EvolDir

September 1, 2005

Month in Review

Forward

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

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

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

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Conferences

ClemsonU SEEPAGE Sept23-25 2

SEEPAGE 2005-SEPTEMBER 23-25 South-East Ecology, PopulAtion Genetics and Evolution 31st Annual Meeting

Hosted by Clemson University, Department of Biological Sciences

SEEPAGE, first organized in 1974 by Drs. James Murray, Janis Antonovics and David West, serves as a forum for the presentation and discussion of a wide range of both empirical and theoretical research in ecology, evolution, genetics and organismal biology. The Southeast portion of the name derives from the regional location of the meeting, but does not mean it's an exclusive atmosphere. The meeting is open to all scientists from any geographic region and research from around the world. Postdocs and graduate students are especially encouraged to present contributed talks (15 min) in a friendly and low-key environment of collegial exchange.

This year's annual meeting will be held at Camp Kanuga, Hendersonville, North Carolina, USA (http://www.kanuga.org/ - for more info about the camp)

SATURDAY NIGHT KEYNOTE SPEAKER: Dr. David McCauley, Vanderbilt University SPECIAL GUEST SPEAKER: Dr. Felix Breden, Simon Fraser University

The weekend will also include contributed 15-minute talks, a poster session, and spirits!

Visit the webpage for updates, details and registration form! (http://people.clemson.edu/~mptacek/ - click on SEEPAGE 2005)

REGISTER NOW! Registration deadline is August 31, 2005

NOTE - For questions or more information email Michele (kittell@clemson.edu) or Margaret: (mptacek@clemson.edu).

"Margaret B. Ptacek" <mptacek@CLEMSON.EDU>

ClemsonU SEEPAGE Sept23-25 3

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"Margaret B. Ptacek" <mptacek@CLEMSON.EDU>

KansasCity EcolGenomics Nov4-6

Registration is now open <https://www.dce.ksu.edu/cgi-bin/conf/ecological_genomics.cgi> ! Plan now to attend the 3rd Annual Ecological Genomics Symposium on November 4-6, 2005, at the Radisson Hotel in the Lenexa-Overland Park area of Kansas City. The Genes in Ecology, Ecology in Genes Symposium will begin on Friday, Nov. 4, at 7:00 p.m. and conclude on Sunday, Nov. 6, at noon. For a complete brochure, registration, hotel, and poster abstract information, visit our Symposium website, www.ksu.edu/ecogen/symp2005.html <http://www.ksu.edu/ecogen/symp2005.html> .

Ecological Genomics is an emerging field at the interface of ecology, evolution and genomics that seeks to place the functional significance of genes and genomics into an ecological and evolutionary context. Participants will also learn about the Ecological Genomics research initiative in Kansas that includes 37 faculty members in 10 departments from 3 Kansas universities.

Featured speakers:

Toby Bradshaw University of Washington The genetic basis of adaptive evolution in natural plant populations John Kenneth Colbourne Indiana University Finding genes linked to the ecological success of Daphnia Edward F. DeLong Massachusetts Institute of Technology Exploring the natural microbial world, from genomes to biomes Martin E. Feder The University of Chicago Transposition and heat-shock genes: a genomic scan for evolvability of transcription Jan Kammenga Wageningen University Genomical approaches for understanding life-history adaptation to temperature in natural populations of C. elegans Trudy F. C. Mackay North Carolina State University The genetic architecture of complex traits: Lessons from Drosophila Thomas Mitchell-Olds Max-Planck Institute of Chemical Ecology Functional evolutionary genomics of ecologically important variation Johanna Schmitt Brown University Adaptive evolution of seasonal timing in Arabidopsis thaliana Jack C. Schultz Penn State University Whole-genome microarray analysis reveals species-specific responses by Arabidopsis to insect herbivores Charles W. Whitfield University of Illinois Genomic dissection of naturally occurring behavioral maturation in the honey bee

Participants are invited to share their own research at poster sessions on Friday night and Saturday. Please follow the abstract submission guidelines <http://www.ksu.edu/ecogen/Poster%20Abstract%20Guidelines.htm> and submit online <https://www.dce.ksu.edu/cgi-bin/conf/eco_proposal.cgi> before September 15, 2005. A limited number of submitted poster abstracts will be selected for oral presentation. Poster topics should be related to the field of Ecological Genomics.

Please share this announcement with colleagues and students who are interested in learning more about the emerging field of Ecological Genomics. If you have any questions, please contact us at (785) 532-3482 or ecogen@ksu.edu. Additional information about this interdisciplinary research initiative is available at www.ksu.edu/ecogen <http://www.ksu.edu/ecogen> .

DEADLINES: 9/15/05 Poster Abstracts due <https://www.dce.ksu.edu/cgi-bin/conf/eco_proposal.cgi> (Guidelines: http://www.ksu.edu/ecogen/Poster Abstract Guidelines.htm <http://www.ksu.edu/ecogen/Poster%20Abstract%20Guidelines.htm>) 9/30/05 Early Registration <https://www.dce.ksu.edu/cgi-bin/conf/ecological_genomics.cgi> (https://www.dce.ksu.edu/cgi-bin/conf/ecological_genomics.cgi) 10/15/05 Hotel Reservation <http://www.radisson.com/ecogen> (http://www.radisson.com/ecogen)

Project Directors include: Dr. Loretta Johnson, Kansas State University Ecosystem Biology Dr. Mike Herman, Kansas State University Developmental Genetics Dr. Robert Cohen, University of Kansas Developmental Genetics Dr. Daniel Crawford, University of Kansas Ecology and Evolutionary Biology

Funding for this symposium is provided by Kansas NSF EPSCoR, The Kansas Technology Enterprise Corporation, and Kansas State University.

Doris Merrill Ecological Genomics, KSU Biology 785-532-3482, dmerrill@ksu.edu

dmerrill@ksu.edu

MNHNParis ArthropodPhylogeny Sept23-24

Meeting : Development and Phylogeny of Arthropods

September, 23-24, 2005 Museum National d'Histoire Naturelle (MNHN), Paris.

Organizers: Jean DEUTSCH, Michel VEUILLE.

Invited speakers: Wim DAMEN, Claude DESPLAN, Alessandro MINELLI, Ariel CHIPMAN, Ronald JENNER, Cyrille D'HAESE, Gerhard SCHOLTZ, Jean DEUTSCH, Patricia SIMPSON, Angelika STOLLEWERK, Frank SIMONNET, Michael MANUEL, David CRIBBS.

Information, program and registration : http://ifr-bi.snv.jussieu.fr/vie_ifr/Evo-devo2005/program.html Michel Veuille <veuille@mnhn.fr>

Marseilles EvolBiol Sept21-23 2

9th Evolutionary biology meeting at Marseille This year the meeting will take place to a very convenient place very close to the center of the city. at "Centre Régional de Documentation Pédagogique" 31, boulevard of Athenes 13001 Marseilles which is just at the bottom of the train station stairs . more inforamtion are available at http://www.up.univ-mrs.fr/evol/congres/- The precize plan and the the final program will be send directly to the participant at the end of next week Best regards

– Pierre Pontarotti EA 3781 EGEE (Evolution Génome Environnement) Université d'Aix Marseille I Centre St Charles 3 Place Victor Hugo 13331 Marseille Cedex 3 33491106489 http://www.up.univ-mrs.fr/evol We are organizing the 9th Evolutionary Biology Meeting at Marseille http://www.up.univ-mrs.fr/evol/congres/ Pierre.Pontarotti@up.univ-mrs.fr

NHM London Evol Sept16

London Evolutionary Research Network (L.E.R.N.) Third Annual Conference

16th September 2005 National History Museum (Flett Theatre) London, UK

With guest speakers Prof. Linda Partridge (Evolutionary Genomics, UCL) and Dr. Lars Chittka (Sensory and Behavioural Ecology, QMUL)

The London Evolutionary Research Network (L.E.R.N.) is holding its third one day conference, funded by the NHM, to celebrate the wide range of evolutionary- based research currently taking place in London. It will provide a chance for students of natural history to present their research to a peer audience and meet other students studying in London.

For further information on the conference contact Nehal Saleh at n.saleh@qmul.ac.uk or Emily Hornett at e.hornett@ucl.ac.uk

Or see website - http://www.anat.ucl.ac.uk/research/-lern/index.html

NHM London Evol Sept16 extension

The London Evolutionary Research Network: Third Annual Conference

Call for posters (and attendees) from postgraduate and postdoctoral research students

The deadline has been extended for attendance and poster presentations for this event until August 31st, 2005. We currently have over 50 participants and it promises to be a very exciting event!

Each year we celebrate the range of evolutionary research taking place in London. The conference is a friendly venue where young scientists can gain experience giving presentations in a conference setting, as well as networking with other researchers. We would like to promote appreciation for all disciplines and facilitate lateral thinking and synthesis of different disciplines. Therefore, we invite students from any discipline working on any aspect related to evolutionary biology. [For university students: this is an excellent opportunity to get credit points towards your degree]. Prizes for best poster and oral presentation will be awarded.

Confirmed invited speakers are: Professor Linda Partridge (Evolutionary Genomics, UCL) and Prof. Lars Chittka (Behavioural and Sensory Ecology, QMUL)

The conference is FREE and will take place Friday September 16, 2005 at the Natural History Museum. For more information please contact Nehal Saleh (n.saleh@qmul.ac.uk) or visit our website (www.anat.ucl.ac.uk/research/lern/index.html) for a registration form.

Deadline for registering your attendance or poster presentation is August 31 2005.

ULeiden EvolSynthesis Sept16 2

Extending the Synthesis Integrating micro- and macroevolutionary scales

September 16, 2005, 1-Day Symposium in Leiden, The Netherlands

Speakers: Niles Eldredge, John Thompson, Paul Brakefield, Sergey Gavrilets, Ryan Gregory, David Jablonski, Rich Lenski, William Miller.

This Symposium has grown out of a Working Group organized by Niles Eldredge and John Thompson at the National Center for Ecological Analysis and Synthesis, Santa Barbara, California.

Place: Large Lecture Theatre, Institute of Biology, Leiden University, Kaiserstraat 63, Leiden from 9.45 to 17.30. Maps etc: http://biology.leidenuniv.nl/-ibl Further information and registration: brakefield@rulsfb.leidenuniv.nl. Light lunch will be organized for registered attendees; Indonesian Dinner with the speakers is available at 25 Euros per head for registration by 5 September.

