http://www.genomics.ucr.edu/). The Institute also operates a Core Instrumentation Facility, providing centralized, shared-use equipment in genomics, proteomics, microscopy and imaging, and bioinformatics. The successful candidate would be expected to establish and maintain a vigorous, innovative research program, and have a strong commitment to excellence in teaching at the undergraduate and graduate levels. Applicants must hold a Ph.D., and postdoctoral experience is essential for candidates at the assistant level. Review of applications will begin January 1, 2005, with appointment as early as July 1, 2005. Applications will be accepted until the position is filled. Applications should include a curriculum vita, statement of research and teaching interests, and have letters of three references sent (assistant level) or provide names and addresses of three references (associate and full level) to: Dr. Jian-Kang Zhu, Director, Institute for Integrative Genome Biology, 2132 Batchelor Hall, University of California, Riverside, CA 92521. The University of California is an Equal Opportunity/Affirmative Action Employer.

Norman Ellstrand <ellstrand@ucr.edu>

UCanterbury GeneticsConservationEvolution

UNIVERSITY OF CANTERBURY

School of Biological Sciences Christchurch, New Zealand

Lecturer in Genetics, Conservation and Evolutionary Biology

The School is seeking to a make a fixed-term appointment in Genetics, Conservation and Evolutionary Biology to enhance its teaching and research capacity in these areas while the permanent staff fulfil their research grant commitments. The successful applicant will be expected to demonstrate academic excellence in their teaching and research by carrying out innovative and effective lectures and laboratory classes, publishing their research at the highest level as assessed by peer-reviewed publications, generating external research funding, and aiding the supervision of postgraduate students.

The School of Biological Sciences has a high national and international profile. We have an excellent teaching and research infrastructure and in a recent government survey, we were judged among the top research departments at the University of Canterbury . For more information on the School of Biological Sciences see the webpage www.biol.canterbury.ac.nz .

Further details about the position are available at http://www.canterbury.ac.nz/hr/vacancies/science/bs13701_0105.shtml .

For more information on the position please contact Professor Paula Jameson email: paula.jameson@canterbury.ac.nz

For information on the City of Christchurch see www.ccc.govt.nz . Applications should include the official application form, curriculum vitae, together with separate statements of: recent research achievements; research goals; expected teaching contributions, including a list of the courses within the School the applicant could teach into; and the names and contact information of three referees.

The closing date is 10 January 2005. Anticipated start date 1 March 2005.

All applications should be sent to The Human Resources Administrator, College of Science , University of Canterbury , Private Bag 4800, Christchurch , New Zealand . Email: hr@science.canterbury.ac.nz .

Bruce Waldman <bruce.waldman@canterbury.ac.nz>

UConnecticut Bioinformatics

Bioinformatics Scientist Academic Assistant II/III

The University of Connecticut seeks a Bioinformatics Scientist Academic Assistant II/III) to serve the biological science community by working within a newly formed Bioinformatics Facility in the Biotechnology/Bioservices Center. Qualifications include a M.S. or Ph.D. in bioinformatics and experience or the equivalent skills to handle problems in genomics, gene and protein expression analysis, database mining, molecular modeling and programming, and structure- function domain analysis. Highly desirable are 2 years post M.S. work experience. The successful candidate will have an excellent command of verbal and written communication skills and must use them effectively. Salary commensurate with qualifications. Please go to our website: http://www.ucc.uconn.edu/˜wwwbiotc/bioinfrm.html for a detailed job description. This position is subject to annual renewal. Screening of candidates will begin January 3, 2005.

Interested candidates should submit a cover letter, curriculum vitae, and have three letters from professional referees sent to: Sue Levesque, Search Committee Secretary,Biotechnology/Bioservices Center, University of Connecticut, 91 North Eagleville Road, Unit 3149, Storrs, CT 06269-3149. The University of Connecticut actively solicits applications from minorities, women, and people with disabilities.

biotctr1@uconnvm.uconn.edu

UConnecticut EvolGenomics ResTech

RESEARCH ASSISTANT II:

The Townsend Laboratory and the Center for Applied Genetics and Technology are seeking a full time (40 hours per week) Research Assistant II.

Responsibilities Include: Technical assistance in the operation of the Center's two microarray systems, and participation in research projects utilizing them, under the general direction of the two Microarray Instrumentation Supervisors. The ideal candidate will be able to: independently carry out established methods; test and modify or custom-design equipment under supervision; perform a variety of specialized and standard molecular biological tasks; operate, maintain, calibrate, trouble-shoot and resolve ordinary problems with complex instruments and equipment which may require substantial training and judgment to use safely and proficiently; and maintain adequate inventory of supplies.

Qualifications Include: Minimum qualification is a Bachelor's degree in biology/genetics/microbiology or equivalent combination of education and experience, with one to three years experience in a similar position. A Master's of Science degree in a biological or technical field, or experience with microarray technology is desirable.

Application Process: Please send cover letter, resume, and the names and telephone numbers of three references to: Dr. Linda Strausbaugh, University of Connecticut, Department of Molecular and Cell Biology, 354 Mansfield Road, Unit 2131, Storrs, CT 06269-2131. Application deadline is January 1, 2005.

Jeffrey P. Townsend, Ph.D.

Assistant Professor Molecular and Cell Biology Department University of Connecticut Storrs, CT 06269 Storrs, CT 06269

UNICAMP Brazil EvolGenetics

Faculty position in Genetics and Evolution at UNICAMP (Brazil)

Deadline for applications: December 23, 2004

The "Departamento de Genética e Evoluão" of the State University of Campinas (UNICAMP, SP, Brazil) invites applications for a tenure track position in Genetics and Evolution. The minimum requirements are a PhD degree and population genetics knowledge. The evaluation process will take place between January and March 2005, and will include an exam and interview in Portuguese.

For further information and inquiries see the website:

http://www.sg.unicamp.br/procsel/-ConsultaProcessoST.asp Sónia Cristina da Silva Andrade Pós graduaão em Genética e Biologia Molecular Laboratório de Diversidade Genética Depto. de Genética e Evoluão IB-UNICAMP CxP 6109 CEP 13083-970 fax +551937886235

e-mail: soniac@unicamp.br soniacsandrade@hotmail.com

UOxford Ornithology

UNIVERSITY OF OXFORD

Edward Grey Institute

Department of Zoology

Research Fellow in Ornithology Salary on the RS1A Scale (range: £19460 - £29128)

Applications are invited for a position as Research Fellow in Ornithology, as part of the Edward Grey Institute of Field Ornithology in the Department of Zoology (see http://egizoosrv.zoo.ox.ac.uk/EGI/-EGIHome.htm). The main duties of the post holder will be to conduct research into ornithology that complements the existing strengths and interests of the institute, and to develop an independently-funded research programme in ornithology. The successful applicant will have a strong research record in any area of ornithology with relevance to behaviour, conservation, ecology or evolution of wild populations. Candidates from other fields, but with a strong desire to work in ornithology, and with clearly transferable skills, may also apply. Candidates should possess a doctorate in ornithology or a related subject, but have no more than four years' postdoctoral experience by 30 September 2005.

The position is available for two years with the possibility of extension for a further two years. The starting date is negotiable, but it is expected that the successful candidate will be in position from May 2005.

Further particulars are available from lisa.harris@zoo.ox.ac.uk or from our website http://-www.zoo.ox.ac.uk/ (click on the jobs link). Applications (electronic copies are acceptable) should include a full curriculum vitae, copies of three of the applicant's most significant publications, and a 2000 word proposal giving details of the applicant's past (500 words) and proposed (1500 words) research, together with the names and full contact details for three referees. Applications should be addressed to the Head of Department, Professor P.H. Harvey FRS, Department of Zoology, Tinbergen Building, South Parks Road, Oxford OX1 3PS (e-mail: lisa.harris@zoology.oxford.ac.uk), quoting reference number AT04056. Informal enquiries can be addressed to Professor Ben Sheldon (ben.sheldon@zoology.oxford.ac.uk). The closing date for applications is 21 January 2005. Interviews are likely to take place early in February 2005; those interviewed will be expected to give a brief presentation of their research achievements and objectives.

UPennsylvania DiseaseEcolEvol

Position in Disease Ecology and Evolution, University of Pennsylvania

The advertisement below recently appeared in Science and Nature and on Evoldir. In reposting to Evoldir we would like to emphasize that this search is very broad-minded and we would welcome applicants working in any aspect of disease ecology and evolution, on any organisms. Also, although the target date for applications is 10 January, please note that we will continue to consider applications until the position is filled.

Faculty Position in Disease Ecology Department of Biology University of Pennsylvania

The Department of Biology at The University of Pennsylvania expects to make a tenure track appointment in Ecology with a starting date of July 2006. We are seeking a broadly trained scientist whose research addresses the ecology of diseases of natural animal or plant populations. The ideal individual would possess empirical and theoretical strengths in ecology that are complemented by molecular and microbiological approaches. Specific areas of interest include, but are not limited to, epidemiology and ecology of emerging diseases, ecology of microbial pathogens, and molecular evolution of pathogens in natural populations. The successful candidate will interact with existing faculty whose strengths lie in population and community ecology, evolutionary biology, microbial biology, genomics, and the traditional areas of cell and molecular biology.

Candidates will be expected to teach at the undergraduate and graduate levels in addition to maintaining a vigorous, independent research program. It is anticipated that this appointment will be made at the Assistant Professor level. An appointment at the associate or full professor level with tenure might be available for an exceptionally well-qualified candidate. Applicants should submit statements of research and teaching, curriculum vitae, and representative reprints or manuscripts to:

Chair, Ecology Search Committee Department of Biology University of Pennsylvania Philadelphia, PA 19104-6018

Applicants for this position at the Assistant Professor level should also arrange to have 3 letters of recommendation sent to the search committee. Review of applications will begin January 10, 2005 and continue until the position is filled. Further information about the Department of Biology can be found at www.bio.upenn.edu . The University of Pennsylvania is an Affirmative Action/Equal Opportunity Employer. Women and minorities are encouraged to apply.

paulsnie@sas.upenn.edu paulsnie@sas.upenn.edu

UPennsylvania DiseaseEvol

Faculty Position in Disease Ecology Department of Biology University of Pennsylvania

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Chair, Ecology Search Committee Department of Biology University of Pennsylvania Philadelphia, PA 19104-6018

Applicants for this position at the Assistant Professor level should also arrange to have 3 letters of recommendation sent to the search committee. Deadline for the receipt of applications is 10 January 2005. Further information about the Department of Biology can be found at www.bio.upenn.edu The University of Pennsylvania is an Affirmative Action/Equal Opportunity Employer. Women and minorities are encouraged to apply.

paulsnie@sas.upenn.edu paulsnie@sas.upenn.edu

USheffield microsats

The following research assistant post was advertised in New Scientist on 9 and 16 December 2004.

