
E v o l D i r

December 1, 2004

M o n t h i n R e v i e w

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

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Maastricht EvolEconomics Nov22-23

Since economic activities are important determinants of people's success, economic circumstances will influence the evolutionary selection process, while human diversity will affect economic performance. Combining the biological and economic perspective can improve our insight in both disciplines: What role does human diversity play in explaining economic performance and how does the human evolution adjust to economic circumstances? Such a genetic and cultural co-evolution can be related to a number of issues concerning human cooperation, sexual selection and parental investments in children.

On 22 and 23 November 2004 we organize a workshop in Maastricht to bring together leading biologists and economists who are interested in the interplay between biology and economics. The workshop is sponsored by the Dutch Science Foundation as a part of their Evolution and Behavior research program.

For further information, see <http://www.merit.unimaas.nl/HDEP/index.html> Lex Borghans Bas ter Weel University of Maastricht

Ido Pen Simon Verhulst Franz Weissing University of Groningen

– Ido Pen Theoretical Biology Centre for Ecological & Evolutionary Studies University of Groningen 9751 NN Haren - The Netherlands Tel +31(0)503638083 Fax +31(0)503633400

Ido Pen <I.R.Pen@biol.rug.nl>

Marseille EvolBiol Sep21-23

The registrations for the next evolutionary biology meeting at Marseille are now opened

see the meeting web site: <http://www.up.univ-mrs.fr/evol/congres/> Best regards

Pierre Pontarotti EA 3781 EGEE (Evolution Génome Environnement) Université d'Aix Marseille I Centre St Charles 3 Place Victor Hugo 13331 Marseille Cedex 3 33491106489 <http://www.up.univ-mrs.fr/evol>

We organize the 9th Evolutionary Biology Meeting at Marseille <http://www.up.univ-mrs.fr/evol/congres/> pierre.pontarotti@up.univ-mrs.fr

McMasterU Origins May24-28

FIRST ANNOUNCEMENT:

ORIGINS INSTITUTE; CONFERENCE and WORKSHOP

“Astrobiology and the Origin of Life”

McMaster University, Hamilton, Ontario. Conference: May 24 - 28 2005 Workshop: May 30 - June 10 2005

The newly formed Origins Institute at McMaster is organizing an interdisciplinary conference and workshop over a three-week period in Spring 2005. We now call for abstracts for contributed talks and posters and for registration at the meeting. See our web site -

<http://origins.mcmaster.ca/> New observations of exo-solar planets, the search for life in solar system, and advances in genomics and biodiversity make astrobiology one of the most exciting and important emergent topics in modern science. Our topic areas can be grouped under two themes: Planetary Science and Evolutionary Biology. Talks on these two themes will be interwoven during the conference week, with an aim of maximizing the degree of communication between different disciplines.

Planetary Theme - Star formation - Planet formation - Observations of exosolar planets - Search for life elsewhere - Mars, Europa ... - Organic molecules in space and delivery of organics to Earth - Geochemistry - energy sources for life

Evolutionary Biology Theme - The tree of life - molecular phylogenetics - The earliest organisms - origin, evolution, metabolism, fossil evidence... - Extremophiles - Cellular evolution - the origin and evolution of eukaryotic cells and organelles - Origin and evolution of multicellular life-forms - Evolutionary theory - complexity, autocatalysis, replicators...

See the conference website for further details, and for a list of keynote speakers:

<http://origins.mcmaster.ca/astrobiology> The conference week is open to all - please register and contribute abstracts for talks and posters. The following two workshop weeks will be for a small group. This will focus on informal discussions and establishing new collaborations between the participants. You are encouraged to bring along your own ideas and propose topics for discussion and new research work that fits somewhere in the broad themes of the meeting. Participants for the workshop will be selected from among those requesting to attend. Financial support is available for those attending the workshop.

Please apply by 1st February 2005 in order to be considered for financial support, contributed talks, or participation in the 2 week workshop.

See you in May at McMaster! Organizing Committee: Ralph Pudritz - Director of the Origins Institute Paul Higgs and James Wadsley -Department of Physics and Astronomy Brian Golding and Jon Stone - Department of Biology

Paul Higgs <higgsp@mcmaster.ca>

MonteVerita Sperm Feb13-18

From February 13th to February 18th we will be holding an international workshop entitled

?Sperm and seminal fluid: what males produce and how females respond?

at the Monte Verità in southern Switzerland (?Centro Stefano Franscini?, <http://www.csf.ethz.ch>). The meeting is being organized by Eric Kubli (Zoological Institute, University of Zurich), Paul Ward (Zoological Museum, University of Zurich) and Paul Schmid-Hempel (ETH-Zürich).

Our aim is to organize a workshop for scientists working in insect reproduction, especially on sperm and seminal fluid and the responses of the females. We would like to cover proximate and ultimate aspects of this field. Our particular aims are:

- To present and discuss the research of the different fields.
- To initiate and promote interactions between individual scientists on theoretical and practical levels
- To provide a stimulating atmosphere supporting the creation of new ideas and the initiation of fruitful collaborations across the disciplines

The scientific program will consist of 10-15 plenary lectures by invited speakers (T. Aigaki, Tokyo; S. Applebaum, Rehovot; G. Arnquist, Uppsala; G. Bernasconi, Lausanne; T. Birkhead, Sheffield; S. Goodwin, Glasgow; B. Hellriegel, Munich; D. Joly, Gif-sur-Yvette; T. Karr, Bath; G. Parker, Liverpool; M. Wolfner, Ithaca), contributed oral and poster presentations and discussion groups. We particularly welcome postdocs and PhD students. Participants are expected to attend the entire workshop and their number is limited to 55.

Program: Registration starts on Sunday, February 13th, 2005, 1500 at the Conference Centre (Hotel Monte Verità, Ascona, Switzerland). Lectures begin on February 14th, 0900 and end on Friday, February 18th at noon.

Registration deadline: 14.12.2004 Conference fee: Swiss Francs 250.- (about 170 Euro/200 \$) Meals and board: Swiss Francs 500.- (about 350 Euro/400 \$)

There are a limited amount of student funds. Since attendance is limited, acceptance will be on a competitive basis. Decisions will be made in December.

Instructions for payment and detailed travel informa-

tion will follow with the letter of acceptance.

Since we do not have a web-page, please follow the instructions below.

To apply, send an e-mail (as a PDF-file) with the following details to the Secretary of the workshop: Rosemarie Keller, Zoological Museum, University of Zurich-Irchel. E-mail: congress@zoolmus.unizh.ch

- Status (Participant/Invited Speaker/Organizer) - Gender (Female, Male) - Title (Prof, Dr., none) - First Name - Last Name - Institution - Department - Street - ZIP code - City - Country - Phone - E-mail - Presentation (Lecture/Poster/None) - Title of your presentation - Co-authors - Short abstract (max. 250 words) - Keywords (5) - Special technical needs

The organizers: Eric Kubli, Paul Ward, Paul Schmid-Hempel

Eric Kubli <ekubli@zool.unizh.ch>

MurciaSpain Carabidologists Sep19-22

Dear Colleagues,

For those interested in ground beetles we have released a Web page <http://www.um.es/eurmecar/>, where you can find preliminary information on the next XII European Carabidologists Meeting, to be held in Murcia (Spain) in September 2005, 19-22.

Best regards.

Prof. José Serrano Universidad de Murcia, Facultad de Veterinaria. Departamento de Zoología Campus de Espinardo. Apto. 4021 30071 Murcia (Spain) phone 34 968 364206 fax 34 968 364147

GradStudentPositions

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Bremerhaven Phaeocystis microsat

PhP studentship available for 3 years from the DFG (German Research Council) to study genetic diversity in the polar haptophyte *Phaeocystis antarctica* using microsatellites. Current knowledge based on ITS sequencing shows that ancestral populations occur in the

ACC (antarctic circumpolar current) and then diverge sequentially in the major continental seas surrounding Antarctica. The goal of this project is to measure gene flow around Antarctica and into the various gyres, such as the Weddell Sea, the Scotia Sea, etc. Excursions to Antarctica are possible. Applications can be made until November 30 2004 quoting 67/11-1 and mailed to the Personnel Dept., Alfred Wegener Institute for Polar and Marine Research, Am Handelshafen 12, D27570 Bremerhaven, Germany. A knowledge of German is not required but molecular biology experience is.

Futher details can be obtained from Dr. Linda Medlin
lmedlin@awi-bremerhanven.de

GeorgiaSouthernU BioInvasions

Seeking Master's Students

I would appreciate if the readers of evodir could let any potentially interested undergraduates know about this opportunity. Thanks.

I am looking for 1-2 students who are interested in conducting research for a Master's degree. The goal of this NSF-funded project is to examine aspects of the ecological genetics of biological invasions using the plant *Silene latifolia*. Thesis research will include working on experimental common gardens in several North American and European sites. Support for this position includes a combination of research and teaching assistantships. Interested students should contact Lorne Wolfe for more information (912-681-0848, wolfe@georgiasouthern.edu, <http://www.bio.georgiasouthern.edu/Bio-home/-wolfe/Wolfe.html>).

wolfe@georgiasouthern.edu

LeidenU Adaptation

Institute of Biology (IBL), Leiden University

Section of Evolutionary Biology

Promovendus(PhD) position (full-time)

Project: "Mechanisms of adaptation: analysis of geographic variation in a polyphenic butterfly"

The Promovendus will work in the Section Evolutionary Biology with Paul Brakefield and Bas Zwaan. One of the model organisms in this group is the tropical seasonal butterfly *Bicyclus anynana* which is eminently suitable for studying the mechanisms of adaptation. This butterfly exhibits high genetic variation as well as adaptive phenotypic plasticity for the suite of traits associated with temperature adaptation. We understand how genetic and phenotypic correlations among life history traits have been shaped by natural selection and how these traits relate to fitness. This project will use

existing clines with latitude in this butterfly to explore the nature of the genetic and developmental changes that might occur in response to changes in temperature. By using a variety of tools to compare populations that differ extensively in their temperature environment and the association with rainfall, we will study the mechanisms of adaptation at the genetical, developmental and physiological levels. Application of this fully integrated approach will provide novel insights into the mechanisms of genetic adaptation, and also into the role of phenotypic plasticity herein. Furthermore, it will address the issues of potential constraints in adaptive evolution and the rates of evolutionary change, especially with respect to responses to man-made change.

The project is funded by N.W.O., Aard- en Levenswetenschappen, for four years.

Requirements: Experience of working with insects in the context of evolutionary genetics would be an advantage. The successful candidate should have an ability to work with whole organisms and large data sets, as well as in the molecular laboratory, but crucially should also have experience with working under (tropical) field situations. They should also be interested in working at the boundaries between different areas of biology. He/she will work in an active research group encompassing a wide variety of different projects.

The appointment is for a maximum of 4 years and is expected to lead to the completion of a dissertation. The gross monthly salary is 1.702 in the first year and increases progressively each year to 2.283 in the fourth year. Salary and fringe benefits conform to the Collective Employment Agreement for Dutch Universities.

Further information:

Dr. Bas J. Zwaan, zwaan@rulsfb.leidenuniv.nl or Prof. dr. Paul M. Brakefield, brakefield@rulsfb.leidenuniv.nl (Web Site: <http://wwwbio.leidenuniv>)

Applications including c.v. should be submitted by e-mail not later than two weeks after publication of this advertisement to either Paul or Bas.

Bas Zwaan <zwaan@rulsfb.leidenuniv.nl>

Madrid MolecularSystematics

A PhD studentship (F.P.I. programme) is available in the Museo Nacional de Ciencias Naturales in Madrid to work on molecular systematics of water beetles, us-

ing species-level phylogenies to characterise patterns of macroevolution in clades of contrasting dispersal abilities. Candidates should have a good degree in biology and (preferably) some experience with basic molecular work. For more information write to:

Dr. Ignacio Ribera Departamento de Biodiversidad y Biología Evolutiva Museo Nacional de Ciencias Naturales José Gutiérrez Abascal 2 28006 Madrid Spain. i.ribera@mncn.csic.es

i.ribera@mncn.csic.es

NCStateU Quantitative Traits

Department of Genetics at North Carolina State University

Research Training Program in the Genetic Architecture of Quantitative Traits

The National Institute of General Medical Sciences of the National Institutes of Health has awarded the Department of Genetics an Institutional Research Training Grant for predoctoral training in "The Genetic Architecture of Quantitative Traits."

Quantitative, or complex, traits are affected by multiple interacting genes, each of which have small effects and are sensitive to the environment. Understanding the molecular nature of genetic variation for quantitative traits will have an enormous impact on medicine, livestock and crop breeding, and the study of evolution. For over half a century North Carolina State University has been a leading center for research in quantitative genetics. To enable future scientists to advance our understanding of the genetic architecture of quantitative traits, we offer a research and training program that integrates quantitative, population, molecular and developmental genetics, statistics and molecular evolution.

Our program offers:

* \$20,772 stipend with tuition and health insurance * Travel allowance and research funds * State-of-the-art research facilities * Internationally recognized faculty with expertise in theoretical and experimental quantitative genetics * A stimulating academic environment near the University of North Carolina at Chapel Hill, Duke University and the Research Triangle Park * A beautiful and affordable location with a pleasant climate between the beaches and the Appalachian mountains

US citizens and permanent residents are eligible for Fellowships. The Department of Genetics is strongly committed to promoting diversity in the scientific community and encourages applications from individuals of historically under-represented minority groups.

Training Faculty

Jose Alonso: Ethylene signal transduction in Arabidopsis; characterization of Arabidopsis genome.

Robert Anholt: Molecular and quantitative genetics of olfaction.

William Atchley: Developmental quantitative genetics and molecular evolution.

Philip Awadalla: Coalescent estimates and the evolutionary significance of recombination.

Patricia Estes: Development of the Central Nervous System (CNS) and cellular and molecular response to hypoxia.

Robert Franks: Development of the carpel margin meristem in Arabidopsis thaliana.

Gregory Gibson: Molecular and quantitative variation in developmental pathways in Drosophila.

Fred Gould: Ecological, genetic and chemical aspects of plant/herbivore interactions, pest management, and behavioral ecology of arthropods.

Patrick Hurban: Elucidation of biological networks.

Todd Klaenhammer: Physiology, metabolism and genetics of lactic acid bacteria.

James Mahaffey: Drosophila developmental genetics.

Trudy Mackay: Molecular quantitative genetics in Drosophila.

Laura Mathies: Genetic control of early gonad development in *C. elegans*.

Michael Purugganan: Molecular genetics of morphological evolution in plants.

Ronald Sederoff: Molecular genetics, quantitative genetics and genomics of pine.

Jeffrey Thorne: Statistical methods for analysis of sequence data.

Bruce Weir: Statistical methods for characterization of population structure, detecting human disease genes and individual identification.

Shaobang Zeng: Theory and statistical methodology for characterizing and analyzing genetic variation.

For information and application materials, contact:

Director of Graduate Programs Department of Ge-

netics North Carolina State University Raleigh, NC 27695-7614 Telephone: 919-515-2292 <http://www.cals.ncsu.edu/genetics/>

Julie Pederson <jdpeders@unity.ncsu.edu>

PurdueU WildlifeGenetics

A graduate assistantship (Ph.D.) in wildlife ecology and genetics in the Department of Forestry and Natural Resources (FNR) at Purdue University is anticipated for fall 2005. The successful candidate will focus on the use of genetic markers to estimate population-level parameters of free-ranging river otters in Indiana and on the use of these data to validate several of the currently used population indices for this species. Extensive experience with extracting and genotyping DNA from otter scat currently exists in our laboratory and a panel of more than 20 polymorphic microsatellite loci, developed by personnel in the Rhodes lab, is available for this research. Strong quantitative skills are required and experience with molecular genetic techniques is highly desirable. Candidates should have a GPA of at least 3.2 and a cumulative GRE score of at least 1200 (V+Q). Please email Dr. Olin E. Rhodes, Jr., Professor, Dept. Forestry and Natural Resources, Purdue University, W. Lafayette, IN 47907-1159 (rhodeso@purdue.edu; 765-494-3601; Website -<http://www.agriculture.purdue.edu/fnr/html/faculty/-Rhodes/index.htm>) for more information regarding this opportunity. Graduate assistantships are currently awarded at \$17,870.00 per year (Ph.D.). Guidelines for application to the FNR Graduate Program can be found at <http://www.agriculture.purdue.edu/fnr/html/graduate.html>. The deadline for receipt of completed applications to be considered for this opportunity is January 5, 2005. Women and minorities are encouraged to apply. Purdue University is an equal opportunity affirmative action employer.

dewoody@purdue.edu

UArkansas EvoBiol

Ph.D. Fellowships in ecology and evolutionary biology, University of Arkansas

Graduate fellowships are available to qualified applicants for \$20-30,000/yr in the Department of Biological Sciences, University of Arkansas, Fayetteville. Details are available at <http://biology.uark.edu/-docfellow.html>. Deadline for Fall 2005 admission is January 15, 2005.

Program faculty and their interests include: Steven J. Beaupre, Physiological ecology Arthur V. Brown, Stream ecology William J. Etges, Population biology, evolution, speciation John L. Gentry, Plant taxonomy, Director of the Herbarium Douglas A. James, Ornithology, ecology David R. Kremenetz, Wildlife ecology and management, biometrics Daniel D. Magoulik, Fisheries and aquatic ecology, conservation biology Cynthia L. Sagers, Evolutionary ecology, plant-insect interactions Jeffrey Silberman, Molecular evolution, systematics in single-celled eukaryotes Kimberly G. Smith, Community ecology, avian ecology Frederick W. Spiegel, Mycology, systematics Steven L. Stephenson, Community ecology, biogeography, mycology James M. Walker, Herpetology, ecology Susan Ziegler, Aquatic microbial ecology, biogeochemistry

The department, degree requirements, faculty contact information, facilities, and life in the Ozarks are described on our websites <http://biology.uark.edu/> and <http://biology.uark.edu/>Please contact William J. Etges (wetges@uark.edu) for details.

— William J. Etges Department of Biological Sciences SCEN 632 University of Arkansas Fayetteville, AR 72701 USA wetges@uark.edu <http://comp.uark.edu/~wetges/wetges.html> office: (479) 575-6358 lab: (479) 575-7437 FAX (479) 575-4010 —

UBerne MatingSystems

PHD POSITION ON THE CHARACTERIZATION OF MATING SYSTEM AND DISPERSAL ABILITIES FROM GENETIC DATA

Applications are invited for PhD position in the Computational and Molecular Population Genetics lab (CMPG, Zoology Institute, University of Berne, Switzerland), starting on January 1, 2005, or soon thereafter.

We are looking for a highly motivated biology student to work on the characterization of mating system and dispersal abilities from genetic data, mainly through Approximate Bayesian Computation (ABC) techniques

(e.g. Beaumont et al. 2002). These techniques involve massive simulations of genetic data, which are then confronted to observations for parameter estimations. The underlying biological/evolutionary models that are simulated can be arbitrarily complex, and will be spatially explicit in our case. We plan to particularly focus on populations that have gone through a recent range expansion (e.g. Ray et al. 2003, Excoffier 2004). The PhD project should have a strong theoretical/modeling/simulation component, but the student will need to apply his/her methodologies on organisms studied in the CMPG lab (e.g. freshwater fishes, voles, humans).

Previous experience in population genetics, statistics and computer programming (C++) are required.

The CMPG lab is well equipped with computational tools including a 40-nodes Linux cluster, on which simulations and computations will be performed.

Applicants should send (before December 1st) a motivation letter, a CV, a publication list, and the names and emails of two references to Laurent Excoffier, CMPG, Zoology Institute, University of Berne, Baltzerstrasse 6, 3012 Berne, Switzerland email: laurent.excoffier@zoo.unibe.ch

References: Beaumont MA, Zhang W, Balding DJ (2002) Approximate Bayesian Computation in Population Genetics. *Genetics* 162:2025-2035 Excoffier L (2004) Patterns of DNA sequence diversity and genetic structure after a range expansion: lessons from the infinite-island model. *Mol Ecol* 13:853-864 Ray N, Currat M, Excoffier L (2003) Intra-Deme Molecular Diversity in Spatially Expanding Populations. *Mol Biol Evol* 20:76-86

The CMPG lab (<http://cmpg.unibe.ch>) and the Zoology Institute (<http://www.zoology.unibe.ch>) offer a very lively intellectual and social environment. Other research fields in the Zoology Institute include Conservation Biology (Raphael Arlettaz), Evolutionary Ecology (Heinz Richner), Behavioral Ecology (Michael Taborsky), Aquatic Ecology (Ole Seehausen), and Community Ecology (Wolfgang Nentwig). Berne is located in the center of Switzerland and Europe. It offers a high quality of life, and beautiful surroundings (see <http://www.bernetourism.ch>).

This mail was sent through IMP at <http://mail.unibe.ch> Laurent Excoffier <laurent.excoffier@zoo.unibe.ch>

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>

UQuebecRimouski EvolBiol

Graduate student position in evolutionary biology

I am looking for an enthusiastic and dedicated person to carry on Ph.D. studies in my laboratory at the Université du Québec à Rimouski. Research in my lab is centered around evolutionary aspects of polyploidy using the cladoceran *Daphnia* as a model organism. Topics of interests include : 1) the evolutionary fate of gene duplication in polyploid *Daphnia* (cDNA-AFLP analyses will be carried out on parental diploid and allopolyploid clones to estimate global rates of gene silencing), 2) cytonuclear interactions in allopolyploids, and 3) the effects of mutation accumulations on phenotypic characters of polyploid and diploid clones. As the genome of *Daphnia pulex* is being sequenced, many genomic tools are now available and will be of great value to carry on the above projects.

Candidates with a M.Sc. or equivalent and with an interest in evolutionary genetics, preferably with an experience in molecular techniques should send via e-mail a letter of motivation, a CV, and the

names and e-mail of one referee to France Dufresne (France.dufresne@uqar.qc.ca).

–

France Dufresne, Ph.D.

