
E v o l D i r

September 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.

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Marseille 8thEuropean

The 8 th evolutionary biology meeting's program is now available on the site www.up.univ-mrs.fr/evol/congres Posters are accepted untill september 1st Best regards
Axelle Pontarotti

Association pour l'Etude de l'Evolution Biologique Université Aix Marseille I case 19, 3 place Victor Hugo 13331 Marseille Cedex 03 France

congres_evolution@hotmail.com

Marseilles EvolBiol Sep22-24 2

Association pour l'étude de l'évolution biologique. Université Aix-Marseille I centre Saint Charles Laboratoire EGEE (Evolution, Génome, Environnement) 3 place Victor Hugo 13331 Marseille cedex 03 FRANCE

Dear colleagues, I inform you that the definitive scientific program of the 8th evolutionary biology meeting at Marseilles as well as the social events are now available on <http://www.up.univ-mrs.fr/evol/congres/> . Moreover, we exceptionally still accept a few inscription for posters. If you were interested, please send us an abstract and register directly on the meeting web site. Best regards,

Pierre Pontarotti. congres_evolution@hotmail.com

SandbjergDenmark EvolStress Aug22-26 3

Due to late withdrawl we have still 3 to 4 places vacant for the ESEB sponsored workshop on environmental stress, adaptation and evolution, Aug. 22-26, Sandbjerg, Denmark; for further information on the symposium see below; if you are interested to attend, send asap an email to Corneel with cc to Kuke and me (for email addresses see below); if you want to give an oral presentation, also send an abstract; we will accept on first come first served basis to fill the last spots. kind regards Kuke and Volker

Symposium:

Progress in Environmental Stress, Adaptation and Evolution

August 22-26, 2004 at Sandbjerg, Denmark

Sponsors:

European Society of Evolutionary Biology (ESEB)

Faculty of Sciences and Center for Environmental Stress Research, University of Aarhus (DK)

Aim:

Most organisms and populations have to cope with hostile environments, threatening their existence. Their ability to respond phenotypically and genetically to these challenges and to evolve adaptive mechanisms is, therefore, crucial. The aim of the symposium is to understand, from an evolutionary perspective, the impact of stress on biological systems. We have invited speakers that at different organizational levels, from genes

to individuals and populations, explore how organisms adapt to (extreme) environments genetically and physiologically, how stress changes genetic structure and affects life histories and how environmental and genetic stress shape selection pressure and causes extinction of populations.

These issues have already been dealt with in a symposium on stress and evolution during the 5th International Congress of Evolutionary Biology and Systematics in Budapest (1966), and in the end resulted in a book edited by us Environmental Stress, Adaptation and Evolution (1997) published in the Birkhäuser EXS series (EXS 83). It is now nearly ten years later and knowledge and (genomic) techniques in this research field have progressed rapidly. Therefore, we are thinking a follow-up to be timely and are organising this small, 3 day symposium on the same issues

Structure:

The number of participants will be limited to around 50, of which 15 are reserved for invited speakers (for list see below). There will be room for maximal 40 presentations of which 25 are open for contributed talks (25 min.). In conjunction with the symposium a special thematic issue of the Journal of Evolutionary Biology will be published on the topic that will contain high quality papers by the invited speakers. In addition, it will be possible for contributed papers to be included in this special issue of JEB. This will ensure that the papers get lots of exposure in this thematic setting. Papers for the special issue will be selected by the organisers of the symposium and the chief editor of JEB, Juha Merila. Mind that all manuscripts, including those of the invited speakers, will not be treated favourably for this special issue. They are subject to normal, rigorous peer-review and scope limits of the journal: they have to address important evolutionary, and not purely functional, problems.

Participation:

Those that are interested in the symposium topic and want to participate and/or present a paper are kindly invited to contact the organisers from now on. Please do send your application asap to Corneel Vermeulen (<<mailto:c.j.vermeulen@biol.rug.nl>> c.j.vermeulen@biol.rug.nl) who will collect and structure applications (but for safety do send also a cc to both Volker Loeschcke (<<mailto:volker.loeschcke@biology.au.dk>> volker.loeschcke@biology.au.dk) and Kuke Bijlsma (<<mailto:r.bijlsma@biol.rug.nl>> r.bijlsma@biol.rug.nl)). As we, in addition to the invited speakers, can only accommodate around 35 participants, the symposium might easily become over-

booked. If this is the case the organisers will select participants and contributions that seem to fit that symposium and the special volume of JEB the best. Therefore it is important that tentative participants provide a few lines about their research interests, and if they want to present a contribution, please provide also a title and a substantial abstract (up to 200 words). Membership of ESEB is not prerequisite, but gives a discount of the conference fee and might give some priority.

Practical information:

Title: Progress in Environmental Stress, Adaptation and Evolution

Date: August 22-26, 2004

Organisers: Volker Loeschcke, Dept. of Ecology and Genetics, University of Aarhus (DK)

Kuke Bijlsma, Evolutionary Genetics, University of Groningen (NL)

Place: Sandbjerg Manor House, in the south of Jutland, Denmark. This is a conference centre of the University of Aarhus in a very nice and rural setting, easily reached by train and plane. For info see:

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

SwannanoaNC SEEPAGE Sep10-12

2nd Announcement

SEEPAGE, 2004 (Southeastern Ecology, Population Genetics, and Evolution) Swannanoa, North Carolina

This is a reminder that the 2004 (and 30th annual) SEEPAGE meeting, will be held on the 10th-12th of September in Swannanoa, North Carolina. SEEPAGE has a long history of providing an informal atmosphere for the presentation and discussion of research in ecology, evolution, and genetics. SEEPAGE is a great place for graduate students to present their thesis research and we encourage attendance and talks by students.

More information and registration details can be found at <http://salamander.uky.edu/SEEPAGE/> Deadline for early registration is 8-31-04

David Weisrock, Ph.D. University of Kentucky

T. H. Morgan School of Biological Sciences
<http://salamander.uky.edu> David Weisrock
 <weisrock@uky.edu>

UArizona DrosophilaCompGenomics Oct30-31

DROSOPHILA COMPARATIVE GENOMICS:
 Progress and Prospects Symposium - October 30 and
 31, 2004 Hosted by the Tucson Drosophila Species
 Stock Center and the Institute for Biomedical Sciences
 and Biotechnology University of Arizona Tucson

The symposium-workshop will begin with a 6:00PM
 dinner at the Arizona Sonoran Desert Museum and
 guest presentation on Saturday night, October 30, and
 end on Sunday, October 31, at 5:00PM. The event has
 two goals:

(1) to inform the community about the progress of
 the genome sequencing projects for twelve Drosophila
 species and the development of related resources such
 as BAC libraries and living stocks; (2) to engage mem-
 bers of the Drosophila community, including represen-
 tatives from the sequencing, BAC, and genome analysis
 centers as well as computational and experimental bi-
 ologists, in synthetic discussions focused upon the uses

of these new resources to address questions of interest.
 Sunday's program will have four components: 1. Sta-
 tus report of the sequencing and BAC projects for all
 twelve species, including assembly, annotation and dis-
 semination of information 2. Presentation of genetic
 and chromosome maps of the twelve species and issues
 of synteny: what we know and what needs to be done
 next? 3. Comparative functional genomics and gene
 expression: What we know and what comes next? 4.
 Open forum regarding how to best make these resources
 useful to the community and what new resources should
 be developed.

The registration fee of \$150 includes the Saturday night
 dinner, attendance at the symposium on Sunday, in-
 cluding morning and afternoon refreshments. Space is
 limited. Persons interested in attending should con-
 tact Sharon Richards, Center for Insect Science at in-
 sects@arl.arizona.edu. The symposium itself will be
 held at the Marriott Hotel University Park in Tucson
 where rooms have been reserved for symposium atten-
 dees.

Therese Ann Markow Regents' Professor of Ecology and
 Evolutionary Biology Director, Center for Insect Sci-
 ence University of Arizona Tucson, AZ 85721

Office: 520-621-3323 Lab: 520-626-
 2772 tmarkow@arl.arizona.edu [http://-](http://-cis.arl.arizona.edu/markow_lab/)
[cis.arl.arizona.edu/markow_lab/](http://-cis.arl.arizona.edu/markow_lab/) Teri Markow
 <tmarkow@public.arl.arizona.edu>

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Leuven FishGenomics

MARINE GENOMICS EUROPE FP6 Network of Ex-
 cellence funded by the European Commission

PhD studentship in bioinformatics and fish genomics

A 3 year PhD studentship funded by the FP6

NoE “Marine Genomics Europe” (<http://www.sb-roscoff.fr/marine-genomics-europe/MGE-PhD-announcement-KULeuven.pdf>) is available at the Laboratory of Aquatic Ecology of the Katholieke Universiteit Leuven starting 1 October 2004. Topic: analysis of EST data from seabass and seabream. Initial training in bioinformatics and programming will be provided at Bielefeld University (Prof. Folker Meyer) and advanced training in genomic analysis at NERC-British Antarctic Survey (dr. Melody Clark). You will have access to the “Marine Genomics Europe” fish EST data and in doing so will work closely with CCMAR, Univ. do Algarve, Faro (Prof. Adelino Canario). You will learn how to automatically analyse, annotate and submit EST data and prepare a database to combine the fish ESTs. Examples of analysis include: overall statistics, gene discovery/diversity ratios, gene content by tissue, gene functional content, comparative analysis of both the seabass and seabream ESTs, cluster analysis, polymorphism screening, plus comparison to publicly available data in Fugu, Zebrafish and Medaka. There will be time to follow a related project of his/her own choosing such as population SNP frequencies.

The K.U.Leuven was founded in 1325 and has a student enrollment of 28,000. Leuven (<http://www.leuven.be/>) is an historical university town with a very high and pleasant standard of living.

Candidates with a M.Sc. or equivalent in either life or engineering sciences and some training in bioinformatics, a very strong academic record, an interest in marine sciences and perfect knowledge of English (TOEFL score of at least 580), should send a letter of motivation, their CV (including course transcripts) and three letters of recommendation before 15 August 2004 to: Prof. Filip Volckaert Katholieke Universiteit Leuven Laboratory of Aquatic Ecology, Research Group on Fish Genetics Ch. de Bériotstraat 32 B-3000 Leuven, BELGIUM Phone: +32 16 32 39 72 (office) or +32 16 32 39 66 (secretariat) Fax: +32 16 32 45 75 <<mailto:filip.volckaert@bio.kuleuven.ac.be>> [Mailto:filip.volckaert@bio.kuleuven.ac.be](mailto:filip.volckaert@bio.kuleuven.ac.be)

URL: <<http://www.kuleuven.ac.be/bio/eco>> <http://www.kuleuven.ac.be/bio/eco>>

MarieCurie research network

Marie Curie Research training network (MRTN) SEX-ASEX - 10 positions available Students and researchers interested in the paradox of sex in evolutionary biology are strongly encouraged to send an expression of interest to work in the European Union Marie Curie Research Training Network SEXASEX. Criteria of eligibility include: EU citizenship, less than 4 years of research experience for Young Researchers (YR), less than 10 years for Experienced Researchers (ER), and a willingness to work in a European country other than the country of origin. We seek candidates who are enthusiastic about evolutionary biology, travelling and living abroad, learning in a multidisciplinary research environment and working in teams. All appointments will be for 3 years, YR are offered PhD positions, ER post-doc positions. YR will be expected to obtain a PhD at the end of the project. The application of female candidates is especially encouraged; detailed information on child care facilities at the different institutions will be provided upon request. Aid can be sought if accompanying spouses also require employment abroad. Project overview: Sex is the queen of evolutionary problems. It will be tackled by SEXASEX in a multidisciplinary approach, providing training and transfer of knowledge for a total of 360 person-months. 10 network researchers (6 young researchers (YR) and 4 experienced researchers (ER)) will receive training in 9 institutions across as many countries. A wide array of research tools will provide excellent training opportunities, for example through individual career development plans, individual tutoring and secondments, which will be supplemented by participation in courses and external workshops. Network-wide training will exploit the extensive experience of the partner institutions through five courses and summer schools for all network researchers. Complementary skills such as management and communication (verbal, written) will be developed, and gender awareness will be raised, in two network-wide meetings. The networks theoretical and empirical research will apply 13 major approaches, including novel genomic and karyological approaches, intraspecific phylogeography, ecology, behavioural studies, GIS analyses and theoretical modelling. With this multidisciplinary toolkit, SEXASEX will investigate why sex exists at all, given its evolutionary costs, using the model organism *Eucypris*

virens, a non-marine ostracod species with both sexual and asexual reproduction. What determines its gender, what are the genomic consequences of long-term asexuality, what is the cohesiveness of a species with mixed reproduction, how do asexuals and sexuals compete and what is their historical zoogeography? The pluralistic approach of SEXASEX is unique and timely, using highly novel methodologies and dealing with cutting edge science based on European excellence and tradition. If you are interested, please contact Dr Isa Schoen, Royal Belgian Institute of Natural Sciences, Freshwater biology, Vautierstraat 29, B-1000 Brussels, Belgium E-mail (Isa.schoen@naturalsciences.be) or fax (0032 2 62 74 113). Correspondence by email is preferred. For PhD position 2 and Postdoc position 1, a full application is asked before the 20th of September 2004. For all other positions, expressions of interest are invited. Applications or expression of interest should include a letter, a CV and addresses of two potential referees. Please state clearly in the letter which position(s) interest you, and why. If there is more than one, rank them according to your preference. The following 10 research positions will become available in the course of the network: PhD position 1: Historical biogeography of sexual and asexual reproduction in freshwater ostracods. Starting date: 1st May 2005 Duration: 36 months Salary: country-specific plus tax-free mobility allowance Persons in charge: Prof. Dr Koen Martens Dr Isa Schoen Location: Brussels, Belgium Place of work: Royal Belgian Institute of Natural Sciences, Freshwater Biology Methods to be applied: estimates of morphological variability, DNA amplification and sequencing of mitochondrial genes, phylogenetic and phylogeographic reconstructions, GIS-based mapping of haplotypes, modelling Candidate profile: B. S., M.S. or equivalent (e.g. Diploma) in Biology, Zoology, Molecular Biology, Genetics, Geography or Evolutionary Biology. Some practical experience with the involved methods or ostracods is advantageous but not necessarily required. Only persons without Belgian nationality are eligible. Ph.D. degree may be either applied for at the Faculty of Biology at the University of Ghent (or another Belgian university) or at a local university adhering to the regulations of external theses. phd position 2: Genetic divergence and isolation amongst sexual and between sexual and asexual lineages of non-marine ostracods. Starting date: 1st November 2005 Duration: 36 months (2x 18 months)

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UHawaii InsectSystematics

Position Announcement

Graduate Research Assistant in Insect Conservation, Ecology and Systematics

Period: To begin approximately January 10, 2005, for 1 year. Renewable annually for up to 3 years, contingent upon progress and availability of funds.

Duties: Assist in the assessment of the impacts of biological control introductions on non-target endemic moths in Hawaii; including assisting with the development of rigorous quantitative field experiments to determine impact of introduced parasitoids. Will be responsible for designing and conducting laboratory experiments, field trials, and other field work, on several of the Hawaiian islands in both agricultural and native forest environments

Minimum Qualifications Bachelor's degree in a biological science from an accredited university or college. Able to perform field work in rough terrain. Must be accepted in the Entomology Graduate Program (MS or PhD) at the University of Hawaii, Manoa.

Minimum Salary: \$15,558 per year MS, \$16,824 per year PhD, plus benefits and tuition waiver.