UNIVERSITY OF SHEFFIELD DEPARTMENT OF ANIMAL & PLANT SCIENCES

A research assistant is required to assist the work of the Sheffield Molecular Genetics Facility, in particular in the development and genotyping of microsatellite markers for a wide range of taxa. Applicants must have a BSc degree or equivalent and significant research experience in molecular genetics or another relevant discipline. The post is available immediately for one year in the first instance. The Facility has been supported by the Natural Environment Research Council since 1998 and its funding was recently renewed for the period through to March 2008. A full-time post is available but applicants who wish to work on a part-time basis will be considered.

Salary on the RA1B scale (minimum UKP19,400 pa)

Closing date: 6 January 2005

Informal enquiries may be made to Professor T A Burke, Tel: 0114 222 0096 (e-mail: t.a.burke@sheffield.ac.uk).

Further information and details on how to make an application can be found at http://www.shef.ac.uk/jobs/ (under Current Vacancies/ Research)

(Post reference R3524)

t.a.burke@sheffield.ac.uk t.a.burke@sheffield.ac.uk

UWisconsinMilwaukee Zebrafish

The following position announcement has been advertised and review of applications will begin soon. We are looking for someone currently working with zebrafish or other small laboratory fishes. Applicants do not need to have experience in the area of environmental health, just a desire to apply fish model systems to this area. If you have questions, please contact Michael Carvan (carvanmj@uwm.edu) or David Petering (petering@uwm.edu).

ZEBRAFISH DEVELOPMENT AND ENVIRONMENTAL HEALTH

The University of Wisconsin-Milwaukee invites applications from outstanding scientists working on the zebrafish model system for a tenure track faculty position open at any rank (Assistant, Associate, or Full Professor) in the Department of Chemistry/ Biochemistry or Biological Sciences. The new faculty member will be part of an interdisciplinary research studying mechanisms of toxicity of chemicals that affect embryonic development and contribute to the onset of chronic disease. He or she will be able to interact with exceptionally strong groups in developmental biology, neuroscience, metal toxicology, signal transduction, endocrine disruption, and genomics affiliated with the NIEHS Marine and Freshwater Biomedical Sciences Center. Additional information can be found at http://www.uwm.edu/Dept/MFB/. Candidates should send their curriculum vitae, research plans, a statement of teaching interests, and three reference letters to: Dr. David Petering, Department of Chemistry and Biochemistry, PO Box 413, University of Wisconsin-Milwaukee, 53201-0413. Application review will begin on December 13, 2004 and continue until the position is filled. UW-Milwaukee is an equal opportunity/affirmative action employer.

Other

BiolMedSociety think tank

Biology, Medicine and Society

Dear colleagues,

I have great pleasure in informing you of the inauguration of a new think-tank in Montpellier on the theme: "Biology, Medicine and Society".

Progress in the biological and medical sciences has been rapid, pressed forward by the explosion in technology, in particular in genetics and genomics. These developments must be accompanied, supported, and put into perspective by parallel deliberation in the arenas of religion, psychology, psychoanalysis, history, philosophy and politics ("Politics" is not meant here in the sense of politicking, but rather as an elaboration of a vision of society and the world).

The dialogue between the hard sciences and the social sciences is a difficult one. Attitudes, sensibilities, and vocabulary differ. This dialogue, freed from all hegemonic temptation on both sides, is nevertheless essential if it is our ambition to draw up a new ethics and epistemology of biology that is truly adapted to our era. I believe that this enterprise responds to the expectations of many (most particularly students, whether they be in the biomedical sciences or the social sciences), and I find they are indispensable to revitalizing scientific thinking that personally I see falling into a state of total decay.

This scientific thought seems to me to be mainly weakened by scientific taboos, the "gurutizing of science" and the proliferation of irrational thinking.

Taboos: all subjects relating more or less to a biological vision of human nature are a priori heretic. Certain taboos have perverted and biased the scientific approach and, in a new "clerical treason" (Benda), have resulted in salvaging ideologies whose good intentions are not much on an excuse. Science has a duty to remain objective and neutral. "Only truth is revolutionary" (Gramsci). A modern ethics/epistemology of biology will be born only if it can be founded on a science liberated of every taboo.

Gurutizing of science: many of our colleagues have succumbed to the "guru" syndrome. Awarded with some title to glory in a very specialized domain, they proclaim themselves omniscient and pronounce oracles to decision-makers who are too easily misled by the aura of the learned scientist on subjects ranging from global warming to reproductive cloning, and the equality/inequality of Man. It is urgent that we return to truly rigorous scientific thinking, that we establish strict hierarchies between what has been solidly (but never definitively) established and the speculative. The credibility of science depends on it, given the:

Proliferation of irrational thinking: Scientific thinking is in decline, and science is in the throes of considerable mistrust from the public, who lend a receptive ear to a wide variety of demagogues. We must undoubtedly banish excessive scientism, smelling sweetly of the 19th century (the belief that science was capable of resolving all of society's problems and that only rational thinking was the source of true knowledge). However, when it is a matter of problems falling within the domain of science (GMOs, global warming, the biological component of human nature), obscurantism, superstition and the irrational should be combatted by revitalized scientific thinking.

The "Biology, Medicine and Society" (BMS) think-tank will be a place for multidisciplinary dialogue, hosting not only specialists (biologists, physicians, psychoanalysts, ethnologists, philosophers, people of letters and religion, historians, politicians, etc.), but it will also be a place for high school and university students, nonspecialist citizens, etc. We intend to make it a place of true debate, able to unite in a spirit of tolerance participants whose convictions may at first seem irreconcilable. A "debate" gathering protagonists who agree on nearly everything is about as exciting as a flat electroencephalogram. If the controversy focuses on the theory of evolution, it seems to me unacceptable not to listen to the point of view of the creationists. If the genetic diversity of the human species is on the table for debate, the holders of inegalitarian ideas should have the right to express themselves, under the strict condition that their attitude remains polite and does not contravene the laws in force. Moreover, a correct attitude will be required of everyone, and, for example, the intolerant and sarcastic behavior of certain scientists toward people of religious faith will not be tolerated in our debates.

The activities of the BMS will consist of oral debates and conferences, with rotating locations. A web site will be set up to accommodate written communications. These communications will be moderated. A true cyberjournal could thus be born. Later, if the group's activities develop encouragingly, the launch of a new scientific journal on the theme will be envisaged. The publisher

— / —

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

Evolution simulator

I was wondering if you are aware of any biomolecular sequence evolution simulator (such as Seq-Gen) that also simulates insertions and deletions.

Thank you.

Luay Nakhleh Dept. of Computer Science Rice University Houston, TX 77005

Luay Nakhleh <nakhleh@cs.rice.edu>

Evolution simulator answers

I received very helpful answers to my inquiry, that I'd like to forward to you so that you post them for those who may be interested.

Thank you very much. Luay

Luay Nakhleh <nakhleh@cs.rice.edu>o

Dear Luay,

I think the standard is ROSE (http://bibiserv.techfak.uni-bielefeld.de/rose/), but you might check out a recent paper by Webb Miller's group (attached) and contact Webb if you are interested in simulating non-coding DNA sequences.

Bests, Jim

Jim Leebens-Mack, PhD Department of Biology and Huck Institutes of the Life Sciences The Pennsylvania State University University Park, PA 16802

Ph: 814-865-3083 FAX:814-865-9131 jhl10@psu.edu

Dear Luay, Barry Hall has one. It's the only one I know of. You can contact him at drbh@mail.rochester.edu Miriam Barlow

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ROSE is published and has a simple mode of gap formation.

http://bibiserv.techfak.uni-bielefeld.de/rose/ I have written another, more powerful, application and am in the process of writting it up for publication.

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Reed A. Cartwright Phone: (706) 542-1448 Doctoral Student Fax: (706) 542-3910 University of Georgia Department of Genetics http://www.dererumnatura.us/ C232 Life Sciences Bldg http://www.pandasthumb.org/ Athens, GA 30602-7223 http://www.georgiascience.org/ ———

Hi, Try http://bibiserv.techfak.uni-bielefeld.de/rose/-best wishes Dr Georg Fuellen fuellen@alum.mit.edu - alum.mit.edu/www/fuellen/ - fax 49 251 83 21631 - fon 21637

Large Phylogenies editing answers

Hello, A month ago I asked two questions regarding large (>200 taxa) phylogenies. First, how to edit large phylogenies, and then how to present them for publication. So many people responded that I have split their replies into two postings. As I or others try out these suggestions, I recommend that we continue the online discussion.

First I asked: First I am seeking advice on software / instructions for converting a NEXUS tree into a publication quality image.

ANSWERS TO QUESTION ONE Answers included: Treeview,

TREEVIEW The program TreeView (http://taxonomy.zoology.gla.ac.uk/rod/treeview.html) can be used to display and save a NEXUS tree.

I most commonly use the printing facilities in PAUP*, but sometimes also use TreeView. I typically pretty-up my images for final presentation in a graphics editor, as I haven't found any tree-printing program that gives me enough flexibility to generate really sophisticated images. With that said, I'd be interested to hear what other folks tell you, and very interested in responses to your question about big trees.

TreeView is a free program that most people I know use to make pretty trees. It's pretty simple but works well. You can download the latest version here: http://darwin.zoology.gla.ac.uk/ ˜ rpage/treeviewx/. One funny thing is that in older versions you could specify a taxon to root the tree and now you can't so I'm going to download an older one also.

Regarding the publication quality image: I'd prepare the diagram with TreeView (http://taxonomy.zoology.gla.ac.uk/rod/treeview.html), then hack it into form as necessary using PowerPoint or Photoshop (rewriting labels, adding bootstrap values, and so on). [I personally have used PowerPoint in this manner and would NOT recommend it just doesnt come out as prettily as CorelDraw and other software JLC]

With respect to editing the trees: I save the picture image in Treeview (Rod Page's application to visualise NEXUS trees) as a windows metafile (yes, unfortunately, I am a windows user for text editing etc purposes...) and then import this file into Powerpoint for editing. You can also use Coreldraw or Adope Photoshop etc. You can then save the image of your tree as a .jpg file and import this one into your paper. If you are a UNIX user, there are even better graphics programs and importing it into Latex should be easy. However, I haven't used that root myself.

