EvolDir

July 1, 2004

Month in Review

Forward

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

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

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

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Conferences

Auckland Bioinformatics Sept

Dear colleagues

This is just a reminder that the early registration deadline for the 2004 International Conference on Bioinformatics is 30 June 04. Please visit the website www.incob.org to register.

We have an exciting line up of speakers, and it is shaping up to be an excellent conference. Students, don't forget that you can submit an abstract for a poster or an oral presentation.

Also, check out the pre-conference workshop on parallel computing in bioinformatics – well worth attending.

The following are just some of the events taking place in Auckland over the period of the conference:

* Self and other - The Expressionist Spirit in New Zealand Art, free, until 10 October 2004 www.aucklandartgallery.govt.nz . * Harbour Cruises aboard Ted Ashby, traditional sailing scow, until 30 December 2004, Tues 12pm-2pm, Thurs 12pm-2pm, Sat-Sun 12pm-2pm, New Zealand National Maritime Museum, Viaduct www.nzmaritime.org . * Unseen Worlds - New Dimensions, the art of science is unveiled in this exhibition of magnified images from our usually unseen world., donation, until 3 October 2004, Auckland War Memorial Museum www.aucklandmuseum.com . * Who's afraid of Virginia Woolf? by Edward Albee - presented by Auckland Theatre Company, directed by Colin McColl starring David McPhail and Jennifer Ludlam, until 18 September 2004, 8pm, Maidment Theatre www.atc.co.nz . * A Festival of Russian Ballet. Following sellout performances of THE NUTCRACKER in 2003 The Imperial Russian Ballet Co return with a stunning and diverse medley.

* The Whale Rider - On Stage is now a new multi-million dollar theatrical production which follows closely the story of the novel taking the audience on a journey between two worlds.

For more information, refer to the following websites:

http://premier.ticketek.co.nz/Ticketek/default.asp http://www.aucklandcity.govt.nz/whatson/events/ http://www.leadingattractions.co.nz/where_to_go/-auckland.htm I look forward to seeing you here in September. Regards,

Allen Rodrigo a.rodrigo@auckland.ac.nz

Hawaii Biocomputing Jan4-8

Call for Papers and Participation

———————————-

Computational Methods for Inferring SNP Function: Integrating Evolutionary, Structural, and Comparative Genomics MANUSCRIPT SUBMISSION DEADLINE: July 19, 2004

A Pacific Symposium on Biocomputing (PSB) 2005 Session January 4-8 at the Fairmont Orchid, Hawaii http://psb.stanford.edu http://psb.stanford.edu/cfp-snps.html Summary ——- Single nucleotide polymorphisms (SNPs) are the most prevalent form of genetic variation within populations. Recent technological advances have enabled the accumulation of massive amounts of data on SNPs (>15 million entries in dbSNP) from within a wide range of species (e.g., human, Drosophila, Anopheles, mouse, dog, Arabidopsis, maize, and Plasmodium). Upcoming sequences of the chimpanzee and rat genomes provide the possibility for comparison of population genetic variation with species divergence at the genome scale.

Although the majority of SNPs are likely to be neutral both evolutionarily and functionally, some SNPs can alter the structure or function of DNA, RNA, or proteins. If these molecular changes affect the organism's phenotype, natural selection can operate on the SNP alleles. Because evolution acts on phenotypes which impact survival and reproduction, the identification of functionally important variation is integral to important research problems ranging from medicine and agriculture to basic genetics.

This session will focus on statistical and computational methods for inferring functional SNPs and their consequences, with an emphasis on novel approaches that merge population and comparative genomics. The recent avalanche of SNP data has led to rapid development of new techniques and models in a variety of research disciplines, and we encourage manuscript submissions that combine approaches from fields such as bioinformatics, computational biology, evolutionary and human genetics, and molecular and cellular biology.

Session Topics ———— Possible manuscript topics include (but are not limited to):

* Comparative genomic methods for detecting SNPs that affect gene regulation * Biophysical studies investigating the effect of SNPs on protein structure and function * Association (linkage) studies pursuing the detection of correlation among SNP variants with specific phenotypes * Population genetic models for detecting natural selection on SNPs * Novel approaches for integrating microarray data and evolutionary analysis

Session Chairs ———— * Carlos Bustamante, Cornell University cdb28@cornell.edu * Shamil Sunyaev, Harvard University ssunyaev@rics.bwh.harvard.edu * Matt Dimmic, Cornell University mwd8@cornell.edu

Papers, Oral Presentations, Posters, and Demonstrations

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The core of the conference consists of peer-reviewed full-length papers reporting on original work. All submitted papers will be subject to rigorous review by several referees, and must represent original, unpublished results which are not currently under consideration elsewhere. Accepted papers will be fully indexed in Medline and published by PSB in its hard-bound archival proceedings. In addition, a limited number of papers will be selected for oral presentation. Because PSB sessions are conducted sequentially, these talks will be presented to the entire conference.

Researchers who wish to present their research without publication in the proceedings are encouraged to share their results and ideas in the poster session. Posters will be displayed throughout the conference, and computer workstations are also available for software demonstrations and Web site presentation. To be included in the poster abstract book distributed at the conference, a one-page abstract must be submitted by November 1 to Larry Altman at altman@smi.stanford.edu. Poster abstracts are not peer-reviewed.

Conference Deadlines ————— * Full manuscript submissions due: July 19, 2004 * Notification of paper acceptance: August 30, 2004 * Poster/demo abstract deadline: November 1, 2004 * Meeting: January 4-8, 2005

For more information, visit the website of the 2005 Pacific Symposium on Biocomputing at http:/-/psb.stanford.edu .

Lyon IPG Oct13-15

Conference: Integrative Post-Genomic IPG'04 - Lyon, France, October 13-15 2004

IPG '04. Call for abstracts. Please disseminate freely.

The goal of IPG'04 is to promote exchanges between scientists from different disciplines (biology, mathematics, computer sciences) who are interested in the extraction of knowledge from the wealth of data generated by genome or post-genome projets.

Topics of interest include (the list is not exhaustive): genome analysis, evolutionary genomics transcriptome and proteome analysis data mining system biology, regulatory networks analysis artificial life, modeling of biological systems

Abstracts presenting results of multidisciplinary approaches will be favored.

Abstracts (maximum 500 words, in English) must be submitted before the 1st september 2004 through the IPG website : http://ipg.insa-lyon.fr/ The notification of selected abstracts (for poster sessions or oral presentations) will be available on 17 september 2004 through the IPG website. –

Laurent Duret Pole BioInformatique Lyonnais Laboratoire BBE - UMR CNRS 5558 Phone : +33 (0) 4 72 44 62 97 Université Claude Bernard - Lyon 1 FAX : +33 (0) 4 72 43 13 88 16 rue Raphaël Dubois F-69622 Villeurbanne Cedex e-mail : duret@biomserv.univ-lyon1.fr France http://pbil.univ-lyon1.fr/

Marseille EvolBiol Abstracts

The first round of accepted abstracts to be presented a the the 8th Evolutionary Biology Meeting at Marseille will be available at the meeting web site

http://www.up.univ-mrs.fr/evol/congres/ the 06/19/2004

the definitive program will be on line the 07/02/2004

Best regards Pierre

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

SanDiego SexSelection Jan4-8

We would just like to draw attention to a symposium within the Society for Integrative and Comparative Biology conference in San Diego, January 4-8, 2005. Online registration opens July 16.

http://www.sicb.org/meetings/2005/index.php3 Symposium: Sexual Selection & Mating Systems in Hermaphrodites Organizer: Janet L. Leonard, University of California-Santa Cruz, jlleonar@cats.ucsc.edu

List of Talks: Janet L. Leonard, University of California-Santa Cruz: Sexual selection in hermaphrodites: what does it look like and where do we find it?

Michael T. Ghiselin, California Academy of Science: “Hermaphroditism: where did our ideas come from?

Manfred Milinski, Max-Planck Institute for Limnology: ”Fitness consequences of selfing and outcrossing in the cestode, Schistocephalus solidus.“

M. C. Lorenzi and Gabriella Sella, University of Turin: Life-history and sex allocation strategies in a simultaneously hermaphroditic polychaete worm”

Colette St. Mary, University of Florida: “Effects of density on sex allocation mediated through changes in mating system rather than sperm competition”

James Thomson, University of Toronto: Tactics for male reproductive success in plants: contrasting insights of sex allocation theory and pollen presentation theory“

Andrew Pemberton and John Bishop, Marine Biological Association, Plymouth: Plant-like mating in sessile animals by the release and uptake of aquatic sperm

Joanne Webster , Imperial College, London and Oxford University: Snails and Schistosomes - Sex and Success

Joris Koene , Free University, Amsterdam: Tales of two snails: mating behavior and sexual selection in Lymnaea stagnalis and Helix aspersa

Raymond T. Bauer, University of Louisiana, Lafayette: ”Same sexual system but variable sociobiology: evolution of protandric simultaneous hermaphroditism in Lysmata shrimps“

Christopher W. Petersen, College of the Atlantic: Sexual conflict and cooperation in hermaphroditic fishes

Stephen C. Weeks, University of Akron: The evolution of androdioecy in the ephemeral pool clam shrimp, Eulimnadia texana

Lynda Delph, Indiana University: Sexually dimorphic traits affecting mate acquisition in gynodioecious plant species

Nico Michiels, University of Münster: ”The transition from hermaphroditism to dioecy“

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SandbjergDenmark EvolStress Aug22-26 2

Second announcement:

Symposium

Progress in Environmental Stress, Adaptation and Evolution

August 22-26, 2004 at Sandbjerg, Denmark

Sponsors:

European Society of Evolutionary Biology (ESEB)

Center for Environmental Stress Research and Faculty of Sciences, 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 evolutionduring 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 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)), not later than the 7th of June. As we, in addition to the invited speakers, can only accommodate around 35 participants, the symposium might easily become full. 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

Deadline: June 7, 2004 (you will hear about acceptance not later than June 15, 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: <http://www.sandbjerg.dk/en/> www.sandbjerg.dk/en/ .

Participants: maximal number approximately 50 (except for some invited speakers allotted to ESEB members).

Costs: The conference fee is Euro 450 for ESEB members Euro 550 for non-members. (Thus ESEB members get a discount of Euro 100, which is more than twice the yearly membership fee including the printed version of

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UQueensland AncientDNA Jul12-16

The Ancient DNA and Associated Biomolecules Conference is being held at The University of Queensland, Brisbane, Australia from the 12-16th of July 2004. The conference focuses on the analysis of DNA and other biomolecules from archaeological, ancient, damaged and or degraded specimens in order to investigate evolution of species, phylochronolgy, phylogeogaphy, taxonomy of extinct species, history and evolution of disease, preservation of DNA and other biomolecules and much more.

We are still accepting abstracts for all session. Abstracts of around 200 words can be submitted by e-mail to abstracts.dna7@uq.edu.au.

For further information about the conference, including some of the abstracts accepted to date, please visit the conference website at http://dna7.ansoc.uq.edu.au or e-mail enquiries.dna7@uq.edu.au

Regards Tamara Brown

On Behalf of the DNA7 Conference Committee The School of Social Science The University of Queensland St Lucia 4067 Australia

Ph: +61 (7) 3365 7252 Fax: +61 (7) 3365 1544 e-mail: enquiries.dna7@uq.edu.au

Register for the DNA7 Conference Online Now at: http://DNA7.ansoc.uq.edu.au DNA7 Conference Committee <enquiries.dna7@uq.edu.au>

Valencia MEEGID Jul19-22

19/06/04

Dear Colleague,

the program of the 7th congress Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases (MEEGID VII), to be held in Valencia, Spain, 19th-22nd July 2004, is now finalized. Human biology related to the transmission and severity of infectious diseases has been given much importance, with 2 plenary lectures and a 3-way debates of 2 hours. Many communications dealing with parasites, bacteria, viruses, vectors, will be held. I recall that MEEGID VII is organized in connection with the 9th European Multicolloquium of Parasitology (EMOP 9). A special issue of Infection, Genetics and Evolution will be published with the abstracts and selected papers.

Still time to register!

Welcome to Valencia.

Michel Tibayrenc, MD, PhD Editor -in-chief Infection, Genetics and Evolution (Elsevier) http://www.elsevier.nl/locate/meegid Director Unit of Research 165 “Genetics and Evolution of Infectious Diseases” UMR CNRS/IRD 2724 IRD, BP 64501 34394 Montpellier cedex 5, France Tel. 33 4 67 41 61 97 (secretary) 33 4 67 41 62 07 (direct) Fax 33 4 67 41 62 99 Email Michel.Tibayrenc@mpl.ird.fr Website http://cepm.mpl.ird.fr Website MEEGID VII: http://www.uv.es/emop9/MEEGID Programme MEEGID VII updated 19th June 2004

Plenary lectures

(1) How Pathogens and other agents of natural selection Generate Human Genetic Diversity and Genetic Load . Henry Harpending, Salt Lake University, USA.

(2) Parasite Escape from Host Immunity by Antigenic Variation. Steve Frank (UC Irvine, California)

(3) Influenza evolution: linking sequence, structure and function. Robin Bush (UC Irvine, California)

(4) Leishmaniasis in India. Shyam Sundar, Institute of Medical Sciences, Benares Hindu University,

(5) The past, present and future of parasite genome sequencing projects. Jane Carlton (The Institute for Genomic Research [TIGR], Rockville, Maryland)

(6) SARS molecular evolution and epidemiology. Michael Stanhope (GlaxoSmithKline, Collegeville, Pennsylvannia)

(7) Symbiosis and evolution: a genomic perspective on bacteria-insect association. Andrès Moya (University of Valencia)

(8) The emerging global threat of viral zoonoses. Brian Mahy (CDC Atlanta)

(9) The HGDP-CEPH Human Genome Diversity Panel, A Resource for Human Population Genetics Research. Howard Can (Fondation Jean Dausset, Paris, France)

(10) The impact of megatechnologies on infectious disease research. Jolyne Drummelsmith (Centre de Recherche en Infectiologie, Université Laval, Québec, Canada)

(11) The population genetics of clonal and partially clonal diploids: analytical and simulation results. Thierry de Meeus (IRD, Montpellier, France)

Symposia (2 hours, 4 to 6 communications)

(1) Cryptosporidium and Giardia molecular epidemiology and evolution. Chair: Andrew Thompson, Murdoch University, Australia and Eduardo Pozio, Roma, Italy

(2) Host/parasite coevolution; methods approaches, questions. Chairs: Jean-Pierre Hugot, Museum National d'Histoire Naturelle, Paris, and Jean-Paul Gonzalez, IRD, Mahidol University, bangkok, Thailand (common with EMOP)

(3) Leishmania: human and parasite genetics Chair: Marie-Anne Shaw, University of Leeds, UK and Anne-Laure Bañuls, IRD, Montrpellier, France.

(4) Mathematical modelling in infectious diseases epidemiology. Chair: Marc Choisy, IRD, Montpellier, France and Olivier Restif, Cambridge University, UK.

(5) Morphometrical approaches in vector studies. Jane Costa, Fiocruz, Rio de Janeiro, Brazil and Jean-Pierre Dujardin, IRD, Montpellier, France

(6) Mycobacterium tuberculosis molecular epidemiology and evolution. Seyed Hasnain, Centre for DNA Fingerprinting and Diagnostics (CDFD), Hyderabad, India, and Philip Supply, Pasteur Institute, Lille, France

(7) Nosocomial infections. Chairs: Christian Carrière and Sylvain Godreuil, Hospital of Montpellier, France.

(8) Plasmodium vivax population biology. Jane Carlton, The Institute for Genomic Research [TIGR], Rockville, Maryland and Franois Renaud, IRD, Montpellier, France

(9) Population genetics and phylogenetic studies of vectors. Chairs: Lola Ochando, University of Valencia,(Spain) and Jean-Pierre Dujardin, IRD, Montpellier, France

(10) Population genetics of Toxoplasma gondii.Chairs: Marie-Laure Dardé, faculty of Medicine, Limoges, France and Andrew Thompson, Murdoch University, Australia

(11) Species concepts in bacteria. Chairs: Fred Cohan, Wesleyan University, Middletown,Connecticut, and Sylvain Brisse, Pasteur Institute, Paris, France

(12) Trypanosoma cruzi: how many divisions? Chairs: Michael Miles, London School of Hygiene and Tropical Medicine, UK and Michel Tibayrenc, IRD, Montpellier, France

Three-way Express debate on human genetic diversity and infectious diseases (2 h, 3 talk of 20 mn followed by a 60 mn free debate)

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GradStudentPositions

DalhousieU LifeHistoryTheory

Ph.D. Project: Risk-Sensitive Life History Theory: When is Gambling Adaptive?

Adaptive trade-offs are normally studied from the point of view of the mean returns to be gained from alternative fitness enhancing options (e.g. mean fitness when producing many small offspring versus few large offspring). However, risk-sensitive foraging has highlighted the importance of variance when considering such adaptive decision-making. Depending on the shape of the fitness function, individuals should be risk-averse (playing it safe) or risk-prone (gamblers). Evidence to support these predictions has been around for a number of years in the foraging literature (see Real & Caraco 1986 Ann. Rev. Ecol. Syst. 17, 371-390). However, few attempts have been made to apply such thinking to a wider range of evolutionary problems. The purpose of this PhD will be to re-examine existing theory and data, and to carry out original experiments to test whether risk-sensitivity has applications outside the study of foraging behaviour.

Prof. Jonathan Wright, Department of Biology, NTNU, 7491 Trondheim, Norway. Phone: +47 735 96070 Fax: +47 735 91309 E-mail: jonathan.wright@bio.ntnu.no

Jonathan Wright <jonathan.wright@bio.ntnu.no>

MississippiStateU PlantSystematics

Two graduate research assistantships in PLANT SYSTEMATICS (PhD preferred) are available beginning August 2004 or January 2005 in the Department of Biological Sciences at Mississippi State University. Students supported on these NSF funded assistantships will participate in ongoing phylogenetic studies of Asclepias (Apocynaceae/Asclepiadaceae) and develop their own independent projects. Applicants with strong backgrounds in molecular biology or computational biology are especially encouraged to apply. Stipends are $16,000 per year and may be renewed for up to three years. Applications will be evaluated as they are received.

Ecology and evolutionary biology comprise a focal area for the Department, with faculty conducting research in plant systematics and evolution, pollination biology, plant ecology, stream ecology, avian ecology, marine ecology, and genomics. Information about the Department and graduate studies can be found at http://www.msstate.edu/dept/biosciences. The Department is also the home of an NSF funded REU program in Conservation biology (http://csmt.msstate.edu/html/REU/). Mississippi State University is located in a rural area in close proximity to a wide variety of natural communities, including prairies; oak-hickory, mixed hardwood, and pine forests; cedar glades; and wetlands. The Gulf of Mexico and southern Appalachians, as well as major cities (New Orleans, Atlanta, Memphis) are within a 5-hour drive.

Interested persons should send a CV, statement of research interests, GRE scores, unofficial transcripts, and names of three references, and arrange for reference letters to be sent to: Dr.Mark Fishbein (fish@biology.msstate.edu; http://www.msstate.edu/dept/biosciences/fishbein/mf.html), Department of Biological Sciences, Box GY, Mississippi State University, Mississippi State, MS, 39762.

Mark Fishbein Assistant Professor Director, Miss. St. Univ. Herbarium (MISSA) Department of Biological Sciences Mississippi State University P.O. Box GY Mississippi State, MS 39762 USA ph: (662) 325-7577, -7570 fax: (662)325-7939 email: fish@biology.msstate.edu

SELouisianaU PlantEvolEcol

Rick Miller's Lab - Grad position - Masters in Plant Evolutionary Ecology and Systematics

My research focuses on the evolutionary ecology and systematics of morning glories. I have an opening for a masters student in my lab at Southeastern Louisiana University in Hammond, LA, which will be supported on an RA (stipend and tuition waiver). I generally view our program as an excellent opportunity for young scientists to carry out independent research before making a commitment to a Ph.D. program. SELU has an excellent and active group of biologists (see Graduate Faculty Research Interests at www.selu.edu/Academics/Depts/Biology) and together we provide an exciting environment to carry out research.