Département de biologie & Centre d'études Nordiques
 Université du Québec à Rimouski 300 allée des ursulines
 Rimouski, G5L 3A1 tel. (418)-723-1986 poste 1223 fax
 (418)-724-1849 courriel: france.dufresne@uqar.qc.ca
http://www.uqar.qc.ca/bcss/bio_evol/About/-France_fr.html France.Dufresne@UQAR.QC.CA

UWisconsinStevensPoint FishGenetics

M.S. Assistantships in Fisheries Genetics and Fisheries Ecology

The Wisconsin Cooperative Fisheries Research Unit (WICFRU) and the College of Natural Resources (CNR) at the University of Wisconsin-Stevens Point has openings for M.S. students in Fisheries Science beginning Spring 2005. Projects include: - Stock structure of lake whitefish in Green Bay and Northern Lake Michigan - Genetic evaluation of broodstock source and selection strategy in Wisconsin's wild trout stocking program - Genetic analysis of remnant Menominee River Lake Sturgeon populations: Implications for rehabilitation and reintroduction - Habitat modeling of smallmouth bass populations in north temperate lakes - Evaluating success of artificial and natural walleye spawning reefs

The program offers educational opportunities integrating field ecology, resource management, and applied scientific research. Resources available to students include use of the Molecular Conservation Genetics Laboratory, computer and AV equipment, SCUBA equipment, and generous travel support. Successful applicants are expected to have completed a B.S./B.A. in a related biological sciences field (i.e., resource management, biology, zoology, botany, microbiology, etc.) with an undergraduate GPA of 3.0 and minimum GRE scores of 1000 (quantitative and verbal). All Wisconsin Cooperative Fishery Research Unit students are expected to attend and participate in scientific meetings, maintain professional memberships in an appropriate society, and communicate with resource agency personnel regarding their research. Students will be part of a diverse CNR graduate program (www.uwsp.edu/cnr) aimed at pro-

viding superior education, communication, and science-based management professionals.

Research assistants of WICFRU receive funding for 2 years at \$18,000/year and paid tuition. Individuals interested in applying to the program should send a letter of interest, resume', 3 references and photocopies of transcripts and GRE scores to Dr. Brian L. Sloss (Conservation genetics: brian.sloss@uwsp.edu) or Dr. Michael A. Bozek (Habitat and population dynamics: Michael.bozek@uwsp.edu) at:

Wisconsin Cooperative Fishery Research Unit College of Natural Resources University of Wisconsin-Stevens Point Stevens Point, Wisconsin 54481

***** Brian L. Sloss Assistant Unit Leader Wisconsin Cooperative Fisheries Research Unit Biological Resources Division - U.S.G.S. College of Natural Resources University of Wisconsin-Stevens Point Stevens Point, WI 54481 715-346-3522 715-346-3624 (Fax) brian.sloss@uwsp.edu *****

WesternKentuckyU ColeopteraSystematics

GRADUATE ASSISTANTSHIP:

INSECT SYSTEMATICS AND ECOLOGY

WESTERN KENTUCKY UNIVERSITY

An NSF funded graduate assistantship beginning fall semester 2005 is available for M.S. research in the department of biology at Western Kentucky University under the direction of Dr. Keith Philips.

The project will involve the study of either dung beetles or spider beetles, depending upon the interest of the successful applicant, and will include one research expedition to Ghana, West Africa. If dung beetles are the selected group, research will include ecological research with a wide variety of potential choices for specific projects and possible taxonomic and phylogenetic work. Spider beetles are potentially one of the poorest known groups of beetles in Africa and work on this taxon will mainly involve both revisionary and phylogenetic studies.

The successful applicant will be affiliated with the Center for Biodiversity Studies. Facilities include a new research building and a biotechnology center. More information on the Center and the Biology Department can be found at <http://bioweb.wku.edu> This as-

sistantship is for a minimum of \$17,000 per year for two years (amount depends upon status and future tuition costs; excludes a fee waiver). For more information or to apply please contact Keith Philips at Keith.Philips@wku.edu. Please send a cover letter in-

cluding research interests and experiences, a CV with GPA and GRE scores (if available), and names and contact information for three references. Applications will be reviewed as received, until the position is filled.

Jobs

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ColoradoStateU EvolVertBiol

EVOLUTIONARY VERTEBRATE BIOLOGIST-
 Colorado State University: The Department of Biology invites applications for a nine-month, tenure-track position as an ASSISTANT PROFESSOR of vertebrate biology, beginning August 2005. We seek a broadly trained biologist who uses molecular and other integrative approaches to understand the physiology or behavior of vertebrate organisms. A Ph.D. in a

relevant field and postdoctoral or similar experience are required. The successful candidate will be expected to establish a creative, externally funded research program, teach at the undergraduate and graduate levels in organismal biology, and participate in graduate training. Applicants should e-mail as PDF files a cover letter, curriculum vitae, statements of research and teaching experience, and three publications to e-mail: biosrch@lamar.colostate.edu. Three letters of recommendation should be sent to: Vertebrate Biologist Search Committee, Department of Biology, 1878 Campus Delivery, Colorado State University, Fort Collins, CO 80523-1878. For full consideration, applications should be received by January 7, 2005,

although applications will be considered until the position is filled. Colorado State University is an Equal Employment Opportunity/Affirmative Action Employer.

Thanks,
Cameron

Cameron Ghalambor Department of Biology and Graduate Degree Program in Ecology Colorado State University Fort Collins, CO 80523 Phone (office): 970-491-2759 Fax: 970-491-0649 Email: cameron1@lamar.colostate.edu

Cameron Ghalambor <cameron1@lamar.colostate.edu>

HarvardU ResTech

Technician Position

Title: Research technician Institution: Organismic and Evolutionary Biology, Harvard University, Cambridge, MA Full time Date posted: 11/23/04

Participate in research in evolutionary ecology and genetics of plant populations. Research will combine work in the field, laboratory, and greenhouse. Duties include plant care; some molecular work (PCR, electrophoresis, AFLP analysis, and genetic mapping); histological preparations; maintenance of field and greenhouse experiments; data collection and organization; assistance in the design and execution of new experiments; instruction of others in basic laboratory techniques and procedures; general lab and clerical tasks; other related duties as required.

A BA/BS in Biological Sciences or related field and 1-3 years of research experience in the field of plant biology, ecology, or genetics are required. Some experience with molecular biology and/or histology and electron microscopy is strongly preferred, and previous experience working with *Arabidopsis thaliana* is a plus.

For more information, please contact: Chris Preheim Cpreheim@oeb.harvard.edu for Kathleen Donohue Department of Organismic and Evolutionary Biology Harvard University

Kathleen Donohue Assistant Professor of Organismic and Evolutionary Biology Harvard University 22 Divinity Avenue Cambridge, MA 02138 USA kdonohue@oeb.harvard.edu Tel: (617) 384-9768 Fax: (617) 495-9484

INRA France PopGenetics

Permanent position in population genetics of grasslands species

A permanent position in the field of population genetics is open for application at the UGAPF (Grasslands and Forage Crops Genetics Research Unit). This position is at the level of first class 'chargé de recherche' in the National Institute for Agricultural Research (INRA) Plant Genetics Department. It is a research position with no teaching load. The position is to be filled in Spring 2005. The position is aimed at reinforcing a research group headed by C. Huyghe working on the genetic changes occurring in grasslands.

Skills : the candidates should have a good background in population genetics and biology, theoretical approaches and modelling.

Research program: to describe, understand and model demographic and genetic changes in perennial grasslands swards focussing on dominant grassland species (forage grasses and legumes) and taking into account competition within and among plant species, sexual reproduction and recruitment of seedlings.

Available technical resources: molecular biology lab, greenhouses and growth rooms, field experiments.

Qualifications include the completion of a Ph.D. and post-doctoral experience along with demonstrated research potential.

For more information, contact Christian Huyghe (huyghe@lusignan.inra.fr).

Full details on the application procedure will soon be available on the INRA web site (www.inra.fr). Applications must include CV, detailed research achievements and a proposal of research project for the offered position.

Christian Huyghe

Christian Huyghe <huyghe@lusignan.inra.fr>

MadisonWI MaizeEvolGenomics

Molecular and Functional Diversity in the Maize Genome Project Manager

We invite applications for the position of project manager for a multi-institutional NSF Plant Genome Project. The project has two foci: (1) analysis of molecular diversity in the genomes of maize and its wild relatives by SNP genotyping with the principal goals of testing several thousand genes for evidence of selection during maize domestication and improvement and better understanding how historical and demographic factors have shaped the maize genome, and (2) testing diverse alleles at one thousand candidate genes for functional variation on agronomically and evolutionarily important phenotypes through a combination of high-throughput linkage and association mapping.

Members of the project include Ed Buckler (USDA/ARS and Cornell University), John Doebley (University of Wisconsin), Brandon Gaut (UC-Irvine), Major Goodman (North Carolina State University), James Holland (USDA/ARS and North Carolina State University), Steve Kresovich (Cornell University), Mike McMullen (USDA/ARS and University of Missouri), Lincoln Stein (Cold Spring Harbor Lab) and Doreen Ware (USDA/ARS and Cold Spring Harbor Lab).

The project manager will have diverse responsibilities related to coordinating activities among the different project groups, working with our informatics group, presenting project accomplishments at national meetings, overseeing budgets, and reporting project results to the National Science Foundation. The project manager will also have opportunity to participate in data analysis and publications. The position is available January 1, 2005, is funded for four years, and will be located in Madison, Wisconsin.

Applicants should have a Ph.D. in the biological sciences with training in either evolution, agronomy, plant biology, genetics, population genetics or related area. We specifically seek individuals with some background or interest in developing expertise in informatics. Strong organizational and communication skills are required. Applications (including a cover letter, CV, publication pdf files, and names, phone numbers and email addresses of three references) and inquiries should be directed by email to John Doebley, Department of Genetics, University of Wisconsin, jdoebley@wisc.edu.

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John Doebley Genetics Department 445 Henry Mall University of Wisconsin Madison, WI 53706 tel: 608-265-5803 lab: 608-265-5804 fax: 608-262-2976 email: jdoebley@wisc.edu <http://www.wisc.edu/teosinte/index.htm>

MaxPlanck EvolBiodemography

Max Planck Institute for Demographic Research

Directors: Prof. James W. Vaupel - Prof. Jan M. Hoem

The Max Planck Institute for Demographic Research is seeking to expand further its activities in the field of

Evolutionary Biodemography

and is recruiting to vacancies at the

PhD, Post-Doc, and Research Scientist levels

The successful candidates will complement an existing research team of 14 staff, working alongside a total of some 80 employees from diverse backgrounds engaged in a range of issues in demography. The team aims to gain a fundamental understanding of demographic processes, and is particularly interested in how these are shaped by evolution. We seek to advance our knowledge of life histories using a variety of field and laboratory based studies, theoretical modeling, and analysis of existing databases. As well as studies on birds, mammals, plants and a range of invertebrate organisms, the institute is particularly well placed to support the quantitative aspects of work in this field. There are ongoing projects on age-specific schedules of mortality, reproduction and growth, on the evolution of senescence, on reproductive effort, parental investment and intergenerational transfers, and on the costs of reproduction and the delayed effects of stress.

We are seeking able scientists from all levels with strong academic track records in life history biology, ecology, demography, mathematics or statistics. Applications should be addressed to Executive Director, Prof. James W. Vaupel and should include a CV with a statement of academic interests and relevant experience, a list of publications and the contact details of 3 referees. All material should be e-mailed to: Evodemo.positions@demogr.mpg.de. See www.demogr.mpg.de for information.

The Max Planck Society wishes to increase the share of women in areas where they are underrepresented, and strongly encourages women to apply.

The Max Planck Society is committed to employing more handicapped individuals and especially encourages them to apply.

Evo-Demo Positions, Attn. Prof. James W. Vau-

pel, Max Planck Institute for Demographic Research, Konrad-Zuse-Strasse 1, D-18057 ROSTOCK, Germany. E-mail: Evodemo.positions@demogr.mpg.de

“Thomson, David” <Thomson@demogr.mpg.de>

MichiganStateU QuantPlantBiol

Faculty Position in Quantitative Plant Biology

Michigan State University

As part of a broad initiative to strengthen quantitative approaches in the biological sciences at Michigan State University, the Department of Plant Biology seeks an individual who will use mathematical or statistical methods to address fundamental biological questions in plant systems. The candidate can work in any biological discipline (e.g. physiology, metabolism, cell biology, development, ecology, or evolution), and at any level of biological organization, from genes to cellular processes to ecosystems. Research experience with plant systems is desirable, but is not a requirement. The successful candidate will be expected to develop an independent research program addressing biological problems in plant systems that is supported by extramural funding, and we are particularly interested in those who will participate in collaborative interdisciplinary research. The successful candidate will have the option of a joint appointment with another suitable department, will contribute to undergraduate teaching, and will develop a graduate course in their area of expertise.

The faculty position is a tenure-track, academic year appointment at the Assistant Professor level. In exceptional cases, an appointment at the associate professor level will be considered. Applicants must have a Ph.D., and postdoctoral research experience is desirable. Applications should include a curriculum vita, a summary of research accomplishments and future research objectives, a brief description of teaching philosophy and goals, and three letters of reference. Information about the Department of Plant Biology can be found at <http://www.plantbiology.msu.edu> <<http://www.plantbiology.msu.edu>>. The review of applications will begin November 30, 2004 and will continue until a suitable candidate is identified. Questions regarding this position may be sent to Douglas Schemske (schem@msu.edu). Application materials can be sent electronically to jtate@msu.edu, or mailed to:

Douglas W. Schemske Chair, Mathematical Plant Biologist Search Department of Plant Biology Michigan State University East Lansing, MI 48824

Michigan State University is an Equal Opportunity/Affirmative Action Employer. Women and minorities are strongly encouraged to apply. Persons with disabilities have the right to request and receive reasonable accommodation.

Rob Tempelman <tempelma@msu.edu>

MississippiStateU EvolBiol

SECOND POSTING: THREE FACULTY POSITIONS IN BIOLOGICAL SCIENCES

The Department of Biological Sciences, Mississippi State University, (<http://www.msstate.edu/dept/biosciences>), invites applications for the following three tenure-track ASSISTANT PROFESSOR positions, as part of an expansion of biological sciences, beginning August 16, 2005.

1. Cell Biologist: Chair: Dr. Dwayne Wise
2. Evolutionary Biologist: Chair: Dr. Walter Diehl
3. Microbiologist: Chair: Dr. Karen Coats

Successful applicants should be able to make use of the University's state-of-the-art infrastructure in proteomics, genomics, and computing capabilities. Qualifications include postdoctoral experience and an established record of research productivity. The successful candidates are required to develop externally funded research programs and to direct graduate students. To apply send curriculum vitae, reprints of three representative publications, a concise statement of current and future research interests, and a statement of teaching interest. Applicants should provide names and addresses of at least three references. Screening will begin December 8, 2004 and will continue until the positions are filled.

Applications should be sent to appropriate search committee chair, Department of Biological Sciences, P.O. Box GY, Mississippi State University, Mississippi State, MS 39762. Mississippi State University is An Affirmative Action/Equal Opportunity Employer

Mark Fishbein, fish@biology.msstate.edu
Mark Fishbein, fish@biology.msstate.edu

Montpellier TheoPopGenet

Permanent position in theoretical population genetics

A permanent position in the field of theoretical population genetics is open for application at the C.B.G.P. (Center for Biology and Management of Population) in Montpellier (France). This position is at the level of first class "chargé de recherche" in the National Institute for Agricultural Research (I.N.R.A.). It is a research position with no teaching load. The position is aimed at reinforcing a research group headed by A. Estoup and J.M. Cornuet, working on the development of statistical methods for the genetic analysis of invading pest populations.

Skills : the candidate should have good expertise in theoretical population genetics including the coalescence theory. He should also be familiar with Bayesian statistical inference methods and random simulation based methods (e.g. importance sampling or Monte Carlo Markov chains). A background in spatial statistics and a good practice of a programming language are also recommended.

Initial research program : Develop statistical methods for coupling coalescence theory with temporal and geographical information. Test applicability and measure performances of these methods on simulated data sets reflecting situations found in species studied at the CBGP. Only neutral traits will be considered in a first step, but as soon as possible, selective processes will be included in the description of demo-genetic models

Available technical means : molecular biology lab, geographical information system and computer cluster.

For more information, contact Arnaud Estoup (estoup@ensam.inra.fr) or Jean-Marie Cornuet (jmcornuet@ensam.inra.fr) or Denis Bourguet (bourguet@ensam.inra.fr)

Denis Bourguet

NorthernMichiganU Geneticist

Biology Faculty Position

Geneticist Posted in the 5 November issue of Science See also: www.higheredjobs.com/institution/-details.cfm?JobCode=175110147

Northern Michigan University invites applications to fill a faculty position at the level of Assistant Professor in Biology beginning August 2005. The position requires a Ph.D. and is tenure earning. We seek a biologist committed to teaching with an interest in contributing to interdisciplinary programs in a comprehensive university. An active research program in genetics involving undergraduate and graduate students is expected. Teaching responsibilities will include genetics, cytogenetics, and introductory biology, and courses in area of specialization.

Application review begins December 6, 2004 and continues until the position is filled. Send curriculum vitae, statements of teaching and research philosophies, and names, addresses, telephone numbers and email addresses of three references to: Chair, Genetics Search Committee, Department of Biology, 1401 Presque Isle Avenue, Marquette, MI 49855-5341. (906) 227-2310 (voice); (906) 227-1063 (fax); email biology@nmu.edu. Detailed selection criteria are available at www.nmu.edu/biology. "NMU is an equal opportunity, affirmative action employer and is strongly committed to increasing the diversity of its faculty."

ABOUT NMU Northern Michigan University is a four-year, public, coeducational university founded in 1899. We offer learning opportunities to approximately 9,300 undergraduate and graduate students. Each incoming student is equipped with a notebook computer as a part of tuition and fees.

The NMU campus is located in an environment unrivaled by any other, on the south shore of Lake Superior in Michigan's Upper Peninsula. Nestled in the town of Marquette, NMU shares an array of breathtaking vistas with the town's 20,000 lucky residents.

Our campus is wired with state-of-the-art technology. We're large enough to offer scenic spaces and 50 quality facilities, such as: nine computer labs; the Glenn T. Seaborg Center; two on-campus radio stations; a public TV station; and the Superior Dome, an 8,000 seat stadium (the largest wooden dome in the world).

OregonStateU BioStatistics

Oregon State University Tenure-Track - Assistant Pro-

fessor

Tenure-track Assistant Professor in Statistics, beginning Fall 2005. Ph.D. in statistics/biostatistics and strong teaching and research potential. Duties include teaching, research, and collaborations in the natural resources and/or bioscience areas. Preferred qualifications include a demonstrable commitment to promoting and enhancing diversity.

Send curriculum vitae and graduate transcripts, and have 3 letters of reference sent to

Search Committee or email: searchA@stat.oregonstate.edu Dept. of Statistics, 44 Kidder Hall, Oregon State Univ., Corvallis, OR 97331-4606

For full consideration apply by Jan. 15, 2005.

For more information: <http://oregonstate.edu/dept/statistics> . OSU is an AA/EEO employer and is responsive to dual-career needs.

qu.annie@hotmail.com

PennStateU EvoBiol

Pennsylvania State University Assistant Professor (or above)

Astrobiology / Evolutionary Biology

The Eberly College of Science at Penn State invites applications for a tenure track faculty position in Astrobiology with the appointment to be made in one of the colleges departments including Biology, Biochemistry and Molecular Biology, and Chemistry (<http://www.science.psu.edu>). We seek a candidate interested in pursuing evolutionary research, with either prokaryotes or eukaryotes, on the early evolution of the Earth's environment and biota. Potential fields of study include, but are not limited to, molecular, cellular and developmental evolution, and paleontology. The appointee will have the opportunity to join our Astrobiology Research Center (<http://psarc.geosc.psu.edu>) and is expected to develop a strong, externally funded research program and participate in undergraduate and graduate teaching. Exceptional candidates at the rank of Associate or Full Professor may be considered. Applicants should send a PDF file containing their CV, statement of research and teaching interests, and contact information for three references to astrobio@email.bio.psu.edu, or mail to:

Chair, Astrobiology Search Department of Biology 208 Mueller Laboratory The Pennsylvania State University University Park, PA 16802-5301

Review of applications begins January 3, 2005 and will continue until a suitable candidate is identified. Penn State is committed to affirmative action, equal opportunity, and the diversity of its workforce.

PennStateU PlantFuncGenomics

PENN STATE UNIVERSITY Huck Institutes of the Life Science Assistant / Associate / Full Professor

FACULTY POSITION

PLANT FUNCTIONAL GENOMICS

The Department of Biology and the Huck Institutes of the Life Sciences invite applications for a faculty position at the Assistant, Associate, or Full Professor level in Plant Functional Genomics. We seek an individual with outstanding research accomplishments who will establish a vigorous and innovative research program in any area of plant genomic or post genomic biology, but particular interests would include genomics, evolutionary and functional analysis of developmentally important genes or gene families, cell-cell signaling, and genomic analysis of regulatory networks. In addition to maintaining a vigorous research program, the successful candidate will have a strong commitment to excellence in teaching. The successful candidate will join a faculty with outstanding research and graduate training groups in plant molecular and cellular biology, molecular evolution, bioinformatics, and ecology, and will occupy state-of-the-art laboratory facilities on a plant genomics floor in the newly constructed Life Sciences Building. Applicants should submit a CV, a summary of research accomplishments and future research plans, a statement of teaching experience and / or teaching interests, copies of major research publications. Applicants for an assistant professor position should request at least three letters of recommendation. Application materials should be sent to:

Plant Genomics Search Committee, Department of Biology, 208 Mueller Laboratory, Penn State University, University Park, PA 16802

– Claude dePamphilis email: cwd3@psu.edu Associate Professor of Biology Department of Biology and phone: 814-863-6412 (office) Huck Institutes of Life Sciences 814-863-6413 (lab) 405B Life Sciences Building fax:

(814) 863-1357 Penn State University website1: <http://depcla4.bio.psu.edu/> University Park, PA 16802 website2: <http://www.floralgenome.org/> University Park, PA 16802 website2: <http://www.floralgenome.org/>

QueensCollegeNY EvoDevo

Dear Brian, I would like to bring to the attention of the evoldir list the following ad that appeared recently in Science for two developmental biologist positions at Queens College, City University of New York. It is not specified in the ad but we strongly encourage applications from developmental biologists who bring an evolutionary perspective into their research ("Evo-Devo").

Sincerely,

Stephane

Stephane Boissinot, Ph.D. Department of Biology Queens College, CUNY

ASSISTANT PROFESSOR DEVELOPMENTAL BIOLOGIST Queens College of the City University of New York

2 POSITIONS AVAILABLE

The Department of Biology at Queens College of the City University of New York seeks two tenure-track Assistant Professors to begin September 1, 2005. We seek candidates with a doctoral degree, at least two years of postdoctoral experience, and a record of research accomplishment in the area of developmental biology with particular interest in individuals working on model organisms. Successful candidates will be expected to establish an externally funded research program and teach at the undergraduate and graduate (M.A./Ph.D.) levels. Please submit CV, a two to three page research plan, and arrange for submission of three letters of recommendation. Candidates should submit materials by January 31, 2005 to: Dr. Corinne A. Michels, Chair, Developmental Biologist Search Committee, Department of Biology, Queens College of CUNY, 65-30 Kissena Blvd., Flushing, NY 11367-1597. An equal opportunity/affirmative action/IRCA/Americans with Disabilities Act Employer

Stephane Boissinot <SBoissin@qc1.qc.edu>

SmithCollegeMA ResTech EukaryoticDiversity

RESEARCH TECHNICIAN: Reconstructing Eukaryotic Phylogeny through Multigene Analyses of Microbial Eukaryotes

An NSF-funded research technician position is available to explore the evolutionary relationships among eukaryotes. The technician will PCR, clone and sequence multiple genes from diverse microbial eukaryotes. In addition, the technician will edit and align sequences, and maintain up-to-date databases.