To Apply: Send letter of application and names and contact information for 3 academic references to Dr. Daniel Rubinoff, Department of Plant and Environmental Protection Sciences, University of Hawaii at Manoa, 3050 Maile Way, Gilmore 310, Honolulu, HI 96822; or by email to rubinoff@hawaii.edu

Closing Date: October 31, 2004

The University of Hawaii is an Equal Opportunity / Affirmative Action Institution

Daniel Rubinoff <rubinoff@hawaii.edu>

UWales OtterPopBiol

A PhD position is likely to be available to study otter populations in Snowdonia and Anglesey, North Wales, UK. This position is available to EU citizens

only and will involve the use of molecular genetic markers in addition to radio-tracking. The supervisors will be Dr. Chris Gliddon (UWB) and Dr. Dorian Moro (CEH & UWB). Further details can be obtained from domo@ceh.ac.uk (since Chris will be on holiday!).

Dr. Chris Gliddon School of Biological Sciences University of Wales, Bangor LL57 2UW United Kingdom

Tel: +44 (0)1248 382533 FAX: +44 (0)1248 382569 Mobile: +44 (0)7941 060423

UWyoming Martens

Ph.D. position vacancy - population genetic studies of martens

Dr. Merav Ben-David and Steven Buskirk, Department of Zoology and Physiology, University of Wyoming, are seeking a Ph.D. student with an M.S. in biological sciences to conduct a study of the population genetic responses of the American marten to insularity and habitat fragmentation in western North America. The study will population genetic structure of martens in relation to taxon, island-mainland location, and fragmentation of habitat. The study are will include, but not be limited to Alexander Archipelago of Southeast Alaska and adjacent island groups. Field studies may be included as well. Interested individuals should contact one of us.

Steven Buskirk <Marten@uwyo.edu>

UnivKwaZulu-Natal Micros

2 MSc Studentships: Genetic markers to tackle illegal trade in wildlife

2 MSc studentships are available (eligible to South African Nationals only) at the University of KwaZulu-Natal, Pietermaritzburg, South African.

The aim of the studentships are to develop microsatellite markers for two species identified as currently threatened by the illegal trade (Cape Parrot and Blue Crane). The two students will be based at the University of KwaZulu-Natal, Pietermaritzburg but will spend up to 6 months at the University of Sheffield in the UK learning the techniques required to develop microsatellites. Returning to the University of KwaZulu-Natal, Pietermaritzburg, to analyse and apply the markers. The illegal trade in wildlife threatens a number of South Africa's species. It is often difficult for the authorities to provide the conclusive evidence, required for successful prosecutions, to prove an animal has been illegally removed from the wild. Genetic techniques offer the potential for conclusive evidence to be provided to assist such prosecutions.

Applications are invited from suitably qualified South African students. Applicants should hold a good honours degree, ideally have studied molecular and population genetics theory at undergraduate level and have had some previous experience working within a laboratory environment. Please apply electronically (if possible) forwarding a letter of motivation with a CV, statement of your research interests and experience (including subjects studied at undergrad/honours with grades and laboratory experience). Plus contact information (including email addresses) for three referees.

Please send applications and/or queries (preferably by email) to: Dr Tiawanna Taylor, School of Botany and Zoology, University of KwaZulu-Natal, Pietermaritzburg, 3209. Email: 201512493@ukzn.ac.za Fax: +27 (0) 33 260 5105

Tiawanna Taylor <TaylorT@ukzn.ac.za>

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BalboaPanama LabAdministrator

A full-time position for collaborating in research of molecular evolution and population genetics is available at the Smithsonian Tropical Research Institute (STRI), located in Balboa, Panama. The position entails the supervision of data gathering in research involving molecular markers to study ecological and evolutionary topics, including phylogeography, gene flow speciation, and the evolution of reproductive isolation in marine organisms. Specific duties include: Overseeing the collection, tabulation, and analysis of DNA sequencing and microsatellite data obtained by two technicians; supervising the technicians' daily work; orienting new pre- and post-doctoral fellows and aiding all people in the lab with molecular techniques and analysis of data; troubleshooting procedures; ensuring that there is an adequate store of supplies; keeping computers and laboratory equipment functioning; maintaining specimen and sequence databases up to date; submitting sequences to GenBank; managing the laboratory's operating budget. Candidates with a degree in biology or a related discipline are invited to apply. A background in both molecular biology and the phylogenetic and population genetic analysis of DNA data is essential. Proficiency in English is required. Knowledge of Spanish is desirable. This is a US permanent federal position at the GS-11 level. It includes generous benefits and co-authorship in publications. The selection will be made without regard to nationality, race, sex, or religious background. For more details about STRI, please consult <http://www.stri.org>. <<http://www.stri.org>. Please, submit your CV, copies of publications (if any) and the names, titles, and e-mail addresses of two people that can be contacted for letters of recommendation to: Dr. H.A. Lessios, Smithsonian Tropical Research Institute, Unit 948, APO AA 34002, e-mail: LessiosH@stri.org. Elec-

tronic submissions are preferred. The position will be available as of October 1, 2004, and the search will continue until a suitable candidate is identified.

H. A. Lessios Smithsonian Tropical Research Institute
Balboa, Panama

Telephone: +507/212-8708 Fax +507/212-8791 Telephone from the US (domestic call): 202/786-2099 x 8708

Mail address: >From the USA: Unit 948 APO AA 34002-9948

>From elsewhere: Box 2072 Balboa, Panama

lessiosh@stri.org

CaliforniaAcademy GeneticTech

Molecular Evolution Laboratory Technician (Molecular Biology), California Academy of Sciences, San Francisco

This one-year position will provide research and analytical support for molecular genetics research on the lowland phylogeography of New Guinea birds. The position is in the Osher Molecular Genetics Laboratory, California Academy of Sciences, located in downtown San Francisco. The technician will conduct laboratory procedures including isolation of DNA from tissues, set-up and running of polymerase chain reactions (PCR), DNA sequencing, sequence editing and alignment, and assisting with analyses of phylogeography. The technician will enter data into computer databases, and assist with running and loading an ABI 3100 Genetic Analyzer, general lab maintenance, preparation of solutions, inventory and stocking of general lab supplies. The technician will be required to attend meetings of laboratory staff. The position requires at least a bach-

elor's degree in a biological or chemical science and experience in basic DNA and laboratory methods.

Our lab is a small genetics lab with PIs from multiple fields, including botany, invertebrate zoology, entomology, herpetology, and ornithology. Most active projects involve molecular systematics and taxonomy, and focal taxa come from around the globe. This would be an ideal position for someone considering graduate school in evolutionary biology and who would like additional laboratory experience. San Francisco is a vibrant city with many scientific and cultural opportunities, and the California Academy of Sciences is centrally located in the Bay Area.

For more information, contact John Dumbacher, Curator and Department Chair, at jdumbacher@calacademy.org, Department of Birds and Mammals, California Academy of Sciences, 875 Howard Street, San Francisco, CA 94103. To apply, send curriculum vitae, statement of interests, and at least two letters of recommendation, preferably by email. Please submit application materials by 1 September 2004. Applications will be reviewed beginning 1 September. The position will be filled as soon after September 1st as possible.

ClarksonU EvolBiol

The Biology Department at Clarkson University is seeking applicants for a tenure-track faculty position in 2005. The successful candidate will possess a Ph.D. and postdoctoral experience, be committed to excellence in undergraduate teaching, and maintain an active externally-funded research program. Teaching and research in the area of evolution, molecular biology, and bioinformatics would complement our interdisciplinary programs emphasizing health, environmental, and biomolecular science. Candidates with expertise in the area of immunology and microbiology will also be considered. Clarkson is a small private university with a mission focused on technology serving humanity. Potsdam is an educational and cultural center in northern New York and is located within two hours of Montreal, Ottawa, Lake Placid, and the Adirondack Park. Applicants should submit curriculum vitae, research and teaching statements, sample reprints and three letters of reference to: Dr. Edward Moczydlowski, Chair, Biology Search Committee, Department of Biology, Clarkson University, Potsdam, NY 13699-5805. All applications received before October 31, 2004, will receive

full consideration. POS#14-04. Clarkson is an Equal Opportunity/Affirmative Action Employer.

ImperialCollege LabTech

Imperial College London Department of Biological Sciences

Molecular Systematics Laboratory Technician

The Molecular Systematics Laboratory based at the Natural History Museum, London, requires a full-time research technician. The successful candidate will be conducting DNA sequencing and assisting in the maintenance of a specimen-tissue database.

Your responsibility will be to provide primary support for a Biotechnology and Biological Sciences Research Council-funded project sequencing insects from Madagascar. The team in this diverse laboratory consists of undergraduate and postgraduate students, post-doctoral researchers and visiting researchers. Routine duties include DNA extraction and purification, large-scale PCR and sequencing using a robotic workstation. You will be required to assist with the maintenance of a comprehensive specimen-tissue-sequence database, help maintain supplies and equipment, occasionally train students and staff in laboratory procedures and equipment operation and also provide regular briefings to the team.

The position will be for up to 18 months and the salary will be £18,908 to £21,541 Level 2B on Technical Services Job Family.

You will have a BSc. or MSc. in biology, genetics, or a related field, and experience with databasing, specimen preparation and storage experience, molecular biology techniques including PCR and sequencing.

The Imperial College Application form can be downloaded from <http://www.imperial.ac.uk/-employment/academicform.htm> and should be accompanied by a copy of your CV.

Completed applications should be sent to Dr. Alfried P. Vogler, Department of Entomology, The Natural History Museum, Cromwell Road, London, SW7 5BD, U.K., or by email to a.vogler@imperial.ac.uk.

Closing date: 17 September 2004

Valuing diversity and committed to equality of oppor-

tunity

m.monaghan@nhm.ac.uk

“m.monaghan@nhm.ac.uk”

<m.monaghan@nhm.ac.uk>

LeidenU Phycologist

SYSTEMATIC PHYCOLOGIST (tenure track) Vacancy number: 4-169

The candidate should have a PhD degree and subsequent experience in the taxonomy and molecular systematics of algae, an excellent publication record, and knowledge of herbarium curation. The candidate should also have experience in integrating molecular data into traditional systematics. The establishment of an active research program and pursuit of external funding is part of the job requirements. A strong commitment to the teaching of undergraduate and graduate students is mandatory. Supervision of the molecular research of PhD and MSc students working on higher plants and macrofungi will also belong to the tasks of the successful candidate. The ability to speak Dutch or the willingness to learn Dutch is required.

Salary in the first two years ranging from EURO 2179,- / 3344,- per month depending on experience. The tenure track formula implies that following a probationary period of two years, a further three year contract with adapted salary scale will lead to tenure if all task elements of the job descriptions are successfully fulfilled.

Please send your application, stating research interests and specific research goals/targets (the research goals should fit into the general mission statement and research programme of the NHN and PCNE (see our website at www.nationaalherbarium.nl), a CV and the names of 3 references to: Prof. dr. P. Baas, Einsteinweg 2, room A216, 2333 CC Leiden The Netherlands or <mailto:BAAS@NHN.leidenuniv.nl>

publicatiedatum WEB: 26-7-2004 closing date: 1 September 2004

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Joe Zuccarello <zuccarello@nhn.leidenuniv.nl>

SyracuseU EvolBiocomplexity

ECOLOGIST. – The Department of Biology at Syracuse University invites applications for a tenure-track position (Assistant to Full Professor) to be filled by August 2005. The successful candidate will have, or will develop, a strong, extramurally funded and highly innovative research program in ecology to join an emerging interdisciplinary research group in biocomplexity. The successful candidate will be one who uses terrestrial or aquatic systems to investigate questions related to plant ecophysiology, plant ecology, microbial ecology, trophic interactions, or ecosystem dynamics. Successful applicants will complement current research strengths within the department and university related to functioning of complex biological systems in different environments. The Department and the University place a high priority on effective teaching. Successful candidates will be expected to teach at undergraduate and graduate levels.

Successful candidates will join a highly productive faculty with strong links to other programs at Syracuse University, including engineering, environmental policy, biochemistry and earth sciences. The Department is in the midst of an exciting growth period, having hired seven new faculty in the past four years. We anticipate hiring six-ten more new faculty over the next five years. Specific information about individual Biology faculty research programs may be found on our website:

<http://biology.syr.edu/facultyresearch/facultyresearch.html>

The Syracuse biocomplexity group also has close intellectual ties to more than 60 other faculty at several other universities including the nearby State University of New York Environmental Science and Forestry school (SUNY-ESF) and Cornell University. Collaborations among the faculty in this group would allow successful applicants to explore several new interdisciplinary funding initiatives at NSF, including NSF's Biocomplexity Initiative, Emerging Frontiers, and Biology & Mathematics programs.

Applicants should forward a curriculum vitae, a description of past research accomplishments, a clearly focused description of his/her proposed future research goals and a statement of teaching interests. We also request that applicants have at least three letters of reference sent. Please include the name, address, phone number and e-mail address of each of your references.

We invite applicants to submit materials electronically as a single PDF file to: biosearch@cas.syr.edu. The position will be open until filled, but to be assured your application receives full consideration, we urge that you arrange to have all necessary materials to us by October 15, 2004.

Applications and reference letters should be addressed to:

Larry Wolf, Chair, Biocomplexity Faculty Search Department of Biology 130 College Place Syracuse University Syracuse, NY 13244

Syracuse University is an affirmative action/equal opportunity employer with a strong commitment to equality of opportunity and a diverse workforce.

TexasAM EvolBiol

Dear Evoldir Members,

I would like to draw your attention to the job advertisement below (faculty positions in Biology at Texas A&M University), which recently appeared in Science. We expect to make multiple hires from this search, and at least one of them will probably be in evolutionary biology. The hires are part of a major, ongoing expansion of the department, and the infusion of new faculty makes the academic environment in Biology particularly exciting right now. Also, Texas A&M is a great place to study evolution, because a fairly large number of individuals housed in multiple academic departments on campus are interested in evolutionary issues.

Best wishes, Adam G. Jones

Faculty Positions in Biology Texas A&M University

The Department of Biology at Texas A&M University (TAMU) invites applications for faculty positions at the ASSISTANT PROFESSOR level. However, prominent scientists at other academic levels will be given full consideration.

We are particularly interested in outstanding scientists who will enhance our existing programs in Circadian Clocks and Sleep, Cell and Developmental Biology, Evolution, Microbial Genetics and Genomics, Plant Biology, and Neuroscience. We strongly encourage applications from candidates who will increase the exposure of our students to a diverse culture.

The successful candidates will be expected to maintain a vigorous externally funded research program and to

contribute to the teaching of undergraduate and graduate students. We offer a highly interactive research environment, a strong modern infrastructure, and a competitive startup package. More information about our department can be found at www.bio.tamu.edu. Applicants should send a letter of application, curriculum vitae, statement of research and teaching interests, and three letters of recommendation by September 15, 2004 to:

Biology Faculty Search Committee Department of Biology Texas A&M University 3258 TAMU College Station, TX 77843-3258

If you have questions about this search, please direct e-mails to Ms. Lieu Jean, Assistant to the Head, at ljean@bio.tamu.edu

Texas A&M University is an Equal Opportunity Employer and has a policy of being responsive to the needs of dual-career couples.

ajones@mail.bio.tamu.edu ajones@mail.bio.tamu.edu

UArkansas EvolEcologist

ECOLOGIST - The Department of Biological Sciences at the University of Arkansas announces a tenure-track opening at the Assistant level to start 15 August 2005. We seek candidates whose research and teaching expertise focuses on ecology/environmental biology. Examples of relevant areas include but are not limited to biogeochemistry, conservation biology and landscape/ecosystem ecology. Possible areas of specialization include biological invasions, the effects of elevated CO₂, land use change, or nutrient cycling. The successful applicant is expected to establish an externally funded research program and to be actively committed to teaching at both the undergraduate and graduate level.