A wide range of studies related to my current research would make excellent master's projects. Investigations could include such topics as the pattern of selection and constraints affecting life history traits, evolution of reaction norms, phylogenetic systematics, adaptive radiation, and taxonomy. I use morning glories as a model system and have made good progress towards developing a well-resolved phylogeny for groups of these species. It is a morphologically diverse group of plants found in the subtropics and tropics worldwide with perhaps as many as 1000 species.

I have a well-equipped new molecular lab in a new biology building, we have a new greenhouse, growth chambers, and I am in the process of developing experimental gardens.

The natural history of the area is fascinating, including longleaf pine savannas and cypress-tupelo swamps. Hammond is one CD away from New Orleans (you put a CD in the player and when its finished, there you are) with its great music, art, and cuisine.

For further information please contact me by email at rickmiller@selu.edu.

Rick E. Miller, Ph.D. Department of Biological Sciences Southeastern Louisiana University Hammond, LA 70402 985 549-5556 (phone) 985 549-549-3851 (FAX) E-mail: rickmiller@selu.edu Web: http://www.selu.edu/Academics/Faculty/rickmiller

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UAuckland Yeast

PhD scholarships (2)

Research Field: Yeast molecular genetics Research Topic: Wine aroma Institution: University of Auckland Academic supervisors: Prof. Richard Gardner, Dr Mat Goddard

Description: The chemical constituents of some of the major aromas and flavours in Sauvignon Blanc have recently been elucidated. Three of the most dominant aromas are derived from flavour-active volatile thiols. These are formed during the fermentation of the wine by yeast, which convert flavourless, non-volatile precursors (cysteine conjugates) that are present in grape juice. The goal of the project is to develop yeast strains with differing efficiencies of conversion of the various thiol compounds.

PhD student 1 (Supervisor: Richard Gardner) will identify and characterise the genes responsible for uptake and conversion of the thiol precursors.

PhD student 2 (Supervisor: Mat Goddard) will analyse the genetic variation of the trait and the genes among commercial wine yeast strains and natural populations of wine yeasts.

Qualifications: Applicants must have an MSc, BSc hons, or equivalent in a relevant subject. Practical experience of molecular genetics or biochemistry, especially with yeast, is an advantage.

Stipend: The PhD studentships pay $25,000 per annum and full fees.

Start date: After July 1 2004 (PhD1) or after Nov 1 2004 (PhD2).

Applications: Please email cv (including names and email addresses of three referees) and covering letter to Cathy Corbett (c.corbett@auckland.ac.nz). There is no closing date.

Further information: Both students will be based in yeast genetics labs in the School of Biological Sciences at the University of Auckland (www.sbs.auckland.ac.nz). The research maintains close contacts with analytical chemists (Laura Nicolau, Paul Kilmartin) in the wine science programme (www.che.auckland.ac.nz/wine). The work is part of a new, 6-year, FRST-funded project that is currently investigating the potential of New Zealand^{1}s Sauvignon Blanc wines. The project includes expertise in viticulture and sensory science and has strong links with the New Zealand wine industry (www.nzwine.com). More information on the projects can be obtained from r.gardner@auckland.ac.nz or m.goddard@imperial.ac.uk. The University of Auckland is New Zealand^{1}s largest University and SBS is the top-ranked biology department nationally. The University is situated in the heart of the cosmopolitan city of Auckland and provides an exciting and stimulating environment for 26,000 students. Auckland has a population of 1 million people and is located adjacent to harbours and beaches, and within a four hour drive of winter skiing.

Dr. Matthew R Goddard N.E.R.C. Centre for Population Biology Department of Biological Sciences Imperial College at Silwood Park Ascot SL5 7PY U.K.

Tel (Direct): +44 (0)20 7594 2470 Tel (Reception): +44 (0)20 7594 2475 Fax: +44 (0)1344 873173 http://www.cpb.bio.ic.ac.uk/staff/goddard/mgoddard.html m.goddard@imperial.ac.uk

UCanterbury Avian bottlenecks

PH.D. SCHOLARSHIPS to study the effect of population bottlenecks on New Zealand birds. Two scholarships are available at the University of Canterbury, Christchurch, New Zealand to study the consequences of severe population bottleneck size in New Zealand birds. The first project will examine how severe population bottlenecks affect the susceptibility of a population to parasitic infection and disease resistance. The second project will examine how severe population bottlenecks affect reproductive success. Both projects will focus on about 15 species introduced to New Zealand in the 19th century and that have gone through bottlenecks of varying sizes. Applicants for either position require either a B.Sc. Honours or M.Sc. in Biology. Candidates must be prepared to work in the field and travel. Scholarship $20,000 NZ per year for 3 years (plus $4,000 NZ per year for tuition). For more information or to apply contact JAMES BRISKIE (EM: Jim.Briskie@canterbury.ac.nz). Applicants please send cover letter, CV and names of three references via EM only. Application deadline: 25 July 2004. Start date by negotiation but preferably before 1 October 2004. NOTE that most non-residents of New Zealand are subject to full tuition fees.

James Briskie University of Canterbury Christchurch

James Briskie <Jim.Briskie@canterbury.ac.nz>

ULausanne AntGenomics

Université de Lausanne, Switzerland Department of Ecology and Evolution

PhD student position to work on ant genomics

A PhD student position is available for 3 years in the lab of Professor Laurent Keller (http://www.unil.ch/dee/page7717_en.html). Our group is interested in the principles governing the behavior, ecology, and evolution of animal societies. While this is richly described by theory, how this is translated to the molecular level is virtually unknown. One aim of our group is to use genomic techniques to identify candidate genes and pathways that are associated with the biology of social insects. In particular, we are using use cDNA microarrays to examine gene expression in fire ants. Ultimately, our goal is to elucidate the molecular mechanisms underlying these processes. Possible topics include, but are not limited to, social behavior, caste determination, evolution and aging.

Candidates should be highly motivated and have a good background in molecular, genomic or cell biology. Good knowledge of English is required.

Interested applicants should send a short summary of research interests and experiences (in English) a curriculum vitae as well as the names and emails and phone numbers of 2 references to John Wang by email.

email: John.Wang@ie-zea.unil.ch

John.Wang@ie-zea.unil.ch

ULausanne HumanEvolGenet

PHD POSITION: HUMAN EVOLUTIONARY GENOMICS

A PhD position is available immediately in the group of Henrik Kaessmann at the recently founded Center for Integrative Genomics, University of Lausanne, Switzerland.

Currently we focus on the origin and evolution of primate genes and gene structures. New genes originate through various molecular mechanisms such as the classic mechanisms of gene duplication (e.g. tandem gene duplication), gene copying by retroposition, exon/domain shuffling, and gene fusion. We pursue several projects that aim to shed light on the relative importance of these mechanisms in generating primate genes. We are particularly interested in characterizing the (adaptive) evolution of young genes in the human genome that originated recently on the primate lineage and therefore may be relevant in regard to human/hominoid-specific phenotypes. To this end, we explore available data from genomic databases and generate complementary data by experimental analysis.

For more information on the group and our institute more generally, see the website: http://www.unil.ch/cig For this position, I am seeking highly qualified and motivated applicants with a strong interest in human genome evolution and experimental lab work, because we want to identify and characterize functional adaptive changes of newly emerged genes. Thus, dedicated biochemists or molecular biologists with an evolutionary interest are encouraged to apply as well.

The salary is approximately 30,000 Euros per year.

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

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

Applications including a CV, statement of research interest, copies of relevant publications, and two letters of recommendation should be emailed or mailed to me at the address below. Review of applications will begin imme diately.

Henrik Kaessmann, Ph.D. Assistant Professor Center for Integrative Genomics BEP University of Lausanne CH-1015 Lausanne Switzerland Phone : 41-(0)21-692-3907 Fax : 41-(0)21-692-3905 E-mail : Henrik.Kaessmann@cig.unil.ch Internet : http://www.unil.ch/cig

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UOttawa MolEvol

Multiple funded research associate and graduate student positions available immediately to study:

1. Microarray studies of the effect of environmental hormone-like chemicals (steroids) on gene expression of goldfish brains. Strong quantitative and computational skills required to participate in analyzing microarray data and developing software.

2. Molecular phylogenetics: develop and implement new phylogenetic tools

3. Molecular evolution of mitochondrial and prokaryotic genomes.

Best. Xuhua ==== Dr. Xuhua Xia CAREG and Biology Department University of Ottawa 150 Louis Pasteur, P.O. Box 450, Station A Ottawa, Ontario Canada K1N 6N5 Tel: (613) 562-5800 ext 6886 Fax: (613) 562-5486 URL: http://aix1.uottawa.ca/~xxia

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UPotsdam EvolBiol

PhD grant for 30 months (prolongation possible)

A PhD grant for 30 months (prolongation possible) is immediately available in the newly established graduate school “Earth Surface Processes”:

“Recent and fossil DNA as indicators of past environmental change”

In this project, the distribution of limnic organisms will be assessed in lake sediments of differente age (recent to several 10,000 years old), making use of modern molecular genetic techniques. The project objective is to reveal the impact of climatic change on limnic organisms. This is a joint project of the Institute of Biochemistry and Biology and the Institute of Geosciences at the University of Potsdam.

Applicants must hold a university degree (Diplom oder Master of Science, preferably in biology or biochemistry). They should appreciate interdisciplinary research. Familiarity with modern molecular genetic techniques (PCR etc.) is desired.

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 31st of July 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 Potsdam Institut fuer Biochemie und Biologie Evolutionsbiologie/Spezielle Zoologie Karl-Liebknecht-Str. 24-25, Haus 25 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

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URegensburg Communication

PhD: Chemical communication and intracolonial conflict in ants.

A PhD position (3 years) is available at the Zoological Institute of the University of Regensburg, Germany. The successful applicant will work under the supervision of Dr. Patrizia d Ettorre and join the Evolution, Behavior and Genetics group led by Prof. Juergen Heinze. The project intends to achieve an interdisciplinary understanding of the chemical, neurophysiological and evolutionary principles that have shaped chemical communication in insect societies, using ants as model systems. The research will address generally important questions about intracolonial conflict and the reliability of communication signals. The methodology will consist of a combination of behavioural experiments, genetic, chemical, electro- and neurophysiological studies. Field work in the tropics may be possible. Applicants must have a Diploma or Master's degree in biology. Previous experience in behavioural studies, chemical (GC, GC-MS) and molecular techniques (DNA extraction, microsatellite analysis) would be welcome but is not compulsory. Competence in basic statistical analysis is expected. A good knowledge of written and spoken English is required, German would be helpful as the Ph.D. student will take part in supervising undergraduate students in practicals (2 hrs per week). The fundamental requisite for the successful candidate is being enthusiastic and highly motivated. For further information or to apply please contact: patrizia.dettorre@biologie.uni-regensburg.de The application, consisting of curriculum vitae, list of publications, summary of research interests and a letter of recommendation is to be sent by e-mail to Patrizia d Ettorre in a single file. The position is available from October 2004. Deadline for applications: 20 August 2004.

Dr Patrizia D'Ettorre Dep. Biology I University of Regensburg D-93040 Regensburg phone +49 941 943 2996 fax +49 941 943 3304 http://www.biologie.uni-regensburg.de/Zoologie/Heinze/en/staff.html patrizia.dettorre@biologie.uni-regensburg.de

UWisconsin EvolEcol

Graduate student research assistantships

Two graduate student research assistantships (one M.S. and one Ph.D) are available in the laboratory of Dr. Johanne Brunet at the University of Wisconsin-Madison in the area of evolutionary ecology. Research in the laboratory focuses on gene flow and the impact of transgenes on the environment. The assistanships are available as early as fall 2004, but could start in winter or summer 2005. Depending on the interests of the applicants projects with a more ecological, genetical, or theoretical approaches are available. The research assistanships are for $17,430 per year; tuition is covered and some benefits provided.

Information about the University of Wisconsin-Madison can be found at http://www.wisc.edu. Candidates could join either the graduate program in Plant Breeding and Plant Genetics (PBPG), http://www.hort.wisc.edu/pbpg, or in Horticulture, http://www.hort.wisc.edu. Information about graduate school can be found at http://www.grad.wisc.edu . Candidates should have a strong undergraduate background in biology. For more information contact Dr. Brunet at jbrunet@wisc.edu. Interested candidates should send a curriculum vita, copy of undergraduate and graduate transcripts if applicable, GRE scores, a brief statement of research interests, and three reference letters to Dr. Brunet at the address below.

Johanne Brunet Department of Horticulture 1575 Linden Drive University of Wisconsin Madison, WI 53706 jbrunet@wisc.edu (608) 265- 3587 (Office) (608) 262-4743 (Fax)

UppsalaU ComparativeGenomics

UPPSALA UNIVERSITY, SWEDEN

PhD student position in Molecular Evolution: Comparative genome analyses of bacteria associated with animals, plants and insects

Applicants are invited to a four-year graduate student position in Molecular Evolution at the Department of Evolution, Genomics and Systematics, Evolutionary Biology Centre, Uppsala University, focusing on the exploration of similarities and differences between bacteria that live as symbionts and parasites of plants and animals.

Genomics is revolutionizing the field of microbiology. We have sequenced the typhus pathogen genome, one of the first 20 genomes completed worldwide. Additionally, we have sequenced the genome of an aphid endosymbiont (Buchnera) as well as the genomes of pathogens causing the trench fever (Bartonella quintana) and cat-scratch disease (Bartonella henselae). Our studies have shown that the genomes of intracellular pathogens have been extensively reduced in size, whereas soil microorganisms that interact with plants have evolved by expansion of their genetic material. Still, very little is known about the forces and mechanisms that drive reductions and expansions of gene contents and gene functions, and how these relate to the different types of host-cell interactions. We intend to recruit a PhD student to study the origin, diversity and function of proteins and metabolic networks of bacteria that have evolved close relationships with higher eukaryotes. The projects will involve both experimental and bioinformatic analyses. The successful candidate will have the opportunity to interact with our collaborators in Canada. External funding is available for this project from the Swedish Foundation for Strategic Research (SSF) from a collaborative grant with Genome-Canada.

The group belongs to the Department of Evolution, Genomics and Systematics (http://www.egs.uu.se/), which is part of the Evolutionary Biology Centre. Information about this centre and its coordinated postgraduate education is available at http://www.ebc.uu.se/ .The work will be performed within the research group "Comparative microbial genomics". Interested candidates are welcome to contact prof. Siv Andersson http://artedi.ebc.uu.se/molev/staff/staf/people/-siv.html, who is the main supervisor.

Applicants are requested to have a BSc or MSc in molecular biotechnology, biology or a related field, preferably including courses in molecular biology, bioinformatics and microbiology. Please send a written application, including complete curriculum vitae, brief description of career goals, copies of honor's thesis or similar, the names and e-mail addresses of two references, and other relevant documentation, to Siv Andersson, Department of Molecular Evolution, Evolutionary Biology Centre, Uppsala University, Norbyvägen 18C, SE-752 36 Uppsala, Sweden. Siv Andersson (phone +46 18 4714379, Siv.Andersson@ebc.uu.se)

Applications should be received no later than July 31, 2004.

Jobs

ArizonaStateU AvianBehavioralEvol

RESEARCH TECHNICIAN position in avian behavioral ecology through the School of Life Sciences at Arizona State University. Candidates should have earned a B.S. degree in Biology or a related field. He/she will (a) assist in field studies of local songbird populations, (b) coordinate laboratory activities aimed at identifying colorful pigments and assaying immunocompetence in birds, and (c) help maintain and conduct physiological studies on captive birds. For more information about our research on bird coloration, visit http://sols.asu.edu/faculty/-kmcgraw.php .Experience handling and monitoring wild songbirds and laboratory experience in biochemistry or immunology preferred. Target starting date for the position is 1 September 2004. For the official job advertisement, visit http://www.hr.asu.edu/-vacancy_notice/vacancy_posting.asp?id=115559.

Send cover letter summarizing your qualifications and interests, curriculum vitae, and the names and contact information of three references to: Arizona State University, P.O. Box 875612, Tempe, AZ 85287-5612. Reference SR# O-115559 in your application. Email submissions are accepted (resumes@asu.edu). Direct further inquiries about the position to Dr. Kevin McGraw (Kevin.McGraw@asu.edu). Application deadline is 16 June 2004; if not filled, biweekly thereafter until the position is closed. Arizona State University is an Affirmative Action/Equal Opportunity Employer. – Dr. Kevin McGraw Post-doctoral associate Department of Animal Science University of California-Davis One Shields Avenue Davis, CA 95616

Phone: (530) 752-2401 FAX: (530) 752-0175 Email: Kevin.McGraw@asu.edu Webpages: http:/-/sols.asu.edu/faculty/kmcgraw.php http://-lsweb.la.asu.edu/kmcgraw NEW ADDRESS AS OF 15 AUGUST 2004: Dr. Kevin J. McGraw Assistant Professor School of Life Sciences Arizona State University P.O. Box 874501 Tempe, AZ 85287-4501

Kevin McGraw <kjmcgraw@ucdavis.edu>

Austria MolEvolLab

Molecular Laboratory Position

A laboratory position is being offered at the Institute of Zoology, Karl Franzens University of Graz, Graz, Austria. Minimum required skills are both knowledge of, and experience with PCR and genotyping applications, preferably at an advanced level. Additional skills that would be appreciated are experience in optimising multi-plex PCR reactions and basic cloning procedures. The position is being offered in the framework of a multidisciplinary applied research project, financed by various Austrian government authorities, aimed at developing a genotyping test for local populations of Austrian brown trout Salmo trutta The position is fixed for two years, with possible extension dependant on additional funding. The net monthly salary is approximately 1600 Euros (x 14). Approximate starting time is August 1. Applicants may have a technical degree, master's, or PhD, but skills are emphasised over title. The project will be managed by Univ. Prof. Christian Sturmbauer and Univ. Ass. Steven Weiss. Interested applicants should submit a CV immmediately emphasizing their laboratory work experience, or direct questions to:

Steven Weiss E-mail: steven.weiss@uni-graz.at Office phone ++43-(0)316-380-5599 Mobile phone 0699-19675341

Steven Weiss Ass. Prof. Karl-Franzens Universität Graz Institut für Zoologie Universitätsplatz 2 A-8010 Graz, Austria E-mail: steven.weiss@uni-graz.at <mailto:steven.weiss@uni-graz.at> Office phone ++43-(0)316-380-5599 Mobile phone 0699-19675341

Steve Weiss <steven.weiss@uni-graz.at>

ErasmusU HumanEvolution

Research Scientist in Human Molecular Genetics

A Research Scientist position is available immediately in the newly established Department of Forensic Molecular Biology at the Erasmus MC University Medical Centre Rotterdam, The Netherlands. You will be working on identifying the biological / genetic basis of human individual and population differences (such as physical traits). You have a strong background in genetics and /or molecular biology (PhD) with experience in gene mapping techniques both on the theoretical and practical level, preferable QTL mapping. You are highly motivated, scientifically creative and able to work independently. You are expected to start a new line of research and positions for PhD student / technician will be available. You will be officially appointed by the Netherland Forensic Institute, fulltime for a period of two to three years, with potential possibility of elongation, place of work is Erasmus MC. The gross monthly salary, depending on qualifications and experience, is a maximum is a maximum of 3.945.77 full-time. Erasmus MC offers a state-of-art research environment (check: http://www.erasmusmc.nl).

Please send your application with CV, a description of research interests, publication list and names and contact information for two references to Prof. Dr. M. Kayser, Department of Forensic Molecular Biology, Erasmus MC University Medical Center Rotterdam, Medical-Genetic Cluster, PO Box 1738, 3000 DR Rotterdam, The Netherlands, or prefered by e-mail to m.kayser@erasmusmc.nl.

HarvardU Lepidoptera curator

Sorry-this position is only available to US citizens or those already holding work permits.