Paul Brakefield, Institute of Biology, Leiden, The Netherlands

Draft Program:

9.45 am Opening and Introduction by Niles Eldredge

9.50-10.30 The ecology of stasis: Species interactions and the coevolutionary process Prof. John Thompson, Dept. of Ecology and Evolutionary Biology, University of California, Santa Cruz, USA

coffee

11.00-11.45 Macroevolutionary theory and genomes-at-large Ryan Gregory; Dept of Integrative Biology, University of Guelph, Canada

11.45-12.30 Dynamic patterns of adaptive radiation Sergey Gavrilets, Dept of Ecology & Evolutionary Biology, Dept of Mathematics, University of Tennessee, Knoxville, USA

Lunch 12.30-13.45

13.45-14.30 The fossil record and the origin of evolutionary novelties, David Jablonski, Dept. of Geophysical Sciences, University of Chicago, Chicago, USA

14.30-15.15 On species and the rate of speciation in the fossil record, William Miller III, Dept. of Geology, Humboldt State University, Arcata, USA

tea

15.45-16.15 On the role of developmental constraints in morphological evolution, Paul Brakefield, Institute of Biology, Leiden, NL

16.15-17.00 Testing evolutionary predictability and contingency by experiments with E. coli, Richard Lenski, Department of Microbiology and Molecular Genetics, Michigan State University, East Lansing, USA

17.00-17.45 A new synthesis: From ecology and genetics to extinctions and turnovers, Niles Eldredge, American Museum of Natural History, New York, USA

brakefield@rulsfb.leidenuniv.nl

UManchester EvoDevo Sept9 2

Dear colleagues

We are pleased to be able to extend the deadline for registration for the UK Evo-Devo meeting here in Manchester on 9 September 2005.

We will accept registrations on our web site for some additional time. When we approach the capacity of the lecture theatre, we will need to stop registrations and will remove the registration form from the web without further warning. Therefore, please do not procrastinate.

The URL for the meeting web site is http://-www.flywings.org.uk/EvoDevo2005/ I look forward to seeing you in Manchester.

Best wishes, Chris

Christian Peter Klingenberg Faculty of Life Sciences The University of Manchester Michael Smith Building Oxford Road Manchester M13 9PT United Kingdom

Telephone: +44 161 275 3899 Fax: +44 161 275 5082 E-mail: cpk@manchester.ac.uk Web: http://www.flywings.org.uk

Vienna QTL-MAS Sept16-17

Dear colleagues,

This is an announcement for the 10th QTL-MAS workshop, which will be organised by the University of Natural Resources and Applied Life Sciences, BOKU-Vienna.

The workshop will be held from the 16th - 17th of September 2005 in Salzburg Austria, at Salzburg‘s Agrarian Impulse Center Heffterhof.

You can find all the information at http://www.nas.boku.ac.at/5399.html where you can also register online.

(or use the url provided in the signature of this mail and follow the link “courses and workshops” from there)

Deadline for registration and paper submission is the 25th of August.

We are looking forward to welcoming you in Salzburg!!

for further questions please contact marlies.dolezal@boku.ac.at

best regards

Marlies Dolezal

Dipl. Ing. Marlies Dolezal

BOKU-Universität für Bodenkultur Wien Department für Nachhaltige Agrarsysteme Institut für Nutztierwissenschaften Gregor Mendel Str. 33 1180 Wien

BOKU-University of Natural Resources and Applied Life Sciences Vienna Department of Sustainable Agricultural Systems Division of Livestock Sciences

http://www.nas.boku.ac.at/ tel: +43-1-47654-3252 fax: +43-1-47654-3254 marlies.dolezal(at)boku.ac.at marlies.doleza(at)gmx.at

Marlies Alexandra Dolezal <marlies.dolezal@boku.ac.at>

VrijeU AquaticVascularPlantsEvol Jan11-14

International Symposium on Aquatic Vascular Plants: 25 Years After

On 11-14 January 2006, an International Symposium on Aquatic Vascular Plants will be organized again at the Vrije Universiteit Brussel, 25 years after its first edition. The aim is to bring together aquatic plant scientists and ecologists from all over the world, with emphasis on the following topics:

? Molecular phylogeny and evolution

? Phylogeography and patterns of distribution

? Molecular ecology of populations

? Survival strategies, dispersal and establishment

? Autoecology and relationships with environment

? Vegetation analysis and remote sensing applications

? Biotic interactions and stable isotope applications

Original contributions on aquatic vascular plants from freshwater, brackish water and coastal zones are welcomed. New insights using DNA, stable isotopes, remote sensing, modeling etc. are envisaged

25 years ago on 23-25 January 1981, an International Colloquium on Aquatic Vascular Plants was held in Brussels. The aims of the colloquium were to provide contact between botanists working on aquatic plants to present a synthesis of their work and to define key subjects in this field of research. The colloquium was attended by 140 plant scientists and ecologists from 15 countries and 70 presentations were scheduled. The topics covered at that time were pollination mechanisms, morphological variation and development, cytology, photosynthesis, growth and reproductive strategies, primary production, nutrient cycling, decomposition, community analysis, distribution, conservation, introductions and weeds. These contributions were published in a much cited book Symoens J.J., Hooper S. & Comp?re P. (Eds.) (1982) Studies on Aquatic Vascular Plants. Royal Botanical Society of Belgium 424 pp.

The organizers are aiming at a similar success, in honor of Em. Prof. J.J. Symoens http://www.vub.ac.be/APNA/-aquaticplantsymposium2006/welcome.html karolien van <karolienvanpuyvelde@yahoo.com>

GradStudentPositions

Bergen EvolEcology

*** 1 PhD student position in evolutionary ecology in Bergen, Norway ***

Position is available at the Institute of Marine Research in Bergen, Norway, to develop and analyse eco-genetic models of fisheries-induced adaptive change. This modelling framework aims at combining a realistic description of the ecological setting as well as population structure with a description of genetic detail at a level that would still allow predictions on rate of evolutionary change. Potential empirical interfaces include applications to cod, plaice, salmon and oysters.

The post is funded as part of a EU Marie Curie Research Training Network FishACE (Fisheries-induced Adaptive Change in Exploited Stocks). According to fellowship rules (see http://www.iiasa.ac.at/Research/-ADN/FishACE/Positions.html), applicants must be of non-Norwegian nationality and must not have resided in Norway for more than 12 months in the last three years [notice that Norwegian citizens and residents can apply for positions in other teams in this network.] Skills in life history theory, ecological and evolutionary modelling and an interest in fisheries would be an advantage. The work will be carried out in collaboration with other teams in the network, facilitated by short research visits.

FishACE (http://www.iiasa.ac.at/Research/ADN/-FishACE/) is an EU Marie Curie Research Training Network set up to investigate the prevalence and consequences of fisheries-induced adaptive changes in exploited aquatic systems in European waters. The network is coordinated by International Institute for Applied Systems Analysis in Laxenburg, Austria. There are altogether 11 network teams in 8 European countries. Besides training through research, the network provides tailored training courses on relevant methods and skills.

Institute of Marine Research (http://www.imr.no) is a national research centre affiliated with the Norwegian Ministry of Coast and Fisheries. The institute conducts research in the fields of marine environment, marine resources, and aquaculture. IMR, in its area, is one of the largest research institutes in the world, focusing on both applied and fundamental marine research. The main office of IMR is located in Bergen on the west coast of Norway. Bergen is a lively town with rich cultural life, and the surroundings offer excellent opportunities for all sorts of outdoor pursuits.

The PhD position is for 36 months. The fellow will enrol as a PhD student at the Institute of Biology in University of Bergen. Salary, which include travel and mobility allowances, follows the rates prescribed by EC and are competitive. Preferred starting date is in autumn 2005. The review of applications will start September 1 and continue until the positions are filled.

For more information, please contact Mikko Heino (http://www.imr.no/research/heino), preferably via e-mail (mikko@imr.no). An application, consisting of an application letter, curriculum vitae and two references, should be sent to the Personnel Section, Institute of Marine Research, P.O. Box 1870 Nordnes, NO-5817 Bergen, Norway. Mark the application with the reference number "33-05". Please also submit an electronic copy of the application to Mikko Heino by email.

mikko.heino@imr.no mikko.heino@imr.no

UCollegeDublin GenomicImprinting

PhD Studentship

Evolution of a complex receptor and of genomic imprinting

A three-year PhD Studentship, funded by Science Foundation Ireland and commencing in September 2005, is available in the Zoology Department, University College Dublin, Ireland (Catherine M. (aka Kay) Nolan's lab). The research will investigate the cell and molecular biology of the cation-independent mannose 6-phosphate receptor (CI-MPR), also known as the IGF2 receptor (IGF2R). The overall goal of the study is to understand the evolution of this complex receptor and in particular the factors that may have contributed to the evolution of its imprinted status in mammals.

The project will focus on the zebrafish, Danio rerio, and the dog, Canis familiaris, and is part of an ongoing collaboration between the Nolan lab in UCD and Dr Lucy Byrnes (Biochemistry Dept, NUI Galway, Ireland) and Prof. Bass Hassan (Dept of Pathology and Microbiology, School of Medical Sciences, Bristol, UK). The student employed will also spend some time in the collaborating laboratories.

The studentship will provide a stipend and full payment of fees (for a candidate of EU origin). Candidates for this position should have a B.Sc.(Hons) in a relevant discipline (such as Biochemistry, Cell and Molecular Biology, Genetics, Zoology etc), with a minimum of 2.1 Grade, preferably with experience of cell and/or molecular biology techniques. The research will involve training in molecular biology techniques, animal cell culture, ligand-receptor binding assays and the use of reporter assays in analysis of gene expression.

Highly motivated individuals, with an enthusiasm for research and a determination to succeed, should apply by sending a letter of application, together with a curriculum vitae to Kay Nolan, Zoology Dept, University College Dublin, Belfield, Dublin 4, Ireland (Tel +353-1-716 2112)(or by e-mail to Catherine.Nolan@ucd.ie). Please include the names and contact details of two referees.

Further reading Ghosh et al (2003) Mannose 6-phosphate receptors: new twists in the tale. Nature Reviews Molecular Cell Biology 4: 202-212.

Killian, Nolan, et al (2001) Divergent evolution in M6P/IGF2R imprinting from the Jurassic to the Quaternary. Human Molecular Genetics 2001 10, 1721-1728.

Wilkins and Haig (2003) What good is genomic imprinting: the function of parent-specific gene expression. Nature Reviews Genetics 4: 1-10.

Kay Nolan Zoology Dept University College Dublin Belfield Dublin 4 Ireland

Tel: +353-1-716 2112 Fax: +353-1-716 1152

E-mail: catherine.nolan@ucd.ie

catherine.nolan@ucd.ie

UHelsinki TrophicLevels

POST GRADUATE FELLOWSHIP: MULTI-TROPHIC INTERACTIONS IN SPACE

How do species at different trophic levels interact with each other, how are these interactions modified by the spatial setting, and how do spatial effects then reflect into rates of functional processes? If these questions interest you, you are invited to apply for a three-year post graduate fellowship, available from September 2005 onwards in the Metapopulation Research Group (www.helsinki.fi/science/metapop) at the University of Helsinki, Finland. The monthly salary is ca. 1900 EUR and your supervisor will be Tomas Roslin.

The PhD project is aimed at analyzing how herbivorous insects on the pedunculate oak (Quercus robur) interact with trophic levels above and below them in a quantitative manner. Our target taxa encompass the oak and its microlepidoptera, gallwasps, their parasitoids (largely Hymenoptera) and the oak mildew fungus. The project has a strong empirical focus, but allows for interaction with several theoretically-minded members of a broader research group. Finnish PhD projects typically last for four years: hence, the successful candidate should dedicate him-/herself to this project until 2009.