I suppose you will receive this advice 200 times, but I recommend TreeView http://taxonomy.zoology.gla.ac.uk/rod/treeview.html . TREEVIEW - CONVERTIBLE TO NEWICK? This link http://workshop.molecularevolution.org/resources/fileformats/tree_formats.ph p states that treeview (very similar to treetool) will not read Nexus, but the page gives instructions on how a Nexus format tree can be converted to the Newick format. However http://taxonomy.zoology.gla.ac.uk/rod/treeview/help/formats.html states that treeview will read Nexus format trees.

TREEGRAPH You might check into the software program TREEGRAPH. The reference journal article is as follows: Muller, J. and Muller, K. 2004. TREEGRAPH: automated drawing of complex figures using an extensible tree description format. Molecular Ecology Notes (online early - In press).

SAVE FROM MAC SCREEN, EDIT IN GRAPHICS SOFTWARE One option: You can open put your tree into PAUP using the “Get Trees” function. Then from the “Print Trees” window you can preview your tree and save it as a .pict file for use in any drawing program. I should note, however, that I think this will only work in the Macintosh version.

I just saw your message on Evoldir, and I've been struggling with the same issues. There is a simple way to make the trees graphically good (if you are using a Mac). When in Paup, use the command print tree, then instead of printing, press the preview button. A preview of the tree will appear, from there, just press the button “copy to clipboard” and paste the tree either on Corel Draw or Adoba Illustrator. You can edit it there and get very good results.

You could save the nexus tree as a pic in PAUP and then open the file with Adobe Illustrator. Once there you could edit the tree and create a publishable quality figure.

Is that NEXUS tree generated by a MAC or PC? With MACs you can just copy the tree into the clipboard (in the Print Preview window) and paste it in Word. Word will then allow you to make changes in that picture file according to your needs.

— / —

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

Large Phylogenies publishing answers

Hello, A month ago I asked two questions regarding large (>200 taxa) phylogenies. First, how to edit large phylogenies, and then how to present them for publication. So many people responded that I have split their replies into two postings. As I or others try out these suggestions, I recommend that we continue the online discussion.

My second question received not only helpful suggestions but also many emails asking for a copy of any suggestions. I am not the only one out there with this problem!!!!

The question was: Second, my tree contains >200 taxa. How are people handling such phylogenies for publication purposes? This is an issue that has not been adequately addressed by journals, and I am soliciting opinions on what should be done about this (especially since everyday phylogeny size gets larger and larger). Should the image be saved to the internet for download? Publish subtrees of interest with remainder as an online appendix? If so, what type of file?

ANSWERS TO QUESTION TWO

DONT KNOW HOW TO DO THIS Your question is very close to my heart. I am also currently writing a phylogeny paper with >200 taxa. I have not contemplated any solutions other than making the names very small to fit on an A4 size page. [this is just a sample of many similar responses JLC]

ENTIRE TREE AS FOLD-OUT I just published a large phylogeny as a fold out in the journal Phycologia. I will have to do this again as my next tree will have 438 taxa.

OVERVIEW, WITH SELECT SUBTREES I don't think I have ever seen a tree of that size published. Perhaps you can display an overview tree showing how the major groups present in your analysis are related and also show a few select subtrees. Post the complete 200+ member tree and any remaining subtrees as supplemental data on the web. High resolution GIF or PNG format images should provide sufficient image quality for trees at a very reasonable file size.

I've attached an example of a solution I've used for the big tree problem (although, I have only about 100 OTUs). Another option would be to break the tree in half and present it on 2 pages. [Thanks to Dave Weisrock for his trees, which reduced large internal clades to triangles, then presented the tree within the triangle as a separate figure. JLC]

I suggest you put the more interesting parts on the paper, and make a full tree available online (either at your site or as an electronic appendix to the paper at the journal's site). I just saw a paper with an appendix containing a tree that had several hundred taxa and was drawn over three pages.

I would be grateful if you could mail me other suggestions that you would receive. Personally, I would prefer to give a tree with basal relationships and general names of subtrees. Subtrees would then be presented separately. The whole tree should be available for download.

ENTIRE TREE ON MULTIPLE PAGES, DEPENDING ON THE POINT Working at the HIV Databases I routinely deal with phylogenetic trees containing over 1,000 taxa. How to best make a viewer of the tree understand the points I want to address, depends very much on which taxa are included, and what the overall pattern of the tree is. A tree built with 1,200 HIV-1 M group subtype B sequences plus a few subtype D for an outgroup is very "flat" and crowded on the B branch, so it usually requires a 6 or 7 page tree to show for example that sequences from one patient nearly always cluster together, indicating few dual or multiple infections.

On the other hand, a tree that includes a few hundred HIV-1 M group sequences, a few HIV-1 O group, plus SIVs from chimpanzees, sooty mangabeys, red capped mangabeys, African green monkeys and dozens of other non-human primate species does not require labelling of each individual sequence, I can just point to each major clade and label its species of origin.

CHECK THE HIV LITERATURE I think Bette's paper may give you some ideas. I like the way she saved not only the trees but the infiles with site-specific rates of evolution and other parameters pre-calculated. There are at least a hundred other HIV papers that cover trees of more than 1,000 taxa so you could get other ideas from them.

ONLINE APPENDIX, TREEBASE The Chase et al. (1993) phylogeny of angiosperm families has, if I remember, diagrams of the main clades which successively "explode" in on detail. But that takes several pages. (Ann. Mo. Bot. Gard., 80, 528-580.)

But such big phylogenies are no longer such massive news in themselves, and also, everyone working in the field is now likely to have the Internet.

I would go for your option "Publish subtrees of interest with remainder as an online appendix". The online appendix could have the trees in a PDF-format document. This seems to be the only widely useful, fairly system-independent format. (Do check it on a Mac and a PC though, as sometimes, weird things happen with the fonts.)

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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

Major Gene Tests

Dear EVOLDIR,

Does anyone know of a program that performs complex segregation analysis on data from crosses between inbred lines? I have biometric data from parental, F1, F2, and backcross generations from an interspecific cross and wish to test for the presence of a major gene influencing the trait of interest.

Thank you for your help

Nicola Barson

BarsonNJ@cf.ac.uk or nicolabarson@hotmail.com

Mesquite PDTREE

I'm trying to export independent contrasts from the program PDTREE (PDAP package), running in MESQUITE, to excel or SPSS. Anyone knows how to do it? Thanks, Tiana Kohlsdorf

– Tiana Kohlsdorf Department of Ecology and Evolutionary Biology Yale University 165 Prospect St. 06511 New Haven, CT, USA

tiana.kohlsdorf@yale.edu

Microsat cloning

Dear all,

I am currently cloning microsatellite loci for house sporrows, using an enrichment protocol based on biotinylated probes (Hamilton et al, BioTechniques 27:500-507; Paetkau, BioTechniques 26: 690-697; both 1999). Most of my microsatellite repeats are too close to the cloning site, so that I cannot design primers.

I remember that a couple of years ago someone else had similar problems and posted a question either on EvolDir or on the microsat newsgroup. Does anybody have a suggestion why most the repeats are so close to the cloning site, and how this problem could be rectified? Thanks in advance, happy holiday season everyone!

John PS: Please reply to wickie1988@yahoo.com

wickie1988@yahoo.com

Model generator

Hi, We have just completed the development of a fully self-contained substitution model selection application. Modelgenerator supports 28 amino acid models and 24 nucletoide models (base model with three optional rate distributions: Gamma, Invariable sites, and Gamma+Invariable sites). Model selection is performed using both the hLRT and AIK tests (Posada and Crandall, 2001). We have devised a modified hLRT for the amino acid models that has shown to be extremely effective in our simulated data tests (manuscript in preparation). Our tests have also shown the importance of using Modelgenerator when choosing a particular amino acid model - as arbitrarily choosing a model can lead to incorrect or suboptimal phylogenies. Unlike other popular modeltesting software, Modelgenerator does not require the installation of any other software package (e.g. PAUP*).

We invite you to try this application on your datasets and welcome any positive or negative feedback on the application.The application can be downloaded from: http://bioinf.may.ie/software/modelgenerator Cheers, Thomas

Posada, D. and Crandall, K.A. (2001) Selecting the Best-Fit Model of Nucleotide Substitution, Systematic Biology, 50(4), 580601

– Thomas Keane, Bioinformatics and Pharmacogenomics Lab, Department of Biology, National University of Ireland, Maynooth, Ireland.

http://www.cs.may.ie/distributed http://www.cs.may.ie/ ˜ tkeane E: thomas.m.keane@may.ie P: +353 1 708 6043 F: +353 1 708 3845

Outsourcing microsatellites

I would be happy if anyone could send some information about trustworthy companies or institutions dealing with microsatellite library construction (eventually also primer design) on a commercial basis. I believe the same inquiry has been directed to evoldir earlier (and I hope the answers obtained then can be redirected).

Kind regards,

PhD Håvard Kauserud E-mail: haavarka@bio.uio.no Department of Biology, University of Oslo, P.O.Box 1045 Blindern, N-0316 OSLO, NORWAY

Outsourcing sequencing

Dear all,

we are looking for companies or other institutions which would do fragment analysis (e.g. microsatellites) and/or DNA sequencing on a commercial basis.

Do you know of any companies? If so, how expensive are they and how reliable is their service?

I would be very grateful for any information you have. By the way, I intend to post the collected replies on Evoldir for everyone else interested in this topic, so please let me know if your information is open for reposting or whether it is confidential.

Many thanks in advance, best wishes,

Hinrich

Dr. Hinrich Schulenburg Department of Evolutionary Biology Institute for Animal Evolution and Ecology Westphalian Wilhelms-University Hufferstr. 1 48149 Muenster Germany Tel.: +49-251-8321019 or -8324664 Fax: +49-251-8324668 e-mail: hschulen@uni-muenster.de http://www.uni-muenster.de/biologie.evoeco/evolbio/

Hinrich Schulenburg <hschulen@uni-muenster.de>

Outsourcing sequencing answers

Dear all,

please find below the replies on my enquiry of outsourcing fragment analysis and DNA sequencing.