Applicants must be highly motivated to collect and catalog DNA sequence data. Applicants should have experience with PCR, cloning, sequencing as well as basic database maintenance and sequence analysis. Salary will be commensurate with experience. You can learn more about the grant by visiting our newly-launched website: http://www.biology.uiowa.edu/eu_tree/. Applicants should fax or mail: (1) curriculum vitae, (2) description of previous research experience and (3) names and addresses of three references. Applications received by Dec. 15, 2004 will receive full consideration.

Smith College is an equal opportunity employer encouraging excellence through diversity.

For more information, contact:

Laura A. Katz LKatz@Smith.edu

Department of Biological Sciences Smith College Northampton, MA 01063 Phone: 413-585-3825 Fax: 413-585-3786 <http://www.science.smith.edu/departments/Biology/lkatz/>

StAndrewsU EvolGenomics

ACADEMIC FELLOWSHIP IN EVOLUTIONARY AND FUNCTIONAL GENOMICS

Centre for Evolution, Genes & Genomics University of St Andrews

Projected Salary Range: £19460-£29128 per annum
Deadline: Monday, 22 November 2004 Advertised in

Nature, 4 November 2004 (<http://www.nature.com/naturejobs/>)

This position is a research fellowship for 5 years under the Academic Fellowship scheme administered by Research Councils UK. At the end of this period the University will guarantee a permanent academic position following successful completion of the award. To complement our strengths in organismal biology we are seeking candidates using both experimental and/or computational genomic approaches to solve important questions in ecology, evolution, physiology and behaviour. The successful candidate will be based within the Centre for Evolution, Genes and Genomics (tree.st-andrews.ac.uk/cegg) or the Gatty Marine Laboratory (www.st-andrews.ac.uk/~seeb/gatty). You will already have demonstrated outstanding research potential but must not yet have a permanent position. Candidates with an existing independently funded fellowship, which covers the early years of the proposed RCUK Academic Fellowship, are also eligible to apply.

Informal enquiries may be directed to:

Prof Richard Abbott rja@st-and.ac.uk Prof Thomas Meagher trm3@st-and.ac.uk Prof Michael Ritchie mgr@st-and.ac.uk

Application forms and further particulars are available from <http://www.st-andrews.ac.uk/hr/recruitment/vacancies> or from

Human Resources, University of St Andrews, College Gate, North Street, St Andrews, Fife KY16 9AJ, tel: 01334 462571, fax: 01334 462570, or by e-mail: Jobline@st-andrews.ac.uk

Ref: SK70 / 04

Richard Abbott Professor of Plant Evolution Mitchell Building School of Biology University of St Andrews St Andrews Fife KY16 9TH UK

Tel: 0 1334 463350 Fax: 0 1334 463366 <http://biology.st-and.ac.uk/staff/abbott.html> <http://www.st-and.ac.uk/~hmbldg/abb.htm>

TexasStateUSanMarcos Chair

Position Announcement: Chair, Department of Biology
The College of Science at Texas State University-San Marcos, Texas, is inviting applications for the position of Chair in the Biology Department.

Position: The chair is the chief academic, administrative and fiscal officer of the department assuming a broad range of responsibilities. For more information about these functions of department chairs at Texas State, visit www.txstate.edu/academicaffairs/-pps/pps1/1-10.html. Nationally competitive salary and teaching load are negotiable.

Department: The Biology Department, the largest unit within the College of Science, has 31 tenure-track faculty, over 1000 undergraduate majors, 133 Master's and 20 doctoral students. We have filled 10 positions in the past 4 years and will continue adding new tenured and tenure-track positions. The Department covers the full spectrum of the biological sciences, with a strong commitment to organismal and field biology (see www.bio.txstate.edu). Funded research, representing all the disciplinary areas of our faculty, is supported by state and federal resource management agencies, as well as federal, state and private research agencies. The Department offers Master's Degrees in Biology, Aquatic Biology, Wildlife Ecology, Education, and Population and Conservation Biology (pending), plus a comprehensive Ph.D. in Aquatic Resources.

University: Texas State is a large university (over 26,000) with a commitment to quality instruction and an increasing emphasis on scholarship and research. Additional resources associated with the Department include the 4200 acre Freeman Ranch, Aquarena Center, and state and federal fish hatcheries. San Marcos, an historic town of 40,000, is centrally located within Texas at the edge of the scenic Hill Country 30 miles south of Austin.

Qualifications: Applicants must have a sustained record of professional achievement in a Ph.D.-granting program and be tenureable at the level of Full Professor. Desirable experience includes a record of building interdisciplinary programs, working effectively with many constituencies, and developing and strengthening research programs and facilities.

Application: Consideration of applications will begin February 15, 2005, and continue until the position is filled. Interested candidates should submit, by mail, a CV, statements of research interests, academic vision and administrative style, copies of representative publications, and the names and addresses of five references. Submit materials to:

Dr. James R. Crawford, Chair, Biology Chair Search Committee RFM 3240 Texas State University-San Marcos 601 University Drive San Marcos, TX 78666

Phone: 512-245-2131 Fax: 512-245-8233 Email: jc03@txstate.edu

Texas State University-San Marcos is an equal opportunity educational institution and as such does not discriminate on grounds of race, color, sex, national origin, age, sexual orientation or status as a disabled or Vietnam era veteran. Texas State is committed to increasing the diversity of its faculty and senior administrative positions. Texas State University-San Marcos is a member of the Texas State University System.

Caitlin R. Gabor Assistant Professor Department of Biology Texas State University (Formerly SWT) San Marcos, TX 78666 (512) 245-3387

Caitlin Gabor <gabor@txstate.edu>

TowsonU EvolMammalogist

MAMMALOGIST

The Department of Biological Sciences, Towson University, seeks applicants for a tenure-track position at the Assistant Professor level to begin mid-August, 2005. Candidates must have a strong commitment to excellence in both teaching and research. Initial teaching responsibilities will include the following: basic human anatomy and physiology, majors' introductory course in ecology, evolution and behavior, upper-level undergraduate/graduate-level mammalogy and another course in the candidate's area of specialization. The candidate is expected to develop an active research program involving undergraduate and graduate students. Pursuit of extramural funding is also required. Preference will be given to individuals whose research is at least partly field-oriented and involves the ecology, evolution, behavior, conservation, and/or management of mammals. A Ph.D. in an appropriate field is required. Teaching and post-doctoral experience is desirable. Qualified applicants should send letter of interest, C.V., teaching philosophy, research plans, photocopies of all transcripts, and three letters of recommendation (hard copies of all documents only) to: Dr. L. Scott Johnson/Chair, Mammalogist Search Committee/Department of Biological Sciences/Towson University/Towson MD 21252 USA Towson University is an Equal Opportunity/Affirmative Action Employer and has a strong institutional commitment to diversity. Women, minorities, persons with disabilities and veterans are encouraged to apply. Review of applications will begin 29 Nov 2004 and will continue until a suitable applicant is found. Much additional informa-

tion on this position, Towson University and its Department of Biological Sciences can be found at: <http://wwwnew.towson.edu/biology/> or can be requested from the search chair at sjohnson@towson.edu

UBath Bioinformatics

University of Bath

Research Councils Academic Fellowship in Bioinformatics

This Fellowship will provide a clear career path for the successful candidate, from a research focused post into an academic position (<http://www.rcuk.ac.uk/-acfellow>). The research can be in any area of bioinformatics, with this defined broadly as any area of biosciences that is dominantly computational. This includes evolutionary/comparative genomics and systems biology.

The Fellowship is in the Department of Biology and Biochemistry and is part of a joint initiative in Post-Genomic Biosciences with the Department of Pharmacy and Pharmacology. The two departments are respectively RAE grade 5 and 5* and are well equipped for work in the molecular life sciences.

Initially, the Fellow's time will be devoted mostly to research and s/he will be expected to establish an independent and externally funded programme. There will be a gradual increase in teaching duties as well as some outreach to schools. The Fellowship period is five years and is expected to lead to a permanent academic appointment.

Salary range £21,640 - £29,128 or, exceptionally, for a candidate with existing Fellowship support, up to £35,883.

Informal enquiries may be made to Professor Laurence Hurst (email l.d.hurst@bath.ac.uk)

Application forms and further particulars may be obtained from the Dept of Human Resources, University of Bath, Claverton Down, Bath, BA2 7AY, (tel 01225 386873; fax 01225 386559; email H.M.Keogh@bath.ac.uk) or phone the 24 hour answerphone service on Bath (01225) 386924, textphone (01225) 396039, quoting reference 04/359

Closing date: 09 December 2004

An Equal Opportunities Employer

– ----- Laurence D. Hurst, Professor of Evolutionary Genetics, Department of Biology and Biochemistry, University of Bath, Claverton Down, Bath, Somerset BA2 7AY, UK Tel. (01225) 386424 Fax: (01225) 386779 email: l.d.hurst@bath.ac.uk -----

UBerne EvolPopGenetics

ADVANCED POSTDOC POSITION IN EVOLUTIONARY BIOLOGY/POPULATION GENETICS

Applications are invited for an advanced post-doc position in the Computational and Molecular Population Genetics lab (CMPG, Zoology Institute, University of Berne, Switzerland), starting on March 1st 2005.

We are looking for a highly motivated evolutionary biologist/population geneticist to lead a small research group in our lab. The position is initially for 2 years, with the possibility of extension for up to 4 additional years, which would make it comparable to an Assistant Professor position without tenure.

Potential research field is relatively open, and could be within Evolutionary Genomics, Theoretical Population Genetics, Population Genomics, Statistical Genetics, or Molecular Ecology, but the successful candidate will have a strong background in population genetics, statistics and data analysis.

The CMPG lab is well equipped with molecular biology facilities including PCR machines, ABI 3100 16 capillaries sequencer, and a liquid-handling robot, as well as with computational tools including a 40-nodes Linux cluster.

Preference will be given to a candidate showing potential for excellence in research, group leadership, and developing an externally funded research program.

The successful candidate will have to participate to teaching in both Bsc and Msc programs, and to supervise both undergraduate and graduate students. Scientific language of the lab is English, but notions of German or French could be useful. Salaries will be in the range 40-50,000 \$ per year depending on the age and the experience.

Applicants should send (before January 9th 2005) a CV, a publication list, and the names and emails of two references to:

Laurent Excoffier, CMPG, Zoology Institute, University of Berne, Baltzerstrasse 6, 3012 Berne, Switzerland

(email: laurent.excoffier@zoo.unibe.ch)

The CMPG lab (<http://cmpg.unibe.ch>) and the Zoology Institute (<http://www.zoology.unibe.ch>) offer a very lively intellectual and social environment. Other research fields in the Zoology Institute include Conservation Biology (Raphael Arlettaz), Evolutionary Ecology (Heinz Richner), Behavioral Ecology (Michael Taborsky), Aquatic Ecology (Ole Seehausen), and Community Ecology (Wolfgang Nentwig). Berne is located in the center of Switzerland and Europe. It offers a high quality of life, and beautiful surroundings (see <http://www.bernetourism.ch>).

Laurent Excoffier <laurent.excoffier@zoo.unibe.ch>

UCBerkeley EvolEcolEmergingDiseases

The Division of Insect Biology, in the Department of Environmental Science, Policy, and Management, at the University of California, Berkeley is advertising for the position of Assistant Professor in the Ecology of Emerging Infectious Diseases.

Please post and distribute this advertisement widely.

Thank you, Penny Hines

Penny Hines Academic Personnel Analyst University of California ESPM: Insect Biology 201 Wellman Hall Berkeley, CA 94720-3112 510-643-9405 Fax: 510-642-7428

phines@nature.berkeley.edu

UCaliforniaBerkeley VertEvolBiol

UNIVERSITY OF CALIFORNIA, BERKELEY

Faculty Position in Vertebrate Evolutionary Biology

The Department of Integrative Biology and the Museum of Vertebrate Zoology seek a colleague at the Assistant Professor and Assistant Curator level in the area of Vertebrate Evolutionary Biology, to serve as Curator of either extant birds or mammals in the Museum of Vertebrate Zoology, and to develop an outstanding teaching and research program. We expect the suc-

successful candidate to have an intellectual commitment to collection-based research, expertise in one of the two aforementioned taxonomic groups, the capacity to achieve intellectual leadership in the area of research specialization, and to contribute to interactions among the diverse faculty of Integrative Biology. Candidates should have a strong commitment to both undergraduate and graduate teaching.

The position is available 1 July 2005. Applicants should submit a curriculum vitae and a statement of research and teaching objectives, including a vision for the future of natural history museums such as the MVZ. Applicants should also arrange for at least three letters of recommendation to be sent directly to the search committee and should refer their reviewers to the UC Berkeley Statement of Confidentiality at <http://apo.chance.berkeley.edu/evalltr.html>. Applications should be sent to: Search Committee, Vertebrate Evolutionary Biology Search (Position ID# 954), Department of Integrative Biology, 3060 VLSB, University of California, Berkeley, CA 94720-3140. The deadline for receipt of applications is 15 January 2005.

Further information about the department, the MVZ, and this faculty position can be found at <http://ib.berkeley.edu/> and <http://mvz.berkeley.edu>. The University of California, Berkeley, is an Equal Opportunity Employer committed to excellence through diversity.

–

Robert Dudley Professor Department of Integrative Biology University of California, Berkeley Berkeley, CA 94720 U.S.A. 510-642-1555; FAX 510-643-6264 wings@socrates.berkeley.edu

Robert Dudley <wings@socrates.Berkeley.EDU>

UCaliforniaLA HumanGenetics

Faculty Position in Bioinformatics/Computational or Mathematical Biology/Statistical Genetics:

The Department of Human Genetics at the David Geffen School of Medicine, University of California Los Angeles, is accepting applications for a state-funded, tenure-track faculty position. Starting academic rank and salary will be based on level of experience. The applicant would be part of a faculty of 7 computational geneticists in the Department of Human Genetics led by Department Chair Kenneth Lange. They would in-

teract, through their research and teaching, with a diverse faculty of applied mathematicians and biomathematicians at UCLA. The applicant will be expected to carry out an active and independent research program in bioinformatics, computational/mathematical biology or statistical genetics and participate in graduate student education. Applicants should send their CV's, a statement of research and teaching interests, reprints of three significant publications and the names of three professional references to:

Janet Sinsheimer, Ph.D., Search Committee Chair; c/o Ms. Nancy Hards; Department of Human Genetics; The David Geffen School of Medicine at UCLA; 695 Charles E. Young Drive South; Los Angeles, CA 90095-7088.

UCLA is an Affirmative Action/Equal Opportunity Employer.

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>

UChicago EvoBiol

Martin Kreitman University of Chicago Ecology and Evolution

The Department of Ecology & Evolution seeks candidates for at least one open rank appointment on the tenure track. All qualified applicants, especially women and minorities, are encouraged to apply.

We are interested in applicants from all disciplines in ecology and evolution that complement and extend our existing strengths. We are particularly interested in identifying individuals whose research addresses novel problems or employs new approaches and methods. Research that bridges or draws from other disciplines is especially attractive.

Applicants should have outstanding records of research achievement, commensurate with rank, and are expected to have or develop strong, extramurally supported research programs. The appointee is expected to contribute to teaching and departmental functions.

Applications will be reviewed beginning on November 15 and accepted until the position(s) are filled. Mail hard copies of curriculum vitae, statement of research and teaching interests, and three letters of reference (mailed directly by the referees) to:

Martin Kreitman Ecology & Evolution Search Department of Ecology & Evolution 1101 E. 57th St. Chicago, IL 60637 mkre@midway.uchicago.edu mkre@midway.uchicago.edu

UColorado VertebrateCurator

COLLECTIONS MANAGER, VERTEBRATE ZOOLOGY University of Colorado Museum, USA

The University of Colorado Museum (CU Museum) is a world-class natural history museum nestled against the foothills of the Rocky Mountains in Boulder, Colorado. The CU Museum has an extensive Vertebrate Zoology collection and we are looking for a collections manager to guide the continued growth and management of the collections. Strengths of the collection include extensive herpetological and mammal material from the Rocky Mountains and adjacent plains as well as important bird and fish holdings.

Job Classification: Professional Exempt

Minimum Qualifications: M.S. degree in relevant field (Biology, Zoology, Museum and Field Studies) or equivalent experience and education is required. Prior experience in collection management (or closely related work) is not required but will be given high priority. Prior supervisory experience preferred.

Duties Include: Assists curator(s) in the management of zoological collections including specimen preparation, cataloguing and database management; systematic arrangement and storage; conservation; routine collections tasks (i.e., sectional correspondence, assistance to visitors, response to requests for information, and processing of loans); museum and local community service (such as general inquiries and collection tours); training and supervision of students and volunteers.

Salary: \$28,500 per year at 75% time (30 hrs./week)

To Apply: Send curriculum vitae, letter of interest and names and contact information for three references to Collections Manager Search Committee, c/o Karen Hebbel, CU Museum of Natural History, 218 UCB, Boulder, Colorado, 80309-0265. Review of applications will begin December 15, 2004 and continue until the position is filled.

CU Museum of Natural History: <<http://cumuseum.colorado.edu/>><http://cumuseum.colorado.edu/> CU Museum: Zoology Section: <<http://cumuseum.colorado.edu/Research/Zoology/>><http://cumuseum.colorado.edu/Research/Zoology/>

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

Jason Knouft <Jason.Knouft@colorado.edu>

UEdinburgh QuantGenet

Tools for the Genetic Analysis of Complex traits

Opportunities at the Roslin Institute and the University of Edinburgh

The University of Edinburgh and the Roslin Institute (Edinburgh) have been at the forefront for developing methods to detect quantitative trait loci (QTL) and making those available to the genetics community via QTL Express (<http://qtl.cap.ed.ac.uk>). In collaboration with the National eScience Centre, we have recently been awarded a BBSRC grant to expand the functionality of QTL Express and move it to a GRID platform.

For this project, we are looking for two post-docs with experience in quantitative genetics or bioinformatics. One Post-Doc will be appointed at the Roslin Institute and the other one at the University of Edinburgh. The posts encompass the development and implementation of novel methods that require strong genetics and scientific computing skills, and will involve innovation in the field of quantitative genetics and bioinformatics.

The University of Edinburgh will also be looking for a software engineer within the same project.

The posts are initially for 4 years and projected starting date is December 2004, but later starting dates would also be considered.

More details about the position at Roslin can be found on <http://www.roslin.ac.uk/jobs/>. Alternatively, contact Chris Haley (Chris.Haley@bbsrc.ac.uk) or Dirk-Jan de Koning (DJ.deKoning@bbsrc.ac.uk).

For more information about the opportunities at the University of Edinburgh, please contact Sara Knott (s.knott@ed.ac.uk). All jobs will be advertised on jobs.ac.uk as well.

The closing date is December 6.

DJ de Koning ***** Roslin Institute Genetics and Genomics Roslin, Midlothian, EH25 9PS UK New phone +44(0)131 5274258 fax: +44 (0)131 4400434 e-mail: DJ.DeKoning@bbsrc.ac.uk *****

UGroningen EvolutionaryStudies

Tenure-Track Positions for Women at the University of Groningen-NL

As indicated in the official advertisement below, the University of Groningen has 20 tenure-track positions

available for outstanding women scholars through the Rosalind Franklin Programme. Five of these positions will be filled in the Natural Sciences Faculty.

If you are a senior post-doc with sterling credentials, now is your chance to develop your own permanent research line. Unlike a normal job-search, the Rosalind Franklin programme is open. We are simply looking for the best. Prospective applicants should feel free to contact groups for further information on how your research might fit within the broader goals of the institute/group.

In particular, I would like to call your attention to the Centre for Ecological and Evolutionary Studies (CEES:

<http://www.rug.nl/biologie/onderzoek/-onderzoeksinstituten/cees>

This research institute comprises seven research groups (Animal Ecology, Marine Biology, Evolutionary Genetics, Theoretical Biology, Microbial Ecology, Community and Conservation Ecology, Plant Ecophysiology.

Official advertisement that appeared last week in Nature follows:

Rosalind Franklin Fellowships for women in Arts and Sciences

(tenure-track)

Rijksuniversiteit Groningen, the Netherlands

To promote the participation of women in Liberal Arts and Natural Sciences the University of Groningen offers a prestigious fellowship programme, named after Rosalind Franklin, whose X-ray studies of DNA were crucial to solving its structure. Five fellowships are available in the Faculty of Mathematics and Natural Sciences. For further information see <http://www.rug.nl/-fwn/nieuws/pr/wnrff/index?lang=en>

APPLICANTS MUST HAVE:

- a Ph.D and post-doctoral experience, preferably in different research institutions (Dutch applicants should have post-doctoral experience outside the Netherlands).
- publications in top international scientific journals
- experience in supervising research projects
- the ability to successfully compete for external research funding
- affinity to teaching
- evidence of international recognition

Successful candidates will be expected to establish an independent, externally funded research program in collaboration with colleagues at the University of Groningen and elsewhere. They will also be expected to par-

ticipate in and contribute to the development of the teaching programme of the Faculty.

The 5-year fellowship comprises an annual starting salary of 50000 EURO gross (full time position), and an accompanying research grant of 200000 EURO. During these five years the fellow will be expected to concentrate on research with teaching duties comprising at most 20% of the time.

Following a favourable evaluation at the end of the first 5 years the fellow will be awarded tenure and promotion to the rank of Associate Professor. After a further 5 years another evaluation will take place and if this proves favourable, promotion to full professor will follow.

APPLICANTS SHOULD SUBMIT:

- a complete curriculum vitae including a complete list of publications
- a list of five self-selected "best papers" (not copies of the papers)
- up to 5 keywords describing your research area
- a 3 page statement of research accomplishments and future research goals
- a letter of motivation
- a list of names, addresses (including e-mail) and telephone numbers of three persons who can be contacted for a letter of recommendation.

APPLICATIONS SHOULD BE SENT TO:

Dr. L.J.A. van Putten (e-mail: L.J.A.van.Putten@fwn.rug.nl) Faculty of Mathematics and Natural Sciences University of Groningen Nijenborgh 4 NL-9747 AG Groningen The Netherlands

THE DEADLINE is January 15, 2005

***** Dr. Jeanine L. Olsen Professor Department of Marine Biology Biological Centre, RUG PO Box 14 NL-9750 AA Haren The Netherlands tel: +31-50-3632250 (work); +31-50-3131832 (home) fax: +31-50-3632261 e-mail: j.l.olsen@biol.rug.nl <http://www.biol.rug.nl/-marbio/> *****

UMaryland Genomics

PLEASE NOTE THAT THE DATE FOR BEST CONSIDERATION OF APPLICATIONS FOR THE FOLLOWING POSITION IS DECEMBER 1

TENURE-TRACK FACULTY POSITIONS IN COMPARATIVE OR FUNCTIONAL GENOMICS (RANK OPEN)

The Department of Biology at the University of Maryland, College Park, is seeking tenure-track faculty working within the field of genomics, broadly defined. This includes, but is not limited to, the molecular basis of adaptation, the origin of species, genome evolution and organization, comparative studies of gene expression or function and the evolution of biodiversity. We seek outstanding candidates who are taking empirical, experimental or theoretical approaches.