Some experience with identifying insects in general, and parasitic Hymenoptera in particular, will be regarded as a major advantage (but by no means as a prerequisite for applying). You will also need a strong will to learn and to experiment with new techniques, since your work will involve a range of target organisms studied both under field and laboratory conditions.

Applications including a short CV and two letters of recommendation should be submitted by 15 September 2005 to Dr. Tomas Roslin by email, tomas.roslin@helsinki.fi. Please ask your referees to send their letters directly to this address, not to yourself.

For further information, please start by visiting http://www.helsinki.fi/science/metapop/, then direct more specific queries to Tomas Roslin (tomas.roslin@helsinki.fi, phone +358 9 191 57750), Metapopulation Research Group, Department of Biological and Environmental Sciences, PO Box 65 (Viikinkaari 1), 00014 University of Helsinki, Finland.

tomas.roslin@helsinki.fi

UManchester Bioinformatics

MARIE CURIE TRAINING FELLOWSHIP IN BIOINFORMATICS

Background: Applications are invited from PhD students across Europe to spend up to 12 months undertaking research at the Marie Curie Site for Bioinformatics Education and Research at the University of Manchester. Details on this training site can be found at: http://mc-opportunities.cordis.lu/showPRJ.cfm?obj_id=836

Project Title: Marie Curie Training Site for Bioinformatics, Education and Research

Job Title: Marie Curie Fellow to work on comparative genomics and bioinformatics of noncoding DNA sequences.

Project details: A vacancy is available to work on the development and application of methods to analyse the function and evolution of non-protein-coding DNA sequences in genome sequences, with a special emphasis on the cis-regulatory elements that control transcription in eukaryotes. It is now well appreciated that the vast majority of DNA in the genome sequences of higher eukaryotes is non-protein-coding, yet the function of this noncoding DNA remains largely unknown. An explosion of data and methods are now available to identify functional elements in noncoding sequences, many involving comparative approaches. This vacancy will use comparative genomic data in model organisms (yeast, flies, worms, and/or mammals) to identify signatures of noncoding sequence evolution that are characteristic of cis-regulatory elements such as promoters and enhancers, capitalizing on experience and resources developed in Drosophila (Bergman et al. Genome Biology 2002; Bergman et al. Bioinformatics 2005). Successful applicants will contribute to the overall objective of the group to develop predictive models of cis-regulatory sequences using comparative data, but other project proposals will be considered. Projects will be tailored to the experience and objectives of the applicant and can combine data analysis, text mining, development and/or evaluation of methods.

The project is for 3-12 months and will be under the supervision of Dr. Casey Bergman in the Faculty of Life Sciences at the University of Manchester. Applicants should have a background in biology or computer science, ideally with experience of large-scale data analysis and/or modeling techniques and programming experience in PERL or JAVA. Trainees will be given complementary training in genome informatics, comparative genomics and data-mining and be able to interact with bioinformatics and wet-lab groups in the Faculty working in field of gene expression. For further details, please contact casey.bergman@manchester.ac.uk or visit http://umber.sbs.man.ac.uk/bergman . Position: Doctorate Number of Positions: 2 Deadline: 31/10/2005 Start Date: 01/12/2005 (flexible) Salary: 1200 Euros per fellow (monthly) Supervisor: Dr. Casey Bergman (casey.bergman@manchester.ac.uk)

Submission of applications to: Dr. Maria Cristina Merlotti Faculty of Life Sciences University of Manchester Michael Smith Building Oxford Road Manchester M13 9PT, UK

mqbsscbf@icon.man.ac.uk mqbsscbf@icon.man.ac.uk

UWaterloo SalmonMateChoice

PhD studentship available: Influence of mate choice on immune function of Chinook salmon: Dr Brian Dixon at the University of Waterloo is seeking a strongly independent PhD student to study the effect of mate choice on immune function in aquaculture salmon. The project will involve in vivo and in vitro immune assays as well as a molecular characterization of Major Histocompatibility allele inheritance in salmon bred using both traditional and mate-choice enhanced methods. Fieldwork at the partner salmon farm in British Columbia will also be required. Skills should include a background in molecular biology, population biology or immunology. Candidates who can start by or before January are preferred. Interested parties should contact:

Dr Brian Dixon Department of Biology University of Waterloo 200 University Ave West Waterloo, Ontario Canada N2L 3G1 Ph. (519) 888-4567 x2665 Fax. (519) 746-0614 bdixon@uwaterloo.ca

dheath@uwindsor.ca

UWuerzburg EvolEcol

Ph.D.position available in chemical ecology at Wuerzburg University in Germany

Plant characteristics and pest resistance under UV-influence

The chemical ecology group at University of Wuerzburg is seeking a well-qualified and highly motivated doctoral candidate for a position at the University. The position is for three years, beginning September 2005, provided funding will be allotted. The position will be funded by the BMBF ('Bundesministerium fuer Bildung und Forschung') and is part of a project in which four different parties are involved. In the project, innovative green-house shields will be investigated to study the effects on the resistance of cultivated plants. The doctoral candidate at Wuerzburg will study the effect of different light conditions on plant quality, how this further affects herbivorous insects, and how this again in turn finally influences plant fitness. The successful candidate is well trained in analytical chemistry and has a keen interest in insect-plant-interactions.

Interested candidates should submit a Curriculum vitae along with a list of three references by email or post to Caroline Mueller.

Dr. Caroline Mueller Julius-von-Sachs-Institute for Biosciences Chemical Ecology group University of Wuerzburg Julius-von-Sachs-Platz 3 D-97082 Wuerzburg Germany Phone: + 49 / (0) 931 - 888 62 21 Fax: + 49 / (0) 931 - 888 62 35 E-mail: cmueller@botanik.uni-wuerzburg.de <mailto:cmueller@botanik.uni-wuerzburg.de> http://www.biozentrum.uni-wuerzburg.de/bot2/mueller/caroline_mueller_en.html

"\"Dr. Caroline Müller\"" <cmueller@botanik.uni-wuerzburg.de>

UZurich EvolBiol

Doctoral position available in Evolutionary Biology and Biodiversity in the Zoological Museum at the University of Zurich in Switzerland

The research group in Evolutionary Biology and Biodiversity led by Professor Tony Wilson in the Zoological Museum (<http://www.unizh.ch/zoolmus>www.unizh.ch/zoolmus) is seeking a well-qualified and highly motivated doctoral candidate for a position at the University of Zurich. The position is for three years, beginning in November 2005 and with a salary of ca. 40,000 Swiss Francs. A Masters degree (or equivalent) is a prerequisite for acceptance into the Ph.D. program at the University of Zürich.

Our group concentrates on the role of sexual selection and environmental variation in the speciation process. Integrating molecular phylogenetic, population genetic and functional genomic approaches, our work spans a broad temporal scale in an effort to derive testable hypotheses on the evolution of taxonomic diversity. Over the past several years, our research has concentrated on syngnathid fishes (seahorses and pipefish), a group of particular interest due to specialized morphological adaptations for male parental care and female-dominated competition for access to mates. Our work involves ongoing collaborations with researchers in America, Europe and Australia.

We have recently installed three 5000L climate-controlled aquarium facilities, offering unparalleled opportunities for common garden experiments and observations of mating behaviour under controlled conditions. Our state-of-the art laboratory facilities include a MJ Tetrad PCR machine and an ABI 3100 sequencer, with access to a high-throughput ABI 3730 48-capillary machine. In addition, our Functional Genomics center (<http://www.fgcz.unizh.ch/>www.fgcz.unizh.ch) offers extensive facilities for proteomics and bioinformatics. The University has recently upgraded its core bioinformatics facility, which now consists of two 4 processor Opteron Servers and an 8 TB file system capable of running all Unix-based bioinformatics and phylogenetics software packages.

The University is one of the top comprehensive institutions in Europe and the Zoological Museum is a center of excellence in behavioural ecology, population genetics and evolution. With a critical mass of researchers in Ecology and Evolutionary Biology at the University and the neighbouring Swiss Federal Institute of Technology (ETH Zurich), Zurich offers an exceptional academic environment for research and study.

Zurich is an international city of 350,000 located at the heart of Europe, with world-class facilities for sport, music and theatre. With its location at the head of Lake Zurich and its proximity to the Swiss Alps, there are incredible opportunities for sailing, skiing, hiking and mountaineering in the region. Zurich was recently ranked the top city in the world for quality of living.

Interested candidates should submit a Curriculum vitae and statement of research interests, along with a list of two references, by email or post to Rosemarie Keller, Institute Secretary (<mailto:kellerro@zoolmus.unizh.ch>kellerro@zoolmus.unizh.ch) by September 15, 2005. Any questions on the position should be directed to Prof. Wilson (<mailto:tony.wilson@zoolmus.unizh.ch>tony.wilson@zoolmus.unizh.c

Tony Wilson Zoological Museum University of Zürich Winterthurerstrasse 190 CH 8057 Zürich Switzerland Tel: 41 44 635 4790 Fax: 41 44 635 4780 tony.wilson@zoolmus.unizh.ch

Jobs

AMNatHist Bioinformatics

The American Museum of Natural History seeks candidates with expertise in computer programming, particularly parallel processing. Candidates should have BS or MS degree in Computer Science or engineering, with at least 5 years of experience in scientific computation. Knowledge of at least one functional language (ML, Lisp, Haskell) is required, preferably Ocaml or ML and the C language. Experience in parallel computing desirable. Experience in UNIX/LINUX environments necessary.

Send cover letter, CV, representative publications and names, addresses, phone numbers/e-mail addresses of 3 references to: Dr. Ward Wheeler Division of Invertebrate Zoology American Museum of Natural History Central Park West at 79th Street New York, New York 10024 Ph: 212.769.5754 wheeler@amnh.org

Susan Perkins <perkins@amnh.org>

AMNatHist LabTech

The American Museum of Natural History is seeking candidates for an open position as a laboratory technician. Experience in molecular genetic methods including DNA isolation, PCR, automated sequencing are required and prior work in genomics and/or phylogenetics are highly desired. Candidates with experience in viral genetics are especially encouraged to apply.

Competitive salary and benefits.

Position available Fall 2005.

Send cover letter, CV, representative publications and names, addresses, phone numbers/e-mail addresses of 3 references to:

Susan L. Perkins, Ph.D. Asisistant Curator, Microbial Systematics and Genomics Division of Invertebrate Zoology American Museum of Natural History Central Park West at 79th Street New York, New York 10024 Ph: 212.313.7646 Web: http://research.amnh.org/~perkins perkins@amnh.org

Susan Perkins <perkins@amnh.org>

AMNatHist SystemsManager

The American Museum of Natural History seeks candidates to fill an open position to manage a computing cluster. Applicants should have a Ph.D. and five years experience in scientific computing, hardware and software maintenance. Strategic planning, specification and purchasing of hardware, grant writing, training of personnel are key skills.