The University has state of the art facilities to support environmental research including the University of Arkansas Stable Isotope Laboratory (UASIL: <http://www.uark.edu/ua/isotope>) and the Center for Advanced Spatial Technologies (CAST: www.cast.uark.edu), a GIS and remote sensing facility. The University has doctoral programs in Biology, Environmental Dynamics, and Cellular and Molecular Biology. The candidate will be expected to contribute to the development and the strengthening of these programs and to have an active research laboratory sup-

ported by extramural grants. Applicants must have a Ph.D., and postdoctoral (or equivalent professional) experience is preferred.

Please send a statement of research and teaching interests and goals, curriculum vitae, and three letters of reference to Dr. Cindy Sagers, Chair, Ecology Search, Department of Biological Sciences, University of Arkansas, Fayetteville, AR 72701. For further information, visit the Biological Sciences website at: <http://biology.uark.edu/bisc.html>, or contact C. Sagers at csagers@uark.edu, or (479) 575-7195. Target date for receipt of applications is 15 October, 2004, but applications will be reviewed until the position is filled.

The University of Arkansas is an Affirmative Action, Equal Opportunity, Title IX employer. Women and minorities are encouraged to apply.

csagers@uark.edu

UArkansas ResAssist

A research technician position is available at the University of Arkansas for medical Sciences (UAMS), Department of Obstetrics and Gynecology. Continuation of employment is dependent upon program/operational needs, satisfactory work performance, and availability of funds.

Applicant must have a MS degree or a B.S. honor degree with laboratory experience, and broad experience in molecular, histological and cellular techniques. Salary: 30-35K pa. Ideal Qualifications: Six to twelve (6-12) months of research experience in cell culture, immunohistochemistry, Western blotting, Northern blotting, RT-PCR situ hybridization and cDNA library construction. Other routine duties: Assist in ordering, purchasing and inventory of supplies, maintaining and replenishing chemical solutions for routine use, DNA & RNA extraction and qualification, genetic analyses using Polymerase Chain Reaction (PCR), gel electrophoresis, computer-based data analyses, and summarizing laboratory data for reports.

Minimum Qualifications: Basic knowledge in the principles of molecular genetics, including but not limited to, a working knowledge of computer programs used for DNA sequence analysis. Able to organize and complete multiple laboratory procedures on a daily basis. Able to safely handle chemicals and work with high attention to detail for completion and verification of laboratory

procedures. Willingness to assist in routine laboratory functions, including ordering and inventory of supplies, and maintenance of laboratory equipment. Ability to maintain and update databases for records and data storage. Able to successfully perform multi-task duties as described. If interested, please contact:

Stephen Tsoi, Ph.D. Assistant Professor Department of Obstetrics and Gynecology College of Medicine University of Arkansas for Medical Sciences (Office) 501-526-7679 Application deadline: Review of applications will begin now and continue until the position is filled. Send CV, cover letter including personal details, narrative of your qualifications for position and salary history; names, phone numbers and addresses of two supervisory references to stsoi@uams.edu

Tsoi Stephen <cmtsoi@yahoo.com>

ULausanne Bioinformatics

The Faculty of Biology and Medicine of the University of Lausanne invites applications for the position of

Assistant Professor (tenure track) Or Associate Professor (tenured) in bioinformatics

As part of the vigorous development of the life sciences and in parallel with the creation of the Center for Integrative Genomics at the University of Lausanne, we offer a full-time position in bioinformatics starting in Autumn 2005. Candidates should have demonstrated their potential to develop an innovative research program in bioinformatics with a strong interest in biological or medical applications. Specific research areas include genomics, molecular sequence analysis, molecular evolution, protein structure, gene expression, network analysis, computational proteomics, computational genetics, or structural and functional genomics and data visualization. The successful candidate is expected to conduct an independent research program funded by external resources, to establish strong collaborations within the Faculty, and to become affiliated to the Swiss Institute of Bioinformatics. He/she will be responsible of coordinating the teaching of bioinformatics to biology and medical students at the under- and post-graduate levels. Teaching in French is required, but a period of adjustment can be granted. Specifications are listed at: <http://www.unil.ch/fbm/page2295_fr.html>www.unil.ch/fbm/page2295_fr.html. For further information, please contact Prof. J. Dubochet

(<mailto:jacques.dubochet@lau.unil.ch>)jacques.dubochet@lau.unil.ch
 Applications including a full CV, a list of publications with a copy of the 5 most relevant ones, a brief statement of the research program and teaching experiences, and at least three names of reference, should be addressed before November 15th 2004, to Prof. P. Mangin, Dean of the Faculty of Biology and Medicine, Bugnon 21, CH-1005 Lausanne. Applications from female candidates are strongly encouraged.

Prof. Jérôme GOUDET Dep. Ecology & Evolution, Biol. Building Uni. Lausanne, CH-1015 Lausanne Switzerland NEW <http://www.unil.ch/dee> <http://www.unil.ch/popgen> Tel: +41 21 692 42 42 Fax: +41 21 692 42 65 Secr:+41 21 692 42 60 NEW jerome.goudet@unil.ch

Jérôme GOUDET Dep. Ecology & Evolution, Biol. Building Uni. Lausanne, CH-1015 Lausanne Switzerland NEW <http://www.unil.ch/dee> <http://www.unil.ch/popgen> Tel: +41 21 692 42 42 Fax: +41 21 692 42 65 Secr:+41 21 692 42 60 NEW jerome.goudet@unil.ch

ULausanne TheoEvolBiol

The Department of Ecology & Evolution (University of Lausanne, Switzerland) seeks a highly motivated evolutionary biologist with a strong background in statistics and computing or a statistician/theoretician with a strong interest in evolutionary questions to lead a new research group in our department. The position is initially for 2 years, with the possibility of extension for further 4 years. The successful candidate is expected to develop an externally funded research program, and to participate to teaching in both the Msc program and 3rd year of Bsc.

Applicants should send a CV, publication list, and names and addresses of two referees to:

Jérôme Goudet Dept of Ecology & Evolution Biology Building University of Lausanne CH-1015 Lausanne Switzerland email: jerome.goudet@unil.ch

The consideration of candidates will start as soon as possible, and will be continued until the position is filled.

The Department of Ecology and Evolution of the University of Lausanne, Switzerland (<http://www.unil.ch/dee>), provides a very lively intellectual and social environment. Lausanne, located in Switzerland at the shore of Lake Geneva, offers very high quality of life and outstandingly beautiful surroundings (Alps, Jura mountains, Lake; see <http://www.lausanne-tourisme.ch/>).

informal enquiries can be obtained from the adress above

UMassachusettsAmherst EvolMedEntomology

The Division of Entomology in the Department of Plant, Soil & Insect Sciences at the University of Massachusetts-Amherst seeks applications for a tenure-track faculty position in Medical Entomology at the Assistant Professorship level. Research specialties may include epidemiology, ecology, behavior, physiology, population genetics or molecular genetics of medically important arthropods. The successful applicant will be expected to establish an outstanding, extramurally funded research program, and to develop excellent graduate and undergraduate entomology courses. A PhD is required and postdoctoral experience is preferred. Our department prizes interdisciplinary research, especially the synergy between fundamental and applied research questions and between laboratory and field approaches.

Priority deadline is November 15, 2004, and the search will continue until the position is filled. Applicants should send a curriculum vita, statements of research and teaching interests, three letters of reference and up to five reprints to:

Medical Entomology Search Department of Plant, Soil and Insect Sciences Division of Entomology Fernald Hall rm 102 270 Stockbridge Road University of Massachusetts Amherst, MA 01003 USA

The University of Massachusetts is an Affirmative Action/Equal Opportunity Employer. Women and members of minority groups are encouraged to apply.

Adam Porter Department of Plant, Soil and Insect Sciences & Graduate Program in Organismic and Evolutionary Biology Fernald Hall rm 102 270 Stockbridge Rd University of Massachusetts Amherst MA 01003-9320 USA <http://www-unix.oit.umass.edu/~aporter/> Adam Porter <aporter@ent.umass.edu>

UMinnesota EvolBehavBiology

University of Minnesota—Department of Ecology, Evolution and Behavior—Faculty Position in Experimental Behavioral Biology

The Department of Ecology, Evolution and Behavior invites applications for a faculty position in experimental behavioral biology. The expected appointment is at the Assistant Professor level, but Associate Professors will also be considered. The successful candidate will have expertise in experimental approaches that address key questions in behavioral ecology; interests that bridge the gap between evolutionary and mechanistic studies of behavior; and demonstrated potential to build collaborative connections with other departments (such as entomology, fisheries and wildlife, neuroscience and psychology). Candidates working in any area of behavioral ecology will be considered, but expertise in animal communication, reproductive behavior, or social behavior is especially welcome. The successful candidate will develop an innovative, extramurally funded research program. In addition, the successful candidate will teach an undergraduate course in introductory animal behavior, and develop a more advanced course in his or her area of expertise. A Ph.D. is required and postdoctoral experience is preferred. The Department of EEB is a dynamic, nationally and internationally recognized group of 29 faculty mentoring nearly 100 graduate students and postdocs. Faculty research encompasses ecology, evolution, and behavior with strengths in integrative, interdisciplinary studies. For more information about the Department of Ecology, Evolution and Behavior, please visit our web site at <http://www.cbs.umn.edu/eeb/>. The University of Minnesota is a large, metropolitan institution with excellent opportunities for interdisciplinary research with faculty from the Medical and Veterinary Schools, College of Natural Resources, College of Agriculture, Food and the Environment, Institute of Technology, and the Microbial and Plant Genomics Center.

Review of applications will begin October 1, 2004 with interviews expected to start in mid-January. To apply, send a cover letter, curriculum vitae, a single page statement of research interests, a single page statement of teaching interests, up to five publications, and arrange to have three letters of recommendation sent to Behavior Search, Department of Ecology, Evolution

and Behavior, University of Minnesota, 1987 Upper Buford Circle, Rm 100, Ecology Building, St. Paul, MN 55108. Application packages cannot be accepted by email. The University of Minnesota is an Equal Opportunity Educator and Employer.

Claudia Neuhauser Professor, Head, and Director of Graduate Studies Ecology, Evolution and Behavior University of Minnesota 1987 Upper Buford Circle VOICE 612-624-6291 St. Paul, MN 55108 FAX 612-624-6777 <http://biosci.cbs.umn.edu/eeb/-faculty/NeuhauserClaudia.html> Claudia Neuhauser <CNeuhaus@cbs.umn.edu>

UMinnesota EvolBiology

University of Minnesota—Department of Ecology, Evolution and Behavior—Faculty Position in Evolutionary Biology

The Department of Ecology, Evolution and Behavior invites applications for a position in any area of evolutionary biology. The department will consider applicants at both the tenure-track assistant and tenured associate professor level, but the assistant professor level will be preferred. The successful candidate will be expected to establish a vigorous, extramurally funded research program, contribute to the educational and teaching mission of the College of Biological Sciences at the undergraduate and graduate level, and to provide academic service within and outside of the university. We seek an innovative and productive scientist whose research complements the active and growing group of evolutionary biologists in several departments and in the Bell Museum of Natural History at the University of Minnesota. A Ph.D. is required and postdoctoral experience is preferred. The Department of EEB is a dynamic, nationally and internationally recognized group of 29 faculty mentoring nearly 100 graduate students and postdocs. Faculty research encompasses ecology, evolution, and behavior with strengths in integrative, interdisciplinary studies. For more information about the Department of Ecology, Evolution and Behavior, please visit our web site at <http://www.cbs.umn.edu/eeb/>. The University of Minnesota is a large, metropolitan institution with excellent opportunities for interdisciplinary research with faculty from the Medical and Veterinary Schools, College of Natural Resources, College of Agriculture, Food and the Environment, Institute of Technology, and the Microbial and Plant Genomics Center.

Review of applications will begin October 1, 2004 with interviews expected to start in mid-November or early December. To apply, send a cover letter, curriculum vitae, statements of research and teaching interests, up to five publications, and arrange to have three letters of recommendation sent to Evolutionary Biology Search, Department of Ecology, Evolution and Behavior, University of Minnesota, 1987 Upper Buford Circle, Rm 100, Ecology Building, St. Paul, MN 55108. Application packages cannot be accepted by email. The University of Minnesota is an Equal Opportunity Educator and Employer.

Claudia Neuhauser Professor, Head, and Director of Graduate Studies Ecology, Evolution and Behavior University of Minnesota 1987 Upper Buford Circle VOICE 612-624-6291 St. Paul, MN 55108 FAX 612-624-6777 <http://biosci.cbs.umn.edu/eeb/faculty/NeuhauserClaudia.html> Claudia Neuhauser <CNeuhaus@cbs.umn.edu>

UNebraska MolecularEvol

MOLECULAR ECOLOGIST OR EVOLUTIONARY BIOLOGIST University of Nebraska. The School of Biological Sciences invites applications for a tenure-track faculty position at the Assistant Professor level with expertise in using molecular techniques to investigate evolutionary and/or ecological questions with an emphasis in organismal biology. Candidates will be expected to develop a rigorous research program and assume teaching responsibilities in undergraduate courses in the areas of biological diversity and/or ecology and evolution, and at the graduate level in their area of expertise. A Ph.D. in the life sciences is required and post-doctoral experience is preferred. To apply send a curriculum vita and copies of representative publications along with statement of research interests and teaching interests and philosophy. Also arrange for three letters of reference to be sent by September 30 to Jack Morris, School of Biological Sciences, University of Nebraska-Lincoln, 348 Manter Hall, Lincoln, NE 68588-0118. The position will remain open until a suitable candidate is selected. UNL is committed to a pluralistic campus community through affirmative action and equal opportunity, and is responsive to the needs of dual career couples. We assure responsible accommodation under the Americans with Disabilities Act. For further information contact Jack Morris at 402-472-6676 for assistance.

Guillermo Orti School of Biological Sciences University

of Nebraska 314 Manter Hall, Lincoln, NE 68588-0118, USA

Tel: 402-472-3433 – Fax: 402-472-2083 <http://golab.unl.edu> <http://deepfin.org>

URegina AnimalEvolPhysiology

Animal Physiologist Department of Biology, University of Regina

Animal Physiologist. The Department of Biology at the University of Regina invites applications for an Assistant Professor tenure-track position, effective July 1, 2005. We are seeking an individual who uses modern methods to study animal physiology (fish, amphibians or aquatic invertebrates). Candidates must have a PhD, a productive research record, and post-doctoral experience is an asset. As well as establishing an externally-funded research program, the successful candidate will teach undergraduate and graduate courses, and develop an advanced undergraduate course in his/her area of expertise. Start-up research funds will be provided, as well as a reduced teaching load in the first two years. The Faculty of Science has an excellent stable isotope facility (see <http://uregina.ca/eqal/>), and the Biology Department has a first-rate aquatic sciences laboratory, including aquatic organism holding facilities. To apply for the position, submit a letter of application outlining research and teaching goals, a curriculum vitae, samples of research publications, and arrange for three letters of reference to be sent to: Dr. W. Chapco, Head, Department of Biology, University of Regina, Regina, SK, S4S 0A2 Canada. (fax 306-585-4894; phone 306-585-4231; e-mail William.Chapco@uregina.ca). The closing date for applications is October 15, 2005. Further information about the department is available at: <http://www.uregina.ca/science/biology>. All qualified candidates are encouraged to apply; however, Canadian citizens and permanent residents will be given priority. The University of Regina is committed to the principles of employment equity.