Curatorial Assistant II (Lepidoptera) Museum of Comparative Zoology, Department of Entomology Harvard University Cambridge, Massachusetts

A position is available as Curatorial Assistant in the Museum of Comparative Zoology, Department of Entomology, specializing in Lepidoptera. The job reports to the Curatorial Associate in the Department, and involves working closely with the Curator of Lepidoptera on the DNA and Tissues collection. This requires characterizing specimens using molecular systematic techniques, incorporating DNA samples and other molecular materials into the collection, developing protocols and maintaining the database of molecular specimens, and overseeing, preparing and maintaining loans and exchanges of materials and primers. The person in this position serves as a principal source of information on the molecular systematics facility and the collection to visiting scholars, faculty, staff, students and general public, and addresses technical problems and procedures, including preservation, developments in specimen conservation, and preparation and identification techniques. Additional tasks include budget maintenance and reconciliation, ordering supplies from vendors, tracking orders, processing invoices, etc., and performing related duties as required, such as assisting with curatorial needs of the main insect collection. The job is varied, interesting and fun, and involves meeting and interacting daily with a great many undergraduates,graduate students, and postdoctoral fellows.

Qualifications: A minimum of a college background in biology. Familiarity with museum collections, entomology (especially Lepidoptera), sequencing and computer programs used in DNA sequence analysis and systematics, such as Sequencher and PAUP would be preferred.

The position is full time at 35 hours a week, and comes with attractive health and educational benefits.

Start date is flexible, but preferably before August 1.

The formal job description and additional details can be found at: http://jobs.harvard.edu/jobs/summ_req?in_post_id=22090

It is possible to apply for this position on line at the url above, but applicants should also send a CV, short statement of research interests and experience, and contact information for three referees to:

Naomi E. Pierce Hessel Professor of Biology Curator of Lepidoptera MCZ Labs 26 Oxford Street Harvard University Cambridge, MA email: npierce@oeb.harvard.edu (preferred means of communication) tel: (617) 495 2576 –

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

LancasterU StatGenetics

LANCASTER UNIVERSITY

DEPARTMENT OF MATHEMATICS AND STATISTICS

RESEARCH ASSOCIATE POSITIONS IN SPATIAL STATISTICS/STATISTICAL GENETICS

Two positions are available within a programme of collaborative research between the Lancaster Statistics Group and the Veterinary School at Liverpool University. Within the Statistics Group, the research will be led by Prof. Peter Diggle, Prof. Gareth Roberts and Dr. Paul Fearnhead.

The Department: The Lancaster Statistics Group is one of the strongest in the UK (RAE Grade 6*) with an emphasis on the development and application of methodology motivated by substantive applications, and particular strengths in spatial and longitudinal statistics, statistical genetics and computationally intensive statistical methods. The Group currently includes 16 academic staff positions and around 30 research students and research associates.

The research programme: The overall aim of the research is to further our understanding of the transmission and evolution of food-borne zoonotic pathogens.

A specific aim is to model the spatio-temporal distribution and genetic evolution of human Campylobacter infections, using data derived from all recorded cases of human campylobacter gastroenteritis in the Preston district since 1993.

Position 1: spatial epidemiology. The primary focus of the post-holder will be to develop novel methods of spatio-temporal statistical analysis which can take account of genetic information on individual cases, and to apply these, and existing methods, to the Preston data-set. The post-holder will also be expected to assist with general statistical input to the wider programme of collaborative research, which is likely to involve the innovative application of existing spatial and/or longitudinal statistical methods.

This position is available for a four-year period, beginning 1 April 2005.

Position 2: statistical genetics. The primary focus of the post-holder will be to develop suitable stochastic models and inference methods for population genetic data from pathogens such as Campylobacter, and to apply such methods to learn about the biological factors which affect the evolution of Campylobacter. The methods for analysing the population genetic data will involve the use of modern, computationally-intensive statistical methods.

This position is available for a two-year period, beginning 1 April 2005.

The applicant: Applicants should have a higher degree in statistics, a commitment to collaborative research and either a track-record or clear potential for research in statistics. For Position 1, previous experience of epidemiological research or spatial statistics are desirable. For Position 2, experience of computationally-intensive statistical methods and good computing skills are desirable. Background in population genetics would also be useful but is not essential.

Salary: Both appointments will be made on the RA1A scale, currently 18,893to 28,279 pounds per year. Initial salary will depend on the age and experience of the appointee.

Application procedure: To apply or receive further information online, please visit http://www.lancs.ac.uk/-depts/personnel/jobs Alternatively, telephone Personnel Services, quoting reference A282, on answerphone 01524 846549. Informal inquiries can be made to Prof Peter Diggle (p.diggle@lancaster.ac.uk).

Closing date for both positions: Friday 25 June 2004.

NorthernArizonaU EnvGenomics

Assistant Professor/Assistant Director, Environmental Genetics and Genomics Facility (EnGGEN).

The Department of Biological Sciences at Northern Arizona University (NAU; http://www.3.nau.edu/-biology/) invites applications for a tenure-track position to oversee the operations of and provide instruction in NAU's newly established Environmental Genetics and Genomics Facility (EnGGEN). The facility contains DNA preparation, sequencing, and analysis facilities for use by researchers on the Colorado Plateau. Supervision of operations will include coordinating use of the facilities, organizing maintenance, and overseeing supplies. Education and training will consist of the development and/or coordination of theory-oriented seminar courses, technique-oriented workshops, and informal consultation and training on EnGGEN facilities. We anticipate that these activities will take up ~75% of the assistant director?s time (50% management and 25% teaching) with the remainder devoted to establishment of an externally funded research program. The appointment includes nine months of salary support with additional salary to be generated through extramural funding. Qualifications include a Ph.D. in a relevant field and experience working with molecular methods such as DNA extraction, PCR, DNA sequencing using a capillary system, AFLP's and analysis of DNA data.

Please submit C.V., a description of research interests, a statement of teaching philosophy, a statement that describes your commitment to (and/or evidence of) working effectively with diverse student, faculty, and staff populations, and three letters of recommendation to: EnGGEN Search Committee, NAU, Box 5640, Flagstaff, AZ, 86011-5640. E-mail Catherine.Gehring@nau.edu if you have questions. Position is open until filled and subject to availability of funding. Review of applications will begin 8/1/04. NAU is an Equal Opportunity Affirmative Action Institution. Minorities, Women, Persons with Disabilities and Veterans are encouraged to apply.

Amy V. Whipple Merriam-Powell Center for Environmental Research Hanley Hall, Bldg 7 Northern Arizona University Flagstaff, AZ 86011 Fax: 928-523-8223 Phone:(w) 928-523-8727 (h) 928-714-0409 e-mail: amy.whipple@nau.edu http://www.mpcer.nau.edu

ParisMNHN PlantEvol

Professorship in Botany and Plant Evolution in Paris

The National Museum of Natural History (MNHN) in Paris is looking for a permanent Full Professor in Botany and Plant Evolution to start in September 2005. The Dept of Systematics and Evolution at the MNHN holds major zoological and botanical collections, including the Paris herbarium. This department will host the jobholder and provide additional staff for the research group, e.g. research assistants.

The successful candidate will be expected to develop a strong research program in plant biodiversity, possibly including emerging fields such as evo-devo and DNA taxonomy or phylogenetics. Teaching duties will not exceed 40 hours per year.

Knowledge of French is not a requirement. A PhD in biology is essential and managerial and research postdoctoral experience is desirable. The MNHN is an equal opportunity employer. Starting salary is 35 K euros per year, and includes medical care. France provides free education.

As French regulations require that professors at the MNHN first qualify with the National Council of Universities, the present application is set up in two stages (qualification and final interviews). Interested candidates should send a letter of motivation, a 2000-word research programme, cv, list of publications and contact details of two referees as a single electronic pdf file to systevol@mnhn.fr by 13 July 2004 quoting reference BPE2005. Interviews are scheduled for spring 2005.

Michel Veuille <veuille@mnhn.fr>

Smithsonian EvolLabTech

Biological Science Laboratory Technicians (Molecular Biology), Smithsonian Institution

We are looking for technicians to provide research and analytical support for molecular genetics research in the Genetics Program of the Smithsonian Institution, Washington, DC. The technician will conduct laboratory procedures including isolation of DNA from tissues, set-up and running of polymerase chain reactions (PCR), analysis of microsatellites, DNA sequencing, and assisting with the development and screening of genomic libraries for development of microsatellite markers. The technician will enter data into computer databases, and assist with 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 a bachelor's degree in a biological or chemical science, and experience in basic molecular biology methods.

Remuneration will be in the range of $24-28,000 per year, depending on level of experience. Applications will be reviewed beginning15 June 2004, and we expect the position to commence no later than 15 July 2004. Send a letter of application detailing experience in laboratory molecular genetics; current curriculum vitae; and names, addresses and phone numbers of at least three references to: Robert C. Fleischer, Genetics Program, Smithsonian Institution, 3001 Connecticut Ave., NW, Washington, DC 20008. Phone: 202-673-4842; email: fleischer.robert@nmnh.si.edu.

Robert C. Fleischer Genetics Program Department of Zoology National Museum of Natural History Smithsonian Institution 3001 Connecticut Ave., NW Washington, DC 20008-0551, USA phone 202-673-4842; fax 202-673-0040 fleischer.robert@nmnh.si.edu USE STREET ADDRESS

Sydney EvolMuscleDevelopment

A senior or junior technical position is available for a highly motivated scientist to work within the Muscle Development Laboratory of the Victor Chang Cardiac Research Institute headed by Peter Currie, Sydney Australia. The successful applicant will support research studying the genetics of muscle development using zebrafish as a model system. A familiarity with zebrafish as a model system is desirable but not essential. A working knowledge of developmental biology, immunohistochemistry and histological techniques is however required. Applicants can either be a graduate or hold a PhD, given the appropriate expertise, with salary commensurate with experience and qualifications. Interested applicants should contact: Peter Currie p.currie@victorchang.unsw.edu.au –

– Assoc. Prof. Pete Currie Developmental Biology Laboratory head Wellcome Trust Senior International Research Fellow Victor Chang Cardiac Research Institute 384 Victoria Street Darlinghurst Sydney 2010 Australia tel +61 2 9295 8536 fax +61 2 9295 8537

p.currie@victorchang.unsw.edu.au

UAmsterdam SystematicZoology

The University of Amsterdam is seeking candidates for a full professorship in Systematic and Geographic Zoology. The search committee is especially interested in candidates with the ambition to link expertise in systematics to modern developments (for instance advances in molecular phylogenetic reconstruction, evo-devo, the comparative method, usage of bio-informatics in biodiversity assessment). If you would like to know more about the position yourself, or would like to suggest suitable candidates, please send an e-mail to Peter van Tienderen at tienderen@science.uva.nl, preferably before 12 June 2004.

Prof. Dr. Peter H. van Tienderen Institute for Biodiversity and Ecosystem Dynamics (IBED) University of Amsterdam Postal address: P.O. Box 94062, 1090 GB Amsterdam, The Netherlands Visiting address: Kruislaan 318 (building I, room B06), 1098 SM Amsterdam.

E-mail: tienderen@science.uva.nl Website: www.science.uva.nl/ ˜ tiendere Tel: +31(0)20 525 7821

UCDavis Biodemography

BIODEMOGRAPHY

Postdoctoral position in biodemography available on NIH/NIA-funded program project. Background in ecology, evolution and/or demography preferred though consider applicants with other backgrounds. Successful applicant will based at UC Davis and become a member of the collaborative research program "Biodemographic Detemriants of Life Span" (UC Davis, UC Berkeley, Stanford University) Position is on 'aging in the wild' using new and creative field and laboratory approaches. Work on any model system will be considered though invertebrate systems such as fruit flies (drosophila; tephritid) or nematode (C. elegans) preferred. Send resume and names of 2 references to:

James R. Carey, Professor and Program Director Biodemographic Determinants of Life Span c/o Department of Entomology One Shields Ave. University of California Davis, CA 95616 530-752-6217 jrcarey@ucdavis.edu

Olav Rueppell <olav_rueppell@uncg.edu>

UEdinburgh EvolTech

I am looking for someone to fill a half-time BBSRC-funded research technician post, studying the genetic basis of colour patterns in mimetic Heliconius butterflies.

Contact me (chris.jiggins@ed.ac.uk) or follow this link for more details: https://www.jobs.ed.ac.uk/jobs/index.cfm?action=jobdet&jobid=3001909

Project description: Heliconius erato and H. melpomene have evolved over 20 distinct geographic races that are convergent between the species due to mimicry, offering an excellent opportunity to study the genetic basis of phenotypic adaptation. This project aims to identify genomic regions controlling the radiation of H. melpomene using linkage mapping. The project will develop ESTs from wing tissue sampled at different stages in development. Genes likely to be involved in wing pattern and pigment formation or identified as being differentially expressed between different pigment types, will be included in the map, and linkage to the loci controlling mimicry phenotypes established.

Experience in pcr and standard molecular biology techniques is required.

Chris Jiggins Institute of Cell, Animal and Population Biology University of Edinburgh Edinburgh EH9 3JT Scotland UK Tel: (+44)(0)131 650 8624 Fax: (+44)(0)131 650 6564 http://neruda.cap.ed.ac.uk/ Chris Jiggins <chris.jiggins@ed.ac.uk>

UGuelph TheoEvolBiol

Theoretical Evolutionary Biology

We seek individuals with expertise in evolutionary bioinformatics and/or theoretical approaches to evolutionary ecology and population genetics, evolutionary ecology and molecular systematics. Opportunities exist to participate in a new graduate program in Bioinformatics, and in a variety of multidisciplinary research initiatives including the Biodiversity Institute of Ontario and a CFI-funded initiative in Applied Evolution. Exceptional state-of- the-science facilities are available for computing and data storage (SHARCNet, and the Biodiversity Institute of Ontario), and for genomics and proteomics. Contact Dr. T. Crease, email tcrease@uoguelph.ca

Applicants should submit three copies of their curriculum vitae, including the names of three referees, and a letter of application to the Dean's Office, College of Biological Science, McNally House, University of Guelph, Guelph, ON, Canada N1G 2W1. We will BEGIN reviewing applications on 1st August 2004. General enquiries can be made to the Dean, Professor Michael Emes (email memes@uoguelph.ca) tel. (519) 824-4120 ext. 56102.

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

Dr. Brian Husband and Dr. Chris Caruso will be at the SSEB/ASN meeting in Colorado in late June if you want to discuss this position with them.

UNIVERSITY of GUELPH Full ad as seen in the 11 June issue of Science is below:

College of Biological Science, 12 Tenure Track Positions

The College of Biological Science is the largest unified bioscience institution in Canada and comprises over 90 faculty including nine Canada Research Chairs, 3,000 graduate and undergraduate students, and with an external research income in excess of $ 17.5M. The College will shortly begin occupation of a 375,000 sq ft Science Complex, with outstanding facilities for research and teaching including an Advanced Analysis Centre for proteomics, genomics and bioimaging. As part of a strategic plan to maintain the College at the forefront of life science, we are seeking to recruit outstanding individuals to a series of targeted, tenure-track positions at the Assistant Professor level. Successful applicants will be expected to establish a strong, independent research program involving innovative approaches and contribute to wider, interdisciplinary research goals. The College takes pride in the excellence of its students, and applicants should be able to articulate a commitment to the highest standards of pedagogy and will be expected to participate in undergraduate and graduate education. Candidates must have a PhD, preferably with postdoctoral experience, a strong record of publications in peer-reviewed journals, and ideally some experience in undergraduate/graduate teaching. Further details on specific positions can be obtained by contacting the individuals indicated next to each area. Structural Biology (two positions)

We seek candidates of exceptional promise who apply structural biology approaches to investigate leading edge biological questions in eukaryotic (animals, plants, protozoa, fungi) or prokaryotic systems. Successful candidates will have a strong record of published contributions and a demonstrated potential to develop a competitive and innovative independent research program using X-ray crystallography, cryo-electron microscopy, or NMR approaches. Contact Dr. C. Whitfield email: cwhitfie@uoguelph.ca

Human Health, Nutrition and Metabolism (two positions)

Candidates are sought with proven experience in the area of nutrition and metabolism in relation to human health. For one position, expertise in areas such as endocrinology, cytokine biology and inter-tissue metabolic regulation/communication is preferred as is formal training in nutritional sciences and/or exercise physiology. The applicant must have the ability to address questions related to human health with a combination of molecular and physiological techniques. For the second post, candidates will have interests in exploring the interaction of nutrition and genetics in relation to cardiovascular disease. The candidate will have experience in human nutraceutical supplementation trials. The service component of this position will include a leadership role in the Human Nutraceutical Research Unit. Contact Dr. T. Graham email: terrygra@uoguelph.ca

Developmental Biology (two positions) For one position, candidates are sought with proven experience in research into the regulation of plant development at the cellular and molecular levels. The

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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

UManchester Bioinformatics

LECTURESHIP OPPORTUNITY

University of Manchester, School of Biological Sciences

Bioinformatics Lectureship: Systems Biology/Network Modelling/Comparative Genomics/Bioinformatics (Reference: 589/04)

We invite applications for a Lectureship in Bioinformatics. In particular, we are interested in candidates in the area of systems biology, network modelling and/or comparative genomics, who can exploit the information gained from genome sequencing projects and downstream large scale data gathering projects involving transcriptomic, genomic, metabolomic and proteomic approaches.

Individuals working in other areas of Bioinformatics that seek to exploit or apply computer-based approaches to biological research may also apply.

Initial informal enquiries may be made to Andy Sharrocks. E-mail: a.d.sharrocks@man.ac.uk.

*** Closing date: 9 July 2004. ***

Further particulars and an application form can be obtained from http://www.man.ac.uk/news/vacancies/-academic.html#589 robertson@bioinf.man.ac.uk robertson@bioinf.man.ac.uk

UMontreal programmer

Company/Institution: Robert-Cedergren Centre for Bioinformatics & Genomics, Universite de Montreal

Job Title: Development Programmer

Job Description: The position entails primary responsibility for the maintenance and development of web interfaces for the two bioinformatics databases GOBASE (http://megasun.bch.umontreal.ca/gobase/) and PEPdb (http://amoebidia.bcm.umontreal.ca/public/-pepdb/agrm.php), written principally in PHP but also involving Java. The candidate will further be responsible for the maintenance of existing bioinformatics-related software and development of new code, including Perl scripts and C programs. The development will occur in a primarily Linux-based environment. The successful candidate will be a member of a closely integrated development team comprised of other programmers and database curators.

Requirements:

At least 3 years' programming experience Proficiency in Perl/PHP and SQL Familiarity with C and Java Strong Linux background Good communication skills A working familiarity with the concepts of molecular biology would be highly useful

Availability: The position is available immediately.

Contact:

Emmet A. O'Brien, Database Group Leader Departement de Biochimie Universite de Montreal Pavillon Roger Gaudry (P. principal) H-307-13 2900 Edouard-Montpetit Montreal QC, H3T 1J4 eobrien@bch.umontreal.ca

Emmet O'Brien <eobrien@BCH.UMontreal.CA>

UOregon EvolBiol Tech

RESEARCH ASSOCIATE OR ASSISTANT. Full-time research position available at the University of Oregon, Eugene. Candidates having a B.S., M.S. or Ph.D. are invited to apply. We seek a highly motivated and responsible individual who enjoys participating in an interactive intellectual environment to join us in our studies of questions in evolutionary genetics and physiological ecology using the nematode Caenorhabditis elegans as a model system. The candidate will be responsible for coordinating long-term selection projects, conducting thermal preference experiments, and general laboratory management/maintenance. Yearly appointment at $23,000 to $25,000, with salary commensurate with education and experience. Position open immediately and search will continue until a suitable candidate can be identified. Please send CV and names of three references to: Patrick Phillips, Ph.D., Center for Ecology and Evolutionary Biology, 5289 University of Oregon, Eugene, OR 97403-5289 or PPhil@uoregon.edu. Further details are available at http://www.uoregon.edu/-~pphil. The University of Oregon is an EOAA Institution committed to cultural diversity and compliance with the ADA.