Successful candidates will join a vibrant group of researchers in neuroscience, behavior, development, evolution and ecology. Candidates should have developed, or demonstrate the potential to develop, an outstanding research program and a record of extramural funding. We will provide competitive startup packages. The Department of Biology expects to continue hiring in this area as it expands into laboratory space within a new 155,000 sq. ft. Bioscience Research Building. The University of Maryland, College Park is the flagship campus of the University of Maryland System and one of the most rapidly advancing public research universities in the country. Our close proximity to Washington, Baltimore, and the Maryland Biotechnology Corridor facilitates interactions with an extraordinary range of major research institutions, including the NIH, FDA, Smithsonian Institution, USDA, and TIGR. For more information visit our web site at www.life.umd.edu/-biology. To apply send a curriculum vitae, statements of research and teaching interests, sample publications, and the names and addresses (mail and email) of three references to: Comparative or Functional Genomics Search Committee, Department of Biology, University of Maryland, College Park, MD 20742, USA. For best consideration, submit materials no later than Dec. 1 2004. The University of Maryland is an equal opportunity/affirmative action employer. Applications from minorities and women are encouraged.

tishkoff@umd.edu

UMarylandBC EvoPlantBiol

PLANT BIOLOGY University of Maryland Baltimore County, UMBC

The Department of Biological Sciences seeks to recruit a tenure-track Assistant Professor using inno-

vative approaches to fundamental problems bridging plant-microbe interactions and plant development.

The successful applicant will have a doctoral degree in biology or a related field, post-doctoral experience and will be expected to establish a vigorous, extramurally funded research program. Other obligations include outstanding graduate training, and teaching in the undergraduate curriculum.

Applications should include a cover letter, summary of current research, curriculum vitae, brief summary of future research plans, a statement of potential teaching interests, and a minimum of three letters of reference sent directly to the Department. All materials should be sent to: Chair, Plant Biology Search Committee, Department of Biological Sciences, University of Maryland Baltimore County, 1000 Hilltop Circle, Baltimore, MD 21250 or submitted via e-mail: sschneid@umbc.edu. Review of applications will begin immediately and highest priority will be given to complete applications received by December 1, 2004.

Information on our Department and graduate programs can be found at <http://www.umbc.edu/biosci/>. The University of Maryland Baltimore County is an Affirmative Action/Equal Opportunity Employer. Women, members of ethnic minority groups and individuals with disabilities are strongly encouraged to apply.

omland@umbc.edu

UMunich ResAssist MolEvol

Research Assistant (wissenschaftlicher Assistent), Munich

A research assistant position is available in the group of John Parsch at the University of Munich (LMU). This position is intended for a recent Ph.D. and is best described as something between a postdoc and an assistant professor position. There is an opportunity to conduct independent research and supervise graduate students, however the position is not tenure-track. There is a teaching requirement of roughly one course per semester (teaching may be in German or English). The position is expected to be available beginning March 1, 2005 and have an initial appointment of 3 years, with an opportunity of renewal for up to 6 years total. Requirements are a Ph.D. in biology and a strong interest in molecular evolution and population genetics. According to the German system, candidates are expected to

be under the age of 35 at the time the contract begins. Preference will be given to candidates whose research interests are compatible with current projects in the Parsch group (molecular evolution of *Drosophila* reproductive genes, evolutionary and functional genomics of *Drosophila* gene expression). The University of Munich has a strong, interactive group in evolutionary biology, including theoreticians and experimentalists working on both plant and animal systems. 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:

<http://www.zi.biologie.uni-muenchen.de/institute/zi/-abt/evolutionsbiologie>

Applicants should send a statement of interest and curriculum vitae per email to:

parsch@zi.biologie.uni-muenchen.de

Prof. Dr. John Parsch Department of Biology II University of Munich Grosshaderner Str. 2 82152 Planegg-Martinsried Germany

parsch@zi.biologie.uni-muenchen.de

UNorthCarolina EvolBiol

University of North Carolina, Integrative Organismal Biology

The University of North Carolina at Chapel Hill invites applications for a tenure track position at the level of ASSISTANT PROFESSOR in the Department of Biology. We particularly encourage applications from individuals who use integrative approaches to understand the structure and function of whole organisms. To be effective on or after July 1, 2005. Please submit a curriculum vitae, a statement of research and teaching interests, up to three publications, and four letters of recommendation to: Dr. William M. Kier, Chair, Integrative Organismal Biologist Search Committee, Department of Biology, CB# 3280 Coker Hall, University of North Carolina, Chapel Hill, NC 27599-3280, USA. See <http://www.bio.unc.edu/news/-facultysearch/> for details. Closing date: open until filled; review of applications begins December 15, 2004. The University of North Carolina is an equal opportunity, affirmative action employer and strongly encourages applications from women and minorities.

In addition to the hard copy of your application materials, please send an electronic version in PDF or MS Word format to Mr. David Liesegang: (DavidL@bio.unc.edu)

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Maria Servedio Assistant Professor Department of Biology CB#3280, Coker Hall University of North Carolina at Chapel Hill Chapel Hill, NC 27599-3280 phone: (919) 843-2692 fax: (919) 962-1625 e-mail: servedio@email.unc.edu <http://www.bio.unc.edu/faculty/servedio/Lab/index.htm> <http://www.bio.unc.edu/faculty/servedio/Lab/index.htm>

UNottingham Genetics

The University of Nottingham

RCUK Academic Fellowships

Research Councils UK has recently announced the award of nearly 400 new Academic Fellowships to provide contract researchers with more attractive and stable paths into academia. Each Fellowship offers training and development necessary for the transition from a research focussed post into an academic position within five years, and the guarantee of a permanent academic position at the end of the award (subject to the successful completion of a probationary period).

Following a successful bid, the University of Nottingham invites applications for Academic Fellowships in the research areas of:

Functional Imaging (from single cell to whole organism) (Three Fellowship posts) Organisms and Populations: Genetics and Genomics (Two Fellowship posts)

It is hoped to offer further Fellowships in these areas during 2005/2006.

Over the five-year period of the Fellowship, the successful candidates will mostly carry out research aimed at developing an independent career, but will also undertake teaching experience, outreach activities and training and development relevant to an academic position.

Candidates must have a PhD, or be of postdoctoral standing (someone who can demonstrate equivalent and relevant professional experience), and be able to demonstrate their outstanding research potential.

The partial funding provided by RCUK is flexible

enough to accommodate those who may have their own funding initially (e.g. via existing Fellowship or Research Council grant), but not for the later years of the Academic Fellowship. Applications from such individuals are particularly welcome.

Salary will be within the range £21,460 - £29,128 per annum, depending on qualifications and experience.

Informal enquiries may be addressed to marie.downs@nottingham.ac.uk.

Further details and application forms are available on the WWW at: <http://www.nottingham.ac.uk/rsco/> or from the Research Support and Commercialisation Office, The University of Nottingham, University Park, Nottingham, NG7 2RD. Tel: 0115 846 6418. Fax: 0115 846 7895. Email: marie.downs@nottingham.ac.uk. Please quote ref. AF/04. Closing date: 15 December 2004.

– Dr. Angus Davison

Institute of Genetics The University of Nottingham Queen's Medical Centre Nottingham NG7 2UH

email angus.davison@nott.ac.uk tel 0115 849 3239 (int. 35239) fax 0115 970 9906

www.nottingham.ac.uk/genetics

homepages.ed.ac.uk/adavison

dia.cap.ed.ac.uk/mollusca.html

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USheffield ResAssist Drosophila

Postdoctoral Research Assistant Animal & Plant Sciences, University of Sheffield

Closing date: 30th November 2004 Salary: £19,460 - £24,820 Terms & Conditions: Research Staff

A vacancy now exists for a research assistant to work with Prof. Roger Butlin to investigate the evolution and genetics of sexual signals and responses in *Drosophila virilis* group flies, especially *D. montana*. This is a component project of a Marie Curie Research Training Network (see <http://people.cc.jyu.fi/mirror/-anhoikka/EU/>).

Applicants must have a good grounding in evolutionary biology, the use of a range of laboratory and analytical methods for molecular ecology, and an enthusiasm for interdisciplinary research.

The post is full time for 1 year initially. Only non-UK citizens of the EU are eligible.

Please go to <http://www.shef.ac.uk/jobs/research.html> for project and application details.

Roger Butlin Professor of Evolutionary Biology

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

r.k.butlin@sheffield.ac.uk

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

Jobline@st-andrews.ac.uk

St Andrews HR Ref: SK70 / 04

Professor Thomas R. Meagher Division of Environmental and Evolutionary Biology, School of Biology University of St Andrews St Andrews KY16 9TH UK +44(0)1334 463364 phone +44(0)1334 463366 fax trm3@st-and.ac.uk <http://www.st-and.ac.uk/~hmbldg/meagher.html>

UStAndrews FuncGenomics

Academic Fellowship in Evolutionary and Functional Genomics

Centre for Evolution, Genes & Genomics University of St Andrews

Projected Salary Range: 19460-29128 per annum Deadline: Monday, 22 November 2004 Advertised in Nature, 4 November 2004 (<http://www.nature.com/naturejobs/>)

This position is a research fellowship for 5 years under the Academic Fellowship scheme administered by Research Councils UK. At the end of this period, the University will guarantee a permanent academic position following successful completion of the fellowship. To complement our strengths in organismal biology we are seeking candidates using experimental and/or computational genomic approaches to solve important questions in ecology, evolution, physiology and behaviour. The successful candidate will be based within the Centre for Evolution, Genes and Genomics (tiree.st-andrews.ac.uk/cegg) or the Gatty Marine Laboratory (www.st-andrews.ac.uk/~seeb/gatty). Candidates with an existing independently funded fellowship are eligible to apply.

Informal enquiries may be directed to:

Prof Richard Abbott rja@st-and.ac.uk Prof Thomas Meagher trm3@st-and.ac.uk Prof Michael Ritchie mgr@st-and.ac.uk

Application forms and further particulars are available from

<http://www.st-andrews.ac.uk/hr/recruitment/-vacancies> or from

Human Resources, University of St Andrews, College Gate, North Street, St Andrews, Fife KY16 9AJ, tel: 01334 462571, fax: 01334 462570, or by e-mail:

UTexasSanAntonio EvolPhysicalAnthro

The University of Texas at San Antonio Department of Anthropology, pending budgetary approval, invites applications for a tenure track or tenured position (rank open) in physical anthropology to begin Fall 2005. Applicants should have theoretically motivated research interests focusing on human skeletal biology or human growth and development. Responsibilities include teaching general anthropology, basic courses in physical anthropology and elective courses in area of specialization; on-going research; and service in a dynamic undergraduate and master's program. Courses may be taught at the UTSA North or Downtown campuses, and occasionally at night. Required qualification for the rank of Assistant Professor is a PhD in physical anthropology by December 31, 2004. Preferred qualifications for this rank include promise of developing an ecologically oriented, funded research program in conjunction with area institutions; promise of effective undergraduate teaching; desire and ability to contribute to a graduate-level specialization; ability to complement current faculty specializations. Required qualification for the rank of Associate Professor include a PhD in physical anthropology and attainment the rank of Associate Professor by December 31, 2004; a record of effective undergraduate and graduate teaching; ability to provide guidance and development at the graduate level; a focused research program; a record of funded research; peer-recognized service. Preferred qualifications for this rank include ecologically-oriented research; experience in a doctoral-level program; ability to complement current faculty specializations. Required qualification for the rank of Professor include a PhD in physical anthropology and attainment of the rank of Professor by December 31, 2004; a record of effective undergraduate and graduate teaching; ability to provide guidance and development at the graduate level; a na-

tionally recognized body of research; a record of funded research; service demonstrating peer-recognized leadership. Preferred qualifications for this rank include ecologically-oriented research; experience in a doctoral-level program; ability to complement current faculty specializations. Applicants should submit a letter of application indicating the rank applied for; a statement of teaching and research interests; a C.V.; a writing sample; teaching evaluations (if possible); and the names, phone numbers, and email addresses of three references. All materials must be postmarked by January 7, 2005, and mailed to Search Chair, Department of Anthropology, 6900 North Loop 1604 West, University of Texas at San Antonio, San Antonio, TX 78249-0649. Applicants who are not U.S. citizens must state their current visa and residency status. The University of Texas at San Antonio is an affirmative action, equal employment opportunity employer. Women and minorities are encouraged to apply.

Dr. James H. McDonald Professor & Chair Department of Anthropology University of Texas at San Antonio San Antonio, TX 78249-0649 USA Tel: 210.458.4673 Fax: 210.458.5728 Net: james.mcdonald@utsa.edu

James McDonald <James.McDonald@utsa.edu>

UUtah EvolBiol

EVOLUTIONARY ORGANISMAL BIOLOGY, Department of Biology, University of Utah

The Department of Biology at the University of Utah invites applications for a tenure-track faculty position as Assistant Professor. We seek applicants who are investigating evolutionary adaptation and diversification at the whole-organism level. We are especially interested in research on genetic, developmental, or physiological mechanisms underlying ecologically relevant variation. For an overview of the Department please visit <<http://www.biology.utah.edu/>>. Applicants should submit a curriculum vitae, representative publications, descriptions of research and teaching interests, and have three letters of recommendation sent to Evolution Search Committee, Department of Biology, University of Utah, 257 South 1400 East, Salt Lake City, Utah 84112-0840, USA. Review of applications will begin on December 15, 2004 and will continue until the position is filled. The University of Utah is an Equal Opportunity/Affirmative Action employer and encourages applications from women and minorities and pro-

vides reasonable accommodation to the known disabilities of applicants and employees.

Ann Sherratt annsherratt@bioscience.utah.edu

Department of Biology University of Utah 257 So. 1400 E. Rm. 223 Salt Lake City, UT 84112-0840

Tel 801-585-0622 Fax 801-581-4668

Ann Sherratt <annsherratt@bioscience.utah.edu>

UWesternAustralia EvolEcol

SENIOR LECTURER (REF:) Evolutionary/Behavioural Ecology SCHOOL OF ANIMAL BIOLOGY

Tenurable appointment Salary range: Senior Lecturer Level C AUD\$71,401 - \$82,331 p.a.

In this role you will develop an internationally competitive research program in evolutionary biology, focussing on the interface of mating system evolution and sperm competition and complimenting existing members of the Evolutionary Biology Research Group, see <http://www.zoology.uwa.edu.au/staff/lsimmons/>. A PhD in a relevant discipline is essential. Applicants must include a statement of their suitability for and aspirations in this position, a CV, statement of research program over the next five years; reprints of five career best publications and a teaching portfolio detailing any relevant experience. For further information regarding the position please contact Professor L W Simmons on +61 8 6488 2221 or email lsimmons@cyllene.uwa.edu.au or Head of School, Associate Professor J D Roberts on +61 8 6488 2237 or email droberts@cyllene.uwa.edu.au.

CLOSING DATE: Friday, 10 December 2004

Benefits include generous superannuation, fares to Perth (if applicable) for appointee and dependants, a removals allowance, generous leave provisions and an enviable working environment. These and other benefits will be specified in the offer of employment.

APPLICATION DETAILS: For copies of the selection criteria please access the website <http://jobs.uwa.edu.au/>. Applicants must address the selection criteria. Written applications quoting the reference number, personal contact details, qualifications and experience, along with contact details of three referees should be sent to Director, Human Resources, The University of Western Australia, M350, 35 Stirling Highway, Crawley WA 6009 or emailed to jobs@uwa.edu.au

by the closing date.

Committed to international excellence –

Professor Leigh W. Simmons Zoology Building School of Animal Biology (M092) The University of Western Australia Nedlands Tel: +61 8 6488 2221 WA 6009 FAX: +61 8 6488 1029 Australia

<http://www.zoology.uwa.edu.au/staff/l Simmons>

<http://www.zoology.uwa.edu.au/staff/l Simmons>

UWesternOntario EvolGenetics

THE UNIVERSITY OF WESTERN ONTARIO DEPARTMENT OF BIOLOGY

The Department of Biology at The University of Western Ontario invites applications for the following position effective July 1, 2005:

Geneticist:

Applications are invited for a probationary (tenure track) ASSISTANT or ASSOCIATE PROFESSOR position in genetics. The candidate's research interest should encompass the areas of molecular biology, genetics, evolutionary genetics, and/or genomics. The applicant should have a broad background and training in modern genetic and molecular techniques in order to contribute to the broad range of undergraduate courses offered by this department. Applicants must have a Ph.D. and appropriate postdoctoral training or equivalent expertise and a proven research record, including publications of high quality. The successful applicant will be expected to develop an innovative program of independent, externally funded research and to teach at both the undergraduate and graduate levels. The successful candidate will be a member of the Molecular Genetics Unit within the Department of Biology and have access to a joint core facility and a dynamic research community in London. In particular, we are looking for an enthusiastic individual who is well versed in genetic and molecular principles, able to work well with others and contribute to the undergraduate Honours Program in Genetics and related fields.

Applications, including a curriculum vitae, names and addresses of three referees whom we may contact, copies of recent significant papers and a one page summary of proposed research should be forwarded to:

Dr. Brock Fenton, Chair Department of Biology The

University of Western Ontario London, Ontario N6A 5B7 Canada

Deadline for applications is February 15, 2005.

Position is subject to budget approval. Applicants should have fluent written and oral communication skills in English. All qualified candidates are encouraged to apply; however Canadian Citizens and permanent residents will be given priority. The University of Western Ontario is committed to employment equity and welcomes applications from all qualified women and men, including visible minorities, aboriginal people and persons with disabilities.

UppsalaU SystematicBotany

Uppsala University announces a position as

Chair in Systematic Botany at the Evolutionary Biology Centre of Uppsala University, in the Department of Evolution, Genomics and Systematics, www.egs.uu.se

Description of the subject field: Plant systematics with special emphasis on phylogenetic and evolutionary problems.

Tasks: Comprehensive responsibility for research and postgraduate studies within the area of systematic botany, teaching and supervision of PhD-students and undergraduate students. Research in systematic botany. Information about research and development and planning of new research projects, and administration at department or higher level.

Qualifications: According to Chap. 4, §5 of the Higher Education Ordinance the eligibility criteria for employment as full professor are scientific as well as pedagogic proficiency. According to the employment policy of Uppsala University, the scientific proficiency should be demonstrated through independent research that significantly exceeds the qualifications required for the Swedish "docent" title. Also, experience of scientific planning and leadership is required. The applicant must have the pedagogic proficiency required for the position and, normally, formal pedagogic training relevant for the educational tasks associated with this position. The assessment of pedagogical proficiency will focus on planning, execution and evaluation of teaching, as well as on advisory activities and examination.

The ability to teach in Swedish or English is required. The holder is expected to teach and take part in meetings in Swedish within two years.

Ranking: For this position, the ranking will be based primarily on the scientific and pedagogic proficiencies of the applicants, with special emphasis on scientific proficiency. This order of priorities in the application of the different selection criteria is not absolute. A combined consideration of all grounds of assessment could result, for instance, in an applicant vastly superior regarding pedagogical proficiency being ranked higher than a candidate with superior scientific qualifications who is considered less qualified pedagogically.

In examining the scientific proficiency special attention will be given to research in plant systematics with special emphasis on phylogenetic and evolutionary problems. In examining the pedagogic proficiency, skills and experience in the planning, execution and evaluation of teaching, as well as advisory activities and examination will be considered.

The ranking of applicants for employment as a teacher at Uppsala University is based on an assessment of their proficiencies in the areas required for eligibility for employment.

In addition, administrative and other qualifications relevant to the subject and to the tasks connected to the position will be assessed. Documented ability to attract external funding is essential. Skills in developing and leading research and personnel, in intra- and extramural co-operation and in the communication of research and development will be considered. Personal suitability will also be considered.

The University of Uppsala aims at an equal gender representation. Since most full professors in the Faculty are men, women are encouraged to seek this position.

Personal circumstances that may be of relevance when judging the qualifications, for example parental leave, should be mentioned in the list of qualifications (CV).

For further information, please contact Professor Siv Andersson, tel +46 (0) 18 471 4379, e-mail: Siv.Andersson@ebc.uu.se

How to apply: The application must be written in English. The applicant is required to submit three copies of documents and two copies of publications according to instructions found on the web site <http://www.teknat.uu.se/english/instructions.php> or ordered from Anita.Ljungstrom@uadm.uu.se

Applications should be directed to the Vice-Chancellor and mailed so as to arrive at Uppsala University, Registrars Office, UFV-PA 2004/5234, Box 256, S-751 05 Uppsala, Sweden, or fax +46 (0) 18 471 2000, no later than January 13, 2005. A fax should be followed by a signed application sent within a week of the deadline.

carolin.frank@ebc.uu.se

Vienna LabTech Genetics

Schweiger Teresa t.schweiger@klivv.oew.ac.at
001000

Genetics Laboratory Technician Position Konrad Lorenz Institute for Ethology, Vienna, Austria

We seek a highly organized and motivated genetics laboratory technician to assist with research projects in behavioral ecology and evolutionary biology (In particular, working with Dr. Dustin Penn and his group on the Major Histocompatibility Complex). Applicants should have excellent bench skills using molecular genetic techniques (especially, DNA extractions, PCR, microsatellite development and typing, AFLPs, automatic sequencing, etc.). They should be independent, reliable, and responsible for general laboratory maintenance. The position requires working with other technicians, scientists, and assisting students; therefore, we seek someone who is friendly, and cooperative, as well as having excellent technical and organizational skills. German would be useful but it is not necessary as ours is an international institute that communicates largely in English. Salary depends upon experience, and the position is initially for two years, and it could eventually become permanent depending upon performance. Review of applications begins immediately and will continue until the position is filled, and the starting date is flexible.

The Konrad Lorenz Institute is located in the Vienna Woods, on the outskirts of Vienna (see our website: <http://www.oew.ac.at/klivv/>). There are other laboratories in Vienna that use genetic techniques, including the neighboring Research Institute of Wildlife Ecology (University of Veterinary Medicine). Vienna offers excellent public transportation, excellent schools, cultural activities, and outdoor recreation (<http://www.virtourist.com/europe/vienna/index.html>).

To apply, please send an application letter, a CV, and two letters of reference to the address below.