Send cover letter, CV, representative publications and names, addresses, phone numbers/e-mail addresses of 3 references to:

Dr. Ward Wheeler Division of Invertebrate Zoology American Museum of Natural History Central Park West at 79th Street New York, New York 10024 Ph: 212.769.5754 wheeler@amnh.org

Susan Perkins <perkins@amnh.org>

BathOxford 2 PhylogeneticAnalysis

Two positions in phylogenetic analyses of sexual conflict

We are seeking candidates for a NERC-funded project on Phylogenetic analyses of parental conflict in birds (PIs: Dr T Szekely & Dr R P Freckleton). Two positions are available:

1. Post-doctoral Research Officer (REF 05/300)

Description: The Research Officer will use phylogenetic comparative methods to analyse the causes and consequences of parental conflict including phenotypic rates and macroevolution. Candidates should have a PhD in a relevant field that includes evolutionary biology, animal behaviour or ecology.

Salary: Starting salary is up to £21640 per annum, and the post is for 36 months fixed term.

2. Experimental Officer (REF: 05/301)

Description: The Experimental Officer will collect data from museums, textbooks and online resources. First degree in biology (or a relevant discipline) is required.

Salary: Starting salary is £16071 per annum, and the post is for 18 months fixed term.

Application deadline: 2nd September 2005. Interviews will be in mid-September, and the positions are available from 1 October 2005.

Contact: Application forms and further details may be obtained from the Human Resources Department, University of Bath, Claverton Down, Bath BA2 7AY, email jobs@bath.ac.uk <mailto:jobs@bath.ac.uk> quoting Ref No 05/300 or 05/301. An online application form is accessible from the University of Bath website.

For further information please contact Rob Freckleton (University of Oxford), or Tamas Szekely (University of Bath).

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Dr Tamas Szekely Department of Biology and Biochemistry University of Bath, Bath BA2 7AY, UK 01225 383676 (phone) 01225 386779 (fax) T.Szekely@bath.ac.uk (email) http://www.bath.ac.uk/Departments/BiolBioch/tamas.html http://www.bath.ac.uk/bio-sci/biodiversity-lab/framework.html WORKSHOP

ON SEXUAL SIZE DIMORPHISM - AUGUST 2005 http://www.bath.ac.uk/bio-sci/szekely/-workshop/SSD%20Workshop2%20webmod.htm bssts@bath.ac.uk

ClaremontCA ChairBotany

Director of Research &Chair, Department of Botany

Rancho Santa Ana Botanic Garden, Claremont, California

Rancho Santa Ana Botanic Garden (RSABG) seeks a successful leader, scholar and administrator to direct its research programs and to serve as Chair of the Graduate Program in Botany, Claremont Graduate University.

RSABG is a 78-year-old non-profit organization dedicated to promoting botany, conservation, and horticulture to inspire, inform, and educate the public and the scientific community about California's native flora. The Garden conducts programs in research, graduate education, public and professional education, and rare plant conservation. Facilities include a one-million specimen herbarium with worldwide representation, a living plant collection of over 3,000 species and varieties on 86 acres, research laboratories, greenhouse, nursery, seed storage facilities, and a 50,000-volume research library. The Garden also publishes the scientific journal Aliso.

RSABG has an active, broad-based, internationally recognized research program in systematic and evolutionary botany, and is the Botany Program for Claremont Graduate University by an affiliation agreement, awarding masters and doctorate degrees. Over 90 highly trained students have received Masters of Science or Doctor of Philosophy degrees since inception of the program.

Qualifications: Reporting to the Executive Director, this endowed position will have overall responsibility for management of the Garden's research programs, including oversight of the graduate Botany Program (as Department Chair), as well as supervision of the herbarium and research library. The Director will also participate in teaching graduate-level courses in botany and maintain an active externally-funded research program, with a scientific focus that will complement and strengthen the current research at the institution. The Director of Research will be fully committed to graduate education, a well-regarded researcher, a skilled communicator, and an excellent administrator and manager. Required are a doctorate in botany or a related field, with specialization in some aspect of plant systematics or evolutionary biology preferred, and an excellent and ongoing track record of scientific publication and extramural funding. The Director of Research will be expected to hold an Associate or Full Professorship at Claremont Graduate University, which will be co-terminous with the appointment as Director of Research.

To apply, send a letter of interest and curriculum vita to Patrick S. Larkin, Executive Director, Rancho Santa Ana Botanic Garden, 1500 North College Ave., Claremont, CA 91711. Letters of reference will be requested later. For more information contact Mr. Larkin directly at (909) 625-8767, ext. 220 or by e-mail at Patrick.Larkin@cgu.edu <mailto:Patrick.Larkin@cgu.edu>.

The search will remain open until the position is filled.

The Botanic Garden values a diverse community and is committed to equal opportunity in employment.

Ann Joslin <ann.joslin@cgu.edu>

DuquesneU ChairBiology

The following ad will appear in Science next week. I will be happy to answer any questions about our department (seamanm@duq.edu), or direct them to the search committee chair listed in the ad.

CHAIR OF BIOLOGICAL SCIENCES Duquesne University

The Bayer School of Natural and Environmental Sciences invites applications and nominations for the position of Professor and Chair of the Department of Biological Sciences. Our collegial and dynamic department currently has 14 research faculty, 3 teaching faculty, and 45 graduate students, and over 270 undergraduate Biology majors. Faculty research interests are in the areas of cellular and molecular biology, microbiology, cellular and systems physiology, genetics, and evolution. The Department offers B.S., M.S., and Ph.D. programs with a strong emphasis on research. Additional information regarding our programs and this position can be found at the Department's (www.science.duq.edu/biology/) and the Bayer School's web sites (www.science.duq.edu).

We are seeking an accomplished scientist with imagination and energy, as well as the leadership ability to enable us to continue strengthening our educational and research programs. The preferred candidate will have an excellent record of publication and extramural support, a commitment to education, and strong leadership skills. The Universitys strategic plan identifies biotechnology as a particular focus area for development. The successful candidate will therefore be expected to collaborate with the endowed Edward Fritzky Chair in Biotechnology Leadership and to foster interactions within the University community and with the burgeoning biotechnology initiatives in the Pittsburgh area. Salary will be commensurate with qualifications and experience. Review of applicants will begin September 26 and will continue until the position is filled.

Applicants should submit a letter of interest, curriculum vitae, and a list of three references to:

Dr. Jana Patton-Vogt, Chair Search Committee Department of Biological Sciences Duquesne University Pittsburgh, PA 15282

Founded by the Holy Ghost Fathers, Duquesne University is Catholic in mission and ecumenical in spirit. The University values Equality of Opportunity both as an Educational Institution and as an Employer.

GrinnellCollege 2 EvolBiol

Grinnell College Department of Biology Two Tenure-Track Faculty Positions Microbiology and Plant Biology

Grinnell College invites applications for two tenure-track faculty positions (microbiology and plant biology) at the rank of assistant professor in the Department of Biology. The positions begin in August, 2006. The successful candidates will be expected to teach two courses in our inquiry-based curriculum (Introduction to Biological Inquiry [Bio 150] and either Molecules, Cells, and Organisms [Bio 251] or Organisms, Evolution and Ecology [Bio 252]) and a third course at the upper-level in the candidate's area of specialty. Candidates will be expected to teach in the general education program (e.g. the first-year tutorial) of the college as well. Candidates must have a Ph.D., postdoctoral experience and plan an active research program involving undergraduates. Start-up funds, excellent equipment, new and recently renovated facilities, support for student-faculty research, and a biological field station are available. Grinnell is a highly selective, residential, liberal-arts college with an enrollment of about 1500 students from across the country and around the world. One-third of the college's students major in the sciences, including about 35 biology and 15 biological chemistry graduates in recent years. The department has 12 faculty with active research programs and offers an innovative curriculum centered around research-based learning; for information see http://www.grinnell.edu/academic/biology/. In their letters of application, candidates should discuss their interest in developing as a teacher and scholar in an undergraduate, liberal-arts environment that emphasizes close student-faculty interaction and values diversity; they should also address their ability to teach one of the department's second-year core courses and upper division courses in the areas of either microbiology or plant biology. Send c.v., three letters of recommendation, copies of all transcripts, and other supporting materials to: Charles H. Sullivan, (specify Microbiology or Plant Biology) Search Committee, Department of Biology, Grinnell College, 1116 8th Avenue, Grinnell, IA 50112-1690 (phone 641-269-3042; fax 641-269-4285; biologysearch@grinnell.edu). Electronic applications will not be accepted. To be assured of full consideration, all materials should be received by October 3, 2005.

Grinnell College is an equal opportunity/affirmative action employer committed to attracting and retaining highly qualified individuals who collectively reflect the diversity of the nation. No applicant shall be discriminated against on the basis of race, national or ethnic origin, age, gender, sexual orientation, marital status, religion, creed, or disability. For further information about Grinnell College, see our website at www.grinnell.edu . Jonathan (Jackie) Brown Associate Professor Biology Department Grinnell College Grinnell, IA 50112

ph: 641-269-3096 (office) Web: http://web.grinnell.edu/individuals/brownj/ On leave until August 2006:

641-325-0062 (cell) 808-959-4724 (home) – Mainlanders should note that Hawaii Standard Time is 5 hours EARLIER than Central Daylight Time. Call after noon, your time, yeah?

1271-A Malawaina St Hilo, HI 96720

brownj@grinnell.edu

HunterCollege EvolAnthropology

HunterCollege.BioAnthro

Position Vacancy Notice

Hunter College seeks candidates for an appointment to a tenure track position in physical anthropology effective 01 Sept. 2006. We seek an Assistant Professor, but are authorized to consider appointment at a higher rank, including Professor, for a truly exceptional individual. We seek candidates with an emphasis on hominid paleoanthropology. Subspecialities of interest include (but are not limited to) morphology, development, and life history from an explicitly evolutionary perspective. Candidates must have a strong and active research and publication program, including field and/or laboratory components. The Ph.D. is required at the time of appointment.

Send CV, personal statement and the names of 3 references to Gregory A. Johnson, Chair, Department of Anthropology, Hunter College CUNY, 695 Park Avenue, New York, NY 10021-5085 U.S.A., or by email to gjohnson@hunter.cuny.edu <mailto:gjohnson@hunter.cuny.edu>. Applications should be received by 01 Jan. 2006 to receive full consideration. Visit the department on the Web at http://maxweber.hunter.cuny.edu/anthro/ Hunter College is an Affirmative Action / Equal Opportunity / Americans with Disabilities Act / Immigration Reform and Control Act employer. Women and members of traditionally disadvantaged populations are especially encouraged to apply.