Patrick C. Phillips, Associate Professor of Biology Center for Ecology and Evolutionary Biology Email: pphil@uoregon.edu Phone: (541) 346-0916 | FAX (541) 346-2364 Address: 5289 University of Oregon Eugene, OR 97403-5289 USA Web: Lab http://www.uoregon.edu/ ˜ pphil EvoNet http://www.EvoNet.org CEEB http://evolution.uoregon.edu IGERT http://evodevo.uoregon.edu

USheffield ResTech

Department of Animal and Plant Sciences, University of Sheffield, UK Contract Research Technician

(salary £13,547 pa, full time, 12 months) Closing date 30th June 2004

Applications are invited for the above position to work on a project investigating the evolution and breakdown of C4 photosynthesis. Experience of general lab work is essential, and relevent experience of techniques in plant ecology, physiology or biochemistry, and with the maintenance of plants in controlled environment experiments, would be advantageous. The successful candidate will be expected to undertake a variety of tasks, including general laboratory upkeep, the maintenance and running of controlled environment experiments, routine morphological, physiological and biochemical measurements of plants, and the preparation of data for analysis.

Project details

Mechanisms Driving the Evolution and Breakdown of C4 Photosynthesis

The convergent evolution of C4 photosynthesis in more than 30 plant groups was comparatively recent, but these plants now dominate subtropical ecosystems and account for 25% of global photosynthesis. Despite their importance, the evolutionary mechanisms underpinning the rise of C4 plants are a major unsolved puzzle in biology. The leading hypothesis suggests that past episodes of low atmospheric CO2 selected for the C4 CO2-concentrating mechanism, thereby overcoming the CO2-starvation problem of C3 plants in hot climates. But recent evidence points to a more complex situation involving interactions with growth partitioning, resource-use and plant life history. This project will therefore develop the first explicit experimental test of the CO2-starvation hypothesis, investigating how photosynthetic benefits of C4 plants impact on whole-plant traits in low CO2. Experiments utilizing new state-of-the-art growth facilities at the University of Sheffield will examine the African grass Alloteropsis semialata, a species unique in having C4 and C3 sub-species. Reports of C3-C4 intermediates in A. semialata from high elevations suggest the intriguing additional hypothesis that expression of C4 metabolism may be lost when this plant grows in cool conditions. A further aim of the project will therefore be to test C4 CO2-concentrating efficiency at a range of growth temperatures. The work contributes to research at Sheffield on past, present and future global change.

A full job description can be found on the University of Sheffield website: http://www.shef.ac.uk/jobs/ Informal enquiries may be made to Dr Colin Osborne, Department of Animal and Plant Sciences, University of Sheffield, Sheffield S10 2TN, UK; tel 0114 222 0146; email c.p.osborne@sheffield.ac.uk.

For further background information on this work, please see http://www.palaeobiology.org.uk/projects_05.htm

USheffield tech

Location: Department of Animal and Plant Sciences, University of Sheffield Salary: £13-15k Start Date: 1st September 2004

The post holder will conduct molecular genetic analyses in support of a 36 month NERC-funded research project on North American red squirrels (Tamiasciurus hudsonicus). The candidate will be responsible for optimising and genotyping a T.hudsonicus multiplex microsatellite marker panel, using automated DNA sequencing apparatus. Applicants should have a minimum HNC/HBTEC or degree equivalent, and experience in laboratory work is essential. This post is available from 1 September 2004 for a period of two years.

PIs: Dr Dave Coltman (University of Alberta) & Dr Jon Slate (University of Sheffield) Queries to Jon Slate (j.slate@sheffield.ac.uk)

PROJECT BACKGROUND

The aim of this project is to determine whether changes in breeding time and other fitness related traits that have occurred in response to recent climate change are consequences of adaptive microevolutionary responses or phenotypic plasticity in a natural population of North American red squirrels, Tamiasciurus hudsonicus. Furthermore, we aim to ascertain whether it possible for phenotypic plasticity to evolve under natural selection such as might be mediated by changing environmental conditions and in light of potential genetic and ecological constraints. To address these aims, we will 1) investigate the genetic mechanisms underlying the phenotypic responses to changing environmental conditions in a natural system, and 2) experimentally manipulate individual environmental conditions to alter the potential for evolution in the direction of expected climate change. The Kluane Lake, Yukon red squirrel population that has been monitored for over 15 years in a region that has experienced dramatic changes in spring temperature. The pedigree of this population will be reconstructed using microsatellites to infer relationships and measure relatedness between marked individuals. A postdoctoral researcher supported by the same research grant will conduct the quantitative genetic analyses, and possibly, some of the genotyping. See also: http://www.shef.ac.uk/-misc/groups/molecol/redsquirrels.html RESEARCH TECHNICIAN (FIXED-TERM)

This is an excellent opportunity for an individual to join the University of Sheffields Molecular Ecology Laboratory, which is a newly renovated state-of-the art genetics facility (http://www.sheff.ac.uk/misc/groups/-molecol/) in the Department of Animal and Plant Sciences. APS (www.sheff.ac.uk/aps) is a high profile, research-led department (5* RAE, QAA score: 24 points) and is one of the largest biology departments dedicated to whole organism research in the United Kingdom.

JOB DESCRIPTION

DNA extraction from tissue and hair samples. PCR amplification. DNA fragment analysis using ABI 3730 and associated software. General laboratory duties (preparation of buffers, routine maintenance of laboratory equipment). Data management.

TO APPLY: Visit the University of Sheffield's Jobs and Recruitment page http://www.shef.ac.uk/jobs/- and search for job number PS750

Dr Jon Slate Dept. Animal & Plant Sciences University of Sheffield Western Bank Sheffield S102TN Tel: +44 (0)114 2220048 Fax: +44 (0)114 2220002 www.shef.ac.uk/jon-slate www.shef.ac.uk/-aps/staff-jon-slate.html

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UToronto LabManager

Lab Manager

Laboratory of Professor Mart Gross Department of Zoology, University of Toronto

31 May 2004

Starting Salary: $3000 per month plus 4% vac. pay Location: Department of Zoology, University of Toronto Employment: Full-time Application deadline: until suitable candidate is found.

Position Summary: We are seeking a highly motivated individual to manage a research laboratory in the Department of Zoology. The ideal candidate will possess an interest in conservation biology and have experience in managing a group of researchers. The Lab Manager will serve as the main contact and representative for Prof. Gross.

Duties: - Assist the research of Prof. Gross by working closely with project managers, finding information, organizing meetings and workshops, providing updates on the status of projects, and discussing future projects. - Supervise the office assistant, information technology assistant, various work-study students, and summer undergraduate students. - Manage financial accounts of research grants, confirm the accuracy of monthly PI reports, prepare monthly and yearly budget estimates, search for additional funding sources. - Manage hiring of new staff and students. - Maintain detailed and accurate filing and computer storage of all data obtained by researchers and students.

Qualifications and Skills: - MSc degree in biology with additional training in administrative or managerial office work. BSc applicants with exceptional experience in a research and management environment may also be considered. - Educational background should include ecology and conservation biology, ideally with fishes. - Management experience in a biological field that includes fisheries and conservation; excellent knowledge of research practices; strong written and oral communication; excellent organizational skills; positive interpersonal skills; ability to prioritise and multitask.

Application: Please submit by email: cover letter expressing interest and describing appropriate education, experience and skills; updated CV; transcripts; names and contact information (email and phone) for 3 references to: Lizette Valdmanis Lab Manager, Gross Lab in Conservation Biology Department of Zoology, University of Toronto 25 Harbord St. Toronto, Ontario M5S 3G5 email valdmanis@zoo.utoronto.ca

We thank all applicants for their interest. However, only those applicants selected for an interview will receive responses.

Lizette Valdmanis <valdmanis@zoo.utoronto.ca>

UToronto ManagerGeneBank

Position Available Immediately

Project Manager Evaluation of British Columbia's Living Gene Bank (Steelhead trout)

Laboratory of Professor Mart Gross Department of Zoology, University of Toronto

Salary range: $3000.00 - $3500.00 per month, commensurate with experience. Location: The Project Manager may be able to work from either Vancouver Island, BC or Toronto. Some time in both locations is required. The Project Manager's position is with the Department of Zoology, University of Toronto. Employment length: 1-year position with possibility of extension. Application deadline: until suitable candidate is found.

Position summary: We are seeking a highly skilled and motivated individual with leadership skills to manage a large research project on the scientific evaluation of BC's Living Gene Bank (LGB) project with steelhead trout. The goal of the project is to develop LGB technology into an effective conservation strategy for Canadian fish populations. The project integrates a highly qualified team of scientists, students, and technicians both in Ontario and BC. An NSERC Strategic Grant and BC WLAP are supporting the research. Information about the project can be obtained at: http://www.zoo.utoronto.ca/mgross/research-current2.htm. Responsibilities: - direct multiple studies and staff (in Ontario and BC) - collect, maintain and analyze data - prepare reports and assist with manuscript preparation for publication - interact with external scientists and partners, especially at the BC Ministry of WLAP - prepare and implement new experiments; manage research budget

Candidate Background: The ideal candidate will possess a PhD or MSc in salmonid ecology with knowledge of principles in conservation biology, behaviour, genetics, and evolution. The ideal candidate will have: an understanding of living gene banks, research experience with native BC fish communities, knowledge of hatchery issues and breeding protocols, and excellent skills in statistical analyses. The ideal candidate will have at least two scientific publications to their credit (one with primary authorship). The ideal candidate will have successfully managed a large research program with fishes. Skills include: project management, written and oral communication, analytical/statistical, interpersonal and leadership, ability to prioritise and multitask.

Application: Please submit by email: cover letter expressing interest and describing appropriate education, experience and skills; updated CV; transcripts; names and contact information (email and phone) for 4 references to: Lizette Valdmanis Lab Manager, Gross Lab in Conservation Biology Department of Zoology, University of Toronto 25 Harbord St. Toronto, Ontario M5S 3G5 email valdmanis@zoo.utoronto.ca

We thank all applicants for their interest. However, only those applicants selected for an interview will receive responses.

Lizette Valdmanis <valdmanis@zoo.utoronto.ca>

UZurich PrimateEvol

The Anthropological Institute and Museum at the University of Zürich, Switzerland, is inviting applicants for the position of ^{3}Oberassistierenden 100%^{2} in the area of Evolutionary Genetics of Primates. The position is for a maximum of 6 years, and is available as of September 1, 2004. The successful candidate is expected to:

- Examine patterns of genetic relatedness within and among primate groups and populations, in relation to their socioecological correlates

- Examine the genetic basis of intraspecific variation in functionally relevant adaptive traits, as well as their phylogeographic background

- Direct the Genetics Laboratory

- Participate in teaching at the Institute, especially in the area of Primate Genetics

- Mentor students at bachelor^{1}s and graduate level.

The successful candidate has a PhD in evolutionary genetics, is well versed in genetic laboratory techniques and techniques of analysis of genetic data, and has broad experience in primate genetics and genomics, or a demonstrable willingness to become familiar with this field; as well as the ability to teach in German or a demonstrable willingness to learn to do so within two years.

The appointment is at the level of Oberassistent; salary and benefits are in accordance with the regulations of

Kanton Zürich.

Send your full application (CV, list of publications, addresses of three referees) before June 25 to Prof. Carel van Schaik, Universität Zürich, Anthropologisches Institut und Museum, Winterthurerstrasse 190, 8057 Zürich. For additional information, please contact Ms. Claudia Zebib-Brunner, Tel. ++41 (0) 1 635 54 11, zebib@aim.unizh.ch.

Carel Van Schaik <vschaik@aim.unizh.ch>

Vienna Bioinformatics

The joint search committee of the University Vienna, Medical University Vienna, and the Veterinary University Vienna, invites applications for the position of a

HEAD OF A CENTER FOR INTEGRATIVE BIOINFORMATICS VIENNA - CIBV

Through financial support from the WWTF (Wiener Wirtschafts & Technologie Fonds), and in a competition with Viennese research institutions, the CIBV will be established as a joint effort of three major Universities in Vienna and the private research institutions IMP, GMI and IMBA. The aim is to form a nucleus of innovative and competitive research in quantitative biological modelling and bioinformatics.

Potential candidates should have a strong theoretical and computational background. The prospective head can anticipate close cooperation with the various experimental and theoretical biology groups in Vienna. Interested individuals and in particular female scientists are encouraged to send by e-mail or courier their CV, and a brief statement of research interests and perspectives to Prof. Andrea Barta (Head of Search Committee) at Andrea.Barta@meduniwien.ac.at; Department of Biochemistry, Medical University of Vienna, Dr.Bohrgasse 3/9, A-1030, Vienna, Austria. The deadline to receive the applications is July 31st 2004.

Christian Schlötterer Institut für Tierzucht und Genetik Veterinärmedizinische Universität Wien Josef Baumann Gasse 1 1210 Wien Austria/Europe

phone: +43-1-25077-5603 fax: +43-1-25077-5693 http://i122server.vu-wien.ac.at/

WesternKentuckyU LabCoordinator

The Department of Biology at Western Kentucky University seeks experienced Laboratory Coordinator to operate the Biotechnology Center Core Facility. Candidate must have a MS degree or a B.S. degree with equivalent experience, and broad experience in molecular and cellular techniques. Must be: well organized, able to manage laboratory services and equipment effectively, able to direct student workers and student researchers in the safe application of biotechniques. Salary $33,000/year. Permanent twelve-month full-time position. For more information on the position visit http://biotech.wku.edu/. For full consideration submit letter of application and a resume illustrating experience and skills along with three letters of reference by August 2 to the Department of Human Resources, Wetherby Administration Building, Room 42, Western Kentucky University, 1 Big Red Way, Bowling Green, KY 42101-3576. Internet URL: http://www.wku.edu/Dept/Support/HR/. All qualified individuals are encouraged to apply, including women, minorities, persons with disabilities and disabled veterans. Western Kentucky University is an Affirmative Action/Equal Opportunity Employer.

WoodsHole ResAssist Zerbrafish

Position: RESEARCH ASSISTANT I, Full Time, Non-Exempt

Description: The Marine Biological Laboratory (MBL) is seeking applicants for a full-time, year round Research Assistant I to work on behavioral genetics in zebrafish (Laboratory of Gabriele Gerlach; http://www.mbl.edu/research/labs/gerlach/index.html)

Duties: As part of a research team, this Research Assistant will do PCR automated sequencing, fragment analysis behavioral experiments and zebrafish husbandry.

Conditions: This position is available as early as August 1, 2004.

Education: EDUCATION/EXPERIENCE: A BA/BS and strong skills and documented experience in molecular biology (DNA extraction, PCR, gel electrophoresis, DNA sequencing, etc.). The applicant will also be highly organized, attention to detail and be able to work as an independent part of a team. Background and interest in behavioral ecology is preferred.

Instructions: Applicants should submit a letter of interest highlighting recent relevant experiences, a curriculum vitae, and the names of 3 references including telephone numbers and email address to to: Marine Biological Laboratory, ATTN: Human Resources reference code [RA I ZF GG], 7 MBL Street, Woods Hole, MA 02543-1015, email resume@mbl.edu. An Equal Opportunity/Affirmative Action Employer/Non-smoking workplace.

Gabriele Gerlach, PhD Assoc. Scientist Marine Biological Laboratory 7MBL Street Woods Hole, MA 02543-1015 USA

Telephone office 508 289 7120 Telephone lab 508 289 7391 FAX 508 289 7900 Email ggerlach@mbl.edu <http://www.mbl.edu/research/labs/gerlach/index.html>http://www.mbl.edu/research/labs/gerlach/index.html Gabi Gerlach <ggerlach@mbl.edu>

Other

ABI plates

Dear colleagues,

I was wondering whether it was possible to use custom-made glass plates (from a glazier's shop) on an ABI 377 sequencer. Has anyone had success with anything cheaper than what ABI offers?

Thanks, Kristina

Kristina Sefc Institut für Zoologie Karl Franzens Universität Graz

Kristina Sefc <kristina.sefc@uni-graz.at>

ARG article suggestions

Evolutionary genetics in Annual Review of Genetics

The Editorial Committee of the Annual Review of Genetics will meet at the end of June to discuss topics for inclusion in future volumes in the Annual Review of Genetics and potential authors for review articles. I represent evolutionary genetics on the Committee and would like suggestions for topics and authors. Please give me a paragraph or two describing the topic and the need for a review. Please e-mail me your ideas by June 22, 2004, in order for me to have them for the meeting.

Wyatt Anderson Genetics Department University of Georgia wyatt@fraklin.uga.edu

Wyatt Anderson <wyatt@franklin.uga.edu>

Arabidopsis gnats

I am looking for some info on controlling fungal gnats (Sciarid Flies) infesting Arabidopsis thaliana. We would prefer to avoid pesticides that may affect growth and/or development of our research plants. I have seen hypoaspis miles sold as a commercial predator, but am concerned about any damage they cause to the plant. Any help would be appreciated.

Michael Wierzba Research Specialist Dr. Frans Tax Lab University of Arizona Molecular Cellular Biology Life Sciences South 219 1007 E. Lowell St. Tucson, AZ 85721 520-626-3501 wierzba@u.arizona.edu

Autopolyploids

Dear EvolDir Members,

Does anyone know of sister species (or a clade at any level, whole genus, etc) in which all members are (1) polyploid (2) look like they have inherited that ploidy from a common ancestor, and (3) all have (or are reputed to have, or have anecdotal evidence for) polysomic inheritance?

Or, to ask the question more directly:

Are their any groups of species that have inherited polysomic inheritance from their common ancestor?

and by implication,

Does speciation ever happen faster than polysomic inheritance gives way to disomic inheritance?

– Darren Obbard

Darren Obbard <darren.obbard@plant-sciences.oxford.ac.uk>

Bayesian burn-in

Dear Members, Following are the answers I received regarding determining Burn-in in Bayesian analysis. Some of you requested me to post them. -Jenny

Dear Jenny, It is only the likelihood sampled from the cold chain that matters (the hot chains are used to explore the parameter space). This will be recorded in your '.p' file along with the values of the other continuous parameters. You can either load this into Excel and plot it or you could try our program Tracer:

http://evolve.zoo.ox.ac.uk/software/tracer which is specifically designed for analyzing output from Bayesian MCMC. You can use this to plot posterior distributions of your parameters and look at the trace in order to check for adequate mixing and burn in.

Tracer will also estimate the ESS or effective sample size, a statistic which tells you the equivalent number of independent samples in your output. The samples from an MCMC will be correlated which is why you only sample every (say) 100th generation. If the MCMC is mixing badly or you have a large dataset then even sampling every 100th will produce correlated samples. This is not a problem unless the ESS is very low (say less than 100 or 200). Posterior estimates estimated from runs with very low ESSs will have large errors (these can also be calculated by Tracer - at least for the continuous parameters).

Hope this helps.

Andrew

Jenny, Open the *.p (parameter) file in Excel and graph the gens vs post probs–assuming your data has reasonable structure, it should be quite obvious at what generation the values begin to plateau.

Cheers, Pete

Jenny,

I always run the “sump” command, which gives you a rough plot of how the log likelihood has improved over time. You can set the burnin for the sump command until the log likelihood looks steady over the remaining samples, then use the same burnin value for sumt. Hope that helps,

- Greg

Hi Jenny,

I used version 3 and I think there is a output file that you can see the scores of all four chains. I actually open this file from excel and make a plot, x-axis (generations) vs. y-axis (scores) that you can see where the scores become stabilize. The 'exact' point of burn-in is not easy to find, so I always go some generations after/beyond that so-called stabilizing point just to be safe and not to include any generations when the scores were not stabilized. I am not sure I am answering what you are really asking for, :-)

Fengjie

Jenny, If you go to my web site (url below) and click on "software" in the navigation bar, you will find an "mb-coda" archive with tools you can use to check for convergence using the only diagnostic that we trust, which is the Gelman-Rubin diagnostic (convergence is defined as the convergence of between-chain variance on within-chain variance). The package consists of a Perl script and an R script.

R is an open source implementation of a data analysis language similar to S-Plus. To use mb-coda you must first install R and the R "coda" package of convergence diagnostics. The coda package is the back-end to our software, which just provides a convenient interface with MrBayes output.