Mag. Teresa Schweiger, Secretariat Konrad Lorenz Institute for Ethology Austrian Academy of Sciences Savoyenstrasse 1a A-1160 Vienna, Austria Tel: +43 1 51581 2700 Fax: +43 1 51581 2800 T.Schweiger@klivv.oew.ac.at

Mag. Teresa Schweiger Secretariat Konrad Lorenz In-

stitute for Ethology Savoyenstr. 1a A 1160 Vienna Tel: 01/51581-2700 Fax: 01/51581-2800

Virginia Commonwealth U PlantEvoDevo

Virginia Commonwealth University Plant Evolutionary Development

The Department of Biology invites applications for a faculty position with research interests in the area of plant evolutionary development. Candidates working on any aspect of plant development will be considered, but special consideration will be given to applicants integrating developmental studies into other areas of plant biology (e.g. evolution, physiology, comparative biology). This is a nine-month, tenure-track position

that will be filled pending funding at the rank of Assistant Professor. The successful applicant will be expected to develop a productive, externally funded research program and direct graduate students through the Ph.D. level. Postdoctoral experience is expected and demonstrated evidence of excellence in scholarship and teaching is required. Competitive start-up funds and excellent core facilities are available.

Virginia Commonwealth University has an enrollment of 27,000 students, including over 1000 undergraduate majors and graduate students in Biology. The Biology Department (www.has.vcu.edu/bio) has 32 faculty members with diverse research interests. Faculty members have access to core facilities and with colleagues in the Center for the Study of Biological Complexity (www.vcu.edu/csbc) and the Center for Environmental Studies (<http://www.vcu.edu/cesweb>). Submit vita, statement of research and teaching interests, and three letters of reference by December 3, 2004 to: Stephanie Millican, Department of Biology, Virginia Commonwealth University, Richmond, VA 23284-2012.

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Alcohol alternatives

Dear All, Does any of you know a substance that stains ethanol to some ugly looking colour and/or has ugly smell/taste and does not affect subsequent PCRs of the scat samples stored in it? I'm afraid pure alcohol can be too attractive to some collectors. Simply, I need some repellent. Any suggestions are welcome Best regards Maciek Konopinski

– Institute of Nature Conservation Al. Mickiewicza 33, 31-120 Krakow, POLAND tel. +48-12-6322221 or 6322755 ext. 102, fax. 6322432 – konopinski@iop.krakow.pl

Australasian Evol Society

AES: CALL FOR MEMBERSHIP

The AES was established in 1998 to foster interest and intellectual exchange among those interested in all facets of evolutionary biology. The society intends to realise these aims by holding national meetings, and by encouraging exchanges on its web site. The next formal meeting of the Society will take place in Fremantle, Western Australia in September 2005

Memberships are now due

Full membership \$40.00

Student membership \$20.00

Please take the time to log on to the new web site (www.evolutionau.org), complete and return the membership form, and check out the first announcement for the 2005 meeting. If you have any suggestions for additions to the website or material you would like to be included, please do contact us. Please also forward the attached call for membership to any interested colleagues and pin it on your departmental noticeboard.

Leigh W. Simmons President, Australasian Evolution Society

----- Professor Leigh W. Simmons Zoology Building School of Animal Biology (M092) The University of

Western Australia Nedlands Tel: +61 8 6488 2221 WA 6009 FAX: +61 8 6488 1029 Australia

<http://www.zoology.uwa.edu.au/staff/lsimmons>

Beckman Analyzer experience

Folks:

We are looking into purchasing a capillary-based Automated Sequencing System with both DNA sequencing and fragment genotyping for our Core Sequencing facility. Most of our users are doing DNA sequencing of cloned DNA, but we have several users like myself who sequence mostly PCR products and also do AFLP and microsatellite fragment genotyping. We are looking for a machine with the widest versatility and best resolution for all of these applications.

We are considering the Beckman Coulter CEG 8000 Genetic Analyzer because it is a capillary machine with Sequencing and Fragment Analysis software included in the same package and is considerably cheaper than the ABI 3100 or 3730 (systems that I have used and am familiar with).

So I am looking for feedback (positive or negative) from anyone out there who has experience either with sequencing or fragment analysis using the Beckman system.

We only have a limited fund source to buy a machine, but I want to spend our money wisely.

Please send responses to: Margaret Ptacek (mp-tacek@clemson.edu)

Thanks in advance for any comments.

Cheers, –Margaret Ptacek

“Margaret B. Ptacek” <mptacek@CLEMSON.EDU>

CockerhamWeir model

I am wondering if anyone knows of software suitable for analysis of variance of 'Cockerham-Weir Model' (in

book 'Genetics and Analysis of Quant. Traits'- Lynch M. and Walsh B.), for partition of maternal and paternal effect as well as nuclear and extranuclear effects? It will be disaster if I have to calculate it 'by hand'!

Thanks for all help!

Stevan

stevan@ibiss.bg.ac.yu

DNA from formaldehyde

Dear EvolDir-members,

As part of my PhD-project, I want to make a DNA-based phylogeny of the genus *Diplocephalus* (a dwarf spider genus), using the nuclear rDNA-region (18S, 5.8S and intergenic spacers ITS1 and ITS2).

I am still in the stage of isolating and amplifying the DNA from my spiders, but I have troubles finding specimens of all species I need. Therefore, an easier way to acquire all specimens would be to include material from pitfalls. However, pitfall-traps are usually filled with an aqueous formaldehyde solution (e.g. 4%) and a bit of dishwashing liquid (to break the surface tension), and the formaldehyde seems to have a degrading impact on the DNA. I have tried isolating DNA from pitfall-caught specimens, using my default DNA isolation protocol (Puregene from BIOzym), but this didn't yield any DNA.

If anyone has experience with isolating DNA from formaldehyde-caught specimens, and/or could give me advice on what protocol to use, I would be very pleased to hear.

Also, if anyone would have spare specimens of *Diplocephalus* sp. (Araneae, Linyphiidae, Erigoninae) or could easily collect them, they would be very welcome. Please contact me for details on what species I need most.

Many thanks in advance.

Jeroen jeroen.vandenborre@UGent.be

Jeroen Vanden Borre Ghent University Department of Biology Terrestrial Ecology Unit K. L. Ledeganckstraat 35 B-9000 GENT Belgium phone: +32 9 264 52 58 fax: +32 9 264 87 94 e-mail: Jeroen.VandenBorre@UGent.be www.ecology.UGent.be/terec

DNA ladder answers

A couple of weeks ago, I posted the following message: ----- I am wondering if anyone knows of a commercially available DNA ladder suitable for sizing microsatellites? I am running manual small format 6% acrylamide gels (Sequagel), staining with Sybr-Gold and visualizing under UV light. I would like to know if anyone knows of a commercially available DNA ladder, with fragments sizes from around 80 - 250 bp in increments of 10bp (or less). With fingers crossed! ----- Thanks to all those who replied, I am now trying out the Invitrogen 10 bp ladder. I have compiled the responses I received below:

1/ MOST POPULAR SUGGESTION: Invitrogen 10 bp ladder - catalogue number 10821-015 - 10 bp steps from 30 - 330 bp. (One respondent also said: They also sell a 330 - 30 bp AFLP ladder (cat no. 10832-012) which is exactly the same thing but costs more so buy the former.)

2/ I found two products that could work but I did not try them: Superladder-low 20bp ladder (ABgene) and PCR low ladder (Sigma). Those ladders have 20 bp increments, which may not be enough for your purpose.

3/ 10 bp ladder from GibcoBRL in the past with decent results, which covers your size range. It would depend on your markers, but I also used Gibco's 25 bp ladder with some markers - this one sometimes runs more cleanly. - Kate Teeter

4/ SECOND MOST POPULAR SUGGESTION: the Elchrom M3 marker (www.elchrom.com) might do what you want. The attached poster shows the fragment sizes.

4/ DeWoody JA. Schupp J. Kenefic L. Busch J. Murrill L. Keim P. Universal method for producing ROX-labeled size standards suitable for automated genotyping. [Article] /Biotechniques. 37(3):348+, 2004 Sep. The above techniques requires \$300 buck up front for material and some time, but it beats the exorbitant rates of ABI. Of course you wouldn't need to label the primers since you are using Sybr gold. You would see both DNA stands through, not sure if that would mess up the analysis.

5/ I'd bet that you've thought of this but just incase, would it be practical for you to sequence one of your samples and run the sequence on the same gel? I think

that it is a good idea to sequence at least some of your samples anyway to verify that size polymorphism is a result of different tandem repeat copy number and not flanking indels. A benefit of running a sequence on a microsat gel is of course that the resulting "ladder" has a 1bp resolution. All the best. Cam

Dr Alex Wilson PERT Postdoctoral Fellow Center for Insect Science Department of Ecology and Evolutionary Biology The University of Arizona acwilson@email.arizona.edu <http://cis.arl.arizona.edu/PERT/people/Wilson/index.htm> phone - (520) 626 8661 fax - (520) 621 2590 Mailing address: Department of Ecology and Evolutionary Biology P.O. Box 210088 University of Arizona Tucson, AZ 85721-0088 USA

these, you get a wrong tree by grouping this species with other species but not with its own species. Does anyone have this kind of problem or know a reasonable explanation? Please let me know if there are papers on multiple different copies of mt in an individual, or maybe NUMT?

Sincerely,

Cho, Soowon Department of Plant Medicine Chungbuk National University Cheongju, 361-763 KOREA soowon@chungbuk.ac.kr fax 82-(0)43-271-4414

soowon@chungbuk.ac.kr

Genetics Populations

Genetics of Populations (third edition, 2005) is now available from Jones and Bartlett (<https://www.jbpub.com>). It is expanded from the second edition, published in 2000, and has more coverage of molecular topics and many recent examples. To order a copy, go to <https://www.jbpub.com/cart2004/cart.cfm?bc=4772-6&t=bioscience&CFID=1050325&CFTOKEN=7596777>

or to request a review or complimentary copy, go to <http://www.jbpub.com/reviewcart/cart.cfm?bc=4772-6&t=bioscience&CFID=1050325&CFTOKEN=7596777>

Phil Hedrick, Arizona State University (philip.hedrick@asu.edu)

Philip Hedrick

Heteroplasmy

Dear friends,

I am currently facing a problem of mtDNA sequences. I got two different (similarity is ca 20%) COI sequences from one individual. They are from two different sets of primers to amplify mostly the same region of COI. The same kind of problem occurs in about 10 different specimens now. Of course, if you make a tree from

Heteroplasmy 2

To those who responded promptly, Thank you for all the comments, advice, and your papers. They will be a big help for me.

Some want to know a little more details about the data so here it is.

The sample is giant water bug, a hemipteran insect. I am doing a population study of species A, and I include species B and C that are close to A and species O as an outgroup in the study. The region I sequenced is a part of COI, less than 500bp closer toward 5'. One of the reasons I included B and C is to make a molecular identification marker for these morphologically similar A and C (B is similar but distinguishable).

When I quickly draw NJ tree with these, species A is divided into 3 groups, group 1 with 29 individuals, group 2 with 3 individuals, and group 3 with 4 individuals. In the tree, the group 1 is grouped with the species B, the group 2 is grouped with the species C and together form a sister group of (group 1 and species B), and the group 3 becomes the sister taxon for all the rest.

(((group 1, species B)(group 2, species C))group 3)species O)

The pairwise distances for the 3 groups shows the difference within the group 1, 2, and 3 is 0.00 - 0.02, 0.00 - 0.01, and 0.00 - 0.01, respectively. The difference between group 1 and 2, 1 and 3, and 2 and 3 is 0.29 - 0.32, 0.19 - 0.21, and 0.30 - 0.31, respectively.

In the mean time, the difference between species A and B, A and C, and B and C is about 0.14 - 0.31, 0.30 - 0.35, and 0.30 - 0.31.

Now everything becomes unclear. Furthermore, when

translated into amino acid, I found no stop codons in all of my sequences (except one a.a. missing in the middle if I remember correctly). The 29 individuals from group 1 are from everywhere in Korea, the 3 individuals from group 2 are from two places but the two places are very close: within a couple of miles, but the 4 individuals from group 3 are from three different places and they are far apart (different provinces).

Just before I sent the previous question email two days ago, I amplified the same (actually longer towards 5') region, using with a different 5' primer, from group 2 and 3, one individual each, and then got the same or very similar sequences to those of group 1. This means the group 2 and 3 somehow have two different mtDNA at least partly. I thought I could see at least a few stop codons if they are pseudogenes though the sequence length is not that long. So, are they due to heteroplasmy?

I may do some tests and gene walking to know where they are, but is it worth to publish? Is there anyone who has good experience on it with similar problems in insects?

Sincerely,

Cho, Soowon Department of Plant Medicine Chungbuk National University Cheongju, 361-763 KOREA soowon@chungbuk.ac.kr fax 82-(0)43-271-4414

soowon@chungbuk.ac.kr

ID review

The following review appeared in the November 2004 issue of CHOICE, a review journal taken by many college/university libraries.

Shanks, Niall. God, the devil, and Darwin: a critique of intelligent design theory. Oxford, 2004. 273p bibl index ISBN 0195161998.

Evan B. Hazard, Professor Emeritus of Biology, Bemidji State University, Bemidji, MN 56601-2699 eehazard@paulbunyan.net

Lasergene commercial software

Hi EvolDir! We're interested in purchasing the SeqManII software which is part of the LaserGene software package. It appears to be a very comprehensive program for the analysis of DNA sequence data and assembly into contigs. Could anyone who has experience (good or bad) in using SeqMan or any of the Lasergene programs please get in contact and let me know your thoughts. thanks a lot! mark _____ Mark A Chapman (mark.a.chapman@vanderbilt.edu) Department of Biological Sciences Vanderbilt University VU Station B 351634 Nashville, TN 37235

LongSAGE training

Greetings, I am a graduate student at Oregon State University and am studying gene expression levels relating to migration times between spring and fall chinook salmon. I want to use the LongSAGE approach to analyze it, but as it is technically exhaustive would like to save some time by visiting a lab currently engaged in LongSAGE experiments to learn the process. Is anyone currently working with LongSAGE with animals in a lab in the west coast or rocky mountain areas of the US? If so, would you be receptive to a visitor for a short visit to learn the LongSAGE ropes?

Thanks in advance

Jeremiah Bernier- Graduate Research Assistant ph (541) 867-0291 fax(541) 867-0345 <http://-marinerresearch.oregonstate.edu/genetics/index.htm> Coastal Oregon Marine Experiment Station Hatfield Marine Science Center Marine Fisheries Genetics Program 2030 SE Marine Science Dr. Newport, OR 97365

LowLevel Phylogenetics

Dear colleagues,

I am conducting a survey of literature on nuclear markers for lower-level (intrageneric, family level) phylogenetic analysis in Crustacea. We are working on Peracarida crustaceans, but any universal Arthropod primers for nuclear markers are of interest.

I greatly appreciate your comments and experience in amplifying and sequencing nuclear genes from various creatures!

sincerely,

Asta Audzijonyte (PhD student) Finnish Museum of Natural History & Department of Biological and Environmental Sciences University of Helsinki

asta.audzijonyte@helsinki.fi

Microsat linkage disequilibrium

Dear evoldir Members,

I am working in a tetraploid specie, and I am looking for a software able to calculate linkage disequilibrium among microsatellite loci. So, anybody know a software to estimate linkage disequilibrium in a tetraploid specie?

Thanks in advance,

Miguel Angel

Dr. Miguel Angel González Pérez Departamento de Biología Campus de Tafira Universidad de Las Palmas de Gran Canaria 35017 Las Palmas Canary Islands Spain e-mail: mgonzalez@becarios.ulpgc.es Phone: +34 928 45 45 43 Fax: +34 928 45 29 22

Microsat stutters

Hi,

I am a graduate student attempting to use microsatellites to study population genetics. I have been at it for 2 years now and have thoroughly exhausted all avenues available to me in an attempt to solve a stutter problem on an ABI 377. I am using cattle primers that are known to work on my species and out of 20 have 10 that will amplify up with PCR, but when ran on the ABI 377 I end up with lots of non-specific bands and the desired bands have anywhere from 3 to 7 peaks to them making it impossible to tell the size of the allele. I have checked on a WAVE machine that my primers are in fact the same correct size, tried different taqs, and done optimization with my PCR. Nothing works. My PCR

cycle is 12.5 ul with 40 rounds, an annealing temperature of 58 to 60 followed by a 30 minute extension at 72. I dont think it is an A+ problem because my PCR reaction would more than likely put As on everything given the number of cycles and time around 70 degrees. Furthermore, I dont think this would account for 6 to 7 bands. I have seen the electropherograms of others and they do not have the stutter issue. I use Cambrex gel packs to make my gels, let the gels set up for about 3 hours, run my PCR the day I do it, take 0.5 ul of two separate PCR reactions and add 3 ul of a 5:1:1 mix of formamide:dye:ROX400 ladder, use 96 well membrane combs, add 0.8 ul to each well, and run for 2.5 hours. Does anybody else have stutter issues? Any suggestions to reduce stutters without buying new primers? If I do not get this issue resolved within the next couple of months I will be forced to pursue a different project for my Ph.D. and be extremely disappointed. So any help, advice, or suggestions are welcome since I am at a standstill right now.

Thank you

Microsat stutters 2

For the individual who posted the message regarding microsat stutters, could you please post an email address for members to respond. Thanks.

C. Bettles bettlcmb@dfw.wa.gov

Microsat stutters 3

Please note that Jennifer Schmidt (fsjis@uaf.edu) was the originator of the microsat.stutter posting and to whom replies should be addressed.

My apologies to Kathleen J. Craft for the misunderstanding.

Brian

Microsat stutters answers

RESPONSES TO MICROSAT STUTTERS Below I have grouped the responses so far received to reduce stutters, thank you to everyone who has responded! The most common response was to reduce the number of cycles. Followed by reduce the MgCl concentration. Also a mix of PCR cycle options with a high initial annealing temperature either through a Touch down process or a few said plain heating your PCR before you put the polymerase in. Two-step PCR was mentioned more than just heating your reaction without taq. Also as popular was to reduce the extension time at the end. About 3-4 people said specifically to try hot start taq. After the combined PCR suggestions commonly stated was to just redesign reverse primers according to the Pig-tail method (Brownstein et al. 1996, Biotechniques 20, 1004-1010).

Since then I have reduced the number of cycles, then also shortened the extension time. Then with the shortened number of cycles and extension time varied MgCl from 1.5 to 2.5 because the person who uses them successfully now says not to go out of this range. I have also kept the 2.5 MgCl as original, but added BSA. I am currently looking over the results, but wanted to pass along the feedback I have been getting.

Again THANK YOU very much to all who responded.

PCR REACTION CHANGES Varying Mg++ levels, maybe try a gradient from 1-4mM, lower MgCl helps to reduce stutters. Use hot start Taq Change concentration of your primers. We use a starting concentration of only 0.5uM of our labeled primer and then the reverse (unlabeled) is 2uM. My labmates have found that better bands sometimes come with changing the labeled primer to either 0.3uM or 0.7uM. We were told that it's good to have the reverse primer in higher concentration. Try out t4 polymerase

PCR CYCLE CHANGES Reduce the number of cycles down as low as possible, 40 cycles is excessive and try 25 cycles o "increasing the number of cycles may increase nonspecific background and may lead to artifacts" (source: Qiagen multiplex pcr handbook, 2002, p.33) Use a very stringent annealing temp Set your final extension to 70 degrees or 65 degrees for 45 mins (see Profiler Plus manual for Profiler Plus kit used on humans). I had some loci which were tricky to score until our lab stumbled across the reaction conditions used for Profiler Plus kit. Touch down' PCR program o start Tm at 65C or 67C and the annealing temp reduced 2C per cycle for the next cycles up to TmX, then the remaining cycles at a 58C annealing temperature o start at 60C and within the first 10 cycles down the Ta to 50C, then keep 50C for the next 30 cycles o start at 60C and within the first 10 cycles down the Ta to 50C,

then keep 50C for the next 30 cycles short PCR“ o cycles of 15s at 94, 15s at annealing temperature and 45s at 72 and lower the number of cycles. I've heard people sometimes run only 5s at annealing temperature Hot-start PCR with regular promega taq by performing a first denaturing step with DNA, primers and water and then lower the temperature for about 85C to add the master mix containing taq and all the other reagents. I've performed 12.5 ul reactions, primer concentrations ranging from as low as 0.03 to 1.2uM in multiplexes. Annealing temperatures were 58C for most primer sets and 60C. I also recommend the Quiagen multiplex PCR mix, that provides a taq appropriate for hotstart PCR. No 72C extension step in the cycle (I mean that I have the annealing step followed by the denaturing step and then annealing again, with the Taq extending during the ramp, for microsats is more then necessary), and only 2 minutes of final extension step. Biotechniques suggested abbreviated cycling times for PCR steps. For instance, denature for only 2 seconds, anneal for 2 seconds, extend for 8 seconds. I've often used this "2/2/8" protocol (or some variant, e.g. 3/3/12) to clean up microsatellite stutter. Sometimes it fails miserably, but in about 50% of the cases it helps dramatically. Try heating your PCR without taq in it for 15min @95C, then adding taq Two-step PCR o 30sec at 94C and 80 sec at 50C. Also here is the reference that uses the suggested cycle Here is the reference:  YoshiadK, Awaji M (2000). Improvement of polymerase chain reaction condition to detect polymorphic dinucleotide repeat microsatellite DNA marker in the puffer fish. Fisheries Sciences, 66(2), 397-399. o denaturing at 94 and annealing at 62-65, with no elongation step- this sometime helps

PRIMERS Re-designing the reverse primers the way that you add GTTT to 5'end, i.e. if your original primer has A,G,C, at 5'end add GTTT, if it ends by T, add GTT, if by TT add just GT etc. You may find info in Brownstein et al. 1996, Biotechniques 20, 1004-1010. Also see ABI Prism Linkage Mapping Set User Bulletin for 5 Nov 1997 re: "plus A artifacts".

ADDITIVES There are several additives you could try adding. They include dimethyl

— / —

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>

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 EvoDir 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>

PCR reaction numbers

Dear members of the EvoDir,

I am trying to optimize the number of PCR reactions that can be done with DNA extracted from one single fruit fly. I am not able of performing as many reactions as I need, and that's why I am posting the following questions to the EvoDir:

1- I have the feeling that ethanol purification of DNA is not the most optimal purification method. Do you know of any other method (filters, columns, etc...) that gives a higher yield of DNA per extraction? IMPORTANT: Since I have a quite large number of flies to analyze, a method that uses microtiter plates for the extraction would be more convenient.

2- Have you ever tried to recycle the genomic DNA used in a PCR? if so, what method did you use to re-isolate the genomic DNA from PCR mix? and also, how

reliable are PCR results of reactions using "recycled" DNA?

3- Has anybody experience in Multiplex PCR for population genetics studies? how reliable is the information obtained from multiplex PCR?