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"Michael E. Steiper" <msteiper@hunter.cuny.edu>

IPGRI Rome Bioinformatics

VACANCY ANNOUNCEMENT

INTERNATIONAL PLANT GENETIC RESOURCES INSTITUTE

For further information on IPGRI, consult the Web page at http://www.ipgri.cgiar.org The International Plant Genetic Resources Institute (IPGRI) exists to help poor people in developing countries to make better use of agricultural biodiversity to improve their livelihoods. It is one of the 15 Future Harvest Centres of the Consultative Group on International Agricultural Research (CGIAR). IPGRIs headquarters is just outside Rome in Italy and the organization is active in over 100 countries worldwide, with more than 300 staff working from some 20 country offices. IPGRI is now looking for a well-qualified candidate, to be based at its headquarters, for the position of:

Scientist, Bioinformatics

Under the supervision of the Director, Understanding and Managing Genetic Resources Programme, based at IPGRIs headquarters in Rome, the incumbent will lead IPGRIs bioinformatics activities at the institute level and support the Generation Challenge Programme. More specifically, the appointee will be responsible for the following:

Support the development of a "Genetic Resources Clearing House Mechanism" and coordinate the implementation of its molecular / genomic components including: The development and adoption of bioinformatics standards and ontology The design of a central repository linking phenotype and molecular data The development and use of appropriate web services and applications using BioMOBY and other related technologies The design of user interfaces in collaboration with scientists to phenotype and molecular data Provide support to computational biology projects; Analyze and interpret various data sets including nucleotide and amino acid sequences, protein domains and structures; Represent IPGRI in the various official, strategic and technical areas of bioinformatics; Provide helpdesk support and training to scientists.

Minimum mandatory competencies and qualifications

A PhD in biology, or closely related area or other academic qualifications and experience that are equivalent. At least 3 years professional experience with projects related to genomics, molecular characterization and computational biology and the development and implementation of databases, new algorithms and methods. Knowledge of interoperability standards, methods and tools required. Experience with BioMOBY and related web services technologies are considered an advantage. Knowledge of common bioinformatics programming languages such as Perl and Java; experience with Unix environment would be an advantage. Demonstrated experience and expertise in computational biology, bioinformatics or related field. Knowledge of the conservation and use of plant genetics resources is a considerable advantage. Excellent interpersonal and communication skills and ability to interact effectively with a wide range of collaborators from different cultural backgrounds and across a range of disciplines. High level of initiative, strategic judgment and adaptability. Excellent English, both written and spoken; knowledge of other languages will be an advantage. Motivated and resourceful person with a sustained record of achievement and innovation.

Terms and conditions: IPGRI offers an attractive internationally competitive salary and benefits package. Initial contract will be for a period of three years, renewable.

Applications: Letter of application and curriculum vitae in English, including date of birth, gender and nationality, with names and full contact details of at least three referees, including telephone, fax and email address, should be sent to Ms Ingrid Lambert, Human Resources Manager, IPGRI, Via dei Tre Denari 472/a, 00057 Maccarese, Rome, fax (39) 06 6118341 or preferably online at IPGRI-VACANCY@CGIAR.ORG no later than 16 September, 2005. Note: Please quote source of advertisement. IPGRI is an equal opportunity employer and strives for staff diversity in gender and nationality. Women and candidates from developing countries are particularly encouraged to apply.

Dragos POSTOLACHE <dragospostolache@yahoo.com>

IndianaU EvolBehavior

Animal Behavior - Indiana University, Bloomington

The Department of Biology of Indiana University invites applications for an OPEN RANK tenure-track faculty position in ANIMAL BEHAVIOR. We seek candidates with a conceptually-driven research program to complement existing strengths in the Evolution, Ecology, and Behavior Program. The specific focus within animal behavior is open, but we especially encourage applicants whose research uses evolutionary or ecological approaches to understand the function and diversity of behavior and/or neuroethological, endocrinological, or genetic approaches to understanding the mechanisms of behavior. Indiana University is widely recognized for its outstanding interdisciplinary programs in behavior, including the Center for the Integrative Study for Animal Behavior (http://www.indiana.edu/~animal/) and a new NIH Training Program in Common Themes in Reproductive Diversity (http://www.indiana.edu/~reprodiv/). Strong applicants are expected to have postdoctoral research and/or teaching experience and established research productivity. The successful candidate will be provided with a competitive start-up package and will be expected to establish a vigorous, externally funded research program and to participate in teaching undergraduate and graduate courses. For information about the Biology Department and for links to the campus and the Bloomington community, see website: http://www.bio.indiana.edu. Candidates should send curriculum vitae, a statement of research, and representative publications and should arrange to have three letters of recommendation sent to: Chair, Animal Behavior Search, Department of Biology, Indiana University, 1001 East Third Street, Bloomington, IN 47405-3700. Review of applications will begin October 15, 2005, and will continue until suitable candidates are identified. Indiana University is an Affirmative Action/Equal Opportunity Employer. Women and minority candidates are encouraged to apply.

emartins@indiana.edu

Madrid BotanicalGarden MolecularSystematics

JOB POSITION Full-time 5-year Research Assistant in Plant Sciences

JOB DESCRIPTION Amplified Fragment Length Polymorphism (AFLP) and sequencing analyses

Field work in the Iberian Peninsula and Morocco, DNA extraction, AFLP and sequencing, data collecting. Duties include computer work on phylogeographic and population genetic analyses, annual reports, publications, and interactions with graduate students and interns.

JOB SUPERVISOR Dr. Pablo Vargas Laboratory of Molecular Systematics, Royal Botanical Garden of Madrid, Spain

QUALIFICATIONS Experience in the following techniques and methods: “ DNA plant extraction ” Restriction Fragment Length Polymorphism “ Polymerase Chain Reaction ” Sequencer handling “ DNA sequencing ” Haplotype networking “ Population genetics

DEGREE REQUERIMENTS Masters degree in Plant Sciences (higher degrees most welcome!)

SALARY 30,000 euros per annum pre-tax

SUBMISSION DEADLINE September, 10th for CV and application submission

JOB START DATE November, 1st

Please contact vargas@ma-rjb.csic.es for further info and to send a letter summarizing experience and qualifications, a CV or resume, lists of courses, grades, and publications. Names, phone numbers, and email addresses for 3 references are welcome.

Dr. Pablo Vargas Real Jardín Botánico de Madrid (CSIC) Plaza de Murillo 2, 28014 Madrid (Spain) Phone number: + 34 914203017 (225) Fax number: + 34 914200157

Jardin Botanico de Madrid: un paseo guiado Botanic Garden of Madrid: a guided walk http://www.arbas.org/grupos/tc/Jardin%20botanico%20con%20to-1.pdf Organism, Diversity and Evolution: http://www.urbanfischer.de/journals/ Red Española de Diversidad Biologica, Evolución y Sistemática http://redesmoleculares.csic.es/redesmoleculares/index.jsp Jardín Botánico de Madrid: http://www.rjb.csic.es Consejo Superior de Investigaciones Científicas (CSIC): http://www.csic.es Pablo Vargas <vargas@ma-rjb.csic.es>

PalmerstonNZ PlantSystematics

Lecturer/Senior Lecturer in Plant Systematics and Evolution Position Overview: Applications are invited for a lectureship/senior lectureship in plant systematics and/or plant evolutionary biology. The position is joint with the Institute of Molecular Biosciences (IMBS), and the Allan Wilson Center for Molecular Ecology and Evolution <http://awcmee.massey.ac.nz/>http://awcmee.massey.ac.nz/ Undergraduate teaching is with IMBS, research within the Allan Wilson Center, a center of research excellence.

Our expectations are for someone with both a good basic knowledge of plants, combined with good molecular skills. You will be expected to develop an independent research programme, but also to collaborate with investigators within the Allan Wilson Centre for Molecular Ecology and Evolution and the Institute of Molecular BioSciences. We also request that you submit a research statement with your Curriculum Vitae. For information about the AWC contact <mailto:S.M.Wright@massey.ac.nz>S.M.Wright@massey.ac.nz.

Location: Palmerston North , New Zealand Closing Date: 19 September 2005 Details: http://jobs.massey.ac.nz/positiondetail.asp?p=3420

Important Note. There are other positions in cell biology and plant biotechnology available <http://jobs.massey.ac.nz/positiondetail.asp?p421>http://jobs.massey.ac.nz/positiondetail.asp?p421 <http://jobs.massey.ac.nz/positiondetail.asp?p395>http://jobs.massey.ac.nz/positiondetail.asp?p395

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Susan Wright Executive Officer Allan Wilson Centre for Molecular Ecology and Evolution Massey University Private Bag 11-222 Palmerston North Tel: +64 6 350 5448 New Zealand Fax: +64 6 350 5626

http://AWCMEE.massey.ac.nz
s.m.wright@massey.ac.nz

SyracuseU EvolBiol

Syracuse University Department of Biology Tenure-Track Faculty Position in Ecology & Evolutionary Biology

The Department of Biology at Syracuse University invites applications for a tenure-track position (Assistant or Associate Professor) to be filled by August 2006. The successful candidate will have (Assistant Professor) or will develop (Associate Professor) a strong, extramurally funded and highly innovative research program in ecology and/or evolutionary biology to join an emerging interdisciplinary research group in biocomplexity. Suitable research programs may include theoretical or empirical studies of molecules, organisms or ecosystems. The successful applicant will complement current research strengths within the department and university related to the evolution and functioning of complex adaptive biological systems in different environments. The Department and the University place a high priority on effective undergraduate and graduate teaching.

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

The Biology Department is in the midst of an exciting growth period, having hired nine new faculty in the past five years and with construction beginning on a new Life Sciences Building (anticipated move-in, 2008). We anticipate hiring 6-10 more new faculty over the next five years. Specific information about individual Biology faculty research programs may be found on our website: http://biology.syr.edu/facultyresearch/facultyresearch.html Applicants should forward a curriculum vitae, a description of past research accomplishments, a clearly focused description of his/her proposed future research goals and a statement of teaching interests. We also request that applicants have at least three letters of reference sent. Please include the name, address, phone number and e-mail address of each of your references. We invite applicants to submit materials electronically as a single PDF file to: biosearch@cas.syr.edu. The position will be open until filled, but to be assured your application receives full consideration, we urge that you arrange to have all necessary materials to us by September 16, 2005.

Applications and reference letters should be addressed to: Scott Pitnick, Chair of Eco-Evo Faculty Search, Department of Biology, 130 College Place, Syracuse University, Syracuse, NY 13244

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

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Scott Pitnick Associate Professor & Director of Biology Graduate Program Biology Department Ph. (315) 443-5128 108 College Place Fax (315) 443-2156 Syracuse University sspitnic@syr.edu Syracuse, NY 13244-1270

http://biology.syr.edu/pitnick/index.html Scott Pitnick <sspitnic@syr.edu>

TexasStateU EvolEcol

TEXAS STATE UNIVERSITY, COLLEGE OF SCIENCE

DEPARTMENT OF BIOLOGY

POSITION: Assistant or Associate Professor, Tenure-Track

JOB POSTING #: 2006-14

REVIEW DATE: October 1, 2005

APPOINTMENT DATE: Fall, 2006

Responsibilities

The Department of Biology invites applications for a 9-month tenure-track faculty position in Stream Ecology at the assistant or associate professor level, with both research and teaching responsibilities. Prefer a broadly-trained stream ecologist with strong interest in interdisciplinary research to support our existing Aquatic Biology program and newly-established Ph.D. program in Aquatic Resources, as well as interact in complementary research areas with our diverse faculty.