Many thanks for all the helpful replies, best wishes,

Hinrich

1) Hello, In France we have some corporations that can offer you this kind of prestations... don't you have something like that in Germany? We also have the "CNG" (National Centre for Genotyping) and maybe you could find more informations on their website : http://www.cng.fr/ best wishes Stéphane Fénart

2) Hallo Herr Schulenburg, wir könnten Ihre "auswärtigen Proben" sequenzieren und auch AFLPs laufen lassen. Wir haben hier einen ABI 3100 (16 Kapillaren). Im Moment kann ich Ihnen einen Preis von ca. 6,50 EUR per Primer anbieten, für AFLPs müssten wir erst noch kalkulieren. Sie sollten uns 16 oder ein Vielfaches von 16 schicken. Die Proben sollten wie folgt beschaffen sein: DNA in Wasser (80-100 ng/kb, max. Vol. 5 μl) und Primer (0,8 pmol/μl, 2 μl), zusammen ein max. Volumen von 7 μl. Dazu geben wir dann die Reaktionschemie (1 μl T-Puffer 5x und 2 μl Terminator Ready Reaction Mix) und führen alles weitere (Cycle-Sequencing und Run) durch. Den Preis von 6,50 EUR habe ich wie folgt kalkuliert: ca. 1 EUR für Medien am Sequenzer (Polymer, Kapillaren-Array etc.), ca. 1,50

EUR für Wartungsvertrag und ca. 4 EUR für Reaktionschemie. Wie weit wir das Enzym für Ihre Proben verdünnen können, müssen wir erst austesten - evtl. verringern sich die Kosten für die Chemie noch. Wir liefern Ihnen die ABI-Files per email.

Höre gerne von Ihnen! Mit freundlichen Grüßen Thomas Friedl

3) Dear Hinrich, We usually send our sequences to Macrogen (either PCR products or cloned sequences), and get good quality results; you can negociate godd prices too. Check their website: http://wgs.macrogen.com/ I would be interested in getting feed-back from your question concerning microsatellite services. Best wishes, Malika

4) Dear Hinrich “Macrogen” is a Corean company doing DNA sequencing. The prices seem to be cheap (around 5$ per sample, 7$ if purification needed, express postage paid). From what I’ve heard, results are reliable and given within a week (for customers from France for example). I don’t know if they propose other services. “Wildlife Genetics International” is a Canadian company proposing a wide range of services. See http://www.wildlifegenetics.ca/ This information is open. Regards, Thomas Broquet

5) Hi, I have been using sequencing services of Macrogen at Korea (www.macrogen.com). I am very satisfied with the quality and the price is just $5 if you provide the primers. If you send 10 or more samples, DHL or Fedex services are paid by them. Usually it takes around 8 days to get the results (days of travel included). Unfortunately, they don’t do fragment analysis. Maria Judite Alves, PhD

6) Lieber Hinrich! Wir nutzen den Sequenzierservice der Uni Mainz, der unter dem Firmennamen Genterprise (www.genterprise.de) läuft und sind damit sehr zufrieden. Den genauen Preis pro Sequenz weiss ich jetzt nicht auswendig, ist aber durch Verhandlung variabel - am besten dort anfragen! Mikrosatläufe sind dort ebenfalls möglich, das machen wir aber bei der firma ingenetix (wien, www.ingenetix.com) und sind auch dort sehr zufrieden. Reposting ist ok! Schöne Grüße aus Wien, Heino

7) Lieber Herr Schulenburg, ich lasse seit Jahren fuer diverse Projekte bei GATC Biotech, Konstanz, sequenzieren und bin sehr zufrieden. Die machen einen sehr guten Service, die Prozedur ist sehr komfortabel, und ich weiss, dass sie auch Mikrosatelliten-Analysen anbieten, habe den Service aber noch nicht benutzt. Hier ist der link: http://www.gatc.de/de/index.php Der Listenpreis fuer z.B. single read sequencing ist 17 EUR und umfasst Qualitaetscheck der DNA, bis 750 bp, die Proben werden einen Monat aufgehoben, sodass man eventuell mit anderen Primern spaeter sequenzieren kann, und die Sequenzierreaktion wird einmal wiederholt, falls der erste read nicht gut genug war (wenn man plausibel machen kann, dass da ein Problem bei denen aufgetaucht ist, machen sie es auf Anfrage auch ein drittes Mal. Sie sind sehr kulant und entgegenkommend). Sie koennen je nach Umfang der Auftraege spezielle Konditionen mit ihnen aushandeln. Fuer den Fall, dass Sie dort Kunde werden, waere es nett, wenn Sie erwaehnen koennten, dass ich sie darauf aufmerksam gemacht habe. (Ich kriege KEINE Provision. ;-)) Viele Gruesse, J. Fehrer

8) Hi, This is the place we do large scale sequencing and genotyping. Try to bargain for large scale genotyping. They do the excellent job http://bmr.cribi.unipd.it

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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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PCR reaction numbers answers

Dear members of the Evoldir,

thank you for all the responses to my posting entitled “Optimizing number of PCR reactions”, sent on the 26th Nov.

As many of you requested a copy of the replies, I am sending this email with all the information I got until today.

Thank you,

David ------------

I am extracting DNA from single Daphnia (Crustaceans). They have about the size of a fruit fly. I extract their DNA with the Peqlab kit (only single tubes available), which is among the cheapest silica matrix based kits. It yields 200 ul of which I use 1 ul per reaction and get good results.

A few comments to your questions on evoldir.

1) multiplex-PCR Mulitplex-PCR are used by all forensic genetics labs and the technique is accepted as the standard in our field. The results are reliable and many labs (including ours) have an accreditation after inter-

national standards, and results are acknowledged to be valid in court. At our department (forensic genetics) we have a constant challenge in generating DNA-profiles from low-quality and/or low-quantities of DNA. We do microsatellite-analysis using multiplex-PCR (16 loci pr. reaction) and we do SNP-analysis using multiplex-PCR (sofar a maximum of 52 loci pr. reaction) with high-quality and reproducible results.

2) Re-cycling of genomic DNA We have been doing some experiments with solid-phase PCR using tissue (blood or mouth-swaps) on filter-paper from Whatman called FTA-cards - pretty expensive but very efficient. It is a system with a filter treated in a way that DNA sticks to the paper, and after some washes to clean (we simply use 3x wash with water)you simply run PCR directly on the punch. Works great. To re-use DNA we have been doing experiments with running 1 or 2 PCR-cycles on the filter-punch, remove the punch and continue the PCR on the first generated amplicons. And transfer the punch to a new tube with new primers (after a wash) and run PCR on that. So far we have had good results. We are not using this technique on our case-work samples, just for experiments to investigate how we can use small amount of DNA better.

Try multiplexing. It may need a little tweaking to get it to work, but once it's running I can see no reason why the information should be less reliable than that of single locus pcr. If you have access to a system using differently labelled primers, you can do many loci in one pcr. The manufacturers of such systems typically supply you with a basic “recipe” for multiplexing, which is a good starting point. Maybe also try out how much dna you really need for your pcrs. Maybe you can dilute your extractions and still get good results. That would give you many more pcrs. I had some microsats for which more dilute dna worked even better.

Here's my favorite PCR fly prep that might solve your problem. It's fast, easy and very dirty, but nothing is lost because there are no phenol extractions or precipitations. However, the freezer shelf life of this one is not as good, so you might want to aliquot it if you need it for a long period of time (>3-6 months). I would try systematically increasing the volume in some number of single preps with TE until you lose the signal in your PCR reactions to see how far you can push the number of reactions per fly.

SINGLE-FLY DNA PREPS FOR PCR Greg Gloor and William Engels, Dept. of Genetics, Univ. of Wisconsin, Madison, WI 53706, 608-263-2213, FAX/262-2976, WRENGELS@WISCMACC.BITNET. We have developed a simple method for the rapid and reproducible isolation of DNA from single flies for amplification by the polymerase chain reaction (PCR) (Saiki et al, Science 239: 487), and direct sequencing by asymmetric PCR (Gyllensten and Erlich, Proc. Nat. Acad. Sci. 85: 7652). The simplicity of this procedure means that the problem of contamination with other amplified or cloned DNA is greatly reduced. Sufficient DNA is obtained from one fly for a minimum of 50 PCR analyses, and the DNA is stable for at least one month in the refrigerator. A simple modification of this technique allows the isolation of DNA suitable for use in inverse PCR (Ochman et al, Genetics 120: 621-623). These methods substantially reduce the time involved in DNA isolation, and among other uses, allows the PCR to be used to monitor the segregation of an allele for which there is no phenotype or transposition of an unmarked P element (Engels et al. Cell 62: 515-525). A. DNA PREPARATION PROTOCOL: 1. The squishing buffer (SB) is 10 mM Tris-Cl pH 8.2, 1 mM EDTA, 25 mM NaCl, and 200 ug/ml Proteinase K, with the enzyme diluted fresh from a frozen stock each day. 2. Place one fly in a 0.5 ml tube and mash the fly for 5 - 10 seconds with a pipette tip containing 50 ul of SB, without expelling any liquid (sufficient liquid escapes from the tip). Then expel the remaining SB. 3. Incubate at 25-37[o]C (or room temp.) for 20-30

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PlantMatingSystemDatabase

As part of a literature review, I am updating our plant mating system database previously published in Barrett & Eckert (1990) and Barrett et al. (1996).

In addition to estimates of the outcrossing rate (t = the proportion of seeds outcrossed, as estimated via progeny array analysis), I also want to include estimates of the inbreeding coefficient of reproductively mature plants (parental F, usually estimated from inferred maternal genotypes).

If you have data that you are willing to share I would love to use it in our meta-analysis. Specifically, I am very interested in hearing from you if...

(1) you have published estimates of t but did not include the estimates of F in your paper (note that t and F are usually estimated simultaneously if you used Kermit Ritland's MLTR software);

(2) you have unpublished estimates of t or t & F.

If you would like to send me your estimates, please...

- Indicate plant species - List the estimates by population (we are interested in both the mean and variance among populations) . - Include information on the type (i.e. allozyme, microsat, RAPD, etc.) and number of genetic markers you used. - If you are sending me F's for previously published t's, please indicate the original paper and include population name/codes so that I can match the F's with the t's already in the paper. - I am primarily interested in t based on all marker loci (i.e. the multilocus outcrossing rate tm), but I'm would also like to include average single locus estimates (ts) in the database, if available. - Please email the information to eckertc@biology.queensu.ca

Thank you very much for your help with this.

Chris Eckert

Department of Biology Queen's University Kingston, Ontario, K7L 3N6 Canada

Ph 613-533-6158 Fx 613-533-6617 eckertc@biology.queensu.ca

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Chris Eckert <eckertc@biology.queensu.ca>

Probability estimation

Dear EvolDir members,

I would ask if someone know who to calculate the probability that a new mutation that arise suppose 20 generations ago (and for consequence have a frequency 1/N) raise a frequency equal or higher than 1% in the present day population. I know for each generation the number of individual (N).

many tanks!