Dr. W. Chapco, Head Department of Biology University of Regina Regina, Canada SK S4S 0A2 Phone: 306-585-4478 Fax: 306-337-2410 e-mail: chapco@uregina.ca

URochester ResearchTech

Description: A research technician IV position is available at the University of Rochester, in Rochester New York conducting studies of intracellular bacteria in insects. The position is part of a 5-year NSF funded project to investigate molecular genetics, ecology and evolution of Wolbachia, a widespread and important group of intracellular bacteria found in invertebrates.

Duties/Qualifications: The ideal applicant will be familiar with standard molecular genetic techniques such as DNA and RNA preparations, diagnostic and quantitative PCR, cloning, and sequencing. Some experience with programs for sequence reactions and alignments is desirable. Other duties will include maintenance of insect cultures, ordering supplies, reagent preparation, and other tasks as assigned. Must be able to work independently and maintain good records of work completed. B.S. or M.S. in Biology or related discipline.

Conditions: This position is available now and will be funded through the life of the grant (2003-2008) and possibly beyond.

Instructions: Send resume and cover letter to Cathy Westbrook via email at cwestbro@mail.rochester.edu or mail at the University of Rochester, Dept. of Biology, 226 Hutchison hall, River campus, Rochester, N.Y. 14627-0211. Phone: 585-275-3889. fax 585-275-2070

USDA DavisCA ConservationGenetics

Title: Principal Investigator Conservation Genetics

The Institute of Forest Genetics in Davis, CA is seeking an outstanding individual to join our conservation genetics program at the rank of principal investigator. The successful applicant will develop both an exciting research program addressing the conservation genetics of woodland plants and forest trees, and provide consultation to land managers regarding issues of restoration and conservation. The Institute of Forest Genetics has research programs in Conservation and Population Genetics, Molecular Ge-

netics and Genomics, and Disease Resistance. The Institute has over 75 years of research excellence - more information about the Institute is available at <http://www.fs.fed.us/psw/programs/ifg/>. More information about the position, including how to apply, can be found at <http://jobsearch.usajobs.opm.gov/-getjob.asp?JobID=23222824>

Andrew Groover Project Leader and Geneticist Institute of Forest Genetics USDA Forest Service (530) 758-1060 agroover@fs.fed.us

UTexasAustin LabTech

Lab technician, University of Texas at Austin

We are currently initiated a NSF funded project to explore the evolution of physiological adaptation in *Arabidopsis thaliana*. The goal of the project is to identify and characterize genes underlying naturally-occurring variation in drought adaptation using genome-wide molecular techniques.

A two-year lab technician position associated with this project is available at UT Austin. We are looking for a highly motivated individual with a M.S or B.S degree and with the demonstrated ability to manage labs and carry out research. The individual will be responsible for implementing experiments and high-throughput genotyping of plant material, as well as upkeep of lab equipment, ordering lab supplies, and training students in the lab. The successful candidate must have experience in high-throughput genotyping and a strong background in molecular biology. Preference will be given to candidates with the some of the following skills including DNA and RNA extraction from plant tissue, experience with robotics in PCR setup, DNA sequencing, and SNP genotyping. We also emphasize the ability to interact and work collaboratively with others, as the technician will work closely with post-docs, graduate students, and undergraduate researchers.

Application review begins immediately and will continue until the position is filled. Applications should include a brief cover letter outlining qualifications and interests, curriculum vitae, and the names and email addresses of three references. Send applications to

Tom Juenger Section of Integrative Biology University of Texas at Austin 1 University Station C0930 Austin, Tx 78712 512-232-5751

or via e-mail to tjuenger@mail.utexas.edu.

Preferred start date will be October 2004.

The University of Texas at Austin is an affirmative action, equal opportunity employer committed to excellence through diversity.

“Thomas E. Juenger” <tjuenger@mail.utexas.edu>

WVirginia USGS Genomics

Research Geneticist (Genomics) Position Number:ER-2004-0327

The U.S. Geological Survey, Leetown Science Center (LSC), Aquatic Ecology Branch (Kearneysville, West Virginia), has advertised the permanent position of Research Geneticist (GS-12/13; Salary range: \$60,638 to \$93,742). The ideal candidate would specialize in functional genomics and its applications to ecological issues (i.e., ecological genomics). The selectee will perform the following duties:

- Plan, design and conduct biological research in the areas of genomics, population genetics, and recovery of declining species, with emphasis on aquatic systems.

- Develop techniques to identify and investigate the function and expression of ecologically important genes in species in need of conservation.

- Identify important genetic adaptations to changing environments, and relate population trends to ecological processes, including human interactions.

- Coordinate research work with other federal, state, and academic and private biologists, ecologists, and natural resource managers to identify needed research and plan, organize, execute and report the research results.

The successful applicant is expected to identify and investigate the function and expression of ecologically important genes in species in need of conservation. The scientist will apply genomics investigations to ongoing studies in population genetics, phylogeography, and molecular systematics currently conducted by the Branch. The scientist will also interact with ecologists in the Aquatic Ecology Branch, and with microbial geneticists, molecular biologists, and others at LSC. This interaction is expected to shed light on the relationship between genotypes and phenotypes by understanding the associated genetic and environmental interactions that affect individual fitness. Another line of productive research could extrapolate organismal biology to

population and species evolution to test how regulatory gene networks evolve and how they differ among closely related species (i.e., comparative genomics).

The complete job announcement is copied below. To learn more about the position and to apply on-line: 1) Go to the USAJobs website: www.usajobs.opm.gov; 2) Select: Basic Search; 3) Select: Keyword Search; 4) Enter: ER-2004-0327; and 5) Scroll down and select: Search for Jobs.

Interested candidates may also contact Dr. Tim King [304-724-8340 (ext. 2142); tim.king@usgs.gov] or Dr. Ed Pendleton [304-724-4461; edward.pendleton@usgs.gov] for further insights.

Tim King, Ph.D. USGS-BRD Leetown Science Center Aquatic Ecology Branch 11649 Leetown Road Kearneysville, WV 25430 Phone: (304) 724-8340 ext. 2142 Fax: (304) 725-0351

“The significant problems we face cannot be solved at the same level of thinking we were at when we created them.” Albert Einstein

PLEASE READ ALL INFORMATION CAREFULLY*

POSITION: Research Geneticist, GS-0440 12 / 13, PM-DEU

ANNOUNCEMENT NUMBER: ER-2004-0327

SERIES & GRADE: GS-0440-12/13

SALARY RANGE: 60638 - 93742

PROMOTION POTENTIAL: 15

OPENING DATE: 08/09/2004

CLOSING DATE: 09/08/2004

DUTY LOCATIONS: 1 vacancy Leetown, WV

APPLICATION (RESUME AND QUESTIONNAIRE RESPONSES)

MUST BE RECEIVED ONLINE IN THE USGS ONLINE AUTOMATED RECRUITMENT SYSTEM (OARS)

BEFORE MIDNIGHT EASTERN TIME ON THE CLOSING DATE OF THIS ANNOUNCEMENT TO BE

CONSIDERED. OARS CAN BE ACCESSED AT [HTTP://WWW.USGS.GOV/OHR/OARS/](http://WWW.USGS.GOV/OHR/OARS/).

If selected for this position, a background investigation is required.

Why Is It Great To Work For The USGS?

Become part of the U. S. Geological Survey (USGS), a world leader in the natural sciences. The USGS provides reliable scientific information to describe and understand the Earth; minimize the loss of lives and property from natural disasters; manage biological, water, mineral and energy resources; and enhance and protect our quality of life. For more information about the USGS, visit: <http://www.usgs.gov/ohr/great.html>

Am I Eligible To Apply For This Position? You may apply for this position if you meet the following criteria:

You are a U.S. citizen.

Is This A Permanent Appointment?

Yes

What Are The Major Duties Of This Position?

This position is with the U.S. Geological Survey, Leetown Science Center, Aquatic Ecology Branch, located in Leetown, WV. The selectee will perform the following duties: –Plan, design and conduct biological research in the areas of genomics, population genetics, and recovery of declining species, with emphasis on aquatic systems. –Develop techniques to identify and investigate the function and expression of ecologically important genes in species in need of conservation. –Identify important genetic adaptations to changing environments, and relate population trends to ecological processes, including human interactions. –Coordinate research work with

— / —

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>

WoodsHoleMBL ComputationalBiol

COMPUTATIONAL BIOLOGY RESEARCH ASSISTANT [RAII III SCP], FULL TIME http://www.mbl.edu/inside/what/human_resources/job_search.php?functail&par=job_id32

Josephine Bay Paul Center for Comparative Molecular

Biology and Evolution The Marine Biological Laboratory, Woods Hole, MA

Description: The Marine Biological Laboratory is seeking applicants for a full-time, year round Research Assistant II/III position in the Josephine Bay Paul Center for Comparative Molecular Biology and Evolution as a Scientific Computer Programmer and Database Programmer.

Duties: Duties include but are not limited to design and build relational database for molecular sequences and phylogenetic information. Develop and install high-throughput phylogenetic analysis software that is web-based and accessible to members of the Woods Hole Scientific Community. Consult with scientists who participate in the Woods Hole Center for Oceans and Human Health program. Efforts will be divided into the following areas: Development of databases, including programming, software installation and software development; Development of web-based, high throughput phylogenetic analysis software; Systems administration

Education/Experience: A B.A or M.S. and advanced course work in computer science or have extensive experience working as a Programmer and Systems Administrator. Experience with Linux/UNIX and Beowulf clusters (OSCAR, MAUI), programming languages (C, C++, Perl, Java) and database software (SQL, PHP) is required. The successful candidate must be skilled in design, construction and maintenance of on-line relational databases. Specific skills with web-based graphical interfaces and systems administration of database servers strongly desired. Familiarity with LDAP, intranet structures and management of diverse operating systems a plus. The successful applicant is expected to have good team skills, but be able to work with a high level of independence with broad supervision.

Please apply to: Applicants should submit a cover letter, curriculum vitae, and a list of three references including telephone numbers and email address to to: Marine Biological Laboratory, ATTN: Human Resources reference code [RA II III SCP], 7 MBL Street, Woods Hole, MA 02543-1015, email resume@mbl.edu. An Equal Opportunity/Affirmative Action Employer/Non-smoking workplace.

Deadline: Until a suitable candidate is identified.

amcarthur@mac.com

Other

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AFLP software

my name is Matthias Becker. I'm a coworker of professor Albers, the head of the Department of Classical and Molecular Plant Systematics of the University in Münster, Germany. In the context of my doctor degrees I am looking for a less expensive computer programme to evaluate AFLP patterns. I have already spoken to an agent of the LICOR company. But the presented price of 8500 EUR is to much for us. Do you know about a cheaper alternative?

Thank you very much in advance. With friendly regards,

Matthias Becker

Matthias Becker <beckemat@web.de>

Bayesian analysis morphology

Hello,

Does anyone know of a program to do Bayesian analysis on morphological characters?

Thanks,

William lotar_w@yahoo.com

Cichlid micros

Dear Evol members,

We are initiating a population genetics study with some mexican cichlids (genus Cichlasoma -also known as Thorichthys) and have not been able to find published microsatellites for the genus, and hardly any for the group. If someone has developed microsatellites or is working with this fish group, or else has find success using microsats developed for a different group, I will very much appreciate it if you can contact me.

Thanks a million in advance, Ella

Dra. Ella Vázquez Domínguez

Instituto de Ecología, UNAM Ap. Postal 70-275 Laboratorio de Macroecología Ciudad Universitaria Tel (52) 55- 5622 9002 México DF 04510 MÉXICO Fax (52) 55-5616 1976

evazquez@ecologia.unam.mx

<http://www.ecologia.unam.mx>

Comercial micros

Dear Evoldir members,

I am looking for a biotech company that commercially isolates and develops microsatellite loci. There are a number out there, but I would like to know if some of you have had positive (or negative) experiences, and could suggest one. US and elsewhere.

Thanks a lot for your attention,

Francesco Nardi

University of Siena

North Eagleville Road University of Connecticut Storrs,
CT 06269-3043

chris.simon@uconn.edu Office (860) 486-4640 Lab (860)
486-3947 Fax (860) 486-6364

Home page: <http://www.eeb.uconn.edu/faculty/-simon/simon.htm> with links: Student research opportunities in the Simon lab; the periodical cicada web-searchable data base; Cicada Central with New Zealand cicada and periodical cicada information

Cicada Reprints: <http://collections2.eeb.uconn.edu/-collections/cicadacentral/resources/reprints.html>

EvolDir Instructions

Note that due to the recent escape of two spam messages onto the EvolDir, the rules have been further tightened. In addition to other measures, it is now necessary that for any message sent directly to the EvolDir that its subject header must now have a colon in the text delimiting the category.

That is: Conference: Graduate position: Job: Other:
Postdoc: Workshop: Course:

Messages without this will be sent to my email account and dealt with when I have time.

Brian

Gel Imaging

Dear Evoldir,

My department is looking into gel imaging systems for various DNA analyses. We are considering the Gel Doc EQ system. Does anyone have any experiences good or bad with this system? Other suggestions?

We are also looking into ultracold freezer alarm systems (for a move into a new building) and any suggestions or experiences you could relate would be appreciated.

Send your responses to me and I will compile a summary for the group.

Thanks very much,

Chris

Chris Simon Professor; Editor of Systematic Biology
Department of Ecology & Evolutionary Biology 75

GeneDiversity StdErrs

Hi,

Does anyone know of a program that estimates variance values for observed heterozygosity and gene diversity for use with microsatellite data?

I appreciate any suggestions.

Thanks.

Paulo Russo Almeida

Paulo Antonio Russo Almeida Departamento de Zootecnia Univ. Tras-os-Montes e Alto Douro Apartado 1013 5000-911 Vila Real PORTUGAL e-mail: prusso@utad.pt tel: +351-259350432 fax:+351-259350482

Heritability Likl answers

Hello,

We would like to thank to everybody offering us very helpful information concerning software to compute heritability by maximum likelihood methods, with special mention to Ruth Shaw, Mark D. Camara, Jim Cheverud, Sheena Cotter, Stéphanie Bédhomme and Rick E. Miller. We are attaching all the responses we have received; they might be useful for other researchers trying to compute heritability estimates with their own data sets. Actually, Cecelia Miles, Adam Ehmer and Maciek Konopinski wrote to us asking for them. We will keep you informed if more responses are received.

Thanks again,

Silvina Van der Molen, Neus Martínez-Abadías and Rolando González-José

UNIVERSITAT DE BARCELONA Facultat de Biologia Departament de Biologia Animal Secció d'Antropologia Diagonal 645 08028-Barcelona España Tel: (+34) 93 402 14 59 Fax: (+34) 93 403 57 40 rolandogonzalez@ub.edu neusmartinez@ub.edu southclam@gmail.com

Hi,

I have used recently quercus (developped by Ruth and Frank Shaw) to analyse quantitative genetic data with maximum likelihood. You can also use VCE . You can download these software and others from http://www.math.usu.edu/~vukasino/ANSCI/-soft_anbr.htm Another useful webpage is the one of Lynch and Walsh: <http://nitro.biosci.arizona.edu/-zbook/book.html> I hope, this will help.

Best,

Stéphanie Bédhomme

“Génétique et Evolution des Maladies Infectieuses” UMR CNRS/IRD 2724 IRD, BP 64501 911, avenue d'Agropolis 34394 Montpellier cedex 5 Tel: +33 (0)4 67 41 62 01 fax: +33 (0)4 67 41 62 99 email : bedhomme@mpl.ird.fr

Hello,

There are several programs available. Frank Shaw and I have developed one which we distribute in a package called Quercus. It is available with documentation and sample datasets at:

www.cbs.umn.edu/eeb/events/quercus.shtml I believe Bruce Walsh has also developed a list of quantitative genetics resources on his website.