Qualification Standards

Applicants must have an earned Ph.D. and demonstrate potential to maintain a vigorous research program that complements existing departmental strengths. Area(s) of specialization are flexible, but preference will be given to applicants with research experience involving aquatic macroinvertebrates, a record of extramural funding, postdoctoral research and teaching.

Application Procedures

Qualified applicants are invited to submit a statement of teaching and research interests, curriculum vitae, unofficial transcripts, copies of up to 4 published papers, and names and contact information for four references to:

Dr. Michael Huston Chair, Stream Ecology Search Committee c/o Dr. Joseph Koke, Interim Chair Department of Biology Texas State University-San Marcos 601 University Drive San Marcos, TX 78666

Michael A. Huston Department of Biology Texas State University San Marcos, TX 78666 ph: 512-245-2129 fax:512-245-8713 email:hustonma@txstate.edu

Michael Huston <hustonma@txstate.edu>

TulaneU PhylogeneticSystematics

The Department of Ecology and Evolutionary Biology, Tulane University, invites applications for one tenure-track position in phylogenetic systematics at the level of assistant professor. See the website http://-

www.tulane.edu/ ˜ ebio/News/positions.htm for more details. Send a curriculum vitae, statements of research and teaching interests, selected publications, and names and addresses of three references to Phylogenetic Systematist Search, Department of Ecology and Evolutionary Biology, 310 Dinwiddie Hall, Tulane University, New Orleans, LA 70118-5698. Review of applications will begin October 14, 2005, and the search will remain open until the position is filled. Tulane University is an AA/EEO Employer

Taylor Feild

tfeild@tulane.edu

UCLA EvolBiology

The Department of Ecology and Evolutionary Biology at UCLA invites applications for an OPEN RANK, TENURE-TRACK, FACULTY POSITION in Evolutionary Biology, broadly defined. The expected start date is September, 2006. Candidate must have a Ph.D.; postdoctoral experience is desired. Salary is commensurate with education and experience. Successful candidates are expected to maintain a rigorous research program, and to contribute to undergraduate and graduate teaching. UCLA has outstanding academic support for faculty, including access to the UC Natural Reserve System, a campus-wide Institute of Pure and Applied Mathematics, several departments with computational and evolutionary biology interests, and attractive startup packages. Submit a CV, statements of research and teaching interests, and names and addresses of three references online to http://www.eeb.ucla.edu/-Evolutionist. Please contact Charles Taylor (taylor@biology.ucla.edu) for additional information. Reviews of applications will begin September 30, 2005. The University of California is an Equal Opportunity Employer committed to excellence through diversity.

Charles Taylor <taylor@biology.ucla.edu>

UEdinburgh StatGenomics

UNIVERSITY OF EDINBURGH COLLEGE OF SCIENCE AND ENGINEERING SCHOOL OF BIOLOGICAL SCIENCES and ROSLIN INSTITUTE

READER in STATISTICAL GENOMICS

The Institute of Evolutionary Biology (IEB; http://-www.ieb.org.uk) in the School of Biological Sciences at the University of Edinburgh is a world-leading centre for all aspects of evolutionary genetics extending from quantitative genetics to evolutionary ecology via theoretical and experimental population genetics, speciation, and evolutionary genomics. The Roslin Institute (http://www.ri.bbsrc.ac.uk) is internationally renowned for its research on farm animals with major programmes in molecular and quantitative genetics, genomics, and developmental biology.

With the rapid accumulation of genomic data from humans and many other organisms, these institutions are looking to build on their current strengths by recruiting a dynamic and forward-looking individual with a recognised research reputation to capitalise on the wealth of opportunities available here. The successful candidate, who will have established an innovative research programme in this area, will be based in the University but will be expected to link with collaborators at both Roslin and in the University.

IEB is located in the Ashworth Laboratories, Kings Buildings. It has good collaborative relationships with the College of Medicine and Veterinary Medicine and the MRC Human Genetics Unit as well as the Roslin Institute and the Scottish Agricultural College. All parts of the School of Biological Sciences were graded 5A in the 2001 Research Assessment Exercise, and evolutionary biology received a special commendation.

Informal enquiries about this post may be made to Professors Andrew Leigh Brown, IEB, tel 0131 650 5523, e-mail: A.Leigh-Brown@ed.ac.uk, or Andrew Illius, Head of School, School of Biological Sciences, tel: 0131-650-5525, e-mail hossbs@ed.ac.uk.

Salary scale: £37,558 - £42,573

Applications to http://www.jobs.ed.ac.uk Please quote reference 3004780SI

Closing date: 26th August 2005

“Andrew J. Leigh Brown” <A.Leigh-Brown@ed.ac.uk>

UKansas DrosophilaEvol

The Department of Ecology and Evolutionary is seeking a research assistant by September 12, 2005. The hired individual will join an active research group exploring the evolutionary and behavioral genetics of Drosophila.

Responsibilities: 1. Conduct molecular evolution and behavioral research on Drosophila. Specific duties include, genotyping strains of Drosophila and measuring response to courtship song for quantitative genetic analysis. In addition, there will be analyses of differences gene expression between Drosophila species. Duties include: - Genomic DNA extraction and purification - PCR amplification - Gel electrophoresis and PCR extraction - Sequencing of targeted DNA regions - RNA extraction and analysis - Behavioral assays of courtship song

2. Run and maintain the molecular and behavioral laboratories - Maintenance of Drosophila stocks - Making fly media - Order supplies and equipment

Required qualifications: 1. B.Sc. in biological sciences or related field. 2. Demonstrated experience conducting biological research.

Preferred qualifications: 1. Demonstrated interest in evolutionary behavioral genetics including quantitative genetics. 2. Demonstrated experience working with Drosophila, especially culturing and behavioral experiments. 3. Demonstrated computer skills and experience in statistical analyses. 4. Experience managing a laboratory

The initial appointment is through June 30, 2006. Renewal may be possible contingent on additional funding.

Application Procedures: Apply online at http://-jobs.ku.edu. Questions may be directed to Dr. Jennifer Gleason, Department of Ecology and Evolutionary Biology, 1200 Sunnyside Ave., University of Kansas, Lawrence, KS, 66045, jgleason@ku.edu. Review of applications begins August 19 and will continue until a suitable candidate is found.

The University of Kansas is an Equal Opportunity/Affirmative Action Employer. The University encourages applications from underrepresented group members. Federal and state legislation prohibits discrimination on the basis of race, religion, color, national origin, ancestry, sex, age, disability, and veteran status. In addition, University policies prohibit discrimination on the basis of sexual orientation, marital status, and parental status.

UKentucky Genomics

The following will appear in the Sept 2 issue of Science:

Assistant Professor

Genomics: Quantitative, population, or comparative

The Biology Department at University of Kentucky seeks a tenure-track Assistant Professor with expertise in genomics. Candidates that integrate experimental and computational approaches to study populations, complex traits, or genomes are especially encouraged to apply. The Department will consider applications from a wide range of specializations, including but not limited to, bioinformatics, development, environmental biology, evolution, genetics, and neurobiology. Applicants must provide evidence that they will develop an active, independently funded research program. A commitment to teaching and student training is expected. Applicants should submit a CV and a statement detailing their current and future research plans, and arrange for submission of three letters of recommendation. Please address applications to Randal Voss, Chair Genomics Search Committee, Department of Biology, University of Kentucky, 101 TH Morgan Bldg, Lexington, KY 40506. Applications must be received by October 15, 2005 to ensure full consideration.

Randal Voss, PhD Associate Professor Department of Biology University of Kentucky Lexington, KY 40506

srvoss@uky.edu tel: 859-257-9888 fax: 859-257-1717

Randal Voss <srvoss@uky.edu>

UNCChapelHill Tech EvolGenetics

Evolutionary Genetics in the lab of Chris Willett at UNC-Chapel Hill

I am hiring a RESEARCH TECHNICIAN for my lab in the Department of Biology either in a full-time or part-time capacity as desired by selected applicant. Position is available immediately; initial appointment for one year (potentially extendable) with pay determined by experience level.

RESEARCH SUMMARY: My lab is currently focused on studies of speciation and adaptation using the intertidal copepod Tigriopus californicus. Experiments concentrate on genetic systems involved in reproductive isolation and their physiological consequences. Lab web page (http://www.bio.unc.edu/-faculty/willett/) has more information on research.

REQUIRED EXPERIENCE: A Bachelor's degree in biology or a closely related field and some experience in basic laboratory techniques are required. Additional qualifications desired: experience with molecular biology protocols, experience with handling of organisms, and experience supervising others.

RESPONSIBILITIES: 30% Isolation and molecular analysis of DNA using PCR and other techniques; 20% Physiological assays of enzyme performance in hybrid copepods; 20% Culture maintenance and crossing of copepods; 10% Supervision of undergraduates; 10% Data analysis of results from molecular sequencing; 10% Ordering and laboratory maintenance.

APPLICATION: Please submit a CV or resume, contact information for two references, and a cover letter summarizing your qualifications and interest in the position via email to Chris Willett at: willett4@email.unc.edu. Applications will be evaluated as they arrive.

willett4@email.unc.edu

UNebraska PopulationBiology

I am reposting this ad because we would like to encourage additional applications at all levels, but especially applications from more senior candidates.

POPULATION BIOLOGY and COMMUNITY ECOLOGY FACULTY UNIVERSITY of NEBRASKA

The School of Biological Sciences of the University of Nebraska-Lincoln invites applications for two tenure-track faculty positions. One faculty position will be in the area of Community Ecology. The second position will be in the area of Population Biology, supported by University of Nebraska Program of Excellence funding to the School of Biological Sciences to strengthen research and teaching in Population Biology, through faculty hires and a postdoctoral fellowship program.

The positions are open at the Assistant or Associate Professor level. Candidates will be expected to develop (or to have already developed) a nationally recognized research program in Community Ecology or Population Biology and to teach undergraduate courses in biological diversity and/or ecology and evolution as well as graduate courses in their areas of expertise. Review of applications will begin on August 15, 2005, with an expected start date of Fall, 2006. A Ph.D. in the life sciences is required and post-doctoral experience is preferred. To apply send a CV, representative publications, statements of research and teaching interests, and arrange for three letters of reference to be sent to: Alan C. Kamil, School of Biological Sciences, University of Nebraska-Lincoln, 348 Manter Hall, Lincoln, NE 68588-0118. These positions will remain open until suitable candidates are selected. Email address: biologysearch@unl.edu

UNL is committed to a pluralistic campus community through Affirmative Action and Equal Opportunity, and is responsive to the needs of dual career couples. We assure responsible accommodation under the Americans with Disabilities Act. For further information contact Alan C. Kamil at 402-472-6676 for assistance.

UNewcastle MolBiolTech

Molecular Biology Research Technician A research technician post is available in the division of Biology, University of Newcastle upon Tyne, England. The post is to help run a category II molecular biology laboratory working on eukaryotic molecular evolution. Duties include providing technical and computational assistance for the research group of Prof. T. Martin Embley and Dr Robert Hirt (http://www.ncl.ac.uk/-microbial_eukaryotes/). The post would suit an experienced scientist with good organizational abilities and research experience in modern methods of molecular analysis. The post is available immediately on the salary scale £24,098-£26,327. For further information please contact Prof. Martin Embley email Martin.Embley@ncl.ac.uk. Closing date for applications August 20th 2005.