Cristina Santos

Cristina Santos Unitat d' Antropologia Departament BABVE Edifici C Universitat Autònoma de Barcelona 08193 Bellatterra (Barcelona) Spain

or

Cristina Santos Departamento de Antropologia Universidade de Coimbra 3000 Coimbra Portugal

Cristina.Santos@uab.es

ROX size standards

Dear all

We have been trying to make our own ROX-labelled size standards following the methods described by J. Andrew DeWoody et al. in their published paper "Universal method for producing ROX-labelled size standards suitable for automated genotyping" BioTechniques 37:348-352 (September 2004). We have run into a problem of several extra peaks showing up in the runs (on an Applied Biosystems 3100). The extraneous amplifications are smaller in peak height, but larger in fragment size than the primary amplicon that the primers were supposed to have only produced. This happens in every PCR for the different standard sizes using the pBluescript II SK(+) as template DNA. The standards have been PCR amplified individually and the products pooled prior to loading on the 3100. The extra peaks are present even after increasing the PCR annealing temperature and reducing the number of PCR cycles. Has anybody confronted such a problem in the attempt to produce ones own ROX-labelled size standard using this method or any other methods? I would be grateful for any suggestion or explanation of the problem we have encountered.

Thanks

Seifu Seyoum, Ph.D. Florida Fish and Wildlife Research Institute 100 Eighth Avenue S.E., St. Petersburg, FL 33701 Tel: 727-896-8626 x3100/3212 Fax: 727-823-0166 seifu.seyoum@myfwc.com

ROX size standards answers

Dear all

Thank you to everyone who replied with very helpful suggestions to the problem we were having regarding the production ROX-labeled size standards in our laboratory.. Here is a compilation of the responses to my query for all those who might benefit from these comments. The extra peaks we were seeing on our ABI 3100 were low and messy, randomly spread throughout the run after the target size standard fragment. We seem to have solved the problem, and are now getting good, consistent results. It appears we just needed some further PCR optimization and template dilution. One thing which others might find useful- we actually are not using pfu polymerase. We are using a similar product, Vent polymerase (high fidelity with 3' to 5' proofreading). This product was less than 1/3 the cost of pfu, so we thought we would try it first. The Vent polymerase in conjunction with the methods from the DeWoody et al. paper will result in significant savings in our laboratory. Thank you again to all who responded, and feel free to contact me for additional information. A special thanks to Vaughan Symonds for sending me a copy of his paper “A simple and inespensive method for producing fluorescently labelled size standard”.

Seifu Seyoum, Ph.D. Florida Fish and Wildlife Research Institute 100 Eighth Avenue S.E., St. Petersburg, FL 33701 Tel: 727-896-8626 x3100/3212 Fax: 727-823-0166 seifu.seyoum@myfwc.com

Dear Seifu

Extra peaks show up under denatured conditions, when both strands of the ROX-standard amplicon are labelled. This is true for the commercially available ROX1000 standard delivered by ABI. So, running samples under native conditions could be a first step. Secondly, it is known that pseudo-fragments can be formed after PCR and subsequent restriction of Amplicons in a technique called T-RFLP. See Egert & Friedrich (2003), Applied and Environmental Microbiology 69:2555-2562.

Maybe this helps.

Good luck

Sébastien Wielgoss

PhD Student LS Axel Meyer Zoology and Evolutionary Biology University of Konstanz Germany Hello there, We are in the process of also creating our own ROX-labeled size standard using these same protocols. We have had similar problems with the extra amplification peaks as well on our 310 machine. When I put the sequences into a PrimerSelect program from DNAStar to get the optimal annealing temperature for each fragment and also put in the entire P-Bluescript code, it shows that there are actually more than one region where they can amplify. One of two things must be happening then. Either the problem is simply coming from the multiple sites within the P-Bluescript plasmid that can be amplified by the same primers acting in opposite fashion as they normally do. (CASS Reverse primers acting as forward primers or amplifying other regions). The other option is that simple A-tailing is happening and that the primers are not as specific as they should be, no matter the PCR protocol you use. We use touchdown PCR with exact optimal annealing temperatures for each individual fragment. I'm running the final Size standard product today against 8 samples and also the same 8 with ROX 400HD so we'll test the effectiveness of the final product. Although some fragments do popup (especially on the 200 fragment for us) they don't wind up bothering the system. The dilutions that we have to make to get the peaks to the same relative intensity as ABI's size standard virtually eliminate the smaller peak by lowering it below the threshold reading limit for the Genescan program. Another bonus is that when you actually setup your size standard file in Genescan if this is the program you are using, you can tell it not to use that peak as part of the size standard. Just tell it that 201.5, in our case, is the fragment you want it to use all the time and ignore the other peak. I hope this helps and feel free to contact me further if you discover anything new.

Best Regards, Ben

Benjamin A. Sikes Johnson Controls National Wetlands Research Center/USGS 700 Cajundome Blvd. Lafayette, LA 70506 +1-337-266-8524

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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

Spectrophotometer

Dear evoldir members, I am looking into the purchase of a UV spectrophotometer for routine quantification of RNA, DNA and cells. If any of you has positive or negative experiences to report with equipment purchased during the past five years I would highly appreciate your feedback. Combined feedback will be posted if deemed significant.

Many thanks in advance,

Markus Friedrich

– Markus Friedrich Associate Professor Department of Biological Sciences Department of Anatomy and Cell

Biology Wayne State University 5047 Gullen Mall Detroit, MI 48202

office: 313 577 9612 lab: 313 577 5120 fax: 313 577 6891 web: http://bio.wayne.edu/mf/Markuslab.html

Yeast evol

Dear colleagues,

Does anybody know of a protocol suitable for an introductory genetics lab course the demonstrates random drift and natural selection in yeast? Growth would have to be in flasks or on plates, as we don't have access to a chemostat. I'm thinking, for example, of mixing antibiotic sensitive and resistant haploids and following changes in gene frequencies during growth in the absence of antibiotic.

Bill Birky C. William Birky, Jr. Professor of Ecology and Evolutionary Biology Member, Graduate Interdisciplinary Programs in Genetics Biological Sciences West 1041 E. Lowell University of Arizona Tucson, AZ 85721 Office phone: 520-626-6513 Lab phone: 520-626-5108 Fax: 520-621-9190 Email: birky@u.arizona.edu

real time PCR

Dear EvolDir members,

we would like to replace our standard nematode egg counting procedure from fecal samples by using microscopes (McMaster technique) with a quantification method of nematode eggs from fecal samples based on real-time PCR.

We would be very grateful for any advice or comments on

1) experiences with quantifying parasite eggs by real-time PCR.

2) preferences on real-time PCR machines (Lightcycler was recommended to us) and different approaches that are used (SYBR Green, TaqMan, fluorescence dyes etc) as well on software and associated cost.

Thanks a lot! best,

Simone

PD Dr. Simone Sommer University of Hamburg Biozentrum Grindel Animal Ecology & Conservation Martin-Luther-King-Platz 3 D- 20146 Hamburg Germany Phone +49 40 42838 4226 Fax +49 40 42838 5980 http://www.biologie.uni-hamburg.de/zim/oeko/-sommer/forsch.html Simone.Sommer@zoologie.uni-hamburg.de

real time PCR answers

Dear EvolDir members,

I received very helpful answers to my inquiry. The answers are summarized below.

Thanks a lot!!

Simone

Hallo Simone, ich quanitifiziere Parasiten (Microsporidien) in Wasserflohen mit Real-time PCR. Dazu verwende ich SYBR Green Master Mix von Applied Biosystems, und normale Primer. Damit habe ich gute Erfahrungen gemacht. Es lohnt sich aber unter Umstanden, zum Mix ZUSAETZLICH noch Polymerase (HotStarTaq Polymerase von Qiagen, 0.25 units per 20 ul Reaktion) dazuzugeben. Auch lohnt es sich mehrere Primerpaare (mit Primer3: http://frodo.wi.mit.edu/-cgi-bin/primer3/primer3_www.cgi) zu bestellen und sie zu vergleichen, die Unterschiede konnen betrachtlich sein.

Wir benutzen den Rotor-Gene von Corbett Research. Ich habe vorher mit dem Light-Cycler gearbeitet. Die Maschinen sind gleich gut, aber die Software vom Rotor-Gene bietet mehr (allerdings hat sich der Light-Cycler in der Zwischenzeit wohl auch verbessert) und der Rotor-Gene ist einiges gunstiger im Betrieb (braucht keine speziellen Reaktionsgefasse).

Ich kann mir vorstellen, dass ein Hauptproblem die Inhibitoren in den Fecal Samples sind. Es gibt zwei Publikationen uber die Quanitifizierungen von Microsporidien in Fecal Samples (Menotti et al. 2003a,b).

Viel Gluck, Dominik Dominik Refardt Unit of Ecology & Evolution Department of Biology University of Fribourg chemin du Musee 10 1700 Fribourg Switzerland dominik.refardt@unifr.ch http://www.unifr.ch/-biol/ecology/ebert/group/refardt Fon +41 (0)26 300 88 67 Fax +41 (0)26 300 96 98

Hi Simone In response to your evo-dir enquiry I would recommend that you buy a taqman machine (from ABI gene) instead of a lightcycler from Roche. The reason is that you will need to make standard curves to quantify your mRNA and lightcycler has a limited number of samples per run after you take into account your standard curve (I think it is 24 samples in total per run). Taqman ABI runs off of 96 well plates giving you plenty of sample spaces over and above your standard curve(s). Taqman is a more expensive machine to purchase but it is definately worth the extra money. Software should come with the machine. Regarding methods, FRET probes are more sensitive than SYBR green. However FRET probes are very expensive. Qiagen do a good SYBR green kit. Hope this helps Tracey

Hi Simone, I don't have any experience with your particular application of real-time PCR, but I may be able to help with the different machines/approaches. The real-time machine platform that you choose to use depends on a number of factors - firstly how much money you want to spend and secondly what sort of size runs you will be intending on doing. I have used the applied biosystems 7900 (384 well format), the applied biosystems 7500 (94 well format) and (briefly) the roche lightcycler (32 capillary format). The previous order also corresponds to decreasing cost of the machine! A plate format machine allows you to process large numbers of samples at once and lends itself to automation if you are intending on performing the same run repeatedly - but these machines have traditionally taken around 1-2 hrs to complete a run. In comparison the light cycler is a rapid cycler which takes around 30 minutes, but it is much smaller format than the plates so although faster you may have to do more runs depending on how many

The two detection approaches that I have tried are Taqman and SYBR green. Which one you choose to use depends on how much you are willing to spend and/or play around optimising your process. The Taqman probes are very specific with the specific primers combined with the probe itself. They can also be designed for you by applied biosystems if you use their design service. The only problem with the probes is the cost as you need to purchase the real-time mix from AB too. We were running 384 well plates and worked out that the cost (not including consumables such as plates and seals) was about NZD $1.70 per well. If you were considering a high-throughput assay the Taqman probes would probably work out to be technically easier to use, but alot more expensive! In contrast SYBR works out to be about NZD $0.30c per well. With SYBR for the cost of a pair of primers and some SYBR you can make the real time mix yourself (its just a PCR with SYBR added) and the homemade mix works for me just as well as the comm