Arlin

There is a program called TRACER that can do that for you. Joseph.

—–Original Message—– From: evoldir@evol.biology.mcmaster.ca [mailto:evoldir@evol.biology.mcmaster.ca] Sent: Thursday, May 27, 2004 1:33 AM To: jenny_xiang@ncsu.edu Subject: Other: burn-in in Bayesian analysis

Dear Member, We use MrBayes 3.0 for phylogenetic analysis and have a question about determining the generation of burn in. The Screen output of MrBayes 3.0 does not show a column of summarized likelihood score over the different chains as does in MrBayes 1.0 and 2.0. Does anyone know how to determine the Burin in this case? We need to look at the scores for all four chains to determine the generation when the score starts to be come stabilized (if four chains are run) or if there is a way to see the scores summarized over four chains? Thanks for any help! Sincerely, Jenny Xiang at NCSU, jenny_xiang@ncsu.edu

Jenny Xiang <jenny_xiang@ncsu.edu>

Book donations

Thanks to those of you who donated books or other items to our auction that will be held at this year's Evolution Conference at Colorado State University later this month! Unfortunately, we still have not received very many items. All of the money raised will go into a newly-formed travel fund for students to get to the meetings. This will be particularly important in 2007 when we will be meeting in New Zealand!

Please think about whether you have any items that you could donate to the auction. It could be just about anything - not just books! You could bring a case of your best local microbrew! Do you or your spouse knit? - how about a hand-made sweater? You have a nice framed piece of art that just doesn't fit with your decor? - bring that along and get rid of it! Have some cool old first edition books? - we'd be happy to take those as well! Do you have nice pottery that you bought cause you liked it, but you never use it? - sounds great! We will gratefully accept literally ANYTHING that you think will bring some money! The auction will take place during the BBQ on Monday, June 28th.

Please contact me if you have something you would like to contribute. Be generous! Think about how broke you were when you were a grad student!! Also, don't forget to order a conference-logo or black death t-shirt! You can get them via the T-Shirt link on the conference website, not just at the time of registration. All profits from the shirts will also go to the travel fund.

Thanks, and I look forward to hearing from you! Shanna

If you're not part of the solution, you're part of the precipitate. – Steven Wright

Donuts. Is there anything they can't do?! – Homer Simpson

Back off man. I'm a scientist. – Peter Venkman, Ghostbusters.

It's a mighty poor mind that can only think of one way to spell a word. – Andrew Jackson

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Shanna Carney Department of Biology Colorado State University Fort Collins, CO 80523-1878 970-491-1092 Fax: 970-491-0649 secarney@lamar.colostate.edu http://lamar.colostate.edu/~secarney/

Brinkman vs MJR

Hello, I work in forest disease/population genetics. My question is entirely technical. I have an opportunityt to purchase a Brinkmann Mastercycler gradient thermocycler for nearly the same price as a MJR non-gradient thermocycler. I know MJR's are durable; however, I have no experience or knowledge of the Brinkmann instrument. I need feedback from people who use the Mastercycler.

thanks, Kathie

Kathie Jermstad, Biologist Institute of Forest Genetics 2480 Carson Road Placerville, CA 95667 Phone: (530) 622-1225 http://dendrome.ucdavis.edu/NealeLab Kathie Jermstad <kjermstad@fs.fed.us>

Chrysemys primers

I'm doing paternity analyses on two populations of painted turtle for my Ph.D. research. I'm wondering if anyone is developing/has developed microsatellite primers for Chrysemys picta and would be willing to share (we are currently using the primers published by Pearse and Avise, but would like to try others). I'm also interested in primers developed for congeners of the painted turtle. Thank you, Elinor

Elinor Hughes Department of Zoology University of Guelph ehughes@uoguelph.ca

Divergence with nulls

Hi Everyone, we are working on microsatellites trying to evaluate null alleles effect on population differentiation. Does anyone know any software to test population differentiation taking into account null alleles presence and their estimated frequence? We welcome any suggestions. Thanks in advance! Chiara

Chiara Papetti PhD student (Evolutionary Biology) Biology Dept University Of Padova Via G. Colombo I-35100 Padova Italy e-mail cpapetti@bio.unipd.it chiara.papetti@unipd.it Tel 0039 049 8276222

Drosophila isofemale lines

Dr. Davis were once (February 2001) offering 30 isofemale lines of D. melanogaster originated from the wild nearby Leiden (Netherlands) in Evoldir.

I was wondering if someone still has these 30 isofemale lines, and if so, if I could get a subset of them?

Regards,

Sascha Glinka <glinka@zi.biologie.uni-muenchen.de>

Fragment analysis

Subject: High-throughput fragment analysis

Dear EvolDir readers,

I am a Phd. student from the Netherlands, who would like to gain some experience as a temporary guest at a foreign research institute. I am looking for a molecular lab with high-throughput capabilities (ie. referably robotic DNA extraction, robotic PCR and fragment analysis on automatic sampling sequencer eg. an ABI 3600) in order to make a genetic map of a Senecio population using AFLPs. I am interested in a guest position of approximately four months, beginning in January, 2005 (needless to say, I will pay for the costs of the materials that I will use). I have experience with molecular methods. I have previously run AFLPs on an ABI 377.

If anybody knows of such a lab in Europe, North America, or Australia, I would be greatful to hear from them (kirk@rulsfb.leidenuniv.nl).

Thanks in advance,

Heather Kirk

Plant Ecology Institute of Biology Leiden University

PO Box 9516 2300 RA Leiden The Netherlands

Hexaploid microsatellites

Dear evoldir,

I am a MSc candidate in population genetics and working with Geum triflorum (Prairie smoke) from the Rosaceae family. G. triflorum is an allohexaploid species and I have recently become interested in using nuclear microsatellite markers to study the genetic structure of the species across it's range. Since the species is a hexaploid I am getting from 1 to 6 bands per locus per sample, but I am unsure of how to score the alleles. The parentals are believed to have been two diploid species (Waldesteinia and Coluria) that crossed to make a tetraploid and then backcrossed with a diploid to form the hexaploid. However, I don't think it is known what diploid species the tetraploid was crossed with. I would very much appreciate any incite anyone might have into scoring G. triflorum microsatellites or if it is feasible. Thank-you very much,

Jill Hamilton

Jill Hamilton MSc Candidate Eckert Lab Department of Biology Queen's University Kingston, ON K7L 3N6 (613) 533-6000 ext. 75125 hamiltnj@biology.queensu.ca

Jill Hamilton <hamiltnj@biology.queensu.ca>

Hexaploid software

Dear all,

I am working with a perennial hexaploid species using Inter simple sequence repeat markers (dominant marker 0 or 1). Only moment in time data is available. The species can reproduce both sexually and asexually. This violates Hardy-Weinberg. Is there a a population genetics program I can use to analyze the dominant marker data to obtain genetic diversity measures such as Gst, Hs, Ht, percent polymorphic loci, and Ne? Or is there any better measures that would be appropriate? I would like to use this information to directly compare different populations under different management strategies.

Thanks,

John Starnes starnjh@wku.edu

ItalianEvolBiol census

I apologize for cross-postings, but I am trying to reach as many people as possible.

Dear Colleagues,

I am trying to determine how many Italian-speaking evolutionary biologists are out there and where they are (I am interested in contacting both Italian and foreign nationals doing research in Italy, and Italians working or studying outside of Italy), in order to see if there is interest in the creation of an Italian Society of Evolutionary Biology. During the last couple of years the teaching of evolutionary theory in Italian schools has come under attack from several political groups and movements, and we presently do not have an organization with elected representatives that can speak to the public on behalf of Italian evolutionary biologists to rebuke creationist attacks. All parties that are interested in potentially joining a (yet to be established) Italian Society of Evolutionary Biology, and eventually participating in activities organized by such an entity (annual meetings, workshops, etc.) are warmly invited to please join the list "Biologia Evoluzionistica" and participate in a discussion about how to better organize ourselves.

Instructions on how to join the list are available at http://it.groups.yahoo.com/group/biologia_evoluzionistica/ Please, forward this message to any colleague that might be interested

Many thanks

Francesco Santini

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Cari colleghi,

Vi scrivo per chiedervi di iscrivervi ad una mailing list che ho recentemente creato allo scopo di determinare quanti sono (e dove sono) i biologi evoluzionisti di lingua italiana (intesi questi sia come italiani o stranieri che lavorano in Italia, che come nazionali italiani che lavorano o studiano fuori dall'Italia), e vedere se esiste l'interesse per la creazione di una societa' italiana di biologia evoluzionistica. Durante gli ultimi anni l'insegnamento della biologia evoluzionistica nelle scuole italiane e' stato ripetutamente attaccato da vari movimenti politici, ed al momento attuale non esiste in Italia una organizzazione con rappresentanti eletti dai loro colleghi che possa rappresentare i biologi evoluzionisti italiani e difendere la nostra disciplina dagli attachi dei creazionisti. Tutti coloro che possono essere interessati ad iscriversi e divenire membri di una societa' italiana di biologia evoluzionistica (ed eventualmente partecipare in attivita' organizzate da questa come congressi, discussioni, workshops, etc.) sono invitati ad iscriversi alla lista "Biologia Evoluzionistica" e partecipare ad una discussione su come organizzarci. Le istruzioni su come unirsi alla lista sono disponibili al sito http://it.groups.yahoo.com/group/biologia_evoluzionistica/ Per favore, fate circolare questo messaggio fra tutti i colleghi che potrebbero essere interessati

Grazie per l'attenzione

Francesco Santini

JohnMaynardSmith Book

John Maynard Smith Remembered

Dear Colleagues,

We are putting together a book of memories of the Late and Great John Maynard Smith. We intend to put these together into a bound volume to be presented to John's wife, Sheila. The book will be entitled 'John Maynard Smith Remembered'.

This book will contain reminiscences, anecdotes, stories and recollections about JMS from his colleagues and friends. The contents of the book will also be displayed on the Centre for the Study of Evolution (CSE) website and a copy will be given to John's Archivist.

We really would like you to make a contribution.

To submit your contribution:

Preferred method:

1. Go to the University of Sussex - CSE website and use the online form for automatic submission. You will find a link to the submission page at http://www.lifesci.susx.ac.uk/CSE/members/jms/jmsmemorial.htm 2. Send to me directly by email - noel@sussex.ac.uk

Please remember to include a separate line that answers the question "when and where did you know JMS" (This is important for Sheila).

3. If you do not have access to a computer we will be delighted to take hand-written recollections and process them for you.

Send to

Noel Smith, The John Maynard Smith Building, University of Sussex, BN1 9QG, UK.

Leave extraction

Dear all,

I would appreciate any advice on high throughput DNA extractions from dried leaves.

We have just taken delivery of a 96 well plate shaker-grinder. When combined with the use of a plate spinner this allows us the possibility of using the 96 well extraction kits for high throughput of samples. I have about 1000 silica gel-dried young leaves that I need to extract, so a high-throughput system is clearly preferable!!

If anyone has experience of using a shaker-grinder and/or 96 well kits with dried samples I will be glad to hear of any tips/protocols or problems! I have found that disrupting the dried leaves in liquid nitrogen rather than directly in extraction buffer gives much better DNA quality.

Many thanks in advance!

Alistair Jump

–

Dr. A.S. Jump

Affiliation: Centre de Recerca Ecològica i Aplicacions Forestals (CREAF)

Current address:

Departamento de Genética Molecular IBMB-CSIC C/Jordi Girona 18 08034 Barcelona Spain

Tel: 0034 934006100 ext 256 Fax: 0034 932045904

Lizard samples

Hi,

I am a new postdoc beginning work with the evolution of various diet regulating peptides in lizards and am therefore in need of DNA material from species in Varanus, Lanthanotus, Heloderma, and Anguidae. Samples from other squamates would also be of interest as they could aid in obtaining an overview of the distribution of the peptides within this order. Any help in obtaining samples or DNA would be greatly appreciated.

Best regards,

Marie Skovgaard Computational Biology Unit Bergen Centre for Computational Science University of Bergen N-5020 Bergen Norway maries@ii.uib.no

One Evol book

Greetings,

I would appreciate receiving responses (one per person) to the following scenario (cliche, though it might be):

Were you transported to an isolated island, which was deserted except for a few partiticpants who were enrolled in an 'Advanced Readings in Evolution' course that you were offering, and allowed to bring with you only one published paper or book (other than 'The Origin of Species by means of Natural Selection; or, the Preservation of Favoured Races in the Struggle for Life'), please identify the work that you would choose as the most 'significant', by whatever criteria you consider as important.

with gratitude,

Jon Jon Stone email address: jstoner@mcmaster.ca

Silver staining

Fellow silver-stainers,

We're visualising microsatellites by silver-staining denaturing polyacrylamide gels, following Bassam et al. 1991. Overnight the staining process has stopped working: at the developer stage there is no visible brown stain whatsoever, not even along the top edge of the gel, no matter how long the gel is left in the developer. We've been using this process for a few years and have never had this kind of problem before. We've tried changing reagents without success. Has anyone else encountered (and solved) this kind of problem? Our next step is to try a different water supply (pH is fine though), but I thought I'd get some advice from evoldir readers before running any more gels. Please reply to <p.johnson@bio.gla.ac.uk>.

Thanks for your help, Paul

Paul Johnson Division of Environmental and Evolutionary Biology (DEEB), Graham Kerr Building, Glasgow University, Glasgow, UK, G12 8QQ Tel +44 (0)141 330 6625, Fax +44 (0)141 330 5971, p.johnson@bio.gla.ac.uk

Paul Johnson <p.johnson@bio.gla.ac.uk>

Simulation software

Hi,

I'm looking for software to simulate the effect of selection, mutation and/or migration in a Fisher-Wright population. I want to follow the fate of a single gene linked to several neutral markers, in addition to a polygenic effect (many unlinked genes with small effect). I want to specify the number of generations since the foundation of a population, the initial allele frequencies, population size (constant over time), intensity of selection on the single gene, level of mutation at the gene and markers and possible rate of immigration. I need to recover phenotypes and genotypes at any specified generation.

Thanks

Jules Hernandez-Sanchez Roslin Institute Scotland

jules.hernandez@bbsrc.ac.uk
jules.hernandez@bbsrc.ac.uk

Sloan Research Fellowships

SLOAN RESEARCH FELLOWSHIPS IN COMPUTATIONAL AND EVOLUTIONARY MOLECULAR BIOLOGY

The Alfred P. Sloan Foundation is pleased to invite nominations for Sloan Research Fellowships in Computational and Evolutionary Molecular Biology.

The deadline for receipt of nominations is September 15, 2004. Candidates must be members of the regular faculty (i.e. tenure track) of a college or university in appointments in United States or Canada, and be nominated by a senior scientist. Direct applications are not accepted. The eligibility criteria are quite specific, and are described in appropriate detail in the enclosed brochure, and at www.sloan.org under "Sloan Research Fellowships." Further information may also be obtained from teitelbaum@sloan.org

I invite you and your colleagues to consider nominating any outstanding young scientists who meet the eligibility criteria.

Gwen Knowles Fellowship Administrator

Knowles <Knowles@sloan.org>

Software LAMARC 1 2 1

We have just released version 1.2.1 of the LAMARC program (part of the LAMARC package).

LAMARC uses genetic data from a population to estimate several population parameters: size of subpopulations, subpopulation growth rates, migration rates among subpopulations, and overall recombination rate. The algorithm is Metropolis-Hastings MCMC; we search through a wide space of genealogies representing the possible histories of the data.

Suitable data for this program includes DNA or RNA sequences, SNPs, or microsatellites. Phase may be known or (with some loss of power) unknown.

We had a brief and unsatisfactory release of version 1.2 several months ago, which is why this release is 1.2.1. If you are one of the few people who obtained copies of 1.2, please replace them.

Version 1.2.1 adds:

Population growth and shrinkage. LAMARC can now estimate population growth or shrinkage using an exponential model. In cases with population subdivision, a separate growth rate is estimated for each subpopulation.

GTR model for DNA, RNA and SNP data. LAMARC can now use the General Time-Reversible model of nucleotide sequence evolution. The best way to use this feature is to estimate the GTR rates with a program such as PAUP* and import them into LAMARC.

Performance improvements. Maximization of the likelihood surface is now faster and much more reliable, and the program is faster overall. It has also been updated to recent C++ standards and will compile correctly on a wider variety of systems.

LAMARC is written in C++. We distribute source as well as executables for Linux, Windows and MacOS. To obtain the program or simply learn more about it, visit our web site:

http://evolution.genetics.washington.edu/lamarc.html or our anonymous ftp site:

evolution.genetics.washington.edu, directory /pub/lamarc

The LAMARC development team: lamarc@gs.washington.edu Mary Kuhner Peter Beerli Jon Yamato Eric Rynes Lucian Smith Elizabeth Walkup

Kuhner/Felsenstein Lab Department of Genome Sciences University of Washington Box 357730 Seattle, WA 98195-7730

Software Lamarc 1 2 2

We have just released version 1.2.2 of the LAMARC program (part of the LAMARC package).

LAMARC uses genetic data from a population to estimate several population parameters: size of subpopulations, subpopulation growth rates, migration rates among subpopulations, and overall recombination rate. The algorithm is Metropolis-Hastings MCMC; we search through a wide space of genealogies representing the possible histories of the data.

Suitable data for this program includes DNA or RNA sequences, SNPs, or microsatellites. Phase may be known or (with some loss of power) unknown.

The release of version 1.2.1 from June 1 had a serious bug in the handling of population growth. Any analysis involving growth must be repeated. (In fact, such runs normally crashed.) Other analyses should be fine. We apologize for the inconvenience.

LAMARC is written in C++. We distribute source as well as executables for Linux, Windows and MacOS. To obtain the program or simply learn more about it, visit our web site:

http://evolution.genetics.washington.edu/lamarc.html or our anonymous ftp site:

evolution.genetics.washington.edu, directory /pub/lamarc

The LAMARC development team: lamarc@gs.washington.edu Mary Kuhner Peter Beerli Jon Yamato Eric Rynes Lucian Smith Elizabeth Walkup

Kuhner/Felsenstein Lab Department of Genome Sciences University of Washington Box 357730 Seattle, WA 98195-7730

Tetraploid Microsatellites

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 interprate such types of bands. I would be grateful if anyone can suggest me how to interprate such types of bands and what types genetic variation parameter can be estimated from such types of data using which programme. Thank you in advance for your help in this regard. Sincerely yours,

Madhav Pandey

Madhav PANDEY (Ph.D. Student) Institute of Forest Genetics and Forest Tree Breeding Faculty of Forest Science and Forest Ecology University of Goettingen Buesgenweg 2, D-37077, Goettingen, Germany Tel. +49-551-393539, Fax +49-551-398367 http://www.uni-forst.gwdg.de/forst/fg/index.htm

PostDocs

ArizonaStateU BehavioralEcol

POST-DOCTORAL ASSOCIATE POSITION in avian behavioral ecology in the School of Life Sciences at Arizona State University. Candidates must have earned a Ph.D. in Animal Behavior or a related field. He/she will develop field and laboratory studies on the mechanisms and function of visual and vocal signals in great-tailed grackles (Quiscalus mexicanus). Duties will include monitoring breeding behavior in the local campus population as well as using a variety of biochemical, physiological, and immunological techniques to test the costliness of sexual traits. Position to begin 1 September 2004. Send cover letter summarizing your qualifications and interests, curriculum vitae, up to three representative reprints, and the names and contact information for two references to Dr. Kevin McGraw, School of Life Sciences, Arizona State University, P.O. Box 874501, Tempe, AZ 85287-4501. Email submissions are acceptable (Kevin.McGraw@asu.edu). Application deadline is 1 July 2004; if not filled biweekly thereafter until search is closed. Arizona State University is an Affirmative Action/Equal Opportunity Employer.