Thank you,

David (reply to delorenzo@lmu.de) –

Dr. David De Lorenzo Dep. Biologie II - LMU Grosshaderner Str. 2 82152 Planegg-Martinsried Germany

Phone: (+49 89) 2180 74160 Fax: (+49 89) 2180 74104

<http://www.zi.biologie.uni-muenchen.de/institute/zi/-abt/lgn/evolutionsbiologie>

Pollination

We would like to invite you to subscribe to a new mailing list POLSYND-L This new mailing list is aiming to create an information network among evolutionary-ecologists working on pollination. The goal of the Pollination Syndrome Network would be to enhance communication among researchers in the area of pollinator-mediated floral evolution. We hope to develop this forum as a convenient place for the sharing of knowledge and ideas, in order to revise the generalisation which guide this fascinating discipline of evolutionary biology.

To subscribe, go to: <http://www.lsoft.com/scripts/wl.exe?SL1=POLSYND-L&H=LISTSERV.INDIANA.EDU> Or simply send e-mail to LISTSERV@LISTSERV.INDIANA.EDU with the command: SUBSCRIBE POLSYND-L

Cheers Yuval Sapir and Stacey Smith

– Yuval Sapir, PhD

Dept of Biology Indiana University Bloomington, IN 47405 USA http://www.bio.indiana.edu/~rieseberglab/yuval_sapir.html ysapir@indiana.edu

Pub quality phylogenies

Hello,

Two items: one practical, one discussion oriented.

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

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?

With appreciation, Joel L. Carlin

Visiting Assistant Professor of Biology Whitman College Walla Walla Washington USA

Joel Carlin <carlinjl@whitman.edu>

the idea of no anonymity for reviewers. I believe it would be a positive step forward for scientific communication if reviewers signed their name to their evaluation of manuscripts. It would encourage more thoughtful critiques, reduce cronyism, and bring us a step closer to being accountable as scientists.

I would greatly appreciate it if you could spare the time and cast your vote as follows.

Those in favour of signing your name as a reviewer reply YES

Those in favour of the status quo reply NO

I'll post the results to the list if there is sufficient interest.

Regards

Kelley

K Whitaker Department of Genetics University of Pretoria Hatfield 0002 South Africa

Tel: +27 12 420 3871 Email: kelley.whitaker@up.ac.za

K Whitaker <kelley.whitaker@up.ac.za>

Random samples

Dear Colleagues

I need to randomly select small sub-samples from a series of overly-large data sets. Does anyone know of a program that allows you to randomly select (a predefined number of) specimens from a large list of sample numbers?

Thanking you for your time, Yours sincerely, Stephen Lycett

– Stephen J. Lycett (BA Hons., MSc.) Leverhulme Centre for Human Evolutionary Studies Department of Biological Anthropology University of Cambridge Downing Street Cambridge CB2 3DZ

Telephone (Office): +44 (0)1223 762846 e.mail: s.lycett@human-evol.cam.ac.uk <http://www.human-evol.cam.ac.uk/lycett.htm>

Reviewer Accountability

Dear Colleagues

I would like to gauge whether there is any support for

Rodent EvolEcol

Dear friends and colleagues,

If you are interested in the evolutionary ecology and social behavior of rodents, you might want to read the FSM-TIMES, which can be downloaded at: http://schradin.com/sgm/sm.times_1.pdf The FSM-TIMES provides information about the research on the ecology and behavior of small mammals in Namaqualand, South Africa.

If you would like to receive the FSM-TIMES also in the future, please reply to this email to receive instructions. You will then receive the FSM-TIMES four times a year as email attachment. The FSM-TIMES is free of charge.

The FSM-TIMES has two aims:

1. To provide information about our work at the Succulent Karoo Research Station and the research on small mammals. We aim to provide you with entertaining scientific information, pi that would be enjoyed by everyone interested in nature, and not only (but also) by scientists.
2. To obtain funding for smaller scientific projects from donations of the FSM-TIMES members.

Please forward the FSM-TIMES to anyone who might be interested, e.g. to the mailing list of your department, mailing list of zoological associations or any friend that might be interested.

I apologize in case you got this email more than one time. This could have happened when you are on more than one mailing list.

You can download the FSM-TIMES from the internet at:

http://schradin.com/sgm/sm_times.1.pdf and the German version of it, the SGM-Spiegel at

http://schradin.com/sgm/smg_spiegel.1.pdf

Sincerely yours,

Carsten Schradin

Dr. Carsten Schradin Succulent Karoo Research Station Goegap Nature Reserve Private Bag X1 8240 Springbok

South Africa

Fax: +27 -(0)27- 7181286

(Visiting Researcher at the School of Animal, Plant and Environmental Sciences University of the Witwatersrand)

schradin@mweb.co.za

SSCP DGGE dHPLC

I am attempting to obtain nuclear sequences for my Ph.D. project. I am finding plenty of heterozygosity and am looking for the best methods to separate the alleles for subsequent reamplification via PCR and then sequencing. I've read about the possibility of using a number of methods other than cloning to obtain nuclear haplotype data. Methods that I am considering include SSCP (Single strand conformational polymorphism), DGGE (Denaturing gradient gel electrophoresis), and dHPLC (Denaturing high performance liquid chromatography).

I am looking for individuals who have used any of these techniques to separate alleles for subsequent sequencing. What are the strengths and weaknesses of each approach? How much does it cost to get sequences from one individual for both alleles? What about time commitment? Special equipment?

I will gladly post a summary of replies within the next

week or two.

Thanks for your help!

George Harper gharper@email.unc.edu or harp_unc@hotmail.com

Software Clann

Hi, Just to announce that we have released a new version of Clann at:

<http://bioinf.may.ie/software/clann/> For those that may be unfamiliar with Clann:

Clann is a software program for investigating phylogenetic information through Supertree analyses.

Clann has recently been published in Bioinformatics: <http://bioinformatics.oupjournals.org/cgi/content/abstract/bti020v1> This version of Clann (2.0.3) implements four supertree methods (which are used as optimality criteria):

Matrix Representation using Parsimony (But Paup* is necessary for the parsimony part) Maximum Quartet fit Maximum Split (component) fit Most Similar Supertree Method (A novel method related to the average consensus method with branch lengths set to unity)

For each of these optimality criteria, Clann allows: Searches of supertree-space using Exhaustive or Heuristic searches (NNI & SPR) Searches of User-defined trees. Investigation into the support for various hypotheses through: Bootstrapping (at the source tree level) YAPTP tests (a randomisation test similar to the ptp test)

New Features: Sampling of supertree space before heuristic searches Introduction of Neighbor joining on MRP matrices Readline library for ease of use Several bugs fixed

Clann is freely available to the scientific community at: <http://bioinf.may.ie/software/clann/> -----

Dr. Christopher J. Creevey Bioinformatics and Pharmacogenomics Laboratory, Department of Biology, National University of Ireland, Maynooth Co. Kildare Eire.

e: chris.creevey@may.ie p: + 353 1 708 6043 f: + 353 1 708 3845 w: <http://bioinf.may.ie/>

Software GASP GCMSAnalysisSoftwarePackage

Dear Evoldir

We are releasing a new cross-platform application to organize and align metabolomics data. GASP (GC/MS Analysis Software Package) is a software that allows the comparison of compounds and peaks generated by GC/MS instruments.

It can be run on Windows and Linux machines and is able to deal with large amounts of data. The main aspect of the program is the capability of showing shared and unique compounds in different samples, by aligning the peaks and checking spectra compositions. Usually GC/MS instruments have been used in metabolomics analysis of plants, bacteria, among other biological samples.

GASP accepts inputs from different sources of GC/MS data and as the program uses a NEXUS-like file as main input, the addition of different sources of data is quite straightforward. Also, based on user input it is possible to include new features with ease. GASP is also automatically linked to the statistical package R, using all the calculation power to generate statistics based on peak alignment.

The software is available free of charge (to academics) at

<http://evol.mcmaster.ca/paulo/gasp.php> Two versions are available, Windows and Linux. A chm help file is available also, and it covers basic program usage and some analysis features. Please feel free to download and test it and send us your comments and opinions about it.

Thanks for the interest

Paulo Nuin Post-Doctoral Fellow/Sessional Lecturer
Dept. of Biology McMaster University Hamilton,
ON Canada nuin@terra.com.br nuinp@mcmaster.ca
evol.biology.mcmaster.ca/paulo

Software PopGenetics

I'd like to inform evolutionary biologists about the release of BAPS 3 software for analysis of genetic population structure. Main improvements in the software compared with the earlier versions are: Better usability, faster algorithms (100-1000 times faster, depending on the size of the data set), possibility to do admixture analysis, more informative output, enhanced built-in graphics. The software is freely available at:

<http://www.rni.helsinki.fi/~jic/bapspage.html> Regards

Jukka Corander Department of Mathematics and statistics P.O.BOX 68 00014 University of Helsinki Finland

Jukka Corander <jukka.corander@helsinki.fi>

Software Treefinder

Here is the new world's fastest maximum likelihood phylogeny program on a PC:

www.treefinder.de TREEFINDER has a new tree search algorithm. In my simulations, the new TREEFINDER is three times faster than PHYML, which is the second fastest program. The results are in the manual.

Tree calibration has been extended. Now, TREEFINDER supports multiple calibration points and time intervals. One can specify time boundaries for tips as well as for internal nodes in a tree. I have invented and added two new flavours of rate smoothing to overcome some problems with Sanderson's NPRS: The Global Rate Minimum Deformation method (GRMD), and the Local Rate Minimum Deformation method (LRMD).

I have also improved the utility to check for compositional equilibrium in a sequence alignment. In addition to computing p-values for individual sequences, the tool now visualizes the distribution of base frequencies over sites as well as over species.

Maximum likelihood optimization under the molecular clock is no longer supported. In my opinion, the underlying assumption of a constant rate is unrealistic and not really worth the huge effort on the algorithmic side. For calibration purposes, rate smoothing can achieve the same much easier and has the merit of distinguishing clearly between the time scale and the distance scale. Moreover, one can incorporate explicit as-

sumptions about the rate evolution into the objective function. If you feel that my opinion is wrong, you may try convincing me to re-implement the clock constraint in a future release.

As usual, the program is available for Windows, Linux, MacOS X and Solaris.

Did you know that a German scientist earns less than a worker in car industry, but has studied for years? Obviously, cars are much more useful than most of science. Please note, that I am currently not being paid for my work. I am looking for a position in Munich, where I can continue the TREEFINDER project.

Cheers, Gangolf

Gangolf Jobb <gangolf@treefinder.de>

and discusses TuneClustalX can be downloaded from: www.bellinghamresearchinstitute.com by going to that site, clicking the BRI Reports button, and choosing Report #1.. That report also describes how TuneClustalX was used to determine improved default gap penalties for protein sequence alignments. TuneClustalX for Macintosh, Windows, and Unix platforms is freeware and, together with documentation, can be downloaded from www.bellinghamresearchinstitute.com by clicking the Software navigation button and choosing the appropriate package for your platform.

Barry G. Hall drbh@mail.rochester.edu

“Barry G. Hall” <barryhall@zeninternet.com>

Software TuneClustalX

The previous post had an incorrect email. It is corrected below.

TuneClustalX: A program that facilitates improving the quality of multiple sequence alignments constructed with ClustalX. The quality of a phylogeny is no better than the quality of the underlying data. In the case of phylogenies based upon molecular sequences the underlying data are in the form of a multiple sequence alignment, and the currently most popular tool for multiple sequence alignments is ClustalX, a graphical user interface version of the venerable ClustalW. The most critical factor that affects the quality of the alignment is the proper choice of gap penalties, but most users tend to use the default penalties because it is both difficult and frustrating to attempt to improve the quality of an alignment by modification of those penalties. ClustalX provides a variety of tools for modifying gap penalties and for identifying poorly aligned regions, but it is difficult to evaluate the consequences of changing gap penalties. TuneClustalX uses data that can be output from ClustalX to calculate an average Quality Score. By modifying gap penalties, then using TuneClustalX to calculate the average Quality Score the user can quickly determine whether the modification improves the quality, makes the quality worse, or has no effect upon the quality of the alignment. As a result, the user can begin with the default gap penalties and quickly move toward gap penalties that are optimized for the particular data set. A Bellingham Research Institute report that describes

Software TuneClustalX 2

Below is a patch for TuneClustalX.

```
- #define X(x,y) x##y Peter Cordes ; e-mail:
X(peter@cor , des.ca)
```

“The gods confound the man who first found out how to distinguish the hours! Confound him, too, who in this place set up a sundial, to cut and hack my day so wretchedly into small pieces!” – Plautus, 200 BC

PS. here’s the patch

```
diff -ru TuneClustalX.orig/Makefile
TuneClustalX/Makefile — TuneClustalX.orig/Makefile
Wed Jul 21 01:06:14 2004 TuneClustalX/Makefile Wed
Nov 17 19:45:21 2004 @@ -3,8 +3,9 @@
```

```
LIBS = -lm
```

```
-# Possible options (choose one): -O2 -O3 -O4 -fast
-static -CFLAGS = -O4 +# Possible options (choose
one): -g -Wall -O2 -O3 -O4 -fast -static +#CFLAGS
= -O4 +CFLAGS = -Wall -O4 -march=i686 -fomit-
frame-pointer -ffast-math
```

```
# Possible compilers: cc, gcc, g++ (gcc = MacOS
X) CC = cc @@ -13,19 +14,19 @@ OBJECTS =
TuneClustal.o
```

```
# Give the executable binary a name -PROGS =
TuneClustalX +PROGS = tuneclustalx
```

```
all: $(PROGS)
```

```
# This line begins with program name and ends with
program name (see “all:” above) -TuneClustalX: $(OB-
JECTS) - $(CC) $(CFLAGS) $(OBJECTS) $(LIBS)
-o TuneClustalX +tuneclustalx: $(OBJECTS) +
```



```

$(CC) $(CFLAGS) $(OBJECTS) $(LIBS) -o $@ + /*****/
+TuneClustal.o: TuneClustal.h
# For each .o file a line needs to be made - tells compiler to create a .o file Simulator.o: Simulator.c $(CC) /*****/
$(CFLAGS) -c TuneClustal.c - - /*****/
# This command is invoked either during make (i.e., make clean) or after compiling # Removes the .o files from the directory diff -ru TuneClustalX.orig/TuneClustal.c TuneClustalX/TuneClustal.c -
TuneClustalX.orig/TuneClustal.c Wed Jul 21 01:05:24
2004 TuneClustalX/TuneClustal.c Wed Nov 17
20:28:09 2004 @@ -1,7 +1,17 @@ /* * Copyright
© 2003 Barry G. Hall. All Rights Reserved. * -
+ * cleanups and improvements by Peter Cordes
<peter@cordes.ca> + * 2004 Nov 17: - add command-
line parsing as an alternative to interactive mode + * -
do line-at-a-time I/O, and use scanf instead of parsing
manually + * - use fewer global variables + * - do
more error-checking and safer buffer handling + * +
* This program is probably only useful if you don't
have awk. + * awk '{Q+=$NF} END{print Q/NR}'
R1.qscores + * does the all-positions average, and e.g.
+ * awk 'NR>5 && NR<100{Q+=$NF;count++}'
END{print Q/count}' R1.qscores + * gives the same
result as tuneclustalx R1.qscores 6:99 */
#include <stdlib.h> @@ -11,29 +21,69 @@ #include
"TuneClustal.h"
+/* **** global variables *****/
+/* state set from command line */ +int interac-
tive = 1; +int quiet = 0; +char infilebuf[128] =
""; +char *InFile = infilebuf; +int rangestart =
0, rangeend = 0; + +/* This code is so not re-
entrant anyway, what's another shared temp var :)
*/ +char linebuf[4096]; + +int AlignmentLength;
+int *QScores; +FILE *Input; + +char *banner =
"\n\n\t\t\tTune ClustalX Alignments\n\n"
+"\n\n\t\t\tAn aid to improving alignments with
ClustalX\n\n" +"\n\n\t\t\t Barry G. Hall\n\n"
+"\t\t Copyright 2004 Bellingham Research Institute"
+"\n\n\nCommand line interface by Peter Cordes
<peter@cordes.ca>, Dalhousie University\n\n\n\n";
+ +char *usage = "usage: tuneclustalx [options] [in-
file.qscores [start:end]]\n" + "options: -h -help: print
this help\n" + "-v: version info\n" + "-q: quiet mode
to avoid screen clutter\n" + "infile.qscores: the file to
read\n" + "start:end: the range of alignment positions
to consider\n" + "If infile isn't specified on the com-
mand line, tuneclustalx will be interactive";
- -/*NOTE!! Functions appear AFTER main!*/
+/*NOTE!! Functions appear AFTER main!*/
-int main(void) +int main (int argc, char *argv[]) {
-int i=0; + ParseArgs( argc, argv );
-Initialize(); -Splash(); -GetInfileName(); -
-OpenInputFile(); -GetAlignmentLength(); -
-ReadQScores(); -GetSettings (); + if (!quiet) +
Splash();
+ if (interactive) + GetInfileName( InFile );
-return 0; + Input = OpenInputFile( InFile ); +
GetAlignmentLength( Input ); + ReadQScores( In-
put ); + fclose( Input ); + if (!interactive){ + if(
rangestart ) + printf("The mean Q score for sites %d
through %d is %.4f.\n", + rangestart, rangeend, Av-
erageRange(rangestart, rangeend) ); + else + Aver-
ageAllTheQScores(); + }else{ + while (42){ + Interac-
tiveMenu(); + } + }

```

— / —

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>

Software WinPop

Hello

A new improved version of WinPop 2.0 (v. 2.0.20) is available to download. As you are registered just click on the link below to start the download:

<http://evol.biology.mcmaster.ca/paulo/download.php?file=http://evol.mcmaster.ca/paulo/files/winpop98.zip> A new and improved help file is also available. To download it check WinPop webpage at

<http://evol.mcmaster.ca/paulo/winpop.php> Also there is a survey about the program with the objective of gather user input to improve and correct the program. This survey consists of 25 questions, most of them multiple choice and it can be completed at the following website:

<http://evol.biology.mcmaster.ca/paulo/clipboard/survey.php?surveyid=3> Thanks a lot for the interest.

Paulo Nuin Post-Doctoral Fellow Dept. of
Biology McMaster University Hamilton, ON
Canada nuin@terra.com.br nuinp@mcmaster.ca
evol.biology.mcmaster.ca/paulo

Writer & Photographer ~ www.greendzn.com <<http://www.greendzn.com/>> Ph.D. Student, Rice University, Ecology & Evolutionary Biology Do not go where the path may lead. Go instead where there is no path and leave a trail. – Ralph Waldo Emerson
ecowriter@ev1.net

Speciation with nonsister taxa

I am wondering if anyone has insight into this: what (if anything) can we learn about speciation by studying reproductive isolation between nonsister taxa? I was told recently that you can't learn anything about speciation by studying nonsister taxa, and I am interested in other people's feedback on this.

People have studied hybrid zones as centers to understand speciation for decades and they are certainly not always sister taxa, right?

If most species formed in allopatry anyway, the mechanisms that isolate two species probably arose more by chance, and it is only when species come back together in sympatry that these forces operate. How many times do sister species themselves split and rejoin, as opposed to a species reconnecting (secondary contact) with a nonsister species? I would almost venture to say that much of reinforcement occurs between nonsister taxa (outside of zones where parapatric speciation is occurring). Has anyone ever systematically looked at this?

And how much is known about the biogeography of the distribution of current taxa? If two nonsister species are broadly sympatric, and the sister taxa is in an isolated pocket, then isn't there reason to suspect that these two closely related but nonsister taxa could have influenced one another's isolating mechanisms more than a sister taxa? These two species I'm thinking of have distinct segregated breeding habitats.

Particularly if hybridization is still occurring between these species separated by many or few speciation "events" then we can learn about why speciation has not come to 'completion', at least according to the biological species concept? So it may be more difficult to pinpoint the exact causes in non-incipient or nonsister taxa, but should we restrict all studies of speciation to incipient and/or sister species? Piecing together the puzzle may be more difficult in nonsister taxa but it can still be done, or evidence can be accumulated through experimentation and observation. no?

Best regards, Wendee Holtcamp

Wendee Holtcamp ~ ecowriter@ev1.net Freelance

Supertherm DNA polymerase

Could you give me some information on this enzyme for PCR: SUPER THERM DNA POLYMERASE, this enzyme is distributed for LPI. I need technical information.

Thanks yor for cooperation.

Sincerely,

DOLLY REVELO <girad13@hotmail.com>

Synteny searches

My question concerns synteny searches. I would like to compare within yeast strains and within vertebrate species for protein synteny. But I am not aware of any good and efficient programs that I can use. Could someone give me some tips?

Thank you very much.

Sincerely, Nadja Neumann

Nadja Neumann

Department of Molecular Biology & Functional Genomics Arrhenius Laboratories for Natural Sciences Stockholm University, SE-106 91 Stockholm, Sweden

tel. +46 8 164062

EMAIL: nadja.neumann@molbio.su.se

Nadja Neumann <nadja.neumann@molbio.su.se>

Viruses from tubers

I would like some advice on how to isolate and purify viruses from a diseased tuber of cassava. Especially on the amount of starting material required for a successful isolation and purification.

Thanks

Sharmane Naidoo

Roobavathie Naidoo <Naidooro@ukzn.ac.za>

Winboot

Dear All,

Could anyone indicate where we could get "Winboot" software: A programme for performing bootstrap analysis for binary data to determine the confidence limits of UPGMA based dendrograms (Yap & Nelson, 1996).

Thank you

Prof. Dr. Pedro A. Sosa Department of Biology University of Las Palmas Campus Universitario de Tafira 35017 Las Palmas Canary Islands Spain psoa@dbio.ulpgc.es

adaptation in Moraba

Dear Evoldir reader, For a course dealing with adaptation I am planning to speak about adaptative landscape, and to illustrate the course with the historical example of Moraba Scurra example of Lewontin and White (1960 !). I have 2 questions about this example. First what is the precise relation between the chromosome inversion and the fitness ? Is it known ? Second does some more recent studies about the same material exist ?

Sincely,

Alex Baumel (alex.baumel@univ.u-3mrs.fr)

Alex Baumel Institut Méditerranéen d'Ecologie et de Paléoécologie UMR-CNRS 6116 - Université Aix-Marseille III IMEP - Bat. Villemin Europole de l'Arbois BP80 - 13545 Aix en Provence Cedex 04
Tel. : (33) 04 42 90 84 53 Web : www.imep-cnrs.com/pages/abaumel.htm ALEX BAUMEL <alex.baumel@univ.u-3mrs.fr>

cDNA libraries

Dear Members,

I am interested in hearing comments about cDNA Library Construction Kits. Does anyone have experience with various kits and their performance? Can you comment the advantages and disadvantages of the tested kit? Thanks for your help,

Roxana Yockteng

Roxana YOCKTENG Laboratoire Ecologie, Systématique et Evolution Bâtiment 360 Université Paris-Sud 91405 Orsay Cedex - France Tél. 01-69-15-56-64 - Fax. 01-69-15-73-53

ryockteng@wanadoo.fr

r8s error

Dear EvolDir members,

I have some queries regarding Penalized Likelihood (PL) using the program r8s and would greatly appreciate your feedback:

1) While running cross validation I got the following message several times: MinND returned failure in ConstrOpt on initial search (may restart!).