All of the machines that I have used come with their own associated software. Your assay sounds like an absolute quantification - so the analysis involves comparisons of your unknowns to a standard curve. The software associated with the machines that I have used will do this type of analysis for you - all you need is a good standard curve. There is also a whole variety of resources out there on the internet - a particularly good website

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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

PostDocs

CWilliam Mary EvolPhysiology

Postdoctoral Position, Evolutionary Physiology, College of William and Mary. A postdoctoral position is available immediately, renewable through May 2009, to investigate the evolution of complex neuroendocrine pathways. Applicants should have a PhD prior to November 2004 and experience in one or more of these areas: physiological ecology, neuroendocrinology, behavior, evolutionary biology, physiology, or cell and molecular biology. The research focus is on the contribution of genetic variation and phenotypic plasticity to the evolution of a complex neuroendocrine pathway in mammals. This pathway integrates photoperiod and other environmental information to regulate reproductive, physiological and behavioral responses to seasons. The model system is a wild-derived laboratory colony of white-footed mice. The successful candidate will conduct collaborative research and assist in teaching one course in one semester, probably animal physiology. More details on the research are available at: http://faculty.wm.edu/pdheid. The College of William and Mary is a "Public Ivy" with 5500 undergraduate enrollment, an excellent undergraduate program, and a strong research tradition. Starting salary is $35,000 plus benefits. Please send curriculum vitae, a brief description of research interests/experience, and the names and contact information of three references to: Dr. Paul Heideman, Chair, Department of Biology, P.O. Box 8795, College of William and Mary, Williamsburg, VA 23187-8795; e-mail: pdheid@wm.edu. Review of applications begins immediately and continues until the position is filled. The College of William and Mary is an Affirmative Action/Equal Opportunity Employer.

Paul D. Heideman, Associate Professor and Chair ^^O^^ ^^O^^ Department of Biology email: pdheid@wm.edu College of William and Mary P.O. Box 8795 FAX: 757-221-6483 Williamsburg, VA 23187-8795 Ph: 757-221-2239

http://pdheid.people.wm.edu/ Paul Heideman <pdheid@wm.edu>

FloridaStateU RodentMolSyst

Graduate student and/or post-doc positions in rodent molecular systematics

One to two NSF-funded positions are available for a graduate student and/or post-doctoral fellow beginning Summer or Fall 2005 to work with Scott Steppan at Florida State University on molecular systematics. We are using multiple nuclear genes to infer the phylogeny of the most diverse clade of mammals, the rodent superfamily Muroidea (containing 1/4 of all mammals) with special emphasis on the highly diverse Old World mice and rats (Murinae) and Neotropical mice and rats (Sigmodontinae). These positions are part of a collaborative project with Ronald Adkins at U. Tenn. Memphis (see Steppan et al., 2004. Syst. Biol. 53:533-553). Successful applicants will have opportunities to develop independent research questions involving systematics, molecular evolution, biogeography, macroevolutionary trends, adaptive radiations, or viral coevolution (for example). The Ecology and Evolution program is a highly interactive and supportive environment and now includes computational phylogenetics with the Computational Evolutionary Biology group (including D. Swofford and F. Ronquist).

Post-doc applicants should have a Ph.D. in evolution, systematics, or related field and be proficient in PCR and DNA sequencing. Salary will be competitive. Interested applicants should contact Scott Steppan for more information (steppan@bio.fsu.edu). Deadline for applications is Jan. 15. Additional information on the Steppan Lab is available from http://bio.fsu.edu/ ˜ steppan/, on the Ecology and Evolution group at http://www.bio.fsu.edu/ee/index.html, and the Department (for graduate application, etc) at http://www.bio.fsu.edu/ . For more information, contact, Dr. Scott Steppan; e-mail: steppan@bio.fsu.edu; FAX: (850) 644-9829 or mail to: Dept. of Biological Sciences, Florida State Univ., Tallahassee FL 32306-1100.

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Scott Steppan Department of Biological Science Florida State University Tallahassee, FL 32306-1100 steppan@bio.fsu.edu phone: 850.644.6536 fax: 850.644.9829

http://bio.fsu.edu/˜steppan http://www.bio.fsu.edu/faculty-steppan.php Ecology and Evolution Group at FSU: http://www.bio.fsu.edu/ee/index.html
=
Scott Steppan <steppan@bio.fsu.edu>

GeorgetownU TheoPopGenet

Second posting - note corrected date. Applications due by December 29th, 2004.

Postdoctoral Position in Theoretical Population Genetics

A full-time, NSF-funded postdoctoral research position is available to study the evolution of quantitative traits at Georgetown University, Washington DC.

The successful applicant will collaborate on a project to model the evolution of quantitative traits determined by a finite number of loci (a non-infinitesimal genetic basis), especially in subdivided populations or heterogeneous environments. Desired education and experience: Ph.D. in mathematics, biology or a related field. Mathematical scientists should have background in mathematical modeling or differential equations. Biological scientists should have background in evolutionary biology, population genetics, or quantitative genetics. Experience with statistics or computer simulation preferred.

Position is for two years. Salary will be commensurate with experience; salary range starts at US$40,000 per year. Benefits (including health insurance) are provided. Position is available for fall of 2005. Review of applications will begin on December 29, 2004, and continue until the position is filled.

Applications should include a curriculum vitae, a statement of research interests, and (p)reprints of up to three papers if available. In addition, applicants should arrange for two letters of recommendation to be sent. All materials should be sent by mail to: Prof. Judith R. Miller, Department of Mathematics, Reiss Science Building, Georgetown University, Washington DC 20057 USA.

Interested individuals are encouraged to contact Prof. Miller at jrm32@georgetown.edu or Prof. Matthew Hamilton (biology) at hamiltm1@georgetown.edu.

Georgetown University is an affirmative action/equal opportunity employer.

Matthew B. Hamilton, PhD Associate Professor Georgetown University Department of Biology, Reiss 406 37th and O Streets NW Washington, DC 20057 202-687-5924 (office) 202-687-5662 (fax) http://bioserver.georgetown.edu/faculty/hamilton/

InstitutPasteur EvolMicrobiology

1 post doctoral position, 2 years, begining March 2005

Véronique VINCENT, Senior Scientist Reference Laboratory for Mycobacteria Innstitut Pasteur, Paris vvincent@pasteur.fr

DETECTION OF MYCOBACTERIA IN TAP WATER BY IMMUNOMAGNETIC SELECTION Mycobacteria other than tubercle bacilliare widely present in the environment and specially in tap water. Environmental mycobacteria are a frequent cause of infection and water is a significant vehicle for the transmission of these organisms. We wish to develop immunomagnetic tests for the detection of the mycobacterial species the most frequently present in tap water and biofilms. The ideal postdoctoral candidate will have interest/experience in environmental microbiology and in raising monoclonal/polyclonal antibodies.

– Veronique Vincent Centre National de Reference des Mycobacteries

Laboratoire de Reference des Mycobacteries Institut Pasteur 25 rue du Docteur Roux 75015 Paris Tel: 33 (0)1 45 68 83 60 FAX: 33 (0)1 40 61 31 18 vvincent@pasteur.fr

IowaStateU SalamanderEvol

Postdoctoral Researcher in Evolutionary and Ecological Morphology Iowa State University

A postdoctoral position is available to study the role of ecomorphological variation on the evolution of species interactions and community structure in Plethodon salamanders. The position is part of an NSF-funded CAREER project in the laboratory of Dean Adams, Department of Ecology, Evolution, and Organismal Biology, Iowa State University. The position calls for quantitative analyses of cranial morphology in eastern Plethodon populations across single and multispecies communities, in an effort to quantify patterns of community organization relative to species interactions. Primary responsibilities for this position include: 1) conducting laboratory research in quantitative morphology, 2) maintaining laboratory databases and requesting/retrieving specimens from museum collections, 3) analyzing data and writing manuscripts, and 4) helping to coordinate projects of undergraduate students involved in the project. For additional information concerning this and other research projects, please refer to the laboratory web site (http://www.public.iastate.edu/~dcadams).

Successful applicants should have a Ph.D. in ecology, evolution, or a related field. Strong quantitative and statistical skills are required. Salary is $30,000 plus benefits, and funds are available for two years pending satisfactory progress. The position can begin as early as March 1 2005. Review of applications will begin immediately and continue until a candidate is selected.

To apply, please send a cover letter, CV, and names and e-mail addresses of three references to Dean Adams (dcadams@iastate.edu), Department of Ecology, Evolution, and Organismal Biology, Iowa State University, Ames, IA 50011-3223, USA.

ISU is an equal opportunity/affirmative action employer.

Dean Adams <dcadams@iastate.edu>

MacquarieU MarineConservationGenetics

"POSTDOC IN MARINE CONSERVATION GENETICS, MACQUARIE UNIVERSITY, SYDNEY"

A two-year Postdoctoral position is available to work on dispersal of marine organisms. The successful candidate will join a recently created multi-disciplinary team (Molecular Ecology Group for Marine Research) that will study dispersal in four codistributed groups of marine organisms: sea-urchins, abalones, oysters and sharks. Results from the four individual projects will be combined to address key topics in marine biodiversity, such as design of marine protected areas and conservation and management of marine resources.

Applicants must have a Ph.D. in a relevant area of research, such as conservation genetics or phylogeography. Preference will be given to candidates with strong experience in analyses of gene flow based on microsatellite markers and with a background in marine ecology and/or oceanography. Familiarity with isolation and characterization of microsatellites is desirable but not essential.

The appointee will be responsible for collecting and analyzing data for three of the four projects and supervising activities of a research assistant. In addition, he/she is expected to dynamically communicate and collaborate with other members of our thriving research group (marine biologists, population geneticists and PhD students).

Salary will be established according to Macquarie University guidelines (around $53,500 + 26% on costs per annum). Please e-mail a letter summarizing research interests and experience along with a CV including the names, addresses and e-mails of three referees to Luciano Beheregaray: <mailto:luciano.beheregaray@bio.mq.edu.au> luciano.beheregaray@bio.mq.edu.au

Review of applications will begin immediately and continue until a suitable candidate is identified. The appointee is expected to start in March 2005.

For further information about the lab and related publications please visit our "under construction" web site at <http://www.bio.mq.edu.au/molecularecology>www.bio.mq.edu.au/molecularecology or send an e-mail to the address above.