Dr. T. M. Embley Professor of Evolutionary Molecular Biology School of Biology The Devonshire Building University of Newcastle upon Tyne NE1 7RU UK

Tel 0191 246 4804 Fax 0191 246 4998

New Lab Webpage:

http://www.ncl.ac.uk/microbial_eukaryotes/ Take a look at our Molecular Systematics course Web Page - it is also available in down-loadable (powerpoint) format:

http://www.bioinf.org/molsys/

UQueensland EvolFunctionalGenomics

SCHOOL OF INTEGRATIVE BIOLOGY - St Lucia Campus Major new initiative in ecological and evolutionary functional genomics Two positions available

The School of Integrative Biology at the University of Queensland, Brisbane Australia, provides unique opportunities for study or research in plant and animal biology with research programs spanning ecology, molecular plant sciences, marine biology, insects and parasite interactions, and genetics & evolution.

The School is now undertaking a major new initiative in ecological and evolutionary functional genomics (EEFG) that will consist of 5 new appointments in the next 12 months. We have existing strengths in molecular genetics, developmental genetics, population/quantitative genetics and quantitative/physiological ecology. We now seek two Lecturers/Senior Lecturers in any area of ecological and evolutionary functional genomics that complement our existing strengths in genetics, development and whole-organism ecology/evolution. Newly renovated laboratory facilities under the EEFG initiative, and competitive start-up packages are available.

The successful applicant will be required to deliver undergraduate lectures at all levels, supervise graduate students, and contribute to the administration of the School. Applicants must possess a PhD and have a demonstrated capacity to establish links with industry and government agencies to develop an externally funded research program in the area of their specialty. An outstanding publication record is essential.

This is a continuing, full-time appointment at Academic Level B or C. The remuneration package will be in the range of $71,293 to $84,660 (Lecturer - Level B) or $87,333 to $100,700 (Senior Lecturer - Level C) including employer superannuation contributions of 17%.

Obtain the position description and selection criteria online or contact Ms Monique Atwell +61 7 3365 7946 or m.atwell@mailbox.uq.edu.au. Contact Professor Scott O^{1}Neill, +61 7 3365 2471, scott.oneill@uq.edu.au to discuss the role. Send applications to the Human Resource Officer, Faculty of Biological & Chemical SciencesThe University of Queensland Q 4076or email m.atwell@mailbox.uq.edu.au

Closing date for applications: 06 October 2005

Reference Number: 3012472

Applications are to be sent to the email address specified above or to the name and organisation unit shown at the address: University of Queensland, Brisbane, Qld 4072. Please quote the Reference Number and include a covering letter that includes the vacancy reference number, your contact address and telephone number; a curriculum vitae, that includes details of education and qualifications and the names and contact details of three referees; and a statement addressing how each of the selection criteria have been met. Equal opportunity in employment is University policy

Christine Ballantyne <c.ballantyne@uq.edu.au>

WoodsHole Tech EvolGenomics

The Marine Biological Laboratory in Woods Hole, Mass. is seeking applicants for a full-time RESEARCH ASSISTANT (Technician) position in the Josephine Bay Paul Center in Comparative Molecular Biology and Evolution. This position is available immediately as part of the Center?s Global Infectious Disease Program. Project will explore comparative genomics, molecular diversity, and evolution of virulence in host-associated bacteria.

For more information, please see:

http://www.mbl.edu/inside/what/human_resources/-job_search.php?func=detail&par=job_id=423

Jennifer Wernegreen <jwernegreen@mbl.edu>

WoodsHole MBL ResearchAssist

SENIOR RESEARCH ASSISTANT [JBPC SRA], Josephine Bay Paul Center, Full- time, Exempt

Description: The Marine Biological Laboratory is seeking applicants for a full-time year round Senior Research Assistant Systems Administrator position with the Josephine Bay Paul Center for Comparative Molecular Biology and Evolution as a Computer Systems Administrator. This is a grant funded position.

Duties: Primary duties will include but not be limited to: Management of a large and diverse computing environment dedicated to basic biological research, with an emphasis upon comparative evolution, astrobiology, and genomics. Primary responsibilities include network management (switches, NFS, file synchronization), account and LDAP management, systems security, hardware maintenance, data integrity and back-up strategies, and web site/database development. Secondary responsibilities include telecommunications, including management of PolyCom Video Teleconferencing. Additional responsibilities include basic training of staff in the UNIX operating system.

Conditions: Continuation of this position is contingent upon successful performance and continued grant funding.

Education: The successful applicant should have a B.A. or M.S. and advanced course work in computer science or have extensive experience working as a Programmer and Systems Administrator. Experience with heterogeneous operating systems required (Linux, Mac OS, Windows, etc). Experience with Sun Grid Engine, beowulf clusters or other forms of parallel computing strongly desired. Scientific programming (C, C++, Perl, Java) and web and database software (SQL, PHP) skills a plus. The successful applicant is expected to have good team skills and be able to work with a high level of independence with broad supervision.

Instructions: Send cover letter and the names, addresses, telephone numbers and email addresses of 3 references to: Marine Biological Laboratory, 7 MBL Street, Attn: Human Resources reference code [JBPC SRA], Woods Hole, MA 02543; telephone 508 289 7422; email: resume@mbl.edu An Equal Opportunity/Affirmative Action Employer/Non- smoking workplace.

Deadline: Until a suitable candidate is identified.

Other

ABI377 service

As many of you know, ABI is discontinuing service for 377 sequencers in 2006 to focus exclusively on their capillary sequences. Even though the 377 is a perfectly fine instrument, many of us are likely facing the same dilema of either purchasing a new capillary sequencer that can be serviced, or finding alternative sources of service for our 377's.

Given the number of 377 machines that are likely still out there, I would guess that there are third party companies that may fill the servicing void. However, I do not know if there are any such companies out there. Do any of you know of alternative sources for servicing ABI 377 sequencers? How are other that are using these machines dealing with this problem.

Thanks,

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

Biology Medicine Society

02/08/05

Dear Colleagues,

some of you (below) are fed up with the flood of mails on catholic church and evolution. The think tank "Biology, Medicine and Society" (announcement below) has been specifically designed to welcome this kind of debate. After the meeting on Intelligent Design, scheduled in September, another one will be settled on the topic of religion and evolution. Your contributions are welcome.

Kind regards,

Michel Tibayrenc, MD, PhD Editor -in-chief Infection, Genetics and Evolution (Elsevier) http://www.elsevier.com/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://gemi.mpl.ird.fr Biology, Medicine and Society

Dear colleagues,

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

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

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

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

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

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

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

The "Biology, Medicine and Society" (BMS) think-tank will be a place for multidisciplinary dialogue, hosting not only specialists (biologists, physicians, psychoanalysts, ethnologists, philosophers, people of letters and religion, historians, politicians, etc.), but it will also be a place for high school and university students, non-specialist citizens, etc. We intend to make it a place of true debate, able to unite in a spirit of tolerance participants whose convictions may at first seem irreconcilable. A "debate" gathering protagonists who agree on nearly everything is about as exciting as a flat electroencephalogram. If the controversy focuses on the theory

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

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Bird micros

Dear colleagues,

we are looking for a company that develops new microsatellite primers in bird species at a reasonable price. I know of Ecogenics in Switzerland, but 15,000 Euros for 10 polymorphic microsatellites seems a bit overpriced to me. If you know of any company or have experience in ordering new microsats, please contact h.wolfger@klivv.oeaw.ac.at

thanks a lot for your help, cheers, hubert

Dr. Hubert Wolfger Konrad Lorenz Institute for Ethology Austrian Academy of Sciences Savoyenstraße 1A 1160 Vienna, Austria

Phone: +43-1-515 81-2758 FAX: +43-1-515 81-2800 E-mail: h.wolfger@klivv.oeaw.ac.at

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Bird micros answers

Dear colleagues, thank you so much for your helpful input. As far as I can see, the prices are in the same range at most companies. So, if you have to spend your money carefully, it might be best to develop primers on your own, or - as someone suggested - collaborate with a lab having experience in this field, bring your own student and consumables, make use of their expertise and share the publication.

I have also added a short summary of replies; numbers in parentheses reflect how often an institution has been suggested. Given prices are those people have sent me in their e-mails, I did not check if they are still up to date:

Companies

(6) Genetic Identification Services in Chatsworth, CA http://www.genetic-id-services.com/ USD 10.000,- for enriched library Add USD 2.500,- for 10 primer pairs

(2) Ecogenics http://www.ecogenics.ch/index.html EUR 15.000,- for 10 polymorphic loci

East Malling Research http://www.emr.ac.uk/ EUR 9.000,- + VAT for 10 polymorphic loci

VIB Genetic Service Facility, Antwerp http://www.vibgeneticservicefacility.be/ EUR 10.000,- for 20 loci without polymorphism data

Wildlife Genetics international in Nelson, BC http://www.wildlifegenetics.ca/

Academic institutions

(2) University of Georgia, SREL DNA lab, Travis Glenn List of institutions and companies: http://www.uga.edu/srel/Microsat/Microsat-L.htm they also offer services at all levels of msat development: http://www.uga.edu/srel/Msat_Devmt/Microsatellite_Development.htm

Sheffield Molecular Genetics Facility, Terry Burke http://www.shef.ac.uk/misc/groups/molecol/smgf.html

Thanks again and good luck with your experiments,

Hubert

Dr. Hubert Wolfger Konrad Lorenz Institute for Ethology Austrian Academy of Sciences Savoyenstraße 1A 1160 Vienna, Austria

Phone: +43-1-515 81-2758 FAX: +43-1-515 81-2800 E-mail: h.wolfger@klivv.oeaw.ac.at

Bootstrapping micros

Dear all,

I would be most grateful for ways to construct and bootstrap trees using microsatellite data from individual animals (not populations) as separate data points.

My question concerns the relative relatedness of 33 individuals within a small, interbreeding population of zebras. None of the animals are known parent-offspring pairs. I have tried RELATEDNESS and CERVUS, but to my knowlege, neither program boostraps trees.

Thanks very much, Wenfei

Wenfei Tong Harvard University Museum of Comparative Zoology 26 Oxford Street Cambridge, MA 02138 USA

wenfei.tong@gmail.com

CEQ8000 sequencing costs

Hi All,

Could anyone give me an idea how much one sequencing reaction on CEQ8000 might cost?