Regards, Ruth Shaw

Patrick Phillips has some good software at this website:

<http://darkwing.uoregon.edu/~pphil/software.html>
Mark D. Camara USDA/ARS Aquaculture Genetics OSU - Hatfield Marine Science Center 2030 SE Marine Science Dr. Newport, OR 97365 Office: 541-867-0296 Fax: 541-867-0138 Mailto: Mark.Camara@oregonstate.edu

The program SOLAR available at the Southwest Foundation of Biomedical Research (www.sfbr.org) web site Department of Genetics is widely used in human genet-

ics and well-supported by its authors.

Jim Cheverud

Dear Silvina,

the program VCE, available at <http://w3.tzv.fal.de/-genetik/public.html/> is an excellent maximum likelihood program. VCE itself is freely available but the coding program PEST needs to be purchased. If you want to use it only in an educational non-production setting the license is around \$275 (it may have gone up since I purchased it). PEST can be purchased from Eildert Groeneveld at eg@tzv.fal.de.

Sheena

Sheena Cotter

Postdoctoral Fellow CSIRO Entomology Private Bag 5, Wembley WA 6913, Australia Underwood Ave, Floreat, Western Australia Phone +61 (0) 8 9333 6598 Fax +61 (0) 8 9333 6646 <http://www.ento.csiro.au/staffhome/-scotter.html> *****

Hello: You can do this with SAS (Proc Mixed) and I think Jim Fry has some of the SAS code on his web site laying out the specifics.

Rick E. Miller, Ph.D.

Department of Biological Sciences Southeastern Louisiana University Hammond, LA 70402

Biology Building Room 403 office/ 419 lab phone: (985) 549-5556 FAX: (985) 549-3851 email: rickmiller@selu.edu <http://www.selu.edu/Academics/-Faculty/rickmiller> *****

Hola: Yo tambien estoy muy interesado en computacion de 'heritability' - estudio asimetria fluctuativa (?) de alas de mariposas y quiero comparar 'heritabilities' de varios rasgos. Pueden enviarme todas las repuestas? Saludos,

Maciek Konopinski

Hi-

Could you please be sure to publish the responses to your query?

Thank you very much.

Adam Ehmer Graduate Student Department of Ecology and Evolutionary Biology University of Michigan Natural Science Building 830 North University Avenue Ann Arbor, MI 48109-1048

Hi, I saw your post on evoldir asking about freeware to estimate narrow sense heritability based on maximum likelihood. I was hoping you might share any responses that you got, since I also would like to try this on my data set. Thanks. Cecelia Miles

Cecelia Miles Dept. of Zoology University of Florida
223 Bartram Hall Gainesville, FL 32611

— / —

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>

MTgui software

Hello EvolDir

I have developed a simple interface to be used with ModelTest (by David Posada) called MTgui 0.1. This program works in Windows and Linux (the latter is still not available - I will update it in the next few days) and requires ModelTest 3.5 installed in the machine.

It can be downloaded on

<http://evol.mcmaster.ca/paulo/mtgui.php> It was tested with some score files only, so any errors and problems please send me an email and I will try to solve it quickly. A simple htm help file is included, but I believe is quite user-friendly.

If you want the source code, drop me a note. It was developed in C++ with wxWidgets.

Cheers

Paulo Nuin nuin@terra.com.br

Methylation PCR

Dear all

Two years ago I sent a query to the evoldir list regarding the influence of DNA methylation on PCR efficiency. No clear tendency emerged at that time but several persons seemed interested by this issue.

A little more is known and has been published recently: De Meeûs T., Humair P.F., Delaye C., Grunau C. and

Renaud F. 2004. Non-Mendelian transmission of alleles at microsatellite loci: an example in *Ixodes ricinus*, the vector of Lyme disease. *International Journal for Parasitology* 34: 943-950.

Methylation does not seem to alter PCR amplification (methylated DNA and unmethylated DNA are amplified as efficiently). We however did not test the performance of DNA amplification in heterozygous individuals (heterozygous for methylation and/or for allele size) and we still have no explanation for the short allele dominance that we observed at one locus in *I. ricinus* (see also Wattier, R., Engel, C.R., Saumitou-Laprade, P., Valero, M., 1998. Short allele dominance as a source of heterozygote deficiency at microsatellite loci: experimental evidence at the dinucleotide locus nGvCT in *Gracilaria gracilis* (Rhodophyta). *Mol. Ecol.* 7, 1569-1573).

Thus some things obviously remain to be tested to understand why short allele dominance occur in what kind of locus.

I hope this will be of some help

Thank you again to those who answered to my query two years ago

Of course, any further information will be welcome.

Best regards

Thierry

Thierry de Meeûs Génétique et Evolution des Maladies Infectieuses UMR CNRS/IRD 2724, UR IRD 165 Equipe: Evolution des Systèmes Symbiotiques (ESS) Centre IRD de Montpellier 911 Avenue Agropolis, B.P. 64501 34394 Montpellier Cedex 5, France.

Tel: +33 (0)467 41 63 10 Secrétariat: +33 (0)467 41 61 97 Fax: +33 (0)467 41 62 99 <http://cepm/cepm/-SiteWebESS/Fr/deMeeus/TdeMeeus.html>

Molecular clock

Dear EvolDir members,

I have two queries regarding molecular clock issues and would greatly appreciate your feedback:

1) One of the most common way to test for the molecular clock is by using a LRT of non-clock and clock enforced trees. Looking at several articles it seems to me that the way a ML clock enforced tree is obtained

differs. (a) some people use their ML non-clock tree and re-estimate the likelihood of that tree under a molecular clock enforced, whereas (b) others re-run the entire ML search under the clock constraint. My own observation is that (b) gives better likelihood scores than (a). The consequence may be that using a LRT under (a) the the clock might be rejected, whereas under (b) not. My question would be if (a) is an appropriate way to test the molecular clock? Do the LRT and the Langley-Fitch (as implemented in r8s) method give the same results?

2) When the molecular clock is rejected methods that implement relaxed clock assumptions such as NPRS or PL can be used to reconstruct a chronogram. What is wrong in using these algorithms also to reconstruct a chronogram from a clock-like tree? I would think that the rate smoothing needed would just be very small compared to a non-clock like tree. Are there studies on that? The reason for my question are computational limitations that prevent me for constructing ML clock trees with method (b).

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> mcnlr542@mncn.csic.es

Morphometrics setup

Hi, I am writing to solicit recomendations on software and cameras for a morphometrics setup to measure insect body parts. We are considering using Image J software in conjunction with a Scion CFW-1310 camera. Does anyone have experience with this combination? Alternatively, does anyone have recommendations regarding alternative combinations that have worked well for them in the past?

Any feedback would be greatly appreciated!!

Armin Moczek

Armin P. Moczek Assistant Professor Department of
Biology & Indiana Molecular Biology Institute

Mailing address: Armin P. Moczek Department of Biology Indiana University 915 E. Third Street Myers Hall 150 Bloomington, IN 47405-7107

email: armin@indiana.edu phone: (812) 856-1468 (office) phone: (812) 856-1783 (lab) fax: (812) 855-6082
<http://www.bio.indiana.edu/facultyresearch/faculty/-Moczek.html>

NHGRI BAClibrary

CONTINUATION OF NIH BACTERIAL ARTIFICIAL CHROMOSOME (BAC) LIBRARY PRODUCTION PROGRAM - REQUEST FOR INFORMATION

RELEASE DATE: August 12, 2004

NOTICE: NOT-HG-04-003

National Human Genome Research Institute (NHGRI) (<<http://www.genome.gov>>)

Purpose: The NHGRI is currently assessing the future of the genomic BAC library production program that is part of the NIH BAC Resource Network (<<http://genome.gov/10001844>>) and is, therefore, requesting information from researchers about their awareness of the program, research for which BAC libraries produced through the program have been used, utility of genomic BAC libraries in general, and assessment of future needs for BAC libraries.

Background: The bacterial artificial chromosome (BAC) is a vector system of choice for the construction of the large-insert chromosomal DNA libraries that are needed in genomic studies. The BAC cloning system is more stable than other cloning systems and allows the isolation of genomic DNA fragments that are large enough (80 to >200 kilobases [kb]) to be useful for both targeted genomic sequence determination and for a variety of functional studies. In 2002, three centers were funded for three years (<<http://grants.nih.gov/grants/guide/rfa-files/RFA-HG-01-002.html>>) to produce genomic BAC libraries from multiple organisms and to increase the national capacity for BAC library construction. Both of these goals have been met.

The centers were funded as a production capacity without any decisions of particular organisms (excluding eubacteria, archea and plants) for which to make BAC

libraries. In order to optimally select organisms, the research community was asked to propose species and present a rationale for library construction. Organisms were then chosen based on criteria such as medical relevance and uses for which the BAC library would be put. Through this process 86 organisms have entered the library production pipeline. Library quality is continuously assessed using a standard set of criteria (<http://genome.gov/10001738>) including average insert size and depth of genome coverage. The libraries are also screened for contamination. Libraries are currently available for 36 species (<http://genome.gov/10001852>).

Information Requested: This Request for Information is an attempt to solicit information from the scientific community to better assess the need for future BAC libraries. Information in the following areas will aid in planning future BAC library construction capacity:

- 1) Are you aware of the existence of this program and the opportunity for researchers to propose organisms for BAC library production? If so, have you contributed to a white paper proposing an organism? Would you consider doing so in the future?
- 2) Have you used a BAC clone or library (generated through this program or otherwise) in the course of your research? If so, what was the source and quality of the library and can you please briefly describe how it was used? Did it facilitate your research and if so, how?
- 3) Are there still unmet needs for BAC libraries? If yes, please list the organisms for which you would like to have BAC libraries constructed and state why these organisms are important to study.

This Request for Information is for information and planning purposes only and shall not be construed as a solicitation or as an obligation on the part of the NHGRI. The NHGRI does not intend to award a grant or contract on the basis of responses nor otherwise pay for the preparation of any information submitted or the Government's use of such information. Acknowledgment of receipt of responses will not be made, nor will respondents be notified of the Institute's evaluation of the information received. Responses will be held in a confidential manner. Any proprietary information should be so marked after each response.

Comments should be submitted via email to BAC_Library_Requests@mail.nih.gov <mailto:BAC_Library_Requests@mail.nih.gov>

by Friday, September 3, 2004.

Direct your questions to:

Kris Wetterstrand, M.S. National Human Genome Research Institute 5635 Fishers Lane Suite 4076, MSC 9305 Bethesda, MD 20892-9305 Direct: 301-435-5543 Main: 301-496-7531 Fax: 301-480-2770 Email: wettersk@mail.nih.gov <<mailto:wettersk@mail.nih.gov>>

NeiLeiDistances

Dear Colleagues,

I emailed PAUP tech support and the Paup Forum and did not get a response so I'll try posting my question here.

I am using PAUP with AFLP fragment data from *Carex* spp to create a consensus tree with bootstrap and a neighbor joining tree. I am using the Nei-Li index for a distance measure. The distance measure PAUP gives me differs greatly from what I've calculated in NTsysPC and, for a few samples, by-hand. I first noticed the difference when I compared NJ trees from PAUP vs. NTsys and then compared the numbers in the distance matrices. Am I using the proper syntax (below) in the nexus file? Or is there an extra calculation that happens in PAUP to create the distance matrix?

```
begin paup; dset distance=neili; savedist
format=tabtext file=matrix; set criterion=distance;
hsearch; bootstrap nreps 0 search=nj;
```

Thank-you in advance for you help, Chad Kirschbaum
cdkirschbaum@yahoo.com

Software BEAST v1 1

A new version of BEAST is now available from the BEAST website:

<http://evolve.zoo.ox.ac.uk/beast/> BEAST is a cross-platform program for Bayesian MCMC analysis of molecular sequences. It can be used for many things including:

- * estimating population size
- * estimating changes in population size through time (including bottlenecks)
- * estimating divergence times
- * estimating evolutionary rates
- * analyzing time-stamped data such as viruses

and ancient DNA * reconstructing trees under the assumption of a molecular clock

Its main focus is testing evolutionary hypotheses without conditioning on a single tree topology. BEAST uses MCMC to average over tree space, so that each tree is weighted proportional to its posterior probability.

Amongst the new features in version 1.1 are the following:

* An auto-optimize function that removes the need to perform manual tuning of operators. * Improvement in speed of likelihood calculations for nucleotides. * Now includes BEAUti as part of the BEAST package. BEAUti itself has numerous improvements including new models and options. You can also save the BEAUti settings as separate files for later reloading and modification.

We have also produced a Mac OS X version that has proper OS X applications (although the UNIX version will still work on Mac OS X). The Windows version also now has native Windows applications (.exe files) to run BEAST and BEAUti.

We have also created a new on-line help website:

<http://evolve.zoo.ox.ac.uk/beast/help/> This contains tutorials, documentation and FAQ. There is also a section of the website where users can contribute information, ask questions and the like.

The Tracer package for analysing BEAST output was also recently updated:

<http://evolve.zoo.ox.ac.uk/software/tracer/>

=====

Alexei Drummond & Andrew Rambaut Zoology Department, WWW - <http://evolve.zoo.ox.ac.uk/> University of Oxford, TEL - +44 1865 271261 South Parks Road, Oxford, UK FAX - +44 1865 271249

=====

Taxon sampling

Dear EvoDir members,

Can someone come up with an appropriate way how to measure non-random taxon sampling? Consider we are dealing with a family containing four genera (100/100/10/10 spp, respectively)

1) If we sample 10/10/1/1 or 50/50/5/5 spp, we would

have represented the taxonomic diversity randomly 2) If we sample 30/30/1/1 we have the species rich genera over represented (underdispersed sampling) 3) If we sample 10/10/10/10 we have the species poor genera over represented (overdispersed sampling)

I am looking for an index to illustrate the degree of non-random sampling that also distinguishes between under- and over dispersed sampling e.g. 1) should give a value of one, 2) should give a value smaller than one, and 3) should give a value bigger than one.

Any suggestions will be greatly appreciated. With my best wishes in the meantime, 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> mncnr542@mncn.csic.es

Tetraploid micros answers

Dear Evoldir,

Here are the responses I got for the questions regarding tetraploid microsatellite problem, which I posted in the forum about a month ago. I got some useful suggestions but in my opinion the problem is not yet completely solved. I am very much thankful to all of you who responded my question.

The question I posted was as following:

Dear evoldir,

I am a Ph.D. student in forest genetics and working with a forest tree species called sycamore (*Acer pseudoplatanus*) which is a tetraploid species. I am using nuclear microsatellite marker to study the genetic structure of above mentioned species. Since the species is tetraploid I am getting 1 to 4 bands per locus per sample and to score alleles depending on dosage effects is not working (difficult to differentiate alleles). I am getting difficulties to interpret such types of bands. I would be grateful if anyone can suggest me how to interpret such types of bands and what types genetic variation parameter can be estimated from such types of data using which programme.

ANSWERS:

I already noticed your post at the EvolDir, but did not reply as I was a bit short on time and thought that others might also be able to help you. However, if you did not yet get the answers you needed, I can help you by giving my view on your problem.