Dr. Kevin J. McGraw Assistant Professor School of Life Sciences Arizona State University P.O. Box 874501 Tempe, AZ 85287-4501

Phone: (530) 752-2401 FAX: (530) 752-0175 Email: Kevin.McGraw@asu.edu Webpages: http://sols.asu.edu/faculty/kmcgraw.php http://lsweb.la.asu.edu/kmcgraw Kevin McGraw <Kevin.McGraw@asu.edu>

Biodemography

BIODEMOGRAPHY

Postdoctoral position in biodemography available on NIH/NIA-funded program project. Background in ecology, evolution and/or demography preferred though consider applicants with other backgrounds. Successful applicant will based at UC Davis and become a member of the collaborative research program “Biodemographic Detemriants of Life Span” (UC Davis, UC Berkeley, Stanford University) Position is on ’aging in the wild’ using new and creative field and laboratory approaches. Work on any model system will be considered though invertebrate systems such as fruit flies (drosophila; tephritid) or nematode (C. elegans) preferred. Send resume and names of 2 references to:

James R. Carey, Professor and Program Director Biodemographic Determinants of Life Span c/o Department of Entomology One Shields Ave. University of California Davis, CA 95616 530-752-6217 jrcarey@ucdavis.edu

Olav Rueppell <olav_rueppell@uncg.edu>

Buffalo EnvGenetics

Postdoctoral Position in Environmental Genetics

A new collaborative postdoctoral research and science education position is being established between the Buffalo Museum of Science and the Buffalo State College in the field of environmental genetics. The position is being established to expand the museum’s natural history core to include elements of modern biology and their application to the environmental sciences.

The Buffalo Museum of Science is working to develop and promote science literacy in the community to help the public understand both the process and products of science involving environmental issues of social and community interest. Science and research at the BMS is directed in support of institutional goals to facilitate a quality experience by the public, and to provide real science for a real science experience through museum programs.

This position will be in the Science Section of the BMS under the direction of Dr. John Grehan, Director of Science and Collections. The research program will be under the direction of Dr. Amy McMillan at the Buffalo State College.

This is a one-year, extendable to two year appointment. The salary is $30,000 (plus standard BMS benefits).

Accountabilities

* Participate in a current program on conservation or environmental genetics at Buffalo State College (about 30% time) and lead grant development for research and educational program within a program team (about 65% time).

* Research involving conservation or environmental genetics, including issues such as pollution effects on pop-

ulation genetic structure and diversity, development of genetic markers and genetic analysis for species of interest to NY State and/or to the Buffalo Museum of Science, or development of molecular methods to track migratory species.

* Carry out one or more elements of the research program at the BMS Tifft Nature Preserve.

* Initiate and take the lead in proposed grant development in support of extending research projects.

* Take a lead role in developing funded grant proposals linking research with education, particularly at elementary and high school levels. This project will involve a collaborative relationship with Karen Wallace (BMS Center for Science Learning) and other museum and college science and educational staff. The goal will be, where possible, to establish educational experiences connecting Tifft and the research facilities of the college.

* General supervision of a botanical or zoological collection for collection access, loans, and maintenance (about 5% time, in collaboration with the collections manager).

Requirements

Awarded a PhD in an appropriate field

Demonstrated ability to conduct outdoor, physically demanding fieldwork

Demonstrated IT skills

Interest and ability to collaborate with colleagues in a team environment

Preferred

Experience with instructing pre-college audiences

Experience in the preparation of competitive grant proposals

Application

A letter of application along with cv and three references (preferably by email attachments as well as hard copy) to:

John Grehan

Director of Science and Collections

Buffalo Museum of Science

1020 Humboldt Parkway

Buffalo, New York 14211-1293

Jgrehan@sciencebuff.org

Position to be filled upon determination of suitable candidate.

Dublin GenomeEvolution

Bioinformatics / Molecular Evolution

Postdoctoral Opportunities

Postdoctoral fellowships are available in Prof. Ken Wolfe's group at Trinity College Dublin (Ireland). The projects will involve using bioinformatics and comparative genomics methods to study genome evolution in eukaryotes. Particular interests in the lab include the evolution of polyploid species, clustering of functionally related genes, and fungal genomics.

These fellowships form part of a 5-year research programme supported by Science Foundation Ireland. For further information about the lab, see wolfe.gen.tcd.ie. Very competitive salaries will be available for outstanding applicants.

Previous experience in molecular evolution, bioinformatics, and/or computer programming experience in C / Perl / SQL is essential. Candidates should submit a cover letter and curriculum vitae, including the names of two referees, by mail or e-mail to: Prof. Kenneth H. Wolfe, Department of Genetics, Smurfit Institute, Trinity College, Dublin 2, Ireland (Tel. +353 1 6081253; e-mail khwolfe@tcd.ie). Informal enquiries are welcome. Closing date 8 August 2004.

Trinity College is an Equal Opportunities Employer.

ErasmusU TheoPopGenet

Post-doc in Quantitative Genetics / Theoretical Population Genetics

A Post-doc position is available immediately in the newly established Department of Forensic Molecular Biology at the Erasmus MC University Medical Centre Rotterdam, The Netherlands. You will be working on quantitative genetic / theoretical population genetic issues in projects investigating human individual and population differences with the future aim of predictive use in forensic identification. You have a strong background in statistics /biostatistics (PhD) with experience in quantitative genetics / theoretical population genetics (data analysis, data modeling, model development). Programming skills, experience in data mining and management are needed. You are highly motivated, scientifically creative and able to work independently. Biologists with a strong background in quantitative genetics / theoretical population genetics (PhD), who are able to work independently on statistical issues and have the necessary bioinformatics skills are encouraged to apply as well. You will officially be appointed by the Netherland Forensic Institute (NFI), fulltime for a period of two to three years (with potential possibilities for elongation), place of work is Erasmus MC. The gross monthly salary, depending on qualifications and experience, is a maximum of 3.945.77 full-time. Erasmus MC offers a state-of-art research environment (check: http://www.erasmusmc.nl).

Please send your application with CV, a description of research interests, publication list and names and contact information for two references to Prof. Dr. M. Kayser, Department of Forensic Molecular Biology, Erasmus MC University Medical Center Rotterdam, Medical-Genetic Cluster, PO Box 1738, 3000 DR Rotterdam, The Netherlands, or prefered by e-mail to m.kayser@erasmusmc.nl.

FloridaStateU CompBiol

FOUR POSTDOCS IN COMPUTATIONAL BIOLOGY

The Computational Evolutionary Biology group at the School of Computational Science and Information Technology at Florida State University in Tallahassee will be hiring four new postdocs in the fall. More information about the positions and a printable poster is available at http://www.csit.fsu.edu/employment_opp/CSIT_Ad_4.pdf . We hope to expand through the next couple of years and will be interested to hear of students who might want to join us for postdoctoral research.

Thanks very much,

Peter Beerli Fredrik Ronquist Dave Swofford

—————— http://www.csit.fsu.edu http://www.csit.fsu.edu/ ˜ beerli http://www.bio.fsu.edu/faculty-ronquist.php http://www.bio.fsu.edu/faculty-swofford.php —————— FOUR POSTDOCS IN COMPUTATIONAL BIOLOGY

The Computational Evolutionary Biology group (CEB) is a recent addition to the School of Computational Science and Information Technology (CSIT; http://www.csit.fsu.edu) at the Florida State University in Tallahassee. CSIT is an interdisciplinary school focused on computational applications in fields ranging from mathematics to oceanography. The research focus of CEB is in computational phylogenetics and population genetics. A large portion of the computations in these fields is currently performed by CEB software. CEB has access to excellent computational resources, including clusters and supercomputers.

CEB currently has four openings for postdocs with a background in computer science, statistics and/or biology:

Two computational phylogeneticists: one focused on extending current Bayesian MCMC techniques for phylogenetic inference in an NIH-funded project; the other for the development and implementation of improved heuristic search methods for optimal trees and/or Bayesian MCMC convergence diagnostics. More info: Fredrik Ronquist, ronquist@csit.fsu.edu and Dave Swofford, swofford@csit.fsu.edu.

One computational population geneticist to look at the effects of model violations in population genetics inference using simulations. More info: Peter Beerli beerli@csit.fsu.edu.

One coordinator of image database development/comparative insect morphologist for a Tree of Life project funded by NSF. The successful candidate will work with the phylogenetics of parasitic wasps (Cynipoidea, Ceraphronoidea, and Proctotrupoidea): collect morphological data, perform large-scale phylogenetic analyses, and coordinate the development of a general-purpose image database (MorphBank) for morphological phylogenetics and biodiversity research. More info: Fredrik Ronquist, ronquist@csit.fsu.edu.

For the first three positions, knowledge of a programming language such as C, C++, or Java is essential. The successful candidate should also be familiar with probability theory and statistics and have a genuine interest in biological problems. Algorithm development and large-scale computations will be important components of all three projects. For the last project, a background in insect comparative morphology, SEM imaging and phylogenetics is essential and familiarity with image and biodiversity databasing on the web is desirable. Applicants should submit CV, description of research interests, and name and address of three references. The appointments are for one year at a time up to five years depending on the success of the candidate and funding availability.

Send your application to: Anne Johnson, School of Computational Science and Information Technology, Florida State University, Tallahassee FL 32306-4120. Applications will be reviewed starting on August 9, 2004.

Florida State University is an Equal Opportunity/Affirmative Action Employer and encourages applications from women and members of minority groups. Your application for employment with the Florida State University is subject to public disclosure under the Florida Public Records Act.

Geneva PopGenetics

*_Postdoctoral Research Position Available for a scientist with expertise in Population Genetics / Comparative Genomics _in the Laboratory of S.E. Antonarakis Department of Genetic Medicine and Development University of Geneva Medical School Geneva, Switzerland

The research in the laboratory is funded by grants from the Swiss National Science Foundation, European Union, and the U.S. NIH. The research interests of the lab are the molecular pathophysiology of genetic disorders, and the functional analysis of the human genome (see Nature 420: 578, 2002; Nature 420: 582, 2002; Science 302: 1033, 2003) Please send CV, letters of recommendation, personal statement of research interests and career goals to the address shown at the end of this email.

Geneva offers outstanding living conditions, and the University of Geneva has a competitive salary and fringe benefit package. Geneva University is an equal opportunity employer. *

———————————————–

– Stylianos E Antonarakis MD, DSc Professor and Chairman, Department of Genetic Medicine and Development University of Geneva Medical School, and University Hospitals of Geneva 1 rue Michel-Servet 1211 Geneva, Switzerland tel 41-22-379-5708 fax 41-22-379-5706 Email: Stylianos.Antonarakis@medecine.unige.ch http://medgen.unige.ch/ http://www.frontiers-in-genetics.org Administrative Assistant: Mrs Katia Casada, tel 41-22-379-5707 Email Katia.Casada@medecine.unige.ch

Montpellier Phytopathogens

Post doctoral research position in Montpellier, France: Population Geneticist. Study of adaptive potential of phytopathogenic populations

The detailled announcement is available at: http://www.cirad.fr/fr/empl_formation/poste/766.php (in french) http://www.cirad.fr/en/empl_formation/poste/766.php (in english)

Best regards, Jean Carlier –

Merci de noter mes nouvelles coordonnées Please note my new adress, phone and fax numbers

Jean Carlier

UMR BGPI, CIRAD TA 41 / K, Campus International de Baillarguet 34398 Montpellier Cedex 5

Tél: 33 (0) 4 99 62 48 09, Fax: 33 (0) 4 99 62 48 12 e-mail: jean.carlier@cirad.fr

Bâtiment K, bureau 120

Jean Carlier <jean.carlier@cirad.fr>

NCStateU DiseaseModels

Please use this to replace the previous advertisement from NCSU–vector/disease models

North Carolina State University– Vector/disease models

Posdoctoral Fellowship

Vector/disease models: We need an evolutionary biologist with experience in computer simulation modeling (C++ preferred) to work on an NIH-funded project. The project is aimed at developing spatially explicit models of mosquito population dynamics/genetics that can contribute to assessment of risks and benefits associated with a number of strategies for releasing transgenic mosquitoes to reduce the incidence of human disease. The fellowship is for 3 years. In addition to working on model development and testing, the person in this position will collaborate in an interdisciplinary group composed of mosquito ecologists, disease epidemiologists, molecular biologists, biomathematicians, ethicists, and scientists from disease-endemic countries, in efforts to develop novel transgenic strategies for disease reduction. The person in this position will develop a user-friendly version of the model and will work with the PI in organizing an NIH-funded workshop to teach other researchers to use the model. There will be an opportunity for some empirical research (if desired), and for interactions with other members of the lab working on other evolutionary and modeling research.

An overview of the area of research and an entry point to relevant literature can be found in "Gould, F., and P. Schliekelman. 2004. Population genetics of autocidal control and strain replacement. Ann. Rev. Entomol. 49: 193-217".

North Carolina State University is a leading research institution with a strong commitment to the study of quantitative and population genetics. The University is situated in Raleigh, NC and is within 30 miles of Duke University, UNC-Chapel Hill, NIEHS, an EPA research unit, and the Research Triangle Park. NC State University is an equal opportunity and affirmative action employer.

To apply: Send to Fred_Gould@NCSU.edu 1) A one or two page letter of intent. 2) CV, and 3) Names of 3-4 references. Closing date for applications is August 1, 2004, or until a suitable candidate is found. For further information call Fred Gould at 919-515-1647 or email to above email address.

OhioStateU SongDialects

POSTDOCTORAL POSITION - CULTURAL EVOLUTION OF SONG DIALECTS

We are seeking a postdoctoral researcher to work on an NSF-funded project on the evolution of song dialects in the white-crowned sparrow in collaboration with Doug Nelson (song dialects and learning) and Lisle Gibbs (molecular ecology and behavior) at The Ohio State University. The project involves three months of field work along the Oregon coast between April and June each year, and parentage analysis using microsatellite loci and analysis of field data during the rest of the year at Ohio State. Field work involves capturing and bleeding birds, tape-recording songs, and behavioral observations, often in foul weather. The ideal candidate will have strong interests/experience in animal communication and in molecular methods for the analysis of genetic variation. Initial appointment, beginning around January 2005, is for two years, with two-year extension possible. Starting salary is $30K including full benefits. The Ph.D. degree is required before the position begins. Please send a letter summarizing research experience along with a curriculum vitae including the names, addresses and e-mails of three references to: Dr. Douglas A. Nelson Department of Evolution, Ecology and Organismal Biology The Ohio State University 1315 Kinnear Road Columbus, OH 43212

We will begin screening applications on 1 October 2004. Direct inquiries to Doug Nelson at nelson.228@osu.edu or Lisle Gibbs at gibbs.128@osu.edu.

– H. Lisle Gibbs Associate Professor Department of Evolution, Ecology and Organismal Biology Ohio State University 300 Aronoff Laboratory 318 W. 12th Ave. Columbus, OH 43210-1293

Tel: 614-688-3861, Fax: 614-292-2030 email: gibbs.128@osu.edu http://www.biosci.ohio-state.edu/ ˜ eeob/gibbs/index.html Lisle Gibbs <gibbs.128@osu.edu>

PortlandStateU Arachnid

POSTDOCTORAL POSITION - EVOLUTIONARY GENOMICS AND SYSTEMATICS OF ARACHNIDS

Postdoctoral position available in the laboratory of Susan Masta at Portland State University to study the systematics of arachnids using whole mitochondrial genome sequences. We are using both sequence data and rare genomic changes (such as gene rearrangements and inferred secondary structure changes in tRNAs) to determine the evolutionary history of this ancient group of arthropods. This NSF-funded project is in collaboration with Jeff Boore at the D.O.E. Joint Genome Institute, where most sequencing will be completed. Opportunities exist to extend the project in independent directions. The position is for one year with possibility of extension. Salary is $33,000, plus benefits. The preferred start date is September 2004, although there is some flexibility.

Portland State University is located in beautiful downtown Portland, within close walking distance of a diversity of cultural opportunities, and is served by an excellent public transportation system. Year-round outdoor opportunities exist nearby at the Columbia Gorge, the Cascades, and the Oregon coast.

Please send a statement of research interests, CV, and names and contact information for 3 references via email to smasta@pdx.edu. Applicant review will begin July 12 and continue until the position is filled.

Portland State University is an Affirmative Action, Equal Opportunity employer, and in keeping with the PSU President's diversity initiative, welcomes applications from diverse candidates.

– Susan E. Masta, Assistant Professor Dept. of Biology Portland State University P.O. Box 751 Portland, OR 97207-0751 Phone (503) 725-8505 Web: http://web.pdx.edu/˜smasta/index.html

Sevilla RaptorSpecies

POSTDOC

In Conservation Genetics at Doñana Biological Station (CSIC, Sevilla, Spain)

Funded by Marie-Curie Host Fellowship Programme (E.U.)

We are interested in attracting one post-doctoral fellow combining a good knowledge about general DNA laboratory techniques, such as sequencing and microsatellite typing, as well as the necessary skills to incorporate the resulting data into population genetic models. The successful candidate will be expected to join a research team currently dealing with critically endangered raptorial species including the Spanish imperial eagle and the Egyptian vulture.

This is an opportunity for high quality post-doc students ('Fellows') registered in other EU countries to come and work at our Institute for a period of 1 year. The scheme is well-funded, with travel and subsistence funds for the Fellow and limited funds to cover research costs.

Applicants should have a PhD in genetics or a related field. The successful candidate will also demonstrate proficiency with molecular techniques and a sound publication record. The fellow must be under 37 years of age, a national of a Member State of the Community or an Associated State or residing in the Community for at least the last five years.

If interested, please send CV and 2 support letters to: Dr. Juan Jose Negro Estacion Biologica de Donana, CSIC Avda, Maria Luisa s/n, Pabellon del Perú E-41013 Sevilla, SPAIN negro@ebd.csic.es www.ebd.csic.es/LEM Phone: +34 954232340 Fax: +34 954621125

Juan J. Negro Estación Biológica Doñana (CSIC) Apdo. 1056 41080 Sevilla Spain

negro@ebd.csic.es

TulaneU EvolToolUse

POSTDOCTORAL RESEARCHER

Motor control and kinematics of tool use in humans

Tulane University in New Orleans is seeking applications for an NIH-funded postdoctoral research position to study motor control and kinematics of tool use in infants and young children under the supervision of Dr. Jeffrey Lockman (Department of Psychology) and Dr. Duncan J. Irschick (Department of Ecology and Evolutionary Biology). The primary goal of the project is to study how infant object manipulation and toddler tool use are related in human development. Potential relations will be documented with both 2-D and 3-D kinematic and behavioral techniques. Applicants should have experience with kinematic and/or motor control analysis, preferably in humans, although researchers working with other organisms will be considered. Preference will be given to individuals with a strong publication record and quantitative skills. The researcher will be expected to work closely with both graduate and undergraduate students. Funding is available for up to 5 years. Interested applicants should send a C.V., statement of research goals, contact information for 3 references, and representative publications to:

Dr. Jeffrey J. Lockman, Dept. Psychology, Tulane University, New Orleans, LA 70118.

For further information, contact J. Lockman at lockman@mail.tulane.edu.

UArizona HumanOrigins

University of Arizona Research Associate/Postdoctoral Fellow (Job #30880) Position Summary: A postdoctoral fellow position is open to work on a five-year NSF project (HOMINID) titled "A Novel Genetic Database to Test Models of Human Origins". This project is a collaborative effort between the laboratories of Michael Hammer at the University of Arizona and Jeff Wall at USC to gather new data and design novel analytical methods to answer long-standing questions in human evolution. The successful applicant will participate in experiment design and data collection at the University of Arizona, and analyze data in conjunction with collaborators at USC. The questions to be addressed include the contribution of archaic forms of Homo to the contemporary human gene pool, the degree of subdivision of populations ancestral to modern humans, and the effects of bottlenecks and population expansion on patterns of linkage disequilibrium in the human genome. DNA sequence data will be collected from 90 genomic regions in humans and representatives of great apes. Statistical and computational methods will be developed for rigorously testing the predictions of alternative hypotheses.