I assume it has something to do with the branch length, but since my trees neither contain zero length branches nor polytomies I don't know what is going on.

2) Sometimes, while running cross validation for some smoothing parameters I got a message: "smooth smooth Sq Error Chi Square Error" with all the values and either a (Good) or (Failed) at the end of it. Do I have to worry, when some smoothing parameters failed?

3) In one data sets I observed that the cross validation scores were decreasing gradually under smoothing parameters ranging from 1 to a 1000. Which cross-validation score should be used in this case when cross validation does not really find "a lowest cross-validation score"? Would 1 be ok?

Thank you very much in advance for your kind help and suggestions. With my best wishes, Lukas

Lukas Ruber Museo Nacional de Ciencias Naturales
Jose Gutierrez Abascal 2 28006 Madrid, Spain

Tel. ++34-91-4111328 (ext 1129) (wait for tape-record, dial 1 and then 1129) FAX ++34-91-5645078 Email: ruber@mncn.csic.es URL: <http://www.lukasruber.com>
URL: <http://www.mncn.csic.es>

PostDocs

BrighamYoungU PlantSystematics	45	UChicago Biostatistics	52
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Philadelphia EvolCancer	48	UStAndrews EvolBiol	54
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BrighamYoungU PlantSystematics

Postdoctoral Position in Evolutionary Plant Systematics

An NSF-funded Postdoctoral position is available to pursue species-level phylogenetic reconstruction and evolutionary inference in the Phlox family (Polemoniaceae). Fundamental questions involving species delimitation and non-correspondance between levels of morphological and molecular change are being addressed in a research environment emphasizing low-copy nuclear genes and qualitative & quantitative analysis of morphology. Support is available for up to 2.5 years. Salary is \$30K plus benefits, with the starting date negotiable, on or after 1 January 2005 (preferably by summer 2005). Applications will be considered until the

position is filled. An enthusiastic candidate with good trouble shooting skills is sought. Ideally, this candidate will also possess moderate to advanced molecular biology skills, including primer design/optimization and cloning with thorough familiarity of conceptual issues and methods of phylogenetic inference. Experience with, or the aptitude to learn cDNA/genomic library construction/screening techniques is a plus. The successful candidate will join a lab with graduate and undergraduate students actively involved in evolutionary plant systematics. The Johnson lab is part of an interactive core research group in evolutionary biology at Brigham Young University, with substantial depth in molecular systematics, population genetics, phylogenetics, coevolution, computational biology, and molecular evolution; this postdoctoral position provides opportunities for interaction and potential collaboration on related projects within our growing evolutionary biology faculty (Byron Adams, Keith Crandall, Leigh Johnson, Jerry Johnson, David McClellan,

Duke Rogers, Jack Sites, Michael Whiting), other post docs, and visiting faculty. BYU is well equipped with modern microscopy, automated DNA sequencing, and computer cluster equipment for acquiring and analyzing large data sets. Interested researchers should contact: leigh_johnson@byu.edu for more information.

CornellU PopulationGenetics

POSTDOC IN TRANSMISSION/POPULATION GENETICS OF FUNGI, CORNELL UNIVERSITY

A postdoctoral position is available to study transmission and population genetics of arbuscular mycorrhizal (AM) fungi. With no sexual morphology, AM fungi are hypothesized to reproduce clonally. To test this hypothesis, we are assessing genome organization and population structure of a selected AM fungal species. This work will be paralleled by a cytological study tracing fate of nuclei during AM fungal life cycle, for which we will construct genetically transformed strains expressing a GFP-labeled histone to enable visualization of nuclei in living cells. For more information please consult Pawlowska & Taylor (2004) *Nature* 427: 733-737 and <http://ppathw3.cals.cornell.edu/People/labs/-Pawlowska/Index.html>. Preference will be given to candidates with strong experience in molecular and cell biology and/or in molecular methods for the analysis of genetic variation. A familiarity with arbuscular mycorrhizal fungi is desirable but not essential. The position is for two years with possibility of extension. Applications are due December 15, 2004.

Please e-mail a letter summarizing research interests and experience along with curriculum vitae including the names, addresses and e-mails of three references to: tep8@cornell.edu.

Cornell University is an Affirmative Action, Equal Opportunity employer. –

Teresa E. Pawlowska Assistant Professor Department of Plant Pathology 334 Plant Science Cornell University Ithaca, NY 14853 Phone: (607) 254 8726 Fax: (607) 255 4471 E-mail: tep8@cornell.edu Lab web site: <http://ppathw3.cals.cornell.edu/People/labs/Pawlowska/Index.html> Lab web site: <http://ppathw3.cals.cornell.edu/People/labs/Pawlowska/-Index.html>

GeorgetownU TheoPopGenetics

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 November 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/> hamiltm1@georgetown.edu

Harvard PopulationGenetics

Post doc position in Department of Genetics, Harvard Medical School

“Applying population genetics to find genes for common disease”

I am searching for a post-doctoral candidate who has very strong statistical and mathematical skills-preferably with a background in coalescent theory and population genetic simulations-and is interested in applying these skills to search for genes causing common human disease and for evidence of historical natural selection in the human genome.

This position will require a great deal of creativity. The first project will most likely involve formalization of the test for recent positive selection presented in “Sabeti, Reich et al. (2002) Detecting recent positive selection in the human genome from haplotype structure. *Nature* 419, 832-7.”

Subsequent projects may involve further studies of natural selection in human populations, or extensions of methods recently developed for finding disease genes in populations of mixed ancestry: “Patterson et al. (2004) Methods for high-density admixture mapping of disease genes. *Am J Hum Genet.* 74, 979-1000.”

Please contact David Reich (reich@genetics.med.harvard.edu) for more information <http://www.hms.harvard.edu/dms/bbs/fac/reichda.html> David Reich <reich@genetics.med.harvard.edu>

MaxPlanck AvianEvolBiol

5-year Post-doc Avian Behavioural/Evolutionary Ecologi Avian Behavioural / Evolutionary Ecologist

Applications are invited for a 5-year research position at the Max Planck Institute for Ornithology at the Radolfzell location, starting February 2005. We are looking for a highly motivated scientist who is interested in developing a research program that complements current research done at the Seewiesen location.

Current research there focuses on evolution and function of avian sexual signals including song and plumage colour, reproductive behaviour, including timing of reproduction, hormonal control of sexual behaviour, effects of inbreeding, the neuroendocrine control of song, mate choice, sperm competition, promiscuity, and avian personalities.

The Max Planck Society is an independent, non-profit organization that promotes research in its own institutes. We offer a highly stimulating, international environment, outstanding research facilities (both locally and at Seewiesen) including unique aviary facilities, access to molecular and endocrinological laboratories, access to a long-term ringing scheme and superb logistic support. The working language is English. There are no teaching obligations, but the institute has an active PhD program via connections to the Universities of Konstanz and Munich.

Candidates should send a curriculum vitae, a statement of research interests and scientific goals, and the names and addresses of three referees to the address below. To ensure full consideration, applications should arrive before 3 December 2004. Short-listed candidates will be invited to Radolfzell in January 2005 for a symposium at which they have the opportunity to present their work.

For further information, please contact Prof. Dr. Bart Kempenaers (b.kempenaers@orn.mpg.de) or visit <http://www.ornithol.mpg.de> The Max-Planck Society is an Equal Opportunity Employer

Ms. Heike Gorny Max Planck Institute for Ornithology at Seewiesen Postfach 1564 D-82305 Starnberg Germany E-mail: gorny@erl.ornithol.mpg.de Phone: +49-8157-932334 or -232 Fax: -209

MuseumMankindParis HumanPopGenet

Postdoc: Human population genetics in Paris

A 2-year postdoctoral fellowship is available in Human population genetics at the “Musée de l’Homme” (Museum of Mankind) in Paris (France.) The main objective is to study the impact of history and social organization on the distribution of genetic diversity in Central Asia (Uzbekistan, Tajikistan, Turkmenistan, etc.) This is part of an on-going research project that aims at inferring the past demographic history of these popu-

lations, and understanding the relative role of social organization, linguistic differences, recent migrations and past population settlements in shaping the genetic diversity in this area. We are particularly interested in comparing populations with a past nomadic history with populations of settled agriculturalists.

About 500 individuals from nine different populations have already been sampled and sequenced for the mtDNA hypervariable region I. Most of these have also been typed at 11 microsatellites located on the Y chromosome. In order to complete the project, the postdoc will focus on autosomal microsatellite markers.

The successful applicant should have a Ph.D. in population genetics, and have experience in molecular biology, including standard DNA techniques (DNA extraction, PCR, genotyping, etc.) Ideally, also, he or she would assist with data analysis and address, via analytical methods and/or simulations, the reconstruction of past demography that can explain the level and the distribution of genetic diversity observed in this area.

The position is funded by the Centre National de la Recherche Scientifique (CNRS), but French citizens ARE NOT eligible: Only non-French can apply. Gross salary is 2150/month for a PhD that has just graduated and increases with years of experience. Applicants should send a CV, including a brief statement of research interests, as well as the names, e-mails and postal addresses of two references to Evelyne Heyer (heyer@mnhn.fr)

For further details, please contact:

Evelyne Heyer (heyer@mnhn.fr)

Some recent publications on this project are:

The genetic or mythical ancestry of descent groups: lessons from the Y-chromosome (2004) Chaix R, Austerlitz F, Khedgy T, Jacquesson S, Hammer MF, Heyer E, and Quintana-Murci L. *American Journal of Human Genetics* 75: 1113-1116

Where West meets East: the complex mtDNA landscape of the Southwest and Central Asian corridor (2004) Quintana-Murci L, Chaix R, Wells RS, Behar DM, Sayar H, Scozzari R, et al. *American Journal of Human Genetics* 74: 827-845

----- Pr Evelyne Heyer Unité Eco-anthropologie Equipe "génétique des populations humaines" Musée de l'Homme 17 place du Trocadéro 75116 Paris tel: 33-1-44057252 fax: 33-1-44057241

heyer@mnhn.fr

NatHistMuseumLondon EarlyEukaryoteEvol

Early Eukaryote Evolution

A postdoctoral position funded by the BBSRC is available at the Natural History Museum in London in the molecular systematics of early eukaryotes. The research will be completely in silico. The position would be suitable for someone with an interest in statistical phylogenetics. The successful candidate will use and develop advanced methods, including heterogeneous, covarion, and mixture models, to address questions of the origin and early divergence of the eukaryotes. Applicants should have facility with phylogenetic analysis. Programming ability would be an asset. The position will be for a period of three years. Applications will be accepted until 22 December, 2004. Preferred starting date will be the beginning of February, 2005, although this is flexible. The research will be based mainly at the NHM in London, but will also be closely associated with T.M.Embley and R.P.Hirt at U. Newcastle. Send your CV and names of referees to Peter Foster p.foster@nhm.ac.uk.

Peter Foster <p.foster@nhm.ac.uk>

Philadelphia EvolCancer

There is an opening for a post-doctoral fellow beginning on or after April 2005, to study clonal evolution in carcinogenesis and cancer prevention. An ideal candidate will have cell culture experience in experimental evolution. Expertise in cancer biology preferred. The projects will involve cell/tissue culture competition experiments and drug screens for agents that modulate that competition. Successful completion of the projects will lead to the opening of entirely new fields of cancer prevention. The post-doctoral fellow will be encouraged to develop these projects into his/her own research program when establishing an independent laboratory.

Successful candidate will have a Ph.D. or M.D./Ph.D. in the biological sciences. For consideration, send inquiries to: cmaley@wistar.upenn.edu, or send CV,

cover letter and three letters of recommendation to: Carlo Maley, The Wistar Institute, 3601 Spruce Street, Philadelphia, PA 19104. EOE/AA/M/F/D/V – Carlo C. Maley, Ph.D. Assistant Professor The Wistar Institute 3601 Spruce St. Philadelphia, PA 19104

fax: 206-667-6132 cell: 206-355-7425

http://www.wistar.upenn.edu/research_facilities/-maley/research.htm “Carlo C. Maley”
<cmaley@fhcrc.org>

Philadelphia ExpertimentalEvolCancer

There is an opening for a post-doctoral fellow beginning on or after April 2005, to study clonal evolution in carcinogenesis and cancer prevention. An ideal candidate will have cell culture experience in experimental evolution. Expertise in cancer biology preferred. The projects will involve cell/tissue culture competition experiments and drug screens for agents that modulate that competition. Successful completion of the projects will lead to the opening of entirely new fields of cancer prevention. The post-doctoral fellow will be encouraged to develop these projects into his/her own research program when establishing an independent laboratory.

Successful candidate will have a Ph.D. or M.D./Ph.D. in the biological sciences. For consideration, send inquiries to: cmaley@wistar.upenn.edu, or send CV, cover letter and three letters of recommendation to: Carlo Maley, The Wistar Institute, 3601 Spruce Street, Philadelphia, PA 19104. EOE/AA/M/F/D/V

– Carlo C. Maley, Ph.D. Assistant Professor The Wistar Institute 3601 Spruce St. Philadelphia, PA 19104

fax: 206-667-6132 cell: 206-355-7425

http://www.wistar.upenn.edu/research_facilities/-maley/research.htm cmaley@fhcrc.org

RoscoffFrance MarineInvertEvol

MARINE GENOMICS EUROPE FP6 Network of Excellence funded by the European Commission

Postdoctoral fellowship in molecular identification of marine invertebrate larvae

A 2-year postdoctoral fellowship funded by the FP6 NoE “Marine Genomics Europe” (<http://www.sb-roscoff.fr/marine-genomics-europe>) is immediately available at the CNRS Station Biologique de Roscoff, Roscoff (<http://www.sb-roscoff.fr/>), France, in collaboration with the NERC British Antarctic Survey (BAS) (<http://www.antarctica.ac.uk>), Cambridge, UK.

Topic: To develop and apply to environmental samples in situ hybridization methods to identify single marine invertebrate larvae.

The proposed work aims at developing a method of in situ hybridization on the whole larva, focusing on molluscan larvae, to be applied to identify major species from plankton samples collected in European coastal waters. It will include sequencing, sequence analyses to select putatively diagnostic sequences, and the design of oligonucleotide probes. Designed probes will also be tested to be used in phylogenetic chips, in collaboration with BAS.

The successful candidate is expected to hold a PhD or equivalent in biology or ecology. Relevant experience in molecular biology approaches is required. Especially, experience in in situ hybridization techniques will be appreciated but not necessary. Background in marine ecology will be advantageous.

Candidates should send a letter of motivation, their CV and two letters of recommendation until 20 November 2004 to: Thierry Comtet UMR CNRS-UPMC 7127 Station Biologique Place Georges Teissier BP 74 29682 Roscoff Cedex France Tel: (+33) (0)2 98 29 23 13 Fax: (+33) (0)2 98 29 23 24 Email: comtet@sb-roscoff.fr

Any questions should be addressed to comtet@sb-roscoff.fr — Dr. Thierry Comtet Equipe Ecologie Benthique UMR 7127 CNRS/UPMC Station Biologique BP74 29682 ROSCOFF cedex France

Tel : (33) (0)2 98 29 23 13 Fax : (33) (0)2 98 29 23 24
email : comtet@sb-roscoff.fr

comtet@sb-roscoff.fr

StellenboschU AbaloneEvol

Post Doctoral position available in the Department of Genetics (4 Nov 2004)

A Post Doctoral position in biotechnology is available in the Aquaculture Division, Department of Genetics, Stellenbosch University with the project title "Genetic improvement of the abalone *Haliotis midae*."

Haliotis midae, known locally as 'perlemoen', occurs along the Western, Southern and Eastern shores of South Africa and is the only one of the six species that occurs in South Africa that is commercially exploited. *H. midae* displays a very slow growth rate, taking two to five years to reach market size. This is an obstacle in the profitable farming and global competitiveness of this species. In order to increase the productivity and the profitability of the commercial activity, a research program has been designed that makes use of the modern technology currently applied to other aquaculture species. The research program consists of four main parts: a) induction of triploidy, b) establishment of breeding programs with the assistance of genetic markers, c) generation of linkage maps and QTL identification, d) and the application of gene transfer technology.

The successful candidate will be primarily responsible for establishing gene transfer technology in the perlemoen, *Haliotis midae*. This is an extremely exciting new project that will establish a biotechnology platform for abalone in southern Africa. Furthermore, this will be the first biotechnology application of a species used for commercial application in Africa.

The position is available for 2 years

Interested researchers are requested to send their CV to Dr. Rouvay Roodt-Wilding at roodt@sun.ac.za

Closing date: 6 December 2004.

damato@sun.ac.za

UBritishColumbia Biodiversity

POSITION ANNOUNCEMENT: BIODIVERSITY RESEARCH CENTRE POST-DOC (commencing Sept. 2005)

We seek applicants for a 2-year postdoctoral fellowship in the U.B.C. Biodiversity Research Centre (www.biodiv.ca). The Centre is currently made up of over 40 members of the U.B.C. Science Faculty with interests in ecology, evolution, systematics, biodiversity and conservation. Preference will be given to candidates with bold ideas, demonstrated research ability,

and strong communication skills. The successful candidate will be expected to: conduct original research on core problems in biodiversity, foster interactions within the Centre, run a seminar series and help maintain the Centre's web site. Starting date, 1 September 2005. Salary \$40,000 p.a. Research stipend: \$7,000 p.a. Send curriculum vitae, three letters of reference, and a brief statement of goals to Dolph Schluter, Director, Biodiversity Research Centre, U.B.C., 6270 University Blvd., Vancouver, B.C., Canada V6T 1Z4. (Fax 604-822-0653, e-mail biodiversity.centre@ubc.ca). Closing date for application, 15 November 2004. The University of British Columbia hires on the basis of merit and is committed to employment equity. We encourage all qualified candidates to apply.

Ross Thompson <thompson@zoology.ubc.ca>

UCLosAngeles HumanStatGenetics

POST DOCTORAL POSITIONS IN HUMAN STATISTICAL GENOMICS AT UCLA

I am looking for two post-doctoral fellows with strong computational skills to work in population genetics/gene mapping and in cross-species studies of gene regulation. If interested, send a CV (with publication list), a research statement, any unpublished manuscripts, and three references to Chiara Sabatti at the following e-mail address:

csabatti@mednet.ucla.edu

More information on my lab, department, and university can be found on my web-page:

<http://www.genetics.ucla.edu/labs/sabatti/> Chiara Sabatti <csabatti@mednet.ucla.edu>

UCaliforniaDavis PlantPopGenet

A postdoctoral position in empirical plant population genetics is available at U.C. Irvine. The successful applicant will be expected to analyze large sequence diversity datasets from maize and its wild ancestors. There is a great deal of flexibility in the questions that can be addressed with the data, but possibilities include characterizing genomic patterns of diversity and

LD, estimating the rate of adaptive selection, examining patterns of evolution in candidate genes, assessing migration among taxa, and characterizing population structure in the wild ancestor. This position is funded by a large project funded by the NSF Plant Genome Program; information on the project can be found at www.panzea.org. The Department of Ecology and Evolutionary Biology at UC Irvine has a dynamic group of faculty in evolutionary genetics, including Professors Tony Long, Mike Clegg, Robin Bush, Francisco Ayala and Walter Fitch and others. Information about the department and the campus is available at ecoevo.bio.uci.edu. Information about the lab can be found at gautlab.bio.uci.edu

The successful applicant must have a strong background in population genetics, statistics and data analysis, with programming ability. Applications are due January 1, 2005 and the position will be open until filled. Applicants should submit a curriculum vitae and the name, address and phone number of two references to:

Dr. Brandon S. Gaut Department of Ecology and Evolutionary Biology 321 Steinhaus Hall University of California, Irvine Irvine, CA 92697-2525.

Applications or queries can also be sent to: bgaut@uci.edu.

The University of California, Irvine is an equal opportunity Employer committed to excellence through diversity.

***** Brandon S. Gaut Phone: 949 824-2564 Dept. Ecology and Evolutionary Biology FAX: 949 824-2181 321 Steinhaus Hall e-mail: bgaut@uci.edu U.C. Irvine Irvine, CA 92697-2525 *****

UCanterbury mtDNA

Postdoctoral Fellowship in Evolutionary Genetics Fixed Term for 3 years School of Biological Sciences Vacancy number: BS11711/1204A Closing Date: 1 December 2004

We are currently seeking a postdoctoral fellow with interests in genetics, genomics, and evolution to conduct research on mitochondrial DNA inheritance. Positions are available immediately for a period of 3 years.

Project Description Current dogma holds that mitochondrial DNA (mtDNA) is maternally inherited, in a

clonal form, without recombination. This is clearly untrue, but the frequency and evolutionary significance of paternal inheritance, heteroplasmy and recombination of mtDNA remain to be determined. We propose to look for evidence of paternal inheritance, heteroplasmy and recombination of mtDNA in a hatchery population of New Zealand chinook salmon (*Oncorhynchus tshawytscha*) in order to determine how great an influence these phenomena have on population and evolutionary interpretations of mtDNA data.

The Ideal Candidate The ideal candidate will possess experience in both molecular genetics and population genetics. You will be motivated and organised, with a demonstrated capacity to master the broad skill set necessary for the successful completion of a research program that will span molecular genetics, bioinformatics and biomathematics. You will be a competent laboratory worker, with experience of all routine molecular genetic techniques, particularly genotyping, sequencing and real-time PCR analyses. You should also be computer literate with experience in database management, statistical and population genetic analyses. Most importantly, you will have a desire to forge a career in research science, as witnessed by a track record of publication commensurate with your experience.

The successful applicant will join a thriving Molecular Ecology Group, which uses advanced molecular genetic technologies to elucidate complex ecological and evolutionary problems in organisms ranging from marine invertebrates to marine mammals. The group is well equipped with dedicated sequencing facilities, PCR, microbiology and genomic facilities etc. For more information on the Molecular Ecology Laboratory and the School of Biological Sciences see the web page www.biol.canterbury.ac.nz. Minimum qualifications: PhD in Genetics, Molecular Biology, Genomics, Bioinformatics or equivalent.

Remuneration: NZ\$52,000 per annum

Interested applicants are encouraged to make informal enquires to Dr. Neil Gemmell, in the first instance.

All application materials 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 Applications should include the application form, a curriculum vitae, names and addresses of three referees, university transcripts, a copy of your best paper, and a brief statement of research interests and goals.