Dr Luciano B. Beheregaray Department of Biological Sciences Macquarie University Sydney, NSW 2109 Australia Phone: 61(2)9850 8204 Fax: 61(2)9850 8245 E-mail: Luciano.Beheregaray@bio.mq.edu.au

"Luciano B. Beheregaray" <Luciano.Beheregaray@bio.mq.edu.au>

MaxPlanck BehaviouralEvolEcol

Behavioral Ecologist, postdoctoral research position

The Max-Planck-Institute of Limnology, Plön, Germany, is seeking a behavioral ecologist to join the department of evolutionary ecology.

He/she will work with a team in an integrative project involving immunological, parasitological, population genetic and molecular immunogenetic approaches. Details about the department's research activities can be found under: http://www.mpil-ploen.mpg.de/ The department's major goal is to understand the evolutionary ecology of sexual reproduction and its role in enhancing immune function in the offspring.

The successful candidate's part will be to study experimentally which kind of information about the immunogenetics of both self and potential partners three-spined sticklebacks take into account, in addition to other information, in their mate choice decisions. Experience with experimental techniques to study the behaviour of fishes is required. The candidate will collaborate with the team including PhD students and a scientist who is familiar with stickleback behavior.

Salary will be according to the guidelines of the Max-Planck-Society. This postdoctoral research position is for a two years term and can be extended. For further information please contact Manfred Milinski (milinski@mpil-ploen.mpg.de). Please send your application including a CV, a list of publications and the contact information of three references to the above mentioned e-mail address until February 15.

milinski@alpha1.mpil-ploen.mpg.de

MaxPlanck EvolMolBiol

Molecular Biologist

The Max-Planck-Institute of Limnology, Plön, Germany, is seeking a molecular biologist to join the department of evolutionary ecology.

He/she will work with a team in an integrative project involving immunological, parasitological, population genetic and behavioral approaches. Details about the departments's research activities can be found under: http://www.mpil-ploen.mpg.de/ The department's major goal is to understand the evolutionary ecology of sexual reproduction and its role in enhancing immune function in the offspring.

The specific goal for this position is to identify the molecular correlates of immune challenge and pathogen defence and to explain the functional significance of MHC diversity in the wild.

The successful candidate is expected to further characterize classical MHC loci in the behavioral and ecological model organism three-spined stickleback, with special emphasis on expression analysis.

Experience with modern molecular techniques is expected, in particular molecular cloning by RT-PCR, real-time PCR, expression profiling and subtractive PCR techniques.

The candidate will collaborate with the team including PhD students and one scientist already working on the immunogenetics of the three-spined stickleback.

Salary will be according to the guidelines of the Max-Planck-Society. This postdoctoral research position is for a two years term and can be extended. For further information please contact Thorsten Reusch (reusch@mpil-ploen.mpg.de).

Please send your application including a CV, a list of publications and the contact information of three references by e-mail (milinski@mpil-ploen.mpg.de) until January 31.

–

Prof. Manfred Milinski

Max-Planck-Institute of Limnology Department of Evolutionary Ecology August-Thienemann-Strasse 2 D-24306 Ploen, Germany

direct: +49-(0)4522 763 254 Sec: +49-(0)4522 763 253 Fax: +49-(0)4522 763 310 email: milinski@mpil-ploen.mpg.de http://www.mpil-ploen.mpg.de/ milinski@alpha1.mpil-ploen.mpg.de

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UArizona GenomeEvol

POSTDOCTORAL RESEARCHER GENOME EVOLUTION UNIVERSITY OF ARIZONA

A Postdoctoral Research position is available to study the diverse classes of sequences that reside within bacterial genomes and the process of gene degradation on the evolution and organization of bacterial genomes. Potential projects include both bioinformatic and experimental studies. Applicants could have skills in molecular genetic or microbiological procedures, in bioinformatics or phylogenetic analysis, and/or in evolutionary or population genetics. Candidates trained in the fields of Evolutionary Biology, Microbiology, Computational Biology, Molecular Biology or Genetics are all encouraged to apply. The position is available immediately; however, the starting date is flexible. Salary (in the range of $38K to $45K, plus benefits) will be commensurate with experience.

If you wish to apply, please send a curriculum vita and the names of at least two referees (via e-mail) to:

Howard Ochman Department of Biochemistry and Molecular Biophysics 233 Life Sciences South University of Arizona Tucson, Arizona 85721 USA 520-626-8355 (phone) 520-621-3709 (fax) hochman@email.arizona.edu

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Howard Ochman <hochman@email.arizona.edu>

UCaliforniaLA AncientDNA

Post Doctoral position in Ecology & Evolutionary Biology, University of California, Los Angeles

Ancient DNA Analysis of Mammal Remains from the Arctic Permafrost and Elsewhere

I am searching for a post-doctoral candidate with a good background in molecular techniques to isolate DNA and genetically type remains of mammals from the Arctic Permafrost. This three year NSF sponsored position may also involve other ancient remains from elsewhere in the New and Old World and may include a variety of taxa and questions such as intercontinental migration, climate change, and genetic continuity within populations. Those interested should send a CV to me detailing molecular expertise, as well as accomplishments, publications and contact information for at least three individuals willing to write a letter of support.

Bob Wayne rwayne@ucla.edu

UCopenhagen InsectCommunication

A 1-year postdoctoral position (renewable for another two years) will be available from July 2005 at Faculty of Sciences, University of Copenhagen, Denmark. The position is funded by the European Community via a Marie Curie Excellence Grant. The successful candidate will work in a new research group leaded by Dr. Patrizia D'Ettorre, which will be integrated in the laboratory of Prof. Koos Boomsma.

The research project will focus on Chemical Communication Code of Insect Societies, with a multidisciplinary approach (behavioural, chemical, electro- and neurophysiological analyses and genetics).

Applicants should just have finished their PhD in Biology or related disciplines, and are expected to have a strong background in Evolutionary Biology. Familiarity with general molecular evolutionary techniques, with chemical ecology techniques and neurophysiology is desirable.

Applications should include CV, list of publications, research interests and names and email addresses of two referees, and be sent by email to Patrizia D'Ettorre at patrizia.dettorre@biologie.uni-regensburg.de by January 31st 2005.

Dr. Patrizia D'Ettorre Dep. Biology I University of Regensburg D-93040 Regensburg phone +49 941 943 2996 fax +49 941 943 3304 http://www.biologie.uni-regensburg.de/Zoologie/Heinze/en/staff/dep/dep_e.html patrizia dettorre <patrizia.dettorre@t-online.de>

UGuelph AbaloneLifeStrategy

Post Doctoral position available in the Department of Animal and Poultry Sciences at the University of Guelph, Ontario, Canada. Our research project will develop a selective breeding program for cultured pinto abalone at the Bamfield Huu-Ay-Aht Community Abalone Project (BHCAP) in Bamfield, B.C., Canada. The project is lead by Dr. Elizabeth Boulding (Zoology, U. Guelph) in collaboration with Dr. Ian McMillian (CGIL & APS, U.Guelph) and Dr. Ussif Rashid Sumaila (Fisheries Centre, U.B.C.). This breeding program will apply modern animal breeding methodology to improve the cultured population for economically-important traits, while minimizing inbreeding accumulation. Such a breeding plan is essential because of the potential for rapid inbreeding accumulation resulting from the high fecundity of the abalone and limited rearing space in the hatchery. Dr. Bouldings graduate student on the team will genotype abalone at 12 molecular markers (microsatellites) to monitor inbreeding, estimate genetic parameters, and to identify the parents of potential broodstock. Dr. Sumalias graduate student will help identify important traits to target for selection by predicting the relative economic value of these different traits in the global marketplace. These economic weights will be incorporated into a multitrait selection index that will be used for genetic evaluation of potental broodstock. Pinto, or northern, abalone (_Haliotis kamtschatkana_) is a broadcast-spawning marine gastropod that occurs throughout coastal British Columbia, extending north into Alaska and south to California. In addition to its role as a member of a complex marine ecosystem, pinto abalone is valued as a food and cultural resource by coastal native peoples, and as a food resource by commercial fishermen and recreational divers. Historically, abalone populations were healthy enough to support a traditional fishery by native people and a commercial dive fishery until the late 1980s. In 1990, concern over reduced population levels instigated a closure to all harvesting of abalone, a closure that remains in place today. When populations not only failed to recover under 10 years of protection, but declined further, the species was designated threatened by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC). Dr. McMillan and his post-doctoral fellow will be responsible for quantitative genetic analyses relating to the project. Computer simulation programs will be composed to study alternate selection and mating strategies and predict their effects on genetic progress and inbreeding accumulation. Genetic parameters (heritability and genetic correlations) of the traits measured at BHCAP will be calculated. A selection index will be developed for genetic evaluation of abalone broodstock. Estimated breeding values (EBVs) of broodstock will be calculated for measured traits, and incorporated into the selection index. Research results will be communicated through reports to BHCAP so that they may be implemented into a practical breeding program to improve abalone.

The position is available immediately a term of 2 years. Deadline: Continuous recruitment, applications will be reviewed beginning 15 January 2005 until the position is filled.

Interested researchers are requested to send their CV and two letters of recommendation to Dr. Ian McMillian imcmilla@uoguelph.ca

“Elizabeth G. Boulding” <boulding@uoguelph.ca>

UHertfordshire NetworkModelling

University of Hertfordshire, UK

Post Doctoral Research Fellow: Computational Modelling of Multi-cellular Biochemical Networks

Biocomputation, Algorithms, and Adaptive Systems Research Groups Science and Technology Research Institute (STRI)

(Ref: L6147AC)

Salary: Up to 30k British Pounds.

A post-doctoral research position (Lecturer or Senior Lecturer grade) is available to support further development of an interactive tool for visualizing and simulating the behaviour of multi-cellular biochemical networks. The project is funded by the Wellcome Trust, and involves restructuring the existing NetBuilder program, and design and development of new modules to extend the use of the software. Details of the research in the Biocomputation, Algorithms, and Adaptive Systems Research Groups are featured on the STRI website, http://perseus.herts.ac.uk/uhinfo/research/stri/- , and information on NetBuilder is found on http://-strc.herts.ac.uk/bio/maria/NetBuilder/ . The post is available for two years from January 2005.

A successful candidate will have a background in Biochemistry/Molecular Biology and/or Computer Science, a PhD or equivalent experience in an appropriate field, as well as strong programming skills and experience with at least one of the following languages: C/C++, Python, Java, XML/XSLT. Advantageous would be previous experience with mathematical modelling of biochemical systems, bioinformatics, software design and version control, web development, or a further background in theoretical/evolutionary biology and systems biology/artificial life.

We seek someone who can, as part of a team, think and work independently, who is committed to doing high-quality research, and can demonstrate excellent communication and scientific writing skills in English.