Benefits: Yes Salary: DOE (NIH scale) Hours: Full Time (40 hrs/week) Opening: 6/11/04 Closing: 8/1/04

Application Instructions for Job No. 30880 All applicants must apply on-line using Internet Explorer or Netscape Navigator (see browser settings on the following web site). To apply, please visit https://www.uacareertrack.com/applicants/jsp/shared/frameset/Frameset.jsp?time=1086366632125. Select "Search Postings" and enter job #30880. Select "view" located below the Position Title. Select "Apply to this Posting" and follow instructions. For consideration, complete requested documentation must be received by midnight of the closing date.

Minimum Qualifications * PhD in relevant field * Graduation date no later than 31 July 2004 * Molecular skills and training in theoretical population genetics

Preferred Qualifications * Research experience in molecular population genetics * Computer simulation experience

– Michael Hammer Dept. EEB Biosciences West University of Arizona Tucson AZ 85721 mfh@u.arizona.edu (520) 621-9828

Michael Hammer <mfh@u.arizona.edu>

UArizona phylogenetics

Judith Becerra and I have postdoc funding for someone who can work with us on comparative ecology in a phylogenetic framework. The subject areas are plant-insect interactions and evolution of plant adaptive traits. Ideally we want someone who has familiarity and experience working with the theory and software used in phylogenetic comparative biology. A good background in statistics and computer programming would be a plus. This is a one or two year position, with possibility of renewal for a third. We have a very strong program in ecology and evolutionary biology with may grad students and postdocs, making this a good environment for postdoctoral work. Please contact us at Judith Becerra <becerra@Ag.arizona.edu> or venable@u.arizona.edu

The website with the job posting is: www.UACareerTrack.com/ . Look under Postdocs, Ecology and Evolutionary Biology.

-Larry Venable and Judith Becerra Departments of Ecology & Evolutionary Biology and Entomology University of Arizona Our websites: http://eebweb.arizona.edu/faculty/venable/ http://eebweb.arizona.edu/Faculty/Becerra/ Larry Venable <venable@email.arizona.edu>

UCDavis FlyEvol

A post doctoral position (possibly two) is available in the lab of Sergey Nuzhdin to work in the areas of Molecular Quantitative Genetics, Genomics, and Speciation. You will enjoy stimulating environment of UC Davis Center for Population Biology. We study flies, yeast, mosquitoes and go for answering the most interesting evolutionary questions we can imagine. You will be expected to contribute to NIH and NSF sponsored research, develop your own research directions, and have fun hiking in Sierras, sailing, and enjoying close by urban areas. Info about the lab may be found at nlab.ucdavis.edu

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Charles H. Langley 3342B Storer Hall The Center for Population Biology & The Section of Evolution and Ecology University of California - Davis One Shields Avenue Davis, CA 95616-8554 Phone: (530) 752-4085 - Office (530) 752-4253 - Lab (530) 752-1449 - Fax Email: chlangley@ucdavis.edu

"C.H. Langley" <chlangley@ucdavis.edu>

UCDavis PlantInsect

Post-doc in plant-insect interactions (sensu lato)

A two-year postdoctoral position is available in my lab to study plant-animal interactions. The research topic beyond this general description is extremely flexible and proposed by the applicant. A full range of interests are eligible from use of genomic tools in field studies to the study of microbial impacts on food webs and communities, to anything in between.

Please send a no- longer-than 5 page proposal, 12 point font, CV, and the names and e-mail addresses of three references.

PLEASE send all materials electronically with the subject heading: Postdoc applicant (this will help me to separate spam from good stuff) to systrauss@ucdavis.edu.

Aside from interactions with my lab, there is large group of ecologists and evolutionary biologists here at UC Davis to serve as additional resources. Applicants are encouraged to look at local UC reserves like Bodega Marine Lab, Jepson Prairie, Quail Ridge and Mclaughlin Reserve and other field sites (Yolo Basin) as possible sites for their projects . Website: http://nrs.ucop.edu/publications/reserve-site-spec/info-about-reserves.html I will start evaluating applicants on July 15th. Although there is no strict deadline, applicants are encouraged to have proposals submitted by then for maximal consideration.

Salary: $33,000 plus excellent benefits.

Feel free to contact me if there are any questions.

Position open until filled.

Sharon

Sharon Y. Strauss, Professor Section of Evolution and Ecology, 2320 Storer Hall One Shields Ave, UC Davis, Davis, CA 95616

ph: 530-752-8415 FAX: 530-752-1449 e-mail: systrauss@ucdavis.edu

Sharon Strauss <systrauss@ucdavis.edu>

UCLA TreeGeneFlow

Post-doctoral opening in Plant Population/Conservation Genetics

One year post-doctoral position is available in the research program of Victoria Sork at UCLA who is studying contemporary pollen and seed movement in California Valley Oak. We seek an individual who is interested in data analysis, statistical modeling, and spatial modeling using microsatellite genetic markers of progeny and parents. The post-doc will have the opportunity to interact with Peter Smouse on the modeling components of the project. Other projects in the laboratory include phylogeography of California oaks and seed dispersal in African tropical forests. The position has the potential for continued funding, especially if the individual initiates new projects or becomes involved in other existing research. Position ideally starts in September 2004 but not later than December 2004.

Candidates should send electronically a letter of application, statement of research interests, CV, and names of three references with contact information to Dr. Victoria Sork by email (vlsork@ucla.edu). Please send these documents as attachments in either pdf or Word format and start file names with your initials. Review of applications will start June 2004.

“Victoria L. Sork” <vlsork@ucla.edu>

UCRiverside PlantFitness

Postdoctoral Research Position in Tritrophic Interactions.

A postgraduate research position is available for a highly motivated individual to join an NSF-funded research project to quantify the effects of a trichome dimorphism on plant fitness in a tritrophic context. The primary objective of this position is to test the working hypothesis that the indirect effects of glandular trichomes on natural enemies oppose the direct effects of those trichomes on herbivores. The effects of glandular trichomes on natural enemies may constrain the increase in the frequency of plants with glandular trichomes in natural populations. Measurements of plant fitness in the field in the presence and absence of herbivores and natural enemies will be emphasized. The successful candidate will participate in planned field and laboratory experiments and also will have the opportunity to develop related projects.

The successful applicant must have a PhD. degree, research experience and knowledge in insect ecology and behavior, the design and analysis of field experiments, and insect identification. Excellent oral and verbal communication skills are also required.

Postdoctoral positions start at a salary of $31,044 per year, plus benefits. The position will be available after September 1, 2004. The initial appointment will be for one year with reappointment contingent upon satisfactory performance. To apply, send a description of research interests, curriculum vitae, relevant reprints or manuscripts in press, and the names and e-mail and postal addresses of three references by July 15, 2004 to:

Dr. J. Daniel Hare Department of Entomology University of California Riverside, CA 92521 daniel.hare@ucr.edu. http://faculty.ucr.edu/~harejd/ .

The University of California, Riverside is an Equal Opportunity, Affirmative Action Employer.

UCollegeLondon SexualConflict

Post-Doctoral Research Fellow Department of Biology University College London

Investigation of the mechanisms underlying sexual conflict in a stalk-eyed fly, Cyrtodiopsis dalmanni.

A BBSRC funded post-doctoral position is available for up to 22 months in the stalk-eyed fly research group of Dr Tracey Chapman, Dr Kevin Fowler and Professor Andrew Pomiankowski in the Department of Biology at UCL (http://www.ucl.ac.uk/biology/new/-admin/research.html). Seminal fluid proteins in male insects can reduce female sexual receptivity and increase egg-laying, and may also underlie sexual conflict (e.g. Chapman et al. 1995 Nature 373, 241-244). We will investigate the mechanisms underlying sexual conflict over multiple mating in a stalk-eyed fly, using a species in which females show a preference for mating with males possessing exaggerated eyestalks. We will analyse the functions of male reproductive tract-specific transcripts and determine the functional and evolutionary significance of male accessory glands. The candidate should have experience in molecular biology and flywork. Starting salary is 21,010 GBP per annum prorata (23,144 GBP including London Allowance). To apply and for further information, please send a covering letter and a CV with the names and contact details of 3 referees to Tracey Chapman (t.chapman@ucl.ac.uk) Department of Biology, University College London, Darwin Building, Gower Street, London WC1E 6BT. Tel:020 7679 4393 Fax:020 7679 7096. Applications by email are preferred. Closing date is 24th June 2004.

Tracey Chapman <t.chapman@ucl.ac.uk>

UGlasgow cospeciation

Ancient mariners or recent stowaways?

A three year NERC postdoc is available in Rod Page's lab to in Glasgow study seabird-louse cospeciation in multiple clades of seabirds. The provisional start date is October 1, 2004. The aims of the research are:

1. To establish robust phylogenies for lice from three different seabird orders. 2. To measure the relative frequency of cospeciation, host switching, and other events in the evolution of seabird lice. 3. To determine whether multispecies louse assemblages have evolved in situ on the host, or whether they are the result of independent colonisations. 4. To determine which (if any) host attributes are correlated with louse diversification and degree of cospeciation. 5. To assess the effect of host phylogeny shape on the degree of cospeciation between seabirds and their lice.

Full details of the project can be found at http://-taxonomy.zoology.gla.ac.uk/Jobs/NERC2004/ .

I will be at the Evolution 2004 meetings in Colorado next week, and would be happy to meet anybody interested in the project.

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

Tel: +44 141 330 4778 Fax: +44 141 330 2792 www: http://taxonomy.zoology.gla.ac.uk/rod/-rod.html Roderic Page <r.page@bio.gla.ac.uk>

UKonstanz MolEvol

A Postdoc position in the general area of molecular evolution is available immediately in the

Department of Evolutionary Biology at the University of Konstanz, Germany.

We are looking for a postdoc who is interested in molecular evolution, bioinformatics/genomics or evolutionary developmental biology to augment the evolutionary biology group at the University of Konstanz, Germany.

The great lakes in East Africa house some of the worlds most diverse freshwater ecosystems. Lakes Victoria, Malawi and Tanganyika are particularly well-known for their intriguing species diversity - the adaptive radiations of cichlid fishes are especially well-known. Our research focuses on several aspects of the biology of these fishes. We are interested in the speciation, phylogeography, molecular evolution and molecular phylogenetics of the cichlid fish assemblages of these lakes, we are also interested in identifying and characterizing the function of genes that are involved in the phenotypic diversification and speciation of cichlid fishes. Several molecular biological and "devo-evo" and genomic approaches, including candidate gene approaches, DNA-chip technology, ESTs, in situ hybridization in cichlids and transgenics in zebrafish are used to address these questions. Furthermore, we are interested in evolutionary questions in genomics and the evolution of novel gene functions after gene and genome duplications.

If you are interested in these questions it would be desirable, but not a must, if you already have experience methods in molecular developmental biology, molecular evolution, phylogenetics, or bio-computing.

Funding is available for at least 2 years. Postdoc salaries (BATII/a government payscale) are approximately 40 to 45,000 Euros annually, (depending on marital status, age, etc.) before the deduction of taxes, health insurance and retirement contributions.

The evolutionary biology group is an international group of students and researchers that consists of about 10 different nationalities and about 20 people. The common language for teaching and in the lab is English.

The facilities and instrumentation are state-of-the-art.

The position is open immediately. The review of applications will begin at the end of June 2004 and will continue until this position is filled. To apply, please email or send a curriculum vitae, list of publications, a statement of research interests, and the names and email addresses of two references to:

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

For more information please visit our web page www.evolutionsbiologie.uni-konstanz.de – Axel Meyer, Ph.D. Professor of Zoology and Evolutionary Biology Department of Biology University of Konstanz Universitätsstr. 10 D-78457 Konstanz Germany

email: axel.meyer@uni-konstanz.de

tel. + 49 7531 88 4163 fax. + 49 7531 88 3018 tel. secretary + 49 7531 88 3069 email: (christiane.ehmann@uni-konstanz.de)

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

ULausanne HumanFuncGenomics

POSTDOC POSITION: EVOLUTIONARY FUNCTIONAL GENOMICS OF HUMANS

A Postdoc position is available immediately in the group of Henrik Kaessmann at the recently founded Center for Integrative Genomics, University of Lausanne, Switzerland.

Currently we focus on the origin and evolution of primate genes and gene structures. New genes originate through various molecular mechanisms such as the classic mechanisms of gene duplication (e.g. tandem gene duplication), gene copying by retroposition, exon/domain shuffling, and gene fusion. We pursue several projects that aim to shed light on the relative importance of these mechanisms in generating primate genes. We are particularly interested in characterizing the (adaptive) evolution of young genes in the human genome that originated recently on the primate lineage and therefore may be relevant in regard to human/hominoid-specific phenotypes. To this end, we explore available data from genomic databases and generate complementary data by experimental analysis.

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

cig For this position, I am seeking highly qualified and motivated applicants with a strong interest in human genome evolution, who have strong experimental lab skills, because we want to characterize functional adaptive changes of newly emerged genes. Thus, dedicated biochemists or molecular biologists with an evolutionary interest are encouraged to apply as well.

The position is available for two years, with possible extensions. The salary is approximately 45,000 Euros per year.

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

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

Applications including a CV, statement of research interest, copies of relevant publications, and two letters of recommendation should be emailed or mailed to me at the address below. Review of applications will begin immediately.

Henrik Kaessmann, Ph.D. Assistant Professor Center for Integrative Genomics BEP University of Lausanne CH-1015 Lausanne Switzerland Phone : 41-(0)21-692-3907 Fax : 41-(0)21-692-3905 E-mail : Henrik.Kaessmann@cig.unil.ch Internet : http://-www.unil.ch/cig

UManchester Dipteran olfaction

Comparative behavioural and neuroanatomical studies of olfaction in dipteran larvae

A BBRSC-funded PhD studentship is available at the University of Manchester to study the organisation and functioning of the olfactory response in a simple model system, the Drosophila larva, using mutants and neurogenetic variants created in our laboratory. A comparative aspect testing the findings in other species will also be introduced. The work will be carried out with Dr Matthew Cobb.

Available immediately. Deadline for receipt of complete applications: 15 September 2004.

Candidates should have, or expect to gain, a First Class or Upper Second Class Honours degree in an appropriate subject. Funding is limited to EU citizens. Studentships will cover tuition fees (all EU citizens) and a maintenance grant (UK citizens only).

Informal contact: mcobb@man.ac.uk

Applicants should send a completed application form with two academic references to:-

School of Biological Sciences, The University of Manchester, 1.30 Stopford Building, Oxford Road, Manchester M13 9PT UK

For more details, see http://www.biomed.man.ac.uk/-mcobb Matthew Cobb <mcobb@man.ac.uk>

UManchester FungalFuncGenomics

Please forward the following advert to any PhD students/post-docs who may be interested.

Magnus.

DEPARTMENT OF COMPUTER SCIENCE POSTDOCTORAL RESEARCH ASSOCIATE E-FUNGI: COMPARATIVE FUNCTIONAL GENOMICS REF 679/04

Applications are invited for a BBSRC-ffunded project, available for 3 years from October 2004, to work on a project to develop an e-Science Infrastructure for Comparative Functional Genomics in Fungal Species. The project is collaborative, involving experimental biologists, bioinformaticians and computer scientists at Manchester and Exeter. The successful applicant will be working as part of a team, in particular focusing on the statistical analysis of genomic and functional genomics data.

Applicants should have, or be about to obtain, a PhD in a relevant area. The person appointed must have good team working skills as they will be expected to interact with other members of the team in order to help make the resulting tools available to biologists via a service-based grid infrastructure. The successful applicant must also have good mathematical skills and previous experience in Bioinformatics or computational biology. In addition he/she should have a good appreciation of appropriate statistical and computational methodologies, although some of this experience can be gained during the project. Experience of machine learning or Statistics would be advantageous.

further details are availble from http://-www.man.ac.uk/news/vacancies/research.html#679 Starting salary will be in the range £18,893 up to £24,951 per annum. Informal enquires should be directed to Dr Magnus Rattray (Email: magnus@cs.man.ac.uk) or Prof. Norman Paton (Email: norm@cs.man.ac.uk).

Application forms and further particulars are available from the Office of the Director of Personnel, The University of Manchester, Oxford Road, Manchester M13 9PL tel: +44 (0)161 275 2028; fax: +44 (0)161 275 2471; e-mail: personnel@man.ac.uk. Quote ref 679/04. Closing date 12 July 2004.

UMaryland BehEvolGenetics

Postdoctoral position in behavioral evolutionary genetics and speciation P.I.'s : Drs. Kerry Shaw and Patrick Danley, Department of Biology, University of Maryland, College Park, MD

Research Project: A postdoctoral position is available to join an NSF-funded project to examine the genetic basis of naturally occurring variation in courtship behavior among closely related species of the Hawaiian cricket genus Laupala. While ecologically and morphologically similar, species are easily distinguished by the pulse rates of the male calling song. Male pulse rate has been implicated in mate recognition and the evolution of this behavioral character is thought to have played a large role in the rapid and extensive diversification of this genus. Two focal species, L. paranigra and L. kohalensis, show large differences in the pulse rate of the male calling song and associated female preference, while a third species, L. pruna, sings at an intermediate value. Biometrical and quantitative genetic loci mapping in the focal species indicates that male song is under the genetic control of many loci. We seek to complement these approaches by examining the patterns of gene expression in a large number of genes expressed in the cricket ventral nerve cord via microarray analysis. The rhythmic singing behavior in crickets has been localized to a specific tissue and the development of the rhythmic neuromuscular behavior that generates song has been shown to lie within a specific developmental window. We are probing the link between gene expression and the development of this naturally occurring behavior. The successful candidate would be expected to contribute to this collaborative project while forging an independent research direction. A comparative phylogenetic framework also exists in which to understand behavioral evolution in this genus. Laupala represents a portion of a larger radiation of endemic Hawaiian trigonidiine crickets that is conspicuously characterized by frequent speciation and acoustic signaling evolution. In Laupala, DNA data suggest that the current radiation began on the oldest island where the genus is presently found (Kauai, 5 mya), and radiated into younger island habitats as those islands appeared within the last 5 million years. These data also show that speciation has occurred both within and between islands and that species ranges are limited to single islands. Communities of Laupala occur on all the major Hawaiian Islands and convergent patterns of song evolution among islands, and displaced evolutionary patterns within islands are evident. The three focal species of this study are each endemic to the Big Island of Hawaii and are very closely related. This phylogenetic structure provides a recent evolutionary context in which to study the evolution of genes and behavior.

Requirements: The desired candidate will possess an interest in / experience with a number of bench skills (such as DNA/RNA extraction, PCR, cDNA synthesis, cloning). An interest in the neurological basis of behavior and/or the evolution of premating isolation would be beneficial but no prior knowledge is required.

The University of Maryland's Department of Biology has several labs dedicated to the study of both speciation genetics, neuroethology and evolutionary developmental biology. As such, it provides a rich academic environment for those interested in proximate and ultimate causes of behavioral development, evolution and speciation.

The position can be filled immediately and two years of funding are available. To apply, email a statement of research interests, a curriculum vitae, and the email addresses of three references to Kerry Shaw (ks233@umail.umd.edu). Both Pat and Kerry will be at the SSE/SSB/ASN meeting in Fort Collins, CO and would be happy to meet with potential candidates during the meeting. Please visit poster T115 for further information.

Kerry L. Shaw University of Maryland Dept. of Biology Biology/Psychology Bldg. College Park, MD 20742-4415

tel: (301)405-7503 fax: (301)314-9358 e-mail: ks233@umail.umd.edu

http://www.life.umd.edu/biology/faculty/shaw/index.html http://www.life.umd.edu/biology/faculty/shaw/index.html

UMinnesota PlantEvol

Postdoc: Plant Evolution and Elevated CO2

A post-doctoral position to investigate the effect atmospheric CO2 concentration has on patterns of selection and the genetic basis of phenotypic variation will soon be available in my lab. This research will examine patterns of selection on phenotypic and ecophysiological traits of Arabidopsis thaliana grown in ambient and elevated CO2 environments. The fieldwork will be conducted within an existing free-air CO2 enrichment (FACE) experiment at Cedar Creek Natural History Area near the Univ. of Minnesota. Recombinant inbred lines of A. thaliana will be used to allow for mapping of QTL underlying phenotypic variation. This is an NSF-funded collaboration among Ruth Shaw, Peter Reich, and me.