Further details about the position are available at www.canterbury.ac.nz Dr Neil J. Gemmell Senior Lecturer in Genetics Molecular Ecology Laboratory

School of Biological Science University of Canterbury
Private Bag 4800 Christchurch, New Zealand Phone:
+ 64 (0) 3 364 2009 Fax: +64 (0) 3 364 2590
www.biol.canterbury.ac.nz/people/gemmell.shtml

UChicago Biostatistics

Hello evoldir, I have the following open position..

Biostatistician/Research Fellow

Probe level model development for oligonucleotide tiling microarrays.

Funding is available for 2+ years to develop robust tools for novel uses for tiling arrays in the department of Evolution and Ecology at the University of Chicago. Fellow will lead research and author papers relating to high density polymorphism analysis from RNA and genomic DNA hybridization data for evolutionary genomic problems. This may include improvements and extensions on Single Feature Polymorphism analysis, new gene prediction, alternative splicing, and expression level eQTL analysis, ChIP chip, and methylome analysis. Large Data sets will be generated and are available focusing on the model plant *Arabidopsis thaliana*. Experience with R/Bioconductor, low level microarray analysis, array design, HMM, empirical Bayes, linear models, experimental design, and power analysis/simulations is important. Knowledge of Quantitative genetics, population genetics, and evolutionary genetics is desired and further training will be provided.

Further information is available <http://natural-systems.org/> specifically <http://natural-systems.org/-BorevitzEckerAnnualReview.pdf>

Please email CV and short description of research experience/interests to biostat@pondside.uchicago.edu .

— Justin Borevitz Ecology and Evolution (CLSC 915E) University of Chicago 1101 E. 57th St. Chicago, IL 60637 USA (773) 702-5948 office (773) 702-3172 fax borevitz@uchicago.edu <http://naturalvariation.org>

Justin Borevitz <borevitz@uchicago.edu>

POSTDOCTORAL FELLOWSHIP IN MOLECULAR EVOLUTION AND EVOLUTIONARY GENOMICS, UNIVERSITY OF CONNECTICUT

A NASA-funded postdoctoral fellowship is available starting after January 2005 for a period of up to three years (initial appointment is for one year and renewed based on satisfactory performance) in the laboratory of J. Peter Gogarten, Department of Molecular and Cell Biology, University of Connecticut. This is a collaboration between Gogartens lab and the lab of Lutz Hamel, Computer Science and Statistics Department, University of Rhode Island to improve and develop new tools for comparative analyses of microbial genomes, and to work on deciphering the early evolution of life as provided in the molecular record.

The successful candidate should be a highly motivated individual with a Ph.D. in molecular evolution, computational biology, bioinformatics, or a related area, with programming experience, experience with phylogenetic analyses and at least working knowledge of the UNIX operating system and databases. Some background in mathematics and/or statistics is a plus.

Salary is \$35,000 plus benefits.

Send CV, key publications, a brief statement of research interests and career goals, and the names of at least two referees (or two letters of reference) to:

Prof. J. Peter Gogarten Department of Molecular and Cell Biology University of Connecticut Unit 3125, 91 North Eagleville Road Storrs CT 06269-3125 USA

Phone: (860) 486-4061 Email: bioinf@carrot.mcb.uconn.edu Web: <http://-gogarten.uconn.edu> University of Connecticut is an equal opportunity employer. This position will remain opened until filled.

***** J. Peter Gogarten Professor of Molecular and Cell Biology University of Connecticut Biology/Physics Building, Rooms 404/426/427 Unit 3125 91 North Eagleville Road Storrs CT 06269-3125 USA

Phone: 860 486 4061 (office) 860 486 1887 FAX: 860 486 4331 Email: gogarten@uconn.edu www: <http://-web.uconn.edu/gogarten>

UIdaho PlasmidEvol

UConnecticut MolEvol

Postdoctoral Position in Plasmid Evolution at the University of Idaho:

A postdoctoral position is immediately available for a period of up to two years. The postdoctoral scientist will study how broad-host-range antibiotic resistance plasmids adapt to their host during experimental evolution by characterizing plasmid-encoded genotypic and phenotypic changes (see e.g. De Gelder et al., *Genetics* Nov. 2004). The position offers the opportunity to carry out research in a dynamic and interdisciplinary research environment with excellent resources. The project is part of an NIH COBRE Center for Research on Evolutionary Processes (<http://www.sci.uidaho.edu/biosci/CRePE/index.html>), and the Initiative for Bioinformatics and Evolutionary Studies (<http://styx.ibest.uidaho.edu/ibest/index.html>). The candidate should have a Ph.D. in microbiology, molecular biology, or related discipline, a background in prokaryotic molecular biology or genetics, and the ability to work well in an interdisciplinary team. The candidate should have at least one year of experience in the use of contemporary molecular biology methods, including DNA primers design and DNA sequence analysis. A fundamental understanding of the biology of plasmids and antibiotic resistance and bacterial evolution is a plus, as well as experience with DNA sequence analysis software and statistical analyses.

For more information candidates can write to Dr. Eva M. Top, University of Idaho (evatop@uidaho.edu). Please apply via the website <http://www.hr.uidaho.edu/default.aspx?pid=34234>, send your curriculum vitae to Eva Top, and include the names and contact information of three references. The University of Idaho is an equal opportunity/affirmative action employer

Dr. Eva Top Associate Professor Department of Biological Sciences University of Idaho 347 Life Sciences South Moscow ID 83844-3051 Phone: 1-208-885-5015 Fax: 1-208-885-7905 <http://www.sci.uidaho.edu/biosci/labs/top/> <http://www.sci.uidaho.edu/biosci/labs/top/>

UIowa SexChromEvol

Postdoctoral Scholar, University of Iowa

A postdoctoral position is available on a project investigating sex chromosomes within the genus *Drosophila*. The objective is to examine the tempo of sex chro-

mosome evolution using molecular and cytological approaches within a phylogenetic context. The postdoc will participate in a study of species within the virilirepleta radiation that have chromosomal elements fused with the primary sex chromosomes. Candidates should have a record of publication that demonstrates expertise in techniques of molecular evolution, population genetics, phylogenetics, *Drosophila* genetics, and/or cytology. Appointment will be made for one year with the option of renewal for two additional years. The start date is flexible, but an early 2005 start would be ideal.

A letter of interest, curriculum vitae, representative publications, and three letters of reference should be submitted by December 1, 2004 to:

bryant-mcallister@uiowa.edu

Bryant McAllister Department of Biological Sciences
143 BB University of Iowa Iowa City, IA 52242
www.biology.uiowa.edu/mcallister/

ULeicester HumanEvolGenetics

Research Associate Bioinformatic Analysis of Human Genetic Diversity Data

Department of Genetics

R&AIA scale: GBP 19,460 to 29,128 pa Available until 31 July 2009

Ref: R1502

Applications are invited for a bioinformatics Research Associate to work on a project to investigate how processes at the genome and the population levels act to pattern human genetic diversity. This is part of a five-year Wellcome Trust Senior Fellowship in Basic Biomedical Science awarded to Dr Mark Jobling. Candidates should possess a PhD in bioinformatics or statistical genetics (or equivalent experience) and experience in programming, and database creation and management. Familiarity with human molecular genetics will be an advantage.

Downloadable application forms and further particulars are available from the Personnel Office, email: personnel@le.ac.uk, www.le.ac.uk/personnel/jobs. Please note that CVs will only be accepted in support of a fully completed application form.

Informal enquiries can be made to Mark Jobling, e-mail: maj4@le.ac.uk

Closing date: 19 November 2004.

Mark A. Jobling Department of Genetics University of Leicester University Road Leicester LE1 7RH UK

tel.: +44 (0)116 252 3427/3377 fax: +44 (0)116 252 3378 email: maj4@le.ac.uk web: <http://www.le.ac.uk/-genetics/maj4/maj4.html>

UMarseille BilaterianEvol

Dear all we are a laboratory involved in the understanding of bilaterian evolution. We are looking for CNRS fellow interested in evolution to develop our lab and start new projects Information concerning our research activity are available at our web site <http://www.up.univ-mrs.fr/evol> with my best regards

– Pierre Pontarotti EA 3781 EGEE (Evolution Génome Environnement) Université d'Aix Marseille I Centre St Charles 3 Place Victor Hugo 13331 Marseille Cedex 3 33491106489 <http://www.up.univ-mrs.fr/evol>
We organize the 8th Evolutionary Biology Meeting at Marseille <http://www.up.univ-mrs.fr/evol/congres/pierre.pontarotti@up.univ-mrs.fr>

UOulu FishParasiteEvol

Post doc position in Department of Biology, University of Oulu

“Reproductive biology of monogenean flatworm parasite *Gyrodactylus salaris* on susceptible and tolerant salmon host populations”

We have characterized *Gyrodactylus salaris* as a native and rather harmless parasite in some populations of *Salmo salar* (Lake Onega, the Baltic Sea), while it is highly pathogenic in some other populations (Norway, the White Sea). The field observations indicate that the tolerant salmon host transmits strong negative interference between parasite clones. Mitochondrial DNA has been used as a marker of the clones, but the conclusions need confirmation by nuclear DNA. The details of the reproductive biology of the parasite are not well understood, and comparative studies with other *Gyrodactylus* species will be supported & encouraged.

The task of the post doc will be

1) to develop nuclear DNA markers for *Gyrodactylus*, in particular *G. salaris*, 2) to study the clonal structure of parasites among tolerant and susceptible host populations, and 3) to describe the reproductive biology of the parasite, with emphasis of population genetic and evolutionary consequences 4) to collaborate with the team members who try to characterize properties of tolerant and susceptible salmon.

Recent publications from this project are visible or available on our web site

<http://cc.oulu.fi/~jlumme/> These include papers in *Evolution*, *Int. J. Parasitol.*, *Systematic Parasitology* and *Parasitology*. We have a good background in general phylogeography of North-Eastern Europe.

>From the list of publications you can see that we work in intensive collaboration with Professor Craig Primmer (University of Turku) and with Russian colleagues, thus having access to numerous salmon populations, both susceptible and tolerant.

The environment in University of Oulu is supportive for research in population genetics and evolution. Professor Pekka Pamilo and Professor Outi Savolainen run a national top unit of population genetics.

The position in question is granted from Finnish Academy, and it is planned for a period of two years, starting as soon as possible in 2005.

Jaakko Lumme

Jaakko.Lumme@oulu.fi

Dr. Laura Kvist Docent in molecular ecology and -evolution Department of Biology University of Oulu Linnanmaa 90014-Oulu Finland e-mail laura.kvist@oulu.fi / laura.kvist@csc.fi phone: +358-8-5531802 fax: +358-8-5531061

lkvist@sun3.oulu.fi

UStAndrews EvolBiol

This is a resubmission of an earlier listing that was scrambled due to an apparent email incompatibility.

Postdoctoral position in Plant Evolution Lab of Prof Thomas Meagher School of Biology & Centre for Evo-

lution, Genes & Genomics University of St Andrews

Salary - 19,460 - 23,643 pa pro rata

This 7 month post, which is in the final year of a NERC Environmental Genomics funded project entitled 'Genomic analysis of the relationship between repetitive DNA and phenotypic evolution' is available. The overall aim of this project is to develop and apply methods for quantifying the occurrence of various repetitive DNA in the *Silene* genome and explore the relationship between repetitive DNA, overall nuclear DNA content, and flower size. Techniques involved include flow cytometry and in situ hybridisation analysis. There is also potential for collegial interaction with adjacent labs working on phylogenetic analysis, speciation, and quantitative genetics (including QTL analysis). You should have a PhD and a solid grounding in plant evolutionary biology.

Informal enquiries to Professor Thomas Meagher, Tel: +44 (0) 1334 463364, Fax: +44 (0) 1334 463364, Email: trm3@st-and.ac.uk. Further details about the Meagher lab and the Centre for Evolution, Genes & Genomics from <http://tiree.st-and.ac.uk/-cegg/indexFlash.html> Further details about the NERC program in Environmental Genomics from <http://www.nerc.ac.uk/funding/thematics/envgen/>

Please quote ref: SK85/04 Closing Date: 22 November 2004

Application forms and further particulars are available from <http://www.st-andrews.ac.uk/hr/recruitment/-vacancies> or from Human Resources, University of St Andrews, College Gate, North Street, St Andrews, Fife KY16 9AJ, (tel: 01334 462571, by fax 01334 462570 or by e-mail Jobline@st-andrews.ac.uk).

The University is committed to equality of opportunity.

Professor Thomas R. Meagher Division of Environmental and Evolutionary Biology, School of Biology University of St Andrews St Andrews KY16 9TH UK +44(0)1334 463364 phone +44(0)1334 463366 fax trm3@st-and.ac.uk <http://www.st-and.ac.uk/~hmbldg/meagher.html>

Salary - 19,460 - 23,643 pa pro rata This 7 month post, which is in the final year of a NERC Environmental Genomics funded project entitled 'Genomic analysis of the relationship between repetitive DNA and phenotypic evolution' is available. The overall aim of this project is to develop and apply methods for quantifying the occurrence of various repetitive DNA in the *Silene* genome and explore the relationship between repetitive DNA, overall nuclear DNA content, and flower size. Techniques involved include flow cytometry and in situ hybridisation analysis. There is also potential for collegial interaction with adjacent labs working on phylogenetic analysis, speciation, and quantitative genetics (including QTL analysis). You should have a PhD and a solid grounding in plant evolutionary biology.

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UStAndrews PlantEvol

Postdoctoral position in Plant Evolution Lab of Prof Thomas Meagher School of Biology & Centre for Evolution, Genes & Genomics University of St Andrews

UTexasAustin FishHybridization

A 1-year postdoctoral research position is available at the University of Texas at Austin to work on a study of post-zygotic isolation in a family of North American freshwater fishes, Centrarchidae. The position is full-time and is anticipated to start in winter or early

spring 2005. It may be extended depending on availability of funding. The project seeks to understand the relative importance of different forms of reproductive isolation, and test for breakdown in sex determination in hybrids. The technician will be responsible for collecting live specimens in the field, maintaining fish in the laboratory, carrying out artificial hybridization experiments, and conducting molecular genetic analyses of hybrid progeny.

Candidates must have a Ph.D in evolution or a closely related field, and familiarity with molecular genetic techniques including AFLPs and microsatellites. Experience with field collection techniques for fish, and artificial fertilization techniques, is desirable.

Salary will start at \$30,000 per year plus health benefits.

Interested applicants should send: 1) a brief letter outlining their background, research interests, and long-term goals; 2) a CV; 3) up to three reprints, 4) names and addresses (including telephone number and email addresses) of three references, to:

Dr. Dan Bolnick Section of Integrative Biology, One University Station C0930 University of Texas at Austin Austin, TX 78704 (512) 289-7455

Informal inquiries are welcome and should be directed to Dan Bolnick at danbolnick@mail.utexas.edu

Applications will be reviewed starting December 6, until a suitable candidate is found. The hiring decision will be made no later than January 1. The University of Texas is an EOAA Institution committed to cultural diversity and compliance with the ADA.

Daniel Bolnick <danbolnick@mail.utexas.edu>

Uppsala 2 QuantGenetics

TWO POSTDOCTORAL POSITIONS: QUANTITATIVE GENETICS and COMPUTATIONAL GENOMICS

Linnaeus Centre for Bioinformatics, Biomedical Center, Uppsala University, Uppsala, Sweden.

Two postdoctoral positions are currently available with flexible start dates, funded by the Wallenberg Foundation. Both positions are guaranteed for one year with possible extension of an additional year. We seek independent and motivated individuals to participate in ongoing research projects in two areas:

1) [job code QG] Genetic dissection of multifactorial traits. Applicants are invited to join an ongoing research project focusing on development of analytical methods for mapping of Quantitative Trait Loci (QTL) in the group of Örjan Carlborg. Ongoing research projects include further development of existing bioinformatic tools to identify QTL in experimental crosses using standard genetic models, but also using models including imprinting and epistasis. The project also provides opportunities to collaborate with experimental groups at the Department of Medical Biochemistry and Microbiology (<http://www.imbim.uu.se>), including Professor Leif Andersson working on genetic dissection of multifactorial traits in model organisms. Applicants should have a Ph.D. in genetics, statistics, animal science, bioinformatics, computer science, or a related field, programming skills in UNIX and FORTRAN or C++, and have experience in at least two of the following: statistics, quantitative genetics, and scientific computing. Knowledge of QTL mapping, linkage mapping or genetic association studies is a plus.

2) [job code CG] Correlates of translational selection in prokaryotic genomes. We invite applicants to join an ongoing research project investigating the effects of translational selection for growth and survivorship on prokaryotic genomes, in the group of David Ardell. Research projects include further development and application of existing bioinformatic tools to completely map tRNA and ribosomal operons in completed bacterial and archaeal genomes, model and predict their promoters and associated regulatory sequences, and the statistical and evolutionary comparative analysis of these data in combination with i) associated codon usage patterns ii) tRNA expression data, and iii) amino acid biosynthetic pathways. The project provides the opportunity of collaboration with experimental groups at the Department of Cell and Molecular Biology (<http://www.icm.uu.se>), including Professors Leif A. Kirsebom and Santanu Dasgupta working on the molecular biology and genetics of tRNA expression and processing. Applicants should have a Ph.D. in biology, genetics, bioinformatics, computer science, or a related field, programming skills in UNIX and Perl or Java, and have some experience with biostatistics, genomics, and evolution. Knowledge of the physiology and genetics of translation is a plus.

The Linnaeus Centre for Bioinformatics offers a superb interdisciplinary working environment located at the heart of biomedical research at Uppsala University. Access is available to the Swedish national supercomputing center. Uppsala is located 40 minutes north of Stockholm by train, 20 minutes from Stockholm's international airport. The positions come with full benefits

of employees of the University.

Please submit your CV, a letter describing your research interests and skills, relevant reprints, and contact information for three references. Send all materials by email to:

qg-app@lcb.uu.se (for Quantitative Genetics position)
tRNA-app@lcb.uu.se (for Computational Genomics position)

or by mail to: Linnaeus Centre for Bioinformatics
ATTN: Job Code QG (for Quantitative Genetics position) or ATTN; Job Code CG (for Computational Genomics position) Box 598, Biomedical Center SE- 751 24 Uppsala, Sweden.

For more information, please visit <http://www.lcb.uu.se> and contact Örjan Carlborg (qg@lcb.uu.se, 46 (0) 18 471 6691) or David Ardell (tRNA@lcb.uu.se, 46 (0) 18 471 6694). Screening of applicants will begin November 30, 2004 and will continue until the positions are filled.

dave.ardell@lcb.uu.se

WageningenU ExperimentalEvol

Postdoc position in experimental evolution at Wageningen University

An innovative research incentives grant from the Dutch Organisation for Scientific Research (NWO) was awarded to study the role of antimicrobial compounds and spatial structure in biodiversity. Using populations of bacteria and other microbes that adapt to simple laboratory environments, the process of adaptation has almost exclusively been studied in environments without structure, such as well-mixed batch cultures. However, in nature unstructured environments are rare. Spatially-structured environments also have fundamentally different consequences for adaptation, including the fragmentation of the population into small subpopulations, local interactions with competitors, and slower population dynamics. Recent models have shown that these consequences may be particularly relevant for adaptation by interference competition, e.g. through the production of antimicrobial compounds. The postdoc will address these and other specific consequences of spatial structure for adaptation using evolution experiments with bacteria and fungi.

Profile: We seek someone with a PhD in evolution-

ary biology, microbial ecology or microbial genetics, and experience with basic microbiological and molecular lab techniques and ecological and evolutionary theory. Modeling skills (e.g. cellular automata) are an advantage. Max. salary 3453 per month before tax.

Applications: Submit enquiries or applications (including CV, letter of motivation and names and contact info of two references) before November 19 to Arjan de Visser, arjan.devisser@wur.nl. Wageningen University is a small modern and well-equipped university in the center of the Netherlands, whose research output was top-ranked in a recent survey of Dutch universities. The Department of Genetics was ranked 4.5 (scale 0-5) in another recent international evaluation.

Dr. J. Arjan G.M. de Visser Department of Genetics Wageningen University Arboretumlaan 4 6703 BD Wageningen The Netherlands Phone: (+) 31 317 483144 Mail: arjan.devisser@wur.nl

WashingtonU EvolRegulatoryNetworks

POSTDOCTORAL POSITION AT WASHINGTON UNIVERSITY IN ST. LOUIS

Postdoctoral positions are open to conduct research in the evolution of regulatory networks in enteric bacteria. Our laboratory has been examining the mechanisms by which two-component regulatory systems respond to environmental cues to modify the gene expression patterns of bacterial species. The goals of the project are: (1) to explore the contribution that differences in gene regulation makes to phenotypic differences among closely-related bacterial species; (2) to investigate the genetic origins of regulatory interactions; (3) to study how horizontally-acquired genes become regulated by ancestral regulatory proteins; and (4) to determine the ecological consequences of different regulatory schemes.

These projects will entail the use of a multidisciplinary approach that combines bioinformatics with molecular genetics and microbiology.

Applications should include a curriculum vitae, the names and contact information for three references, and a brief statement of research interests and goals. Applications should be sent to: Eduardo A. Groisman, Howard Hughes Medical Institute, Washington University School of Medicine, Department of Molecular Microbiology, 660 S. Euclid Avenue, Campus Box

8230, St. Louis, Missouri, 63110, USA; E-mail: groisman@borcim.wustl.edu

Sincerely yours,

Eduardo –

Eduardo A. Groisman Howard Hughes Medical Institute Washington University School of Medicine Department of Molecular Microbiology Campus Box 8230 660 S. Euclid Ave. St. Louis, MO 63110-1093

of: (314) 362-3692 lab: (314) 362-3691 fax: (314) 747-8228 e-mail: groisman@borcim.wustl.edu

WesternKentuckyU MolSystematics

INSECT MOLECULAR COLEOPTERA SYSTEMATIST

WESTERN KENTUCKY UNIVERSITY

A two-year NSF funded post-doctoral scientist position is available to conduct molecular phylogenetic studies on the evolution of Coleoptera. Possible projects include research on the Bostrichoidea and Scarabaeinae as well as a group chosen by the successful applicant. This work is in conjunction with biodiversity research

currently being conducted in Ghana, West Africa.

Required qualifications include experience with the collection and analysis of molecular sequence data and excellent communication skills.

Facilities include a Biotechnology Center and additional laboratory space in a newly completed research building. The Center and the Biology Department may be explored online at <http://bioweb.wku.edu>. Please send cover letter, CV and contact information for three references via email to Keith.Philips@wku.edu or through snail mail to:

Dr. Keith Philips,

Department of Biology,

Western Kentucky University,

Bowling Green, KY 42101-3576

270-745-3419

Review of applications begins 1 Jan. 2005 and will continue until the position is filled. Starting date is negotiable. Competitive salary and excellent benefits are offered.

Western Kentucky University is an AA-EOE institution. All qualified individuals are encouraged to apply including women, minorities, persons with disabilities and disabled veterans.

Keith.Philips@wku.edu

Instructions

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