It was nice of Ruzica to suggest my program to you, but I am afraid it might not entirely what you are looking for, though it might be of use, depending on your research question. My program is in principle meant for use with asexually reproducing species, and as most asexuals are polyploid, the program can handle polyploid data. Most of the program's functionality is rather useless if you are working on a sexual species. However, the program does allow you to calculate and export genetic distance matrices (also using Ruzica's method). You can use this matrix then to make a tree (eg. UPGMA) and draw some conclusions from that or to do other things that people usually do with genetic distances. You can find the program on www.science.uva.nl/~meirmans. More useful however would be to forget about my program and do an Amova. In that case you might score your msats as if they were dominant markers and use these as an input file. Someone called JENCZEWSKI published something Amova's on polyploids in Molecular Ecology in 1999, if I remember correctly, but those were on RAPDs. If you do want to use your data as codominant, you would have to think of a way to calculate a chi-square distance matrix for your data to use as an input.

Furthermore there is the excellent program called SPAGEDI, written by Olivier Hardy, that can calculate Fst using polyploid data. However the bias that arises from not knowing the dosage of your alleles is hard to assess, though I know people who have done Fst calculations on data from polyploids like that.

Just out of interest: are all *A. pseudoplatanus* polyploid or are there also diploids somewhere? And something that has been bugging me for quite sometime: is polyploidy as frequent in trees as it is in herbs? I never before heard of polyploid trees, though I never took the effort to look for it...

Hope I have helped you with this, if you have any further questions, don't hesitate to ask.

Greetings, Patrick

Patrick G. Meirmans Institute for Biodiversity and Ecosystem Dynamics Evolutionary Botany University of Amsterdam Kruislaan 318 1098 SM Amsterdam The Netherlands

Tel. +31 (0)20 525 7856 Fax. +31 (0)20 525 7832

<http://www.science.uva.nl/~meirmans>

Hi,

The short answer is:

"There is no standard approach to population genetic stats in a polysomically inheriting polyploid in which you can't identify allele dosage. There is certainly no software to do so."

However,

If you can score allele dosage, then use Spagedi (Hardy and vekemans)

If it has disomic inheritance, then I have an approach (and a beta of a text-interface program) that will give some statistics.

My program will work with a polyploid with polysomic inheritance (i.e. give you numbers), but inference would be harder.

I have attached the (very 'beta') documentation for my program. Included are some helpful references.

Darren

Darren Obbard Plant Sciences, Oxford (Currently residing in Norwich, UK) darren.obbard@plants.ox.ac.uk Mobile: +44 07968 838 635 Home: +44 01603 259 670

I had exactly the same problem when I scored microsatellites in a tetraploid *Echium vulgare*. I did not trust the estimation of number of copies of the alleles, based on the signal intensity. I ended up noting only the presence or absence of amplified alleles. I wrote it in my primer note. Korbecka G, Vrieling K, Squirrell J, et al. (2003) Characterization of six microsatellite

— / —

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>

Wim Scharloo passed away

Professor Willem Scharloo died on 19 August, after a number of difficult years.

Wim Scharloo studied in Utrecht and Leiden, and

held appointments in Groningen and Utrecht (all the Netherlands). He himself worked on canalization, stabilizing selection and disruptive selection; the work of his students diversified into bird studies, studies on enzyme polymorphism in *Drosophila melanogaster* and theoretical models. Wim Scharloo pioneered population genetics and evolutionary genetics in the Netherlands, and has been highly influential; most evolutionary biologist

here are his students or his students' students. He has been Chairman of the European Society of Evolutionary Biology

Wim Scharloo is survived by his wife Tineke (t.h.scharloo@wanadoo.nl), and four children and grandchildren.

Gerdien de Jong G.deJong@bio.uu.nl

PostDocs

AlbertEinsteinCollegeMedicine SystemsBiol	27	UEdinburgh PlantEvol	32
DalhousieU ProtistEvol	28	UHelsinki FunctionalGenomics	32
KonradLorenzInst EvolFishBehaviour	28	UMelbourne InsecticideResistance	33
NorthCarolinaStateU EvolGenomics	29	UMiami EvolBats	33
PurdueU HardwoodTreeEvol	29	UOxford Bioinformatics	33
RichmondVA EcolGenomics	29	UPotsdam EvolBiol	34
StonyBrook InsectPlantEvol	30	USDA MadisonWI PlantPopulationBiol	35
TexasAMU Seahorses	30	USheffield EvolBehaviour	35
UBirmingham SexChromEvol	31	UTexasAustin Arabidopsis	36
UCSantaBarbara PlantGenomics	31		

AlbertEinsteinCollegeMedicine SystemsBiol

Post Doctoral Research Fellow in Evolutionary Systems Biology Seaver Foundation Program in Bioinformatics, Albert Einstein College of Medicine,

Postdoctoral research position is available in Evolutionary Computational/Systems Biology. The program's focus is the study of complex gene networks and their evolution.

Applicants could have skills in any of several areas of evolutionary, molecular, computational, or systems biology and/or genetics, and development biology. We encourage applicants from any of these fields. We particularly encourage applicants working on model organisms with strong background in theoretical and computational biology.

The position is available immediately and for the duration of 1-3 years; Salary (in the range of \$35K to \$40K, plus benefits) will be commensurate with experience.

If interested, please send your curriculum vitae, list of publications, research proposal, and the names of at least three references to:

Prof. Aviv Bergman Department of Pathology Seaver Foundation Program in Bioinformatics, Albert Einstein College of Medicine, Jack and Pearl Resnick Campus, 1300 Morris Park Avenue, Bronx, NY 10461.

E-mail: abergman@aecom.yu.edu

– Aviv Bergman Ph.D. Professor Albert Einstein College of Medicine 1300 Morris Park Ave. Belfer Bldg. Rm. 902 Bronx, NY 10461

Phone: (718) 430-2942 Fax: (718) 430-8541 E-Mail: abergman@aecom.yu.edu

Aviv Bergman <abergman@aecom.yu.edu>

DalhousieU ProtistEvol

POST DOCTORAL POSITION: PROTIST MOLECULAR EVOLUTION/GENOMICS

A two-year post-doctoral position in the molecular evolution of protistan eukaryotes is available immediately, at Dalhousie University, Canada. The project will involve the production and analysis of EST libraries from free-living protists potentially related to the ???deep-branching??? anaerobes *Giardia* and *Trichomonas*. This will include multi-gene analysis of organismal phylogeny, analysis of lateral transfer events, and the identification of mitochondrial-targeted genes.

The successful applicant will work on collaborative research involving the laboratories of Andrew Roger (Dept. Biochemistry) and Alastair Simpson (Dept. Biology), through the Canadian Institute for Advanced Research (CIAR) Program in Evolutionary Biology. See below for some relevant publications.

Applicants will need extensive research experience with laboratory molecular biology and experience with molecular phylogenetics and/or bioinformatics. They will have a strong publication record in international journals. A demonstrated interest in protist evolution would be an asset.

The successful applicant will have the opportunity to interact with world-class phylogenomicists and bioinformaticians at Dalhousie University involved in the CIAR Program and Genome Atlantic. Dalhousie University is the premier research university in maritime Canada, and was judged the best institution outside the US for postdoctoral researchers in a recent survey (*The Scientist* magazine).

Please send a C.V. and contact details for two references to: Alastair Simpson Department of Biology, Dalhousie University, Halifax, B3H 4J1, N.S., Canada Fax: 1 902 494 3736 Email: [alastair.simpson\[at\]dal.ca](mailto:alastair.simpson[at]dal.ca).

by August 30th 2004

Some Relevant Publications:

SIMPSON, A.G.B. and ROGER, A.J. (2004) Protein phylogenies robustly resolve the deep-level relationships within Euglenozoa. *Molecular Phylogenetics and Evolution* 30: 201-212

SIMPSON, A.G.B. MacQuarrie, E.K., and ROGER, A.J. (2002) Early origin of canonical introns. *Nature*

419: 270

SIMPSON, A.G.B. and ROGER, A.J. (2002) Eukaryotic evolution: Getting to the root of the problem. *Current Biology* 12: 691-693.

SIMPSON, A.G.B., ROGER A.J. et al. (2002) Evolutionary history of ???early diverging??? eukaryotes: The excavate taxon *Carpedimemonas* is closely related to *Giardia*. *Molecular Biology and Evolution* 19: 1782-1791.

Baldauf, S.L., ROGER, A.J., Wenk-Siefert, I and Doolittle, W.F. (2000) A kingdom level phylogeny of eukaryotes based on combined protein data. *Science* 290, 972-977.

— Alastair G.B. Simpson, PhD Assistant Professor, Department of Biology, Dalhousie University Canadian Institute for Advanced Research (Program in Evolutionary Biology)

Department of Biology Life Sciences Centre, 1355 Oxford St, Halifax, Nova Scotia, B3H 4J1, Canada

Phone: 902 494 1247 (Country code 1) Fax: 902 494 3736 (Country code 1) Email: alastair.simpson@dal.ca

“Evolutionary speculation...can be considered a relatively harmless habit, like eating peanuts, unless it assumes the form of an obsession; then it becomes a vice” R.Y. Stanier, 1970

Alastair Simpson <Alastair.Simpson@Dal.Ca>

KonradLorenzInst EvolFishBehaviour

POST-DOCTORAL POSITION IN FISH BEHAVIOR

To collaborate with Dr. Richard H. Wagner at the Konrad Lorenz Institute on an experimental study of colony formation in fish funded by the Austrian Science Foundation (FWF). The successful candidate is a behavioral ecologist with a strong theoretical background and experience performing behavioral experiments with fish. The research also entails DNA analysis for assigning paternity, so experience in molecular genetics techniques is an advantage.

The institute has excellent aquarium facilities and a state-of-the-art genetics lab. The position is available for one year with the possibility of a second year.

Applications will be reviewed starting 14 September and the position will be filled as soon as possible af-

ter that date.

Please submit a cover letter describing research experience, a CV and have at least two letters of recommendation sent to:

Dr. Richard H. Wagner, Senior Scientist Konrad Lorenz Institute for Ethology Austrian Academy of Sciences Savoyenstrasse 1a A-1160 Vienna Austria

e-mail: r.wagner@klivv.oeaw.ac.at

phone: +43 1 515 81 27 31 fax: +43 1 515 81 28 00
secretary: +43 1 515 81 27 00

North Carolina State U EvolGenomics

Postdoctoral Position in Evolutionary Genomics

A postdoctoral research associate position in evolutionary and population genomics is available in the Departments of Genetics/Bioinformatics at North Carolina State University in the laboratory of Philip Awadalla. The precise project is flexible. Generally, the interests of the lab include developing and applying models of population genetic inference that address demography and selection, with particular emphasis on, but not limited to, human, drosophila and/or malarial genomes and related species. An individual interested in theoretical, computational or empirical work can apply. The lab is currently involved in strong collaborations with a number of outside groups including individuals at NIAID/NIH in Bethesda as well as the Statistical Genetics Group at Oxford, UK. North Carolina State University provides a dynamic, integrated environment in the area of evolutionary and functional genomics that includes the laboratories of Trudy Mackay, Bruce Weir, Greg Gibson, Zhao Beng-Zeng, Jeff Thorne, Jung-Ying Tzeng, William Atchley, and Michael Purugganan. NCSU is in close proximity to research triangle park (NIEHS, SAS,...), UNC and Duke.

This position will require an independent and motivated individual who has published in genomics and/or population genetics. Mathematical and/or computational modeling skills are not essential but appreciated. Funding is available for two years. The salary is according to NIH pay scale commensurate with experience.

Please contact Philip Awadalla at pawadalla@ncsu.edu

Philip Awadalla, PhD Department of Genetics North Carolina State University Gardner Hall Raleigh, NC

27695-7614

tel:919-513-7680 (Genetics) tel:919-515-1221 (Bioinformatics) fax:919-515-3355

pawadalla@ncsu.edu

PurdueU HardwoodTreeEvol

Van Eck Scholarships: The Hardwood Tree Improvement and Regeneration Center (HTIRC) at Purdue University is seeking outstanding candidates interested in working toward M.S. or Ph.D. degrees or obtaining a post-doctoral position. Areas of research include: development of plant tissue culture and genetic modification technologies for tree improvement; conservation and population genetics; forest tree breeding; and nursery, outplanting, and silvicultural stand management. For full details and application information, please visit:

<http://www.agriculture.purdue.edu/fnr/HTIRC/-job1.html> or email Keith Woeste at:

woeste@purdue.edu

Jeffrey C. Glaubitz Postdoctoral Researcher Purdue University Department of Forestry & Natural Resources 195 Marsteller St (Forestry Bldg) West Lafayette, Indiana , USA 47907-2033 Phone: (765) 494-3609 Fax: (765) 496-2422 Email: glaubitz@fnr.purdue.edu

RichmondVA EcolGenomics

I am not a member of this list and am posting the attached ad for a colleague, Bonnie Brown (blbrown@vcu.edu), who will be out of town until August 15. For specific questions about the position, please reply directly to her; I can answer general questions only.

Postdoctoral Associate, Gene Mapping and Pedigree Analysis

Applications are being considered at Virginia Commonwealth University for an immediate opening for a post-doctoral research position in gene mapping and pedigree analysis. This new position involves research in

quantitative and molecular genetics with the goal of improving growth rate and production of fish broodstock populations through genetic selection. Research involves genetic and performance evaluation of strains and pedigree lines, multiplex analysis of molecular genetic markers, and statistical genomics.

The candidate must have a strong background in statistical methods for determining pedigrees, genetic map construction, and detecting QTLs, as well as hands-on working experience in molecular laboratory techniques such as nucleic acid purification, PCR, and automated genotyping. A Ph.D. degree in quantitative genetics, animal breeding, genomics, or related field is required. The candidate should possess excellent verbal English skills and a demonstrated ability to write technical articles in English. In addition to conducting research and preparing publications for refereed journals and technical reports, the postdoc will supervise and train MS graduate students.

Salary and benefits will be commensurate with qualifications and experience of the successful candidate. Starting date is 15 September 2004 or later; review of applications will continue until the position is filled. Qualified applicants should send resumes by email (mailto:<blbrown@vcu.edu>blbrown@vcu.edu) or surface mail to Dr. Bonnie L. Brown, VCU Dept of Biology, 1000 W. Cary St., Richmond, VA 23284-2012. Include in the resume a description of training and experience relevant to this position, a list of publications, and the names, addresses, emails, and phone numbers of 3 referees.

Virginia Commonwealth University is an equal opportunity/affirmative action institution providing access to education and employment without regard to age, race, color, national origin, gender, religion, sexual orientation, veteran's status, political affiliation, or disability.

— Karen M. Kester, Ph.D. Associate Professor Department of Biology Trani Life Sciences Center 1000 West Cary Street Richmond, VA 23284-2012 phone: (804) 828-0103 fax: (804) 828-0503 email: kmkester@vcu.edu webpage: <http://www.people.vcu.edu/~kmkester/> Karen Kester <kmkester@mail1.vcu.edu>

StonyBrook InsectPlantEvol

Postdoctoral Position in Evolution of Insect/Plant Associations, Stony Brook

A postdoctoral position will be available for two years, starting in January 2005, in the Department of Ecology and Evolution at Stony Brook, New York, for evolutionary studies of associations between herbivorous insects and their host plants. The starting salary will be \$30,000.

The major research themes at this time will be the quantitative genetics of adaptation of insects to normal and novel hosts, and the phylogeography of insect/plant associations. The postdoctoral associate will contribute to one, and preferably both, of these efforts. Experience in molecular phylogeography or phylogenetics, or in experimental study of phytophagous insects, is expected; experience of both kinds will be an advantage.

The research setting is a newly refurbished lab, with excellent computing and greenhouse facilities in the same building. The Department of Ecology and Evolution provides a stimulating, interactive environment, and the University setting provides ready access both to numerous natural areas and to the academic and cultural opportunities in New York City.