The basic requirements are a Ph.D. in some aspect of evolutionary biology or ecology and experience or interest in selection analyses, quantitative genetics, QTL mapping, and large field-experiments. The start date is flexible.

To apply send (e-mail is fine) a CV, a statement of research interests, and names and contact information for three references. Review of applicants will begin August 15th and continue until the position is filled.

If you have questions please contact me (ptiffin@umn.edu). Ruth Shaw and I will also be at the Evolution meetings in Fort Collins.

Peter Tiffin Dept. of Plant Biology University of Minnesota St Paul, MN 55108-1095 USA

Phone: 612 624-7406 FAX: 612 625-1738 ptiffin@umn.edu

The University of Minnesota/Plant Biology is an equal opportunity educator and employer.

UNeuchetel PlantInsect

Proposition de Post-doc sur les Interactions Plantes-Insectes Au laboratoire d'Ecologie Animale et d'Entomologie de l'Université de Neuchâtel en Suisse.

Critères importants pour pouvoir postuler : 1) Parler couramment Franais 2) Avoir une bonne expérience de l'enseignement 3) Disposer de bases solides en entomologie

Nous recherchons un jeune scientifique disposant de solides connaissances dans au moins un des domaines suivants : interactions plantes-insectes, interactions tri-trophiques, écologie chimique et génétique des populations. Toutes les personnes disposant de solides connaissances et d'une bonne expérience en biologie moléculaire dans le domaine de la génétique des populations sont fortement encouragées à postuler. Les recherches développées au sein du laboratoire sont toutes focalisées sur l'écologie et l'évolution des interactions tri-trophiques entre les plantes, leurs ravageurs et leurs parasitoïdes dans des systèmes soit naturels, soit agricoles (pour de plus amples détails voir la page web du laboratoire: http://www.unine.ch/zool/leae/-index.html).

Le domaine de recherche sera défini en accord avec la personne sélectionné et les 3 membres responsables du laboratoire (Martine Rahier, Betty Benrey et Ted Turlings). En plus du travail de recherche, une contribution à l'enseignement principalement d'Entomologie et d'Ecologie sera demandée.

Le poste est initialement prévu pour 1 an à partir d'Octobre 2004, avec une possibilité de prolongation de 3 à 5 ans. Toutes les personnes intéressées sont encouragées à envoyer très rapidement une lettre décrivant leurs parcours et leurs centres d'intérêts tant en recherche qu'en enseignement. Joindre également un CV, une liste de vos publications et les noms avec leurs adresses e-mails et leurs coordonnées téléphoniques et postales de 3 personnalités scientifiques connaissant votre parcours et vos travaux. Envoyer le tout à Martine.Rahier@zool.unine.ch La date de clôture pour recevoir les dossiers de candidature est fixée au 9 Juillet 2004.

UNorthCarolina PlantEvolGenetics

Postdoctoral position in plant molecular and evolutionary genetics PI: Todd Vision, Department of Biology, University of North Carolina at Chapel Hill

Research Focus: A postdoctoral position is available to study the molecular and evolutionary genetics of polygenic traits in plants. Experimental projects in the Vision laboratory include comparative QTL mapping studies of plant water use efficiency, the genetics of domestication in the Solanaceae, and reproductive isolation among species of Mimulus. We are generally interested in the interplay between molecular and phenotypic evolution in polygenic traits. In addition, the laboratory is heavily involved in the development and use of computational tools for comparative genomics. You would be expected to contribute to one or more of these collaborative projects while forging your own research directions. For more information on our laboratory, please visit http://www.bio.unc.edu/faculty/-vision/lab/ Requirements: Applicants with strong laboratory experience in molecular genetics, as well as an interest in population or quantitative genetics, are encouraged to apply. The position would initially be for one year with extension likely. The starting date is flexible. Salary would be commensurate with experience.

The Area: UNC, plus nearby Duke and NC State Universities, collectively host a vibrant community of plant molecular biology and evolutionary genetics researchers. Chapel Hill is located in the culturally rich and cosmopolitan Research Triangle, about equidistant from the Outer Banks and the Appalachian mountains.

To Apply: Email a statement of research interests, a curriculum vitae, and the email addresses of three references to Todd Vision (tjv@bio.unc.edu).

UQuebecRimouski Aquaculture

Postdoc position in aquaculture

A postdoctoral position is available in the laboratory of Dr. France Dufresne in the Biology department of the Université du Québec à Rimouski to pursue a project on the genetic improvement of growth and survival in the giant sea scallop, Placopecten magellanicus. The project will focus on identifying pedigreed scallops in mass spawnings using microsatellite markers and to develop useful biochemical markers of stress resistance that can be integrated into a breeding program.

Candidates are expected to be familiar with molecular techniques such as cloning, PCR, and microsatellites. This position is available immediately.

If interested, please send your curriculum vitae as well as the name and adresses of two referrees to

France Dufresne Département de biologie Université du Québec à Rimouski 300 allée des ursulines Rimouski, Québec, Canada G5L 3A1 tel (418) 723-1986 ext. 1223 fax (418) 724-1849 france_dufresne@uqar.qc.ca

– France Dufresne, Ph.D. Département de biologie Université du Québec à Rimouski 300 allée des ursulines Rimouski, Québec, Canada G5L 3A1 tel (418) 723-1986 ext. 1223 fax (418) 724-1849

france dufresne <rbduffra@jafar.uqar.qc.ca>

USeville FloweringPlants

Dear colleagues,

We are offering a postdoc research position at the University of Seville, Spain. We are looking for a candidate experienced in molecular ecology of flowering plants. More details can be obtained from:

abelardo@us.es Dr. A. Aparicio Dept. Biología Vegetal y Ecología Fac. Farmacia. Univ. Sevilla c/ Prof. Grarcía González n 2 41012 Sevilla. España Tel 954556787 Fax 954233765 http://www.us.es/grnm210

WashingtonU EvolBiol

POSTDOCTORAL FELLOW WASHINGTON UNIVERSITY in ST. LOUIS TYSON RESEARCH CENTER

Washington University in St. Louis, Missouri invites applications for a Postdoctoral Fellowship in Ecology, Environmental Sciences, or Evolutionary Biology to be based at the Tyson Research Center, a 2,000-acre tract of land located 20 miles from campus. The fellow will be responsible for developing

a research program independently or in conjunction with Washington University faculty and involving undergraduates in research conducted at the Center. In addition, the fellow will be expected to teach one course, Conservation Biology, during the school year. This is a twelve-month appointment renewable for a second year. Start date is flexible, but can be no later than Jan. 1, 2005. More information on Tyson can be found at http://www.biology.wustl.edu/tyson/- . Applicants should include a curriculum vitae and a statement of the research to be conducted at the

Center, and arrange to have two letters of recommendation sent on the applicant's behalf. All materials should be sent electronically to Jonathan Losos, Ph.D., (losos@biology.wustl.edu), and to Jon Chase, Ph.D. (jchase@biology2.wustl.edu). Applicant review will begin July 31 and continue until the position is filled.

Washington University is an Equal Opportunity Employer.

Jonathan Chase <jchase@biology2.wustl.edu>

WorkshopsCourses

LundU SensoryEcol Oct11-24

Dear All!

I am happy to inform you that there will be an international PhD student course on Sensory Ecology given at Lund University 11-24 October 2004. You may find more information on program and content of the course at the course web site: www.biol.lu.se/cellorgbiol/sensecol. Participants may sign up at the web site or send an email to Sensory.Ecology@cob.lu.se.

Very welcome!

Susanne Åkesson

Susanne Åkesson PhD, Docent Department of Animal Ecology Lund University Ecology Building SE-223 62 Lund

tel. +46 (0)46-222 3705 fax. +46 (0)46 222 4716 email. susanne.akesson@zooekol.lu.se http://ornlab.ekol.lu.se/birdmigration/

Lyon PopGenet June24-25

TOP OF MESSAGE: Dear Evoldir, an international workshop called "Computational linguistics methods & Population Genetics" will soon be held in Lyon (France) the 24 and 25 June 2004 (next week).

Invited speakers: Peter Forster (McDonald Institute for Archeological Research - Cambridge UK); Russel Gray (University of Auckland - New Zealand); Hans Goebl (University of Salzburg - Austria); Wilbert Heeringa (University of Groningen - The Netherlands); Paul Heggarty (University of Sheffield - UK); Robert McMahon (University of Sheffield - UK); John Nerbonne (University of Groningen - The Netherlands).

Aims: The aim of this workshop is to focus on the possible ways to investigate linguistic variability using computational methods inspired from population genetics and phylogenetics. Several such methods have already been developed in a dialectometric frame, but hardly permeate historical linguistics. The discussion will be restricted to regional scales and to the analysis of similar languages. Clear methodological parallelism can be established between population genetics approaches and linguistic issues. Recently, some of these, median joining network and string alignment for instance, have been introduced in linguistics, but their application is mainly restricted to dialectology. The linguistic community often considers these approaches as heretic, the main stumbling block being the reductionism imposed on the linguistic data to fit models developed for molecular data. To perfect these methods and make them gain acceptance among linguists, some fundamental questions must be answered convincingly: Can these methods also be applied to close languages? How close should these languages be? Are the results reliable? How can this reliability be tested?

Unfortunately, there is no time for other presentations so, please, do not submit abstracts.

Further details concerning the programme, the venue and the registration are available on the website:

http://www.mnhn.fr/mnhn/ecoanthropologie/linguistics/lyon.html END OF MESSAGE

Dr. Franz Manni Maître de conferences / Assistant professor UMR 5145 - Eco- Anthropology Group National Museum of Natural History MNHN - Musée de l'Homme 17, Place du Trocadéro 75016 Paris - France Tel. 0033 1 44 05 72 84 Fax. 0033 1 44 05 72 41 Telex Musethno

Franz Manni <manni@mnhn.fr>

MBL GenomeTechnology Oct5-31

Advances in Genome Technology and Bioinformatics Course Marine Biological Laboratory & The Institute for Genome Research October 5 - October 31, 2004

http://www.mbl.edu/education/courses/special_topics/genome.html ** deadline extended, applications still being accepted

A comprehensive, four-week course in Genome Science that will integrate Bioinformatics with the latest laboratory techniques for genome sequencing, genome analysis, and high throughput gene expression (DNA microarrays). A distinguished faculty from major universities, bioinformatic centers, The Institute for Genomic Research and the Marine Biological Laboratory will train students including postdoctoral students, graduate students and established PI's. This cutting-edge course will integrate a series of lectures with laboratory exercises both at the computer and in a high technology, high throughput facility. Limited to 24 students.

The major instructional modules include (1) Genome Sequencing (vector development, library construction, high throughput sequencing technologies, principles of automation using advanced robotic liquid handlers, genome assembly algorithms and closure strategies); (2) Bioinformatics (Gene prediction algorithms, annotation, database construction and searching, phylogenetics and molecular evolution); and (3) Functional Genomics (DNA microarrays, data analysis). In addition, we will sponsor symposia in topical areas in genome science. Examples of symposia to be offered include: Advances in genome assembly; Genomes and development; Genome science and environmental biology; Genome evolution; Impact of genome science on Drug design; etc. The breadth of topics in genome science and the advanced training based upon advanced laboratory technology, distinguish this course from all other offerings.

Directors: Claire M. Fraser, The Institute for Genomic Research; and Mitchell L. Sogin, The Marine Biological Laboratory, Woods Hole.

Faculty list for 2004:

Mitchell L. Sogin, Claire Fraser (co-directors) Andrew McArthur, Hilary Morrison, Rich Fox, Shanda Birkeland, Michael Cipriano William Niermann, Claudia Reich, Ewan Kirkness, Tamara Feldblyum, John Gill Mihai Pop, David Jaffe, Steve Salzberg, Owen White, Herve Tettelin, John Heidelberg John Quackenbush, Norm Lee, Nirmal Bhagabati, Wei Liang, Alex Saeed, Vasily Sharov Steve Gill, Eric Hoffman, Scott Peterson, Jonathan Eisen, Alex Bateman William Pearson, Gary Olsen Lisa Romano

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Muenster AsexualDiversity Oct6-10

Muenster Asexual Diversity 6-10 Oct

SECOND ANNOUNCEMENT for workshop on "Diversity in asexuals: Patterns and processes" 6.-10. October 2004 Muenster, Germany Organizers: Nico Michiels, Thomas D'Souza, Claus-Peter Stelzer.

TOPIC The workshop covers various aspects of diversity in asexual populations: geographical parthenogenesis, asexual species concepts, phylogenetic constraints, phylogenetic distribution, hybrid zones, niche differentiation, adaptability, genetic diversity, and terminology. Our workshop is one out of four within the Parthenogenesis Network (PARTNER), an initiative funded by the European Science Foundation (ESF). PARTNER is aimed to bring together empiricists and theorists who work in the field of parthenogenesis in botany and zoology (for more information, see http://www.nioo.knaw.nl/networks/partner).

LOCATION Muenster is a charming medieval city in the northwestern part of Germany. An important chapter of history was written here 350 years ago. In 1648, the "Peace of Westphalia" ended the cruelties of the Thirty Years War between Catholics and Protestants. Hence, Muenster's importance as a symbol for conflict resolution in Europe.

CONFIRMED SPEAKERS Michael Mogie (University of Bath, UK), Robert Vrijenhoek (Monterey Bay Aquarium Research Institute, USA), Leo Beukeboom (University of Groningen, Netherlands), Anssi Saura (Umea University, Sweden), Peter van Dijk (Netherlands Institute of Ecology), Hugh Loxdale (Rothamsted Research, Harpenden, UK), Isa Schoen (Royal Belgian Institute of Natural Sciences), Tim Barraclough (Imperial College London, UK) Lawrence Kirkendall (University of Bergen, Norway), Tim Sharbel (Laboratoire IFREMER, France).

APPLICATIONS We are happy to invite ca. 20 additional participants. Each invited attendant is expected to contribute a short oral presentation during the workshop (ca. 15 min). Applications should include a short CV and a brief description of the research interests (together max. two pages). Selection among the applicants will be based on research record and topic. The workshop organization will cover the accommodation costs in the facilities provided by the organization for invited attendants, but cannot cover their travel expenses. Applications, preferably by email, should be submitted before June 15, 2004 to: partner3@uni-muenster.de

The final list of participants and additional information on the workshop will soon be posted on: http://www.partner3.de.ms

RutgersU ReticulatedEvol Sep20-21

DIMACS Workshop on Reticulated Evolution

Call For Papers

September 20 - 21, 2004 DIMACS Center, CoRE Building, Rutgers University

Organizers:

Mel Janowitz, DIMACS, melj@dimacs.rutgers.edu Randy Linder, University of Texas, rlinder@mail.utexas.edu Bernard Moret, University of New Mexico, moret@cs.unm.edu

Presented under the auspices of the Special Focus on Computational Molecular Biology.

Announcing a workshop on reticulate evolution to be held September 20-21, 2004 Registration details and further information for the workshop may be obtained from the website

http://dimacs.rutgers.edu/Workshops/Reticulated
Brief description of the goals of the workshop: Species evolution has long been modeled as a branching process that can uniquely be represented by a tree topology. In such a topology, each species can only be linked to its closest ancestor, while interspecies relationships such as species hybridization or lateral gene transfer in bacteria are not allowed. With the advent of phylogenetic analysis at the molecular level, there is increasing evidence that such a model is inadequate. This workshop will explore the history and latest status of these new models of "reticulate evolution", and will be coupled with a smaller working group meeting designed to explore promising avenues for future research.

The organizers welcome contributed papers that are in the spirit of the above announcement. Abstracts may be submitted to any of the organizers no later than August 1, 2004. Any submissions must be approved by the organizers.

Registration:

Pre-registration deadline: September 13, 2004

Please see website for additional registration information.

Information on participation, registration, accommodations, and travel can be found at:

http://dimacs.rutgers.edu/Workshops/Reticulated/
PLEASE BE SURE TO PRE-REGISTER EARLY

UAlgarve StatGenetics Jul19-28

Please note that there are still some open slots for the Institute! You can sign-up without a late fee until 1 July 2004.

Details:

University of Algarve, Gambelas Campus Faro, Portugal July 19 - 28, 2004

The Institute in Statistical Genetics at North Carolina State University in Raleigh, North Carolina, USA, offers a series of workshops that provide intensive introductions to modern methods of interpreting genomic data. At the invitation of the University of Algarve Marine Science Center, the Institute will conduct a number of its workshops at the Gambelas Campus of the University of Algarve in Faro, Portugal, July 19 - 28, 2004. Each workshop (or module) lasts two and one-half days. Participants may attend modules that fit their backgrounds and interests.

Modules

1: Population Genetic Data Analysis 2: Principles of Quantitative Genetics 3: Interpreting DNA Data 4: Quantitative Trait Locus Mapping 5: Introduction to Genomic Science 6: Behavior Genetics 7: Association Mapping 8: Microarray Analysis 9: Introduction to Bioinformatics 10: Coalescent Theory

Full details on modules/instructors and a registration form can be found at http://statgen.ncsu.edu Bruce Weir <weir@stat.ncsu.edu>

UFribourg ExpEvol Oct4-5

Experimental Evolution Workshop 4-5 October 2004 Fribourg Ecology & Evolution Days 2004

Workshop location: University of Fribourg, Departement of Biology, Fribourg, Switzerland.

When does natural selection favor the evolution of ecological specialization as opposed to a generalist lifestyle, and why? Does conflict between the sexes lead to an evolutionary arms-race? What factors affect the evolution of parasite virulence? Is mutation rate molded by evolution? Is evolution repeatable and reversible? Studying evolution in real time under experimental conditions is a powerful way of addressing these questions.

This workshop will bring together several invited speakers and a number of younger researchers using experimental evolution to address diverse questions. The talks will be followed by plenary discussion. The symposium will be free (no registration fee).

Confirmed invited speakers: * James B. Anderson (University of Toronto, Canada) * Graham Bell (McGill University, Montreal, Canada) * Angus Buckling (University of Bath, UK) * Santiago Elena (University of Valencia, Spain) * William Rice (University of California, Santa Barbara, USA) * Gregory Velicer (Max-Planck Institute of Developmental Biology, Tübingen, Germany)

We have time for about 15 contributed talks of 20 minutes.

Organizers: Tadeusz Kawecki & Dieter Ebert University of Fribourg, Departement of Biology, Fribourg, Switzerland Email: tadeusz.kawecki@unifr.ch dieter.ebert@unifr.ch

For more information on the workshop and for registration check: http://www.unifr.ch/biol/ecology/-expevo04/index.html For more information on Ecology and Evolution in Fribourg check: http://-www.unifr.ch/biol/ecology/index.html The workshop is supported by the University of Fribourg, Switzerland and the TROISIÈME CYCLE de CONFÉRENCE UNIVERSITAIRE DE SUISSE OCCIDENTALE. (http://www.cuso.ch/3e-cycle/biologie.html)

– + Dieter Ebert [Mailto:dieter.ebert@unifr.ch] Université de Fribourg, Departement de Biologie, Ecologie et Evolution, Chemin du Musee 10 1700 Fribourg, Switzerland http://www.unifr.ch/biol/-ecology/index.html Tel. +41-(0)26-300 88 69, Fax +41-(0)26-300 96 98

Please visit the web-page dedicated to the late W.D. (Bill) Hamilton: http://www.unifr.ch/biol/ecology/-hamilton/hamilton.html http://www.unifr.ch/biol/-ecology/hamilton/hamilton.html

Instructions

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

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

To send messages to the EvolDir direct them to the email evoldir@evol.biology.McMaster.CA. Do not include encoded attachments and do not send it as Word files, as HTML files, as LaTeX files, Excel files, etc. ...plain old ASCII will work great and can be read by everyone. Add a subject header that contains 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 preformating is collapsed to save space. At the current time, many features may be incorrectly handled and some email messages may be positively mauled. Although this is being produced by LaTeX do not try to embed LaTeX or TeX in your message (or other formats) since my program will strip these from the message.