Further information and Application Form can be obtained from the Personnel Department, University of Hertfordshire, College Lane, Hatfield, Herts, AL10 9AB, Tel: 01707 284802 (24 hour voicemail). Please quote reference: L6147AC

You can apply on-line at http://-recruitment.herts.ac.uk/recruit/ by Closing Date of 20 December 2004

——— Prof. Dr. Chrystopher L. Nehaniv Professor of Mathematical & Evolutionary Computer Sciences

Adaptive Systems & Algorithms Research Groups School of Computer Science University of Hertfordshire College Lane Hatfield, Hertfordshire AL10 9AB United Kingdom e-mail: C.L.Nehaniv@herts.ac.uk phone: +44-1707-284-470 fax: +44-1707-284-303 URL: http:/-

/homepages.feis.herts.ac.uk/ ˜ nehaniv/welcome.html Director, EPSRC Network on Evolvability in Biological & Software Systems Associate Editor, BioSystems Associate Editor, Interaction Studies

c.l.nehaniv@herts.ac.uk

USheffield QuantGenetics

The following postdoctoral post was advertised in Nature on 9 December 2004. Note that although the initial appointment would be for one year, it would be renewable for upto 3 further years.

UNIVERSITY OF SHEFFIELD DEPARTMENT OF ANIMAL & PLANT SCIENCES

A postdoctoral associate is required to assist with an analysis of components of fitness in the co-operatively breeding Seychelles Warbler.

This is a collaboration between the Universities of Sheffield (Terry Burke), East Anglia (David Richardson), Groningen (Jan Komdeur) and Alberta (David Coltman), in which we will exploit the growing pedigree information on the Cousin island population of Seychelles warblers to obtain new insights on the genetic contribution to behavioural and other traits. This project will produce a rigorous framework for understanding the contribution that environmental and genetic factors, alternative strategies and ecological variables make towards the overall lifetime reproductive success of individuals. A suite of microsatellite markers has been used to deduce the relationships of individuals in the population. Additional genotyping will be carried out by technical staff in Sheffield (and is therefore not a requirement of the postdoc).

Applicants should have a PhD in quantitative genetics or evolutionary ecology and ideally have experience of the analysis of pedigrees using advanced statistical methods. The post is available immediately.

Salary on the RA1A scale (minimum UKP19,400 pa) Closing date: 6 January 2005

Informal enquiries may be made to Professor T A Burke, Tel: 0114 222 0096 (e-mail: t.a.burke@sheffield.ac.uk).

Further information and details on how to make an application can be found at http://www.shef.ac.uk/jobs/ (under Current Vacancies/ Research)

(Post reference R3522)

t.a.burke@sheffield.ac.uk t.a.burke@sheffield.ac.uk

USheffiled miRNA EggHormones

The following postdoctoral post was advertised in Nature on 9 December 2004. Note that although the initial appointment would be for one year, it would be renewable for upto 2 further years.

UNIVERSITY OF SHEFFIELD DEPARTMENT OF ANIMAL & PLANT SCIENCES

The appointee will be required to investigate the role of microRNAs in developmental responses to the environment in birds. The systems to be studied will include hormonal effects on developing embryos and the genetic control of condition-dependent plumage.

A PhD or postdoctoral research experience in molecular genetics, molecular physiology, physiological ecology or another relevant discipline is essential.

Salary on the RA1A scale (minimum UKP19,400 pa) Closing date: 6 January 2005

Informal enquiries may be made to Professor T A Burke, Tel: 0114 222 0096 (e-mail: t.a.burke@sheffield.ac.uk).

Further information and details on how to make an application can be found at http://www.shef.ac.uk/jobs/ (under Current Vacancies/ Research)

(Post reference R3523)

t.a.burke@sheffield.ac.uk t.a.burke@sheffield.ac.uk

WoodsHole 2 MarineEvolBiol

2 POSTDOCTORAL POSITIONS 1 year, beginning ca. February 2005

Roger T. Hanlon, Senior Scientist Marine Biological Laboratory, Woods Hole, MA rhanlon@mbl.edu

CUTTLEFISH CAMOUFLAGE AND VISUAL PERCEPTION OF SUBSTRATES

Cuttlefish (marine mollusks in the class Cephalopoda) have an advanced system of adaptive coloration and seem capable of camouflaging themselves against any background substrate. We are seeking answers to how cuttlefish "decipher" complex visual backgrounds and make the appropriate choice of which camouflage pattern they implement in their skin. We have developed a visual sensorimotor assay in which we present natural and artificial substrates to cuttlefish and we measure the motor response via video of the resultant body pattern they produce in their skin. The ideal postdoctoral candidate will have interest/experience in animal behavior and visual perception, including aspects of psychophysics.

OCTOPUS ARMS AND SUCKERS: SENSORY CAPABILITIES AND MOTION CONTROL

One of nature's most flexible appendage - the octopus arm - is a muscular hydrostat that can extend, retract, bend and rotate anywhere along its length. By studying live octopuses, we have filmed and cataloged many movements. Now we wish to study sensory mechanisms and functions of the arm and suckers, with emphasis on tactile and chemical capabilities. Techniques will include behavioral, neural and anatomical approaches to understand structure and function. Candidates with an interest in animal behavior and sensory neurobiology may find this position particularly rewarding.

Roger Hanlon <rhanlon@mbl.edu>

WorkshopsCourses

NCStateU Statgen

Two 3-credit hour graduate courses in statistical genetics will be offerred online by NC State in the Spring of 2005:

ST 610D: Genetic Data Analysis (using draft of "Genetic Data Analysis III") Taught by Bruce Weir (weir@stat.ncsu.edu)

ST 610F: Statistical Analysis of Pedigree Data (using "Statistical Inference from Genetic Data on Pedigrees") Taught by Elizabeth Thompson (thompson@stat.washington.edu)

Registration is online at http://distance.ncsu.edu
Bruce Weir <weir@stat.ncsu.edu>

Switzerland SexualSize Aug21-26

THE EVOLUTION OF SEXUAL SIZE DIMORPHISM Workshop organized by Wolf Blanckenhorn, Tamas Szekely & Daphne Fairbairn 21-26 August 2005, Switzerland

http://www.bath.ac.uk/bio-sci/szekely/workshop/-SSD%20Workshop2%20webmod.htm We are organizing an international Workshop on sexual size dimorphism (SSD) at the Centro Stefano Franscini Conference Center on Monte Verità, near Locarno in southern Switzerland.

The objectives of the Workshop are to bring together researchers working on various aspects of SSD; overview the pattern of SSD in major animal and plant taxa; investigate the function and mechanisms of SSD.

Our main goal is to adopt a truly interdisciplinary approach, and encourage all participants to go beyond his/her specific research field.

We have invited a group of internationally renowned researchers to the Workshop. In addition, we have space for approximately 35 junior researchers including postgraduate students and post-docs.

The scientific program will consist of about 10 plenary lectures given by invited speakers. There will further be contributed oral and poster presentations, and discussion in groups. We welcome post-docs, MSc and Diploma students, and PhD students. Participants are expected to attend the entire 5-day workshop, and their number is limited to 60.

The cost of Workshop will be approximately 950 Swiss Francs (about 650 Euro or 800 US$) that includes registration fee, accommodation and all meals. For postgraduate participants the Association for the Study of Animal Behaviour (ASAB) has generously provided support to defer the cost of room and full board. To qualify for the ASAB support, please contact one of the organizers.

Abstract submission and registration deadline: 31 March 2005

Please note, that if space is limited applicants offering a presentation will be preferred. One participant is expected to present only one oral paper or poster. Instructions for payment and detailed travel information will follow with the letter of acceptance.

If you are interested in attending, please email the following details to our conference e-mail address after 1 January 2005: congres2@zoolmus.unizh.ch

1. Full name including title

Gender

2. Institution & Department

3. Contact mailing address including street address, city and postcode

Phone Fax Email

4. Proposed presentation

Type of presentation (Talk/Poster)

Title of presentation

Authors including the presenting author (*)

Abstract (max. 250 words)

Keywords (5)

Special technical needs

The Workshop is generously funded by The Centro Stefano Franscini, the Swiss Zoological Society and the Zoological Museum of Zurich.

Best regards,

Wolf Blanckenhorn wolfman@zoolmus.unizh.ch Tamas Szekely T.Szekely@bath.ac.uk Daphne Fairbairn daphne.fairbairn@ucr.edu

T Szekely <bssts@bath.ac.uk>

UReading MolSystematics Apr5-15

The Centre for Plant Diversity and Systematics at The University of Reading is offering an Intensive Course in Molecular Systematics again in 2005. The 10 day course will be held from 5th - 15th April 2005.

The course offers:

in-depth coverage of methods in molecular systematics and comparative sequence analysis

the treatment of theoretical issues in formal lectures alongside hands-on experience in practical workshops

More details from http://www.plantsci.rdg.ac.uk/-molecularcourse05.html or directly from Mrs Grace Barter, Molecular Systematics Intensive Course, Plant Sciences Laboratories, University of Reading, Reading RG6 6AS. email: molecular.systematics@reading.ac.uk

Julie Hawkins <j.a.hawkins@reading.ac.uk>

Instructions

Instructions: To be added to the EvolDir mailing list please send an email message to Golding@McMaster.CA. At this time provide a binary six letter code that determines which messages will be mailed to you. These are listed in the same order as presented here — Conferences; Graduate Student Positions; Jobs; Other; Post-doctoral positions; WorkshopsCourses. For example to receive the listings that concern conferences and post-doctoral positions this would be 100010. Messages are categorized on the basis of their subject headings. If this subject heading is not successfully parsed, the message will be sent to me at Golding@McMaster.CA. In addition, if it originates from 'blackballed' addresses it will be sent to me at Golding@McMaster.CA. These messages will only be read and dealt with when I have time. The code 000000 has all channels turned off and hence gets only a once monthly notifcation of the availability of a monthly review pdf file.

To be removed from the EvolDir mailing list please send an email message to Golding@McMaster.CA. Note that 'on vacation', etc, style messages are automatically filtered and should not be transmitted to the list (I hope), but should you wish to avoid the e-mail's your code can be temporarily changed to 000000.

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains the correct category "Conference:, Graduate position:, Job:, Other:, Postdoc:, Workshop:" and then the message stands a better chance of being correctly parsed. Note that the colon is mandatory.

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. If the message is caught by one of the filters (e.g. a subject header is not correctly formated) the message will be send to me at Golding@McMaster.CA and processed later. In either case, please do not expect an instant response.

Afterward

This program is an attempt to automatically process a broad variety of e-mail messages. Most preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.