Applications should be received by 25 September 2004. Applicants should send a curriculum vitae and a brief letter describing their research experience, interests, and goals, and should arrange to have two letters of reference sent to:

Douglas J. Futuyma

Department of Ecology and Evolution

State University of New York

Stony Brook, NY 11794-5245

e-mail: futuyma@life.bio.sunysb.edu

tel.: (631) 632-1411

Fax: (631) 632-7626

Web: <http://life.bio.sunysb.edu/ee/>

Stony Brook University is an equal opportunity/affirmative action employer.

TexasAMU Seahorses

A POSTDOCTORAL POSITION in molecular evolutionary biology is available in the laboratory of Adam G. Jones at Texas A&M University. The candidate for this position will be expected to contribute to one or both of two major research foci in the laboratory.

The first area of interest involves the use of the phenomenon of male pregnancy in the fish Family Syngnathidae (pipefishes, seahorses and sea dragons) as a model to understand the evolution of morphological innovations. The male's brood pouch is a novel evolutionary structure and it has evolved in parallel in two separate syngnathid lineages. The goal is to use microarrays and other genomics techniques to investigate the evolution of the genes and genetic pathways involved in male pregnancy. The second research area comprises sexual selection and gamete competition in syngnathids. Male pregnancy results in a reversal in the direction of sexual selection in some pipefish, which provides unique opportunities to study gamete competition and cryptic choice (with males rather than females choosing). These studies involve a combination of laboratory-based mating experiments and microsatellite-based parentage analysis.

The start date is flexible, and funding is available for at least two years. The salary will be competitive. Interested individuals should send a C.V., a brief letter (or email) indicating interest, and contact information for 3 references to Adam Jones. Email submissions are preferred (ajones@mail.bio.tamu.edu), but applications can also be sent by regular mail to: Adam G. Jones, Department of Biology, Texas A&M University, 3258 TAMU, College Station, TX 77843. Informal inquiries are welcome.

For representative publications, see my faculty website at: <http://www.bio.tamu.edu/FACMENU/-FACULTY/jones.htm> ajones@mail.bio.tamu.edu
ajones@mail.bio.tamu.edu

UBirmingham SexChromEvol

THE UNIVERSITY OF BIRMINGHAM (United Kingdom) SCHOOL OF BIOSCIENCES

Research Associate/ Fellow

A 35 month NERC-funded postdoctoral position is available in the laboratory of Dr Dmitry Filatov looking at ??? Using Y chromosome haplotype diversity to test for selection within and between natural populations of the plant *Silene latifolia*???. The post will be to work on a project in collaboration with Prof. D. Charlesworth lab at the University of Edinburgh, and is devoted to the study of evolutionary forces playing a major role in the evolution of sex chromosomes.

Applicants should have or be near completion of a PhD in population genetics/molecular evolution and experience in (preferably plant) experimental molecular population genetics and evolution (at least one published paper is required). Experience in programming and database management will be an advantage. The starting salary will be £19,640 - £21,640, dependent on skills, qualifications and experience.

Informal enquiries can be addressed to Dr Dmitry Filatov (D.Filatov@bham.ac.uk, Tel: +44-121-414 2500).

Application forms (returnable by Friday 3rd September 2004) and details from Personnel Services, The University of Birmingham, Edgbaston, Birmingham B15 2TT. Tel: 0121 415 9000, web: www.personnel.bham.ac.uk/-vacancies/ Please quote Ref: H39074

Working towards equal opportunities

– Dmitry Filatov <D.Filatov@bham.ac.uk> University of Birmingham

Dmitry Filatov <D.Filatov@bham.ac.uk>

UCSantaBarbara PlantGenomics

Post-doctoral research associate to study of the genomic basis of adaptations in *Aquilegia*.

We have a two-year position with the possibility of a 1-2 year extension for a recent Ph.D. in an NSF funded project "Genomics of Adaptation to the Biotic and Abiotic environment in *Aquilegia*". This multi-investigator collaboration will study the molecular genetic changes underlying adaptations in the plant genus, *Aquilegia*. This research will examine adaptations to specific pollinators, flowering time and soils/habitats and develop *Aquilegia* as a model organism for evolutionary and ecological functional-genomics studies. Genetic resources and techniques to be developed and utilized include a QTL mapping, EST sequencing, physical map construction, oligonucleotide array expression studies, association mapping, and transformation of candidate genes. PIs include Scott Hodges (UC Santa Barbara), Justin Borevitz (U of Chicago), Elena Kramer (Harvard), Magnus Nordborg (USC) and Jeff Tomkins (Clemson).

The ideal candidate will have experience in molecular biology, quantitative genetics (linkage and association mapping), molecular evolution, adaptation and speciation, as well as statistical and computational skills.

Specific duties will include overseeing the construction of recombinant inbred lines for fine-mapping of traits, linking genetic and physical maps, using oligonucleotide arrays for expression studies and mapping, and conducting field work to quantify habitat associations. Most of the work will be conducted at the University of California, Santa Barbara though the studies will be highly collaborative and likely require short-term visits to other PI's laboratories.

To apply, send a CV, brief statement of research interests/goals, desired start date, and two letters of recommendation to the address below. The start date of the grant awaits final NSF approval but is likely to be October 1, 2004.

Additional information on the *Aquilegia* system can be found at: <http://www.lifesci.ucsb.edu/eemb/faculty/-hodes/research.html> Dr. Scott Hodges Department of Ecology, Evolution and Marine Biology University of California Santa Barbara, CA 93106 805 893-7813 or via email to hodges@lifesci.ucsb.edu

– Scott Hodges Assoc. Professor Dept. of Ecology, Evolution & Marine Biology University of California phone: 805 893-7813 Santa Barbara, CA 93106 fax: 805 893-4724 Santa Barbara, CA 93106 fax: 805 893-4724

UEdinburgh PlantEvol

Postdoctoral position: Plant Evolutionary Molecular Genetics, University of Edinburgh

Institute of Evolutionary Biology, School of Biological Sciences

The position is for a plant population geneticist to work on a NERC funded project (up to 33 months, starting in autumn 2004) to study evolution of sex chromosomal genes in the closely related dioecious plants *Silene latifolia* and *S. dioica*. The project is a collaboration with the group of Dr. D.A. Filatov, University of Birmingham. It will involve studying diversity of genes in natural populations of the two species and testing variants for sex linkage. The Y-linked genes will be used to map the distribution of haplotypes from populations throughout Europe. Microsatellites will then be used to estimate the relative ages of different haplotypes from their intra-haplotype variability, using microsatellite or other genetic markers with high mutation rates.

Requirements: A PhD in biology is essential. Experience is required with all aspects of PCR amplification

and DNA sequencing, and preferably with microsatellite markers, including some familiarity with methods of analyses of sequences and of marker diversity.

For further details, and to apply, see the University of Edinburgh web site

<https://www.jobs.ed.ac.uk/jobs/-index.cfm?action=results> Job Reference 3002347 Salary Scale £ 19460 - £ 29128 – Professor Deborah Charlesworth Institute of Cell, Animal and Population Biology University of Edinburgh Ashworth Lab. King's Buildings, W. Mains Rd., Edinburgh EH9 3JT, UK Tel: (+44)(0)131 650 5751 Fax: (+44)(0)131 650 6564 Fax: (+44)(0)131 650 6564

UHelsinki FunctionalGenomics

Post-doctoral research associate for integration of functional genomics with metapopulation biology

We have a two-year position with the possibility of 1-2 year extension for a recent PhD in a NSF funded "Bio-complexity" project (presently pending final approval). This is a multi-investigator international collaboration that aims to examine physiological and molecular bases of life-history variation in a metapopulation of the Glanville fritillary butterfly (*Melitaea cinxia*), a model system for metapopulation biology. The new research will examine variation in dispersal and fecundity in an integrated fashion, from molecular level to whole-organism traits and to landscape-level metapopulation dynamics. The research group combines expertise in ecology (Hanski), metapopulation theory (Ovaskainen), flight physiology (Marden), molecular endocrinology (Fescemyer) and molecular genetics (Crawford, Frilander).

The ideal candidate will have experience in molecular biology, including standard DNA/RNA techniques, molecular cloning, and an interest in organismal biology and/or ecology. Duties will include: preparation of cDNA libraries, sequencing and construction of a microarray; microarray hybridizations and data analyses; examination of RNA for functional variation in alternative splicing. Most of the work will be performed at the University of Helsinki, along with stints of 1-2 months (preferably winter months) at the RSMAS laboratory of the University of Miami where sequencing will be performed. The work will require additional short-term visits to Penn State University. For information contact the PI's listed below and/or Dr. Mikko Frilander,

University of Helsinki (mikko.frilander@helsinki.fi).

Send CV, brief statement of research interests/goals, desired start date, and two letters of recommendation to either of the principal investigators. Start date of the grant awaits final NSF determination, but is likely to be November, 2004.

Principal investigators: Dr. Jim Marden, Penn State University (jhm10@psu.edu; <http://www.bio.psu.edu/People/Faculty/Marden/index.html>)

Dr. Ilkka Hanski, University of Helsinki (ilkka.hanski@helsinki.fi; <http://www.helsinki.fi/science/metapop/>)

associated with phylogeographic and coalescent-based analyses. Field experience in working with bats is desirable but not necessary. Please send or email a letter of application, current curriculum vitae, and names of three references to: Dr. Theodore H. Fleming, Department of Biology, University of Miami, Coral Gables, FL 33124, USA; email: tfleming@fig.cox.miami.edu.

Ted Fleming Professor and Interim Chairman Department of Biology University of Miami 1301 Memorial Drive Coral Gables, FL 33124 Voice: 305-284-6881 Cell: 305-298-8102 Fax: 305-284-3039 tfleming@fig.cox.miami.edu

UMelbourne InsecticideResistance

Senior Postdoctoral Position

The Department of Genetics at the University of Melbourne is looking for a Research Fellow to actively coordinate and participate in insecticide resistance research, applying molecular genetic and genomics techniques. This is a 3-year joint research program between the Max Planck Institute of Chemical Engineering (Jena, Germany), the University of Melbourne ARC Special Research Centre CESAR (Centre for Environmental Stress and Adaptation Research) and the Bio21 Molecular Science and Biotechnology Institute. Funding is provided by the State of Victoria and the appointee will report to Associate Professor Philip Batterham and Professor David Heckel. Applications close September 24, 2004. For more details see www.hr.unimelb.edu.au/pds/Y0014642.pdf Phil Batterham <P.Batterham@unimelb.edu.au>

UMiami EvolBats

Postdoctoral Position

A Postdoctoral position is available immediately in the Department of Biology, University of Miami to study the phylogeography and historical demography of several species of West Indian bats. Qualifications for this position include a Ph.D. plus laboratory experience working with mtDNA and nuclear microsatellite DNA as well as experience with the analytical tools

UOxford Bioinformatics

2 Postdoctoral Research Assistants (PDRA). Academic-related Research Staff Grade 1A: Salary £19,460 - £29,128

Two postdoctoral research positions of three years duration in Bioinformatics funded by BBSRC are available for working with Jotun Hein. This project will focus on models of sequence evolution that includes a process of insertion-deletion of nucleotides and their implementation. Furthermore, developed methods will be applied to complete genomes as they are determined in coming years. The work will include algorithm development, statistical modelling, software development and large scale comparative analysis of genomes. The research will take place at The Oxford Centre for Gene Function. Earliest starting date is 1st November 2004.

The Research Project: Practical Statistical Alignment.

Although bioinformatics perceived is a new discipline, certain parts have a long history and could be viewed as classical bioinformatics. For example, application of string comparison algorithms to sequence alignment has a history spanning the last three decades. The principle of choosing solutions by minimizing the amount of evolution is also called parsimony and has been widespread in phylogenetic analysis even if there is no alignment problem. Over the last two decades the parsimony method of phylogenetic reconstruction has been severely criticized and has lost terrain to methods based on stochastic modelling of nucleotides, codons or amino acids. The present project will develop, implement and simultaneously apply methods including insertion-deletions of nucleotides/amino acids to give a full model of sequence evolution. At present there are only 2 techniques that can solve these problems -

dynamic programming and MCMC - so that is where our focus lies. We are shifting emphasis from the former to the later; however, this does not mean dynamic programming will be without value. Dynamic programming provides exact solution and MCMC provides only approximation. The former can be used to test the validity of the later on small data sets. The key goals of this project are:

i. Software package: A central aim of the project is to develop a package doing Bayesian statistical alignment for many sequences and performs a series of essential associated analyses: hypothesis testing for molecular clock, phylogeny, mutation rate, selection estimation, assessing ancestral sequences, and structure prediction. It should produce nice graphical outputs of different marginalisation (tree, alignment, structure, ancestral sequences, and posterior distribution of mutation rates) for easy visualization. Prior parameters will be allowed to be set by users. This package of easy to use, biologist-friendly software should be of wide use in the community. A web based server will be developed that researchers can submit jobs to.

ii. Development of better biological models and corresponding algorithms: The TKF91 model allows only single insertions and deletions which is biologically irrelevant. Modelling long insertions and deletions is necessary to make statistical alignment practical. Site heterogeneity and residue-dependent indel rates would also increase the strength of the method.

iii. Structure prediction: Most of the comparative structure prediction methods are based on alignments, which might be misleading when the alignment is wrong. Statistical alignment will improve this.

iv. Comparative genomics: At present the capabilities of our statistical alignment methods matches the growth of mammalian genomes. Several questions are of interest here. Since statistical alignment is based on a general model of molecular evolution including both insertions and deletions, issues related to the nature of these events can be addressed and parameterized. What is the nature of insertions and deletions, their length distribution and rates? There is no reason to assume that insertion process is the time reversed process of deletion as assumed by many models. Quantifying the departure from this assumption would be of great interest. The removal of the intermediate alignment step makes statistical alignment very suited for large scale genomic analysis and question such as departure from the molecular clock and time reversibility of the underlying substitution process can be tested. A good model of neutral molecular evolution also increases the power to detect selection which is central in functional

interpretation of individual genes. An especially interesting question at present is the enigma of the amount of selection outside genes.

The Appointments Applications for the PDRA posts are invited from researchers interested in working on this high-impact project - the development of statistical models, software and the analysis of genomic data. Candidates should have relevant background and research experience in computer

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

UPotsdam EvolBiol

PostDoc position in Evolutionary Biology for 12 months, University of Potsdam

In an EU financed project we look for a qualified Post-Doc to be appointed for 12 month, starting as soon as possible (1st of January 2005 at the latest).

In this project, the successful applicant will have to perform molecular genetic research on population structure and immuno-competence of amphibians. Main objective is to provide qualified advice for management decisions.

Applicants must hold a university degree (Diploma or Master of Science) and a PhD of a relevant topic. They should appreciate interdisciplinary research and cooperation with international project partners. Familiarity with modern molecular genetic techniques (PCR, cloning, marker development) is desired. Experience in research on MHC is beneficial.

The University of Potsdam is an equal opportunity employer. If equally qualified, disabled applicants will be preferably considered. The University of Potsdam aims at increasing the number of female researchers and encourages qualified females to apply.

Please send your application before 15th of September 2004 to: Prof. Dr. Ralph Tiedemann, University of Potsdam, Institute of Biochemistry and Biology, Evolutionary Biology/Systematic Zoology, Karl-Liebknecht-Str. 24-25, Haus 26, D-14476 Potsdam, Germany, Email: tiedeman@rz.uni-potsdam.de

Prof. Dr. Ralph Tiedemann Universitaet Pots-

dam Institut fuer Biochemie und Biologie Evolutions-
biologie/Spezielle Zoologie Karl-Liebknecht-Str. 24-
25, Haus 26 D-14476 Potsdam Germany Tel: +49-
331-977-5249, -5253 (Sekretariat) Fax: +49-331-
977-5070 Email tiedeman@rz.uni-potsdam.de [http://-
www.bio.uni-potsdam.de/spezzoo/index.htm](http://www.bio.uni-potsdam.de/spezzoo/index.htm)

USDA Madison WI Plant Population Biol

POSITION: Plant Population Biologist

LOCATION: Madison, WI

DESCRIPTION OF DUTIES: The position is located in the ARS Vegetable Crops Unit located at the University of Wisconsin. The assignment is part of a long-range research program to study gene flow and the environmental impact of transgenes on the environment. The incumbent will work on estimating gene flow using molecular markers in different plant species and quantifying the impact of different plant characteristics on gene flow. Methods to estimate gene flow will include paternity analyses, and population phylogenies. The long-range plan of this project is to increase our ability to predict gene flow in different crop-native plant systems.

SPECIAL REQUIREMENTS: Recent Ph.D. in plant population biology, plant molecular ecology, plant evolutionary biology, botany, or plant systematic. Previous laboratory experience using molecular markers is required. Previous field experience in native plant populations is highly desirable.

FOR SPECIFIC INFORMATION ON SPECIAL REQUIREMENTS, SALARY, BENEFITS, OR APPLICATION FORMS, CONTACT:

Latania Maise Human Resources Specialist
USDA/ARS/HRD 5601 Sunnyside Avenue Beltsville,
MD 20705-5106 Phone: (301) 504-1583 Fax: (301)
504-1578 Email: lmaise@ars.usda.gov

FOR SPECIFIC INFORMATION ON THE DUTIES AND RESPONSIBILITIES OF THIS POSITION OR TO SUBMIT AN APPLICATION, CONTACT:

Dr. Johanne Brunet USDA, ARS Vegetable Crops
Dept. of Horticulture University of Wisconsin 1575
Linden Drive Madison, WI 53706 Phone: 608 265- 3587
(Office) Fax: 608 262- 4743 Email: jbrunet@wisc.edu

[http://www.afm.ars.usda.gov/divisions/hrd/-](http://www.afm.ars.usda.gov/divisions/hrd/)

hrdhomepage/vacancy/04086.htm Johanne Brunet
<jbrunet@wisc.edu>

USheffield EvolBehaviour

University of Sheffield

Post Doctoral Research Associate in Quantitative Behavioural Genetics and Speciation

Department of Animal and Plant Sciences

P.I.'s: Dr. Rhonda R Snook, University of Sheffield, and Prof. Allen Moore, University of Manchester

A postdoctoral position is available to join a NERC-funded project examining the consequences of mating system structure on genetic architecture and reproductive isolation in *Drosophila pseudoobscura*. We are currently involved in an experimental evolution study in which we have manipulated the mating system of this naturally promiscuous species, by enforcing monogamy and elevating promiscuity. These selection lines are being used to elucidate the adaptive significance of sperm heteromorphism (production of multiple sperm types within a male) and the nature of sexual conflict in this species.

We seek to complement these studies by quantifying how mating system evolution influences the genetic architecture of morphology and behavioural traits that are relevant to reproductive success. This component of the research will employ a quantitative genetics approach using a half-sib design to calculate additive genetic (co)variances within and between the sexes and to determine the relationship to mating system. We will also determine the role of sexual selection and sexual conflict in promoting reproductive isolation by examining pre- and post-copulatory success between and within the selection lines having different mating systems. The project will also take into account any effects of inbreeding by characterizing the effect of selection on genetic diversity using molecular markers.

The Evolution and Behaviour group at Sheffield has been at the forefront of several recent developments in evolutionary and behavioural ecology, including the integration of mechanistic and functional approaches. The postdoc would interact with this large group. Additional interaction would occur with the Integrative Animal Biology group at the University of Manchester, members of which are experts in quantitative genetics.

Candidate requirements:

The desired candidate will have a strong background in evolution, preferably quantitative behavioural genetics. Applicants with experience in one or more of the following will be preferred: microscopy, measurement and dissection techniques; the use of microsatellites. Experience in *Drosophila* culturing is helpful but not essential. The project is based in Sheffield and will require some weekend work.

The closing date for applications is September 8th, 2004. This full time post can be filled immediately although start date is negotiable and is for 1 year initially, renewable for up to a total of 3 years. The proposed salary range is £18,893 - £24,097, commensurate with experience.

For further details and application packs see the University of Sheffield jobs website (posted by August 16th):

<http://www.shef.ac.uk/jobs/> For informal inquiries and further details of the project, please contact either Rhonda Snook (44 114 222 0126; r.snook@shef.ac.uk) or Allen Moore (44 161 275 7221; allen.j.moore@man.ac.uk).

UTexasAustin Arabidopsis

Post-doc on the evolutionary genetics of adaptation in Arabidopsis

An NSF funded Post-doctoral position is available as part of a collaboration to explore the evolution of physiological adaptation in *Arabidopsis thaliana*. The goal of the project is to identify and characterize genes underlying naturally-occurring variation in drought adaptation using genome-wide molecular techniques and whole-plant physiology. Our approach fo-

cuses on screens of *A. thaliana* accessions from around the world, QTL and linkage disequilibrium mapping of a set of core phenotypes, and studies of natural variation in gene expression. A two-year post-doctoral position at UT Austin is available to pursue research on various aspects of evolutionary genetics, including fine-mapping and efforts to characterize and clone ecologically-important QTL.

We are looking for a highly motivated individual with a Ph.D degree and with the demonstrated ability to carry out outstanding research in Plant Genetics. The successful candidate must have experience in high-throughput genotyping and a strong background in molecular biology. Preference will be given to candidates with the following skills needed for map based cloning: DNA sequencing, cloning of PCR products, plant transformation, RT-PCR, and SNP genotyping. We also emphasize the ability to interact and work collaboratively with others. The post-doc will co-ordinate closely with our physiological genetic and computational efforts, as well as a technician, graduate students, and undergraduate researchers at UT Austin.

Application review begins immediately and will continue until the position is filled. Applications should include a brief cover letter outlining qualifications and interests, curriculum vitae, reprints or thesis chapters, and the names and addresses of three references. Send applications to

Tom Juenger Section of Integrative Biology University of Texas at Austin 1 University Station C0930 Austin, Tx 78712 512-232-5751

or via e-mail to tjuenger@mail.utexas.edu.

Preferred start date will be between October 2004 and January 2005.

The University of Texas at Austin is an affirmative action, equal opportunity employer committed to excellence through diversity.

“Thomas E. Juenger” <tjuenger@mail.utexas.edu>

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BertinoroItaly RECOMB ComparativeGenomics

Second Call for Papers

Second RECOMB Satellite Workshop on Comparative Genomics

Location: BICI Bertinoro International Center for Informatics, Bertinoro, Italy, see

<http://www.cs.unibo.it/bici/> The RECOMB Satellite Workshop on Comparative Genomics is a forum on all aspects and components of this field, ranging from new quantitative discoveries about genome structure and process to theorems on the complexity of computational problems inspired by genome comparison.

IMPORTANT DATES: Submission Deadline: August 30, 2004. Notifications to Authors: September 16, 2004. Workshop: October 16-19, 2004 Information on participation, registration, accommodations, and travel can be found at:

<http://www.nada.kth.se/~jensl/recombcg2004.html>
Program committee chair: Jens Lagergren, Stockholm Bioinformatics Center & KTH

Organizers: Jens Lagergren, Stockholm Bioinformatics Center & KTH; Aoife McLysaght, Trinity College; Nancy Moran, University of Arizona Bernard Moret, University of New Mexico; David Sankoff, University of Ottawa.

Accepted papers will be compiled for a volume of Lecture Notes in Bioinformatics (<http://www.springer.de/comp/lncs/index.html>).

David Sankoff <sankoff@uottawa.ca>

Curacao CoralReefs Spring

Hello All:

We have two openings left in a new course we will be teaching the Spring of 2005. It is a 6 credit semester-

long, graduate course where 10 weeks will be spent at CARMABI Marine Laboratory on Curacao (Netherlands Antilles) learning to do field research. This graduate course is open to seniors with adequate background coursework (see list of pre-requisites). It will consist of 5 modules taught by different faculty, and a 3-week period at the end for students to focus on their individual research projects. Undergraduates can concurrently enroll in BIO 480 Field Biology for an additional 6 credits to be fully enrolled (12 credits). Diving certification is required. The full information about the course, the syllabus, the cost structure, as well as the applications forms can be found on my web page [see address in my signature]. Partial scholarships, and special out-of-state tuition rates are available to qualified applicants. The deadline has been extended to August 30th (on web page states Aug 15th). Interested students should contact me immediately.

Thank you for your help in directing this information to students that might be interested in this new offering. We are especially interested in attracting minorities and students from the Caribbean.

Alina Szmant

Dr. Alina M. Szmant Coral Reef Research Group UNCW-Center for Marine Science Presently in Field: 371 Bahia Dr, Key Largo FL 33037
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RiodeJaneiro Phylogeny Nov1-7

Dear all,

Could you please pass this on to anybody that might be interested. We are particularly interested in getting this message out in South and Central America.

EMBO Phylogenetics Course November 1st - November 7th 2004. Fundacao Oswaldo Cruz, Rio de Janeiro.

Applications are sought for this EMBO-funded course on phylogenetic methods for genome analysis. The tuition fees and accommodation and food expenses are being met by EMBO and Fundacao Oswaldo Cruz.

The course will focus on phylogenetic methods and their application in the genome era.

Further information, including timetable can be found at:

<http://bioinf.may.ie/EMBO2004/> Kindest regards,

James

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

UArizona DrosophilaSpeciesID Oct28

Drosophila Species Identification Workshop October 28-30, 2004, University of Arizona

The fourth annual Drosophila Species Identification Workshop will be held at the University of Arizona, Tucson, beginning 8:30 AM Thursday October 28. The workshop lasts three full days and includes participation during a fourth day in the Drosophila Comparative Genomics Symposium on Sunday October 31, a dinner Saturday October 30 at the Arizona Sonoran Desert Museum, and a traditional Mexican meal at the home of Therese Markow on Friday October 29.

Workshop participants will be instructed in Drosophila anatomy and the use of taxonomic keys to identify Drosophila. Following an overview of the species in the genus Drosophila, the workshop will focus on four species groups: melanogaster, obscura, virilis, and repleta. Participants will also receive instruction in the preparation and examination of polytene and metaphase chromosomes. Instructors include Patrick O'Grady, Bryant McAllister, Therese Markow, Marvin Wasserman, Steve Schaeffer, William Heed, Nicolas Gompel.

Space in the workshop is limited to 12 participants and it has filled up quickly in previous years. Those interested in signing up for the workshop should contact Sharon Richards of the Center for Insect Science, University of Arizona at insects@arizona.edu. The fee for attending the workshop is \$350.

Teri Markow <tmarkow@public.arizona.edu>

UAzores MarineMolMarkers Sep1-6

IMAR Institute of Marine Research (DOP-University of the Azores) is organising the following workshop: “use of molecular markers for the study of marine biodiversity” from 1-6 September 2004 and it will be held in Horta (Azores).

This workshop is FREE OF CHARGE for students but please, sort out your flight and accommodation. For further information and applications, please contact Sergio Stefanni at sstefanni@notes.horta.uac.pt

This workshop aims to lead PhD students and young scientists through traditional and more up-to-date methodology of analysing molecular data for the study of marine biodiversity. This subject has become an important issue in the scientific community and the use of molecular tools is of invaluable help. Therefore, with this workshop, we gather together several world-leading experts of marine molecular ecology to give a unique opportunity to students to analyse their own datasets. Seminars followed by tutorials should make the students familiar with the use of designed software's, and the variety of subjects presented by the invited speakers will cover a large spectrum of organisms inhabiting or associated to the sea. Applicants are strongly advised to bring their own datasets as they will analyse them during the workshop. The selection of the candidates is done to equally fill each of the fields of expertise: marine invertebrates (sea urchins, deep sea and hydrothermal vents), fish, sea turtles, marine mammals and seabirds.

The structure of the workshop is as follows: Introduction to mathematical models and building trees/networks techniques applied on molecular data (sequences and microsatellites) Practical exercises on specially prepared datasets for the students. Daily seminars with practicals on the different group of marine or sea associated organisms. Small groups of students, divided according to type of molecular markers used in their projects, with the aim of analysing their own datasets under the supervision of the related field experts. Presentation of students' work based on elaboration of their own datasets is expected to conclude the workshop.

Workshop schedule: Sept 1 9:15-9:30 opening session and welcome (R.S. Santos, Director of Dept. of Oceanography and Fisheries, University of the Azores) 9:30-12:00 lectures (Giorgio Bernardi & Gia-

como Bernardi): - The neo-selectionist theory of evolution: An ultra-Darwinian view - Evolution of coral reef fish *Thalassoma* spp. (Labridae). Molecular phylogeny and biogeography 14:30-17:30 lecture and tutorial (Giacomo Bernardi): - Structural approaches to sequence evolution: Molecules, networks, populations Sept 2 9:00-12:00 lectures (T. Patarnello & H.A. Lessios): - Messinian crisis: macro and micro-evolutionary processes that affected Mediterranean marine fauna - The use of mitochondrial DNA to detect global-scale barriers to Gene Flow of Shallow Water sea urchins 14:30-17:00 lectures (A.R. Hoezel + S. Querouil): - Molecular ecology of marine mammals - Social organization and population genetics of bottlenose dolphins and sperm whales around the Azores Sept 3 9:00-12:00 lectures (S.A. Karl & D.R. Dixon): - Complex population structure in sea turtles - Molecular characterisation of pelagic larvae & molecular biology of hydrothermal vent organisms 14:30-17:00 Tutorials on students' data sets and students' questions Sept 4 10:00-12:00 lectures (R. Bettencourt & S. Stefanni): - Genes that fight infection: what Bivalves say about innate immunity - Phylogeography of two blennies, *Lipophrys pholis* and *Coryphoblennius galerita* and the prospects of two new endemisms for the Azores 14:30-17:00 Tutorials on students data sets and students questions Sept 5 Excursion Sept 6 9:00-12:00 lectures (T.M. Burg & J. Bried): - Review of Seabird Genetics - Combining genetic and demographic data to determine genetic vari-

ability and population structure in the wandering albatross (*Diomedea exulans*) 14:30-17:00 presentations by students and closing session

List of invited speakers: Giacomo Bernardi Associate professor of Molecular Ecology and Evolutionary Biology at the University of California, Santa Cruz. Giorgio Bernardi President of Stazione Zoologica Anton Dohrn, Naples, Italy T. Patarnello Professor of Zoology, Department of Biology, University of Padova, Italy. H.A. Lessios Staff Scientist, Smithsonian Tropical Research Institute, Box 2072, Balboa, Panama, R.A. Hoelzel Reader in Molecular Ecology, Dept of Biological Sciences, University of Durham, UK. S.A. Karl Associate professor Molecular Ecology, Evolution and Conservation Biology at the University of South Florida. D.R. Dixon Group leader of the molecular genetics group, George Deacon Division for Ocean Processes, Southampton Oceanography Centre, University of Southampton, United Kingdom. T.M. Burg Post-doctoral researcher, Dept. of Biology, Queen's University, Kingston, Canada.

List of local speakers: S. Stefanni

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

Instructions

Instructions: To be added to the EvoDir 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 EvoDir 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 EvoDir direct them to the email evodir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as \LaTeX files, Excel files, etc. . . . plain old ASCII will work great and can be read by everyone. Add a subject header that contains one of the keywords

“Conference, Grad, Job, Other:, Postdoc, Workshop” and then the message stands a better chance of being correctly parsed.

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. So 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.