Sincerely,

Volodymyr Dvornyk

Dr. Volodymyr Dvornyk Cunningham Hall, Room 245 Department of Biological Sciences Kent State University P.O. Box 5190 Kent, OH 44242-0001

Tel.: (330) 672-3625 Fax: (330) 672-3713 E-mail: vdvornyk@kent.edu

vdvornyk@kent.edu

Cleaning capillars

Dear all,

I've heard that it is possible to clean capillars for ABI3100 machines, either running only clean polymer (without size standards and anything else) or by cleaning them with TE buffer. I would apreciate any comment on this.

answer to: porozco@science.uva.nl

thanks, Pablo Orozco-terWengel

orozco_terwengel@yahoo.com

Commercial genotyping

Can anyone suggest companies that would be effective and cost efficient to contract for genotyping about 100,000 samples? Thanks. Sandra

Sandra E.Harrington Research Support Specialist 146 Emerson Hall Cornell University Ithaca, NY 14853 USA ph:(607) 255-1206 fax: (607) 255-6683 e-mail: seh15@cornell.edu http://www.Gramene.org seh15@postoffice10.mail.cornell.edu

Commercial genotyping answers

Hello all, Thanks for your suggestions of companies to check for large scale genotyping project. In case anyone else wants the list, here is the summary.

Sandra

www.sym-bio.com <http://www.genomequebec.mcgill.ca/services/genotyping.php>http://www.genomequebec.mcgill.ca/services/genotyping.php http://www.macrogen.com/eng/macrogen/macrogen_main.jsp www.polymorphicdna.com www.prokaria.com . http://www.broad.mit.edu/

http://www.illumina.com/ – Sandra E.Harrington Research Support Specialist 146 Emerson Hall Cornell University Ithaca, NY 14853 USA ph:(607) 255-1206 fax: (607) 255-6683 e-mail: seh15@cornell.edu http://www.Gramene.org seh15@postoffice10.mail.cornell.edu

Crustacean micro problems

Hi, I have been developing microsatellites for 3 species of Galatheidae for the past year and although the developmental process went well and plasmid sequencing gave microsatellites and flanking regions which were sufficient to develop primers I am now having problems with optimisation and amplification. I am somehow amplifying product of incorrect size (as to what the primers were designed for- larger fragments) and am getting multiple bands and lots of background noise when trying to screen samples. Of the two micros that I have managed to optimise the screening concluded that they were uninformative (everything I screened including 19 adult individuals from a single area as well as a mother and 75 eggs where all found to have identical heterozygote bands!). I am confused by this result and was wondering if anyone has had similar problems with crustaceans or could offer advice as to possible problems that could be causing this or how to proceed. Thanking you in advance for any comments you could offer

Deborah

Miss Deborah Bailie 2nd year PhD Student Queens University, Belfast Fisheries Genetics and Molecular Biology Lab Medical Biological Centre 97 Lisburn Road Belfast BT9 7BL Northern Ireland

Tel: 028 90972247 email: d.bailie@qub.ac.uk

d.bailie@Queens-Belfast.AC.UK

Drawing trees

Hello Everyone,

I have been producing trees in PHYLIP (after a long break from tree building), and cannot get the bootstrap values on my plots. From memory I believe that I used to manipulate the trees elsewhere, and add in the values from the output file by hand.

Does anybody know of a programme (for MS system) that will read the PHYLIP files and place the bootstrap values at the nodes?...I have spent the day 'surfing' and cant seem to find anything suitable.

Thank you for any assistance,

E Brede

brede@mpil-ploen.mpg.de

Drawing trees answers

Thank you to all of those who responded so quickly (Prof Maddison,Dr Burg, Dr Dharne, Dr Stern) to my question on 'bootstrap values and tree viewing in other programs'

The suggestions were:- Mesquite (possibly depending on input file) NJplot TREEVIEW32

I chose TREEVIEW and it worked with my PHYLIP file. Be aware when it initially opens not all of the buttons are highlighted. Go to Tree in the upper menu bar and then select 'show internal edge label'....you will then see your bootstrap values.

Thanks once again, E Brede

Drosophila Isofemale Lines

*** NEW DROSOPHILA ISOFEMALE LINES *** The Tucson Drosophila Species Stock Center has recently received new ISOFEMALE lines from different species. These ISOFEMALE lines are available until the last day of September 2005. Please contact us directly if you are interested (stockcenter@arl.arizona.edu).

D. melanogaster: 25 lines Tucson, Arizona 2005

D. pseudoobscura: 32 lines from Chiracahua Mts, Arizona 2005

D. simulans: 1 line Tucson, Arizona 2005

D. arizonae: 4 lines Tucson Arizona 2005

D. arawakana arawakana: 63 lines St. Kitts, Caribbean 2005

D. arawakana (kitts type): 6 lines St. Kitts, Caribbean 2005

Stacy Mazzalupo <smm@email.arizona.edu>

Drosophila stocks

*** NEW DROSOPHILA STOCKS *** The Tucson Drosophila Species Stock Center has incorporated several strains of mutant flies. These strains are now part of our permanent collection. Go to our website for more details or to order (http://stockcenter.arl.arizona.edu/-).

D. ananassae 14024-0371.14 (American Samoa, Pacific Ocean. parthenogenetic, yellow body. 1972).

D. arizonae 15081-1271.25 (Superstition Mountains, Arizona. white-eyes1997).

D. melanogaster 14021-0231.36 (WGS line).

D. simulans 14021-0251.206 (pale red. C. Aquadro).

D. simulans 14021-0251.207 (purple).

D. simulans 14021-0251.208 (cardinal, curled-Sato).

D. simulans 14021-0251.209 (garnet, cinnabar, ebony, ripple).

D. simulans 14021-0251.210 (females yw; males rst. (Attached-X)).

The Tucson Drosophila Species Stock Center has incorporated several strains of wild-type flies. These strains are now part of our permanent collection. Go to our website for more details or to order (http://-stockcenter.arl.arizona.edu/).

MULTIFEMALE STRAINS: D. immigrans 15111-1731.10 (Rocky Point, NY 2004). D. parthenogenetica 15182-2221.04 (Sinaloa, Mexico 2004). D. nigrospiracula 15081-1503.09 (Tucson, AZ 2005). D. melanogaster 14021-0231.38 (Tucson, AZ 2005). D. tolteca 14012-0201.02 (Jalisco, Mexico 2004) D. willistoni 14030-0811.30 (St. Kitts Island, Caribbean Sea 2005). D. robusta 15020-1111.13 (Iowa River, IA 2004).

ISOFEMALE LINES D. affinis 14012-0141.07 (Rocky Point, NY 2004). D. affinis 14012-0141.08 (Rocky Point, NY 2004). D. algonquin 14012-0161.03 (Rocky Point, NY 2004). D. americana americana 15010-0951.16 (Iowa River, Iowa 2004). D. ananassae 14024-0371.15 (St. Kitts Island, Caribbean Sea 2005). D. arawakana arawakana 15182-2261.03 (St. Kitts Island, Caribbean Sea 2005). D. arawakana (kitts type) 15182-2260.00 (St. Kitts Island, Caribbean Sea 2005). D. busckii 13000-0081.30 (Edo. Mexico, Mexico 2004). D. hydei 15085-1641.59 (Oaxaca, Mexico 2003). D. hydei 15085-1641.60 (Edo. Mexico, Mexico 2004). D. hydei 15085-1641.61 (Sinaloa, Mexico 2004). D. immigrans 15111-1731.09 (Rocky Point, NY 2004). D. melanogaster 14021-0231.37 (Tucson, AZ 2005). D. mojavensis 15081-1352.25 (Sinaloa, Mexico 2002). D. nannoptera 15090-1692.12 (Oaxaca, Mexico 2002). D. nebulosa 14030-0761.06 (Sinaloa, Mexico 2004). D. parthenogenetica 15182-2221.03 (Nayarit, Mexico 2004). D. pseudoobscura 14011-0212.118 (Santa Fe, NM 2002). D. putrida 15150-2101.02 (Pennsylvania 2004). D. quinaria 15130-2011.00 (Madison, WI 2004). D. robusta 15020-1111.11 (Madison, WI 2004). D. robusta 15020-1111.12 (Rocky Point, NY 2004). D. tripunctata 15220-2401.12 (Iowa River, IA 2003). D. tripunctata 15220-2401.13 (Madison, WI 2004). D. tripunctata 15220-2401.14 (Madison, WI 2004). D. tropicalis 14030.0801.01 (Jalisco, Mexico, 2004). D. willistoni 14030-0811.29 (St. Kitts Island, Caribbean Sea 2005). D. willistoni 14030-0811.31 (Oaxaca, Mexico 2002).

Stacy Mazzalupo <smm@email.arizona.edu>

Drosophila stocks 2

*** SEQUENCING PROJECT STOCKS *** The following stocks, used in the whole genome sequencing and BAC library projects, are available from the Tucson Stock center. (http://stockcenter.arl.arizona.edu/-sequences.php3)

SPECIES STOCK NUMBER STATUS Whole Genome Sequence (WGS) D. ananassae 14024-0371.13 Complete D. erecta 14021-0224.01 Complete D. grimshawi 15287-2541.00 Complete D. melanogaster 14021-0231.36 Complete D. mojavensis 15081-1352.22 Complete D. persimilis 14011-0111.49 Complete D. pseudoobscura 14011-0121.94 Complete D. sechellia 14021-0248.25 Complete D. simulans 14021-0251.194 Complete (1X coverage) D. simulans 14021-0251.195 Complete (4X coverage) D. simulans 14021-0251.196 Complete (1X coverage) D. simulans 14021-0251.197 Complete (1X coverage) D. simulans 14021-0251.198 Complete (1X coverage) D. willistoni 14030-0811.24 Complete D. virilis 15010-

1051.87 Complete D. yakuba 14021-0261.01 Complete

BAC library only D. americana 15010-0951.15 Complete D. equinoxialis 14030-0741.02 In process D. hydei 15085-1641.58 In process D. littoralis 15010-1001.11 In process D. mercatorum 15082-1521.36 Complete D. novamexicana 15010-1031.14 Complete D. repleta 15084-1611.10 In process D. albomicans On hold

Stacy Mazzalupo <smm@email.arizona.edu>

ESEB and debate on evolution

Dear Colleagues,

ESEB Meeting in Krakow is approaching with great speed. It's been preceded by a laud debate after Cardinal Schönborn remark on evolutionary theory in NY Times. Often I wished I had a babble fish, this ingenious invention of Douglas Adams', or it's visual equivalent I could put on my nose, to understand some of the thought and feeling posted on Evoldir recently. Rather then putting a stick in an ant hill again, I would like to draw your attention to a reaction the Cardinal's letter precipitated in Kraków. Below are a few words of explanation written by Jacek Slusarczyk, who informed me that they can be reprinted or distributed free of charge, providing the logo Tygodnik Powszechny is displayed. The two attached articles were translated Witold Turopolski.

See you in Krakow = Do zobaczenia w Krakowie.

Jacek M. Szymura Jagiellonian University, Kraków, Poland

Cardinal Christoph Schönborn described neo-Darwinism as untrue and incompatible with the teaching of the Church. His op-ed article in The New York Times“, published on 7 July this year, caused a storm in scientific circles. Now the Archbishop of Vienna and one of the main editors of the Catechism of the Catholic Church explains what he meant to say - in ”Tygodnik Powszechny“, a Catholic weekly from Cracow, founded in 1945, with which Karol Wojty a cooperated for years. Cardinal Schönborn's position is countered by Reverend Professor Micha Heller, a philosopher, physicist and cosmologist, a participant of academic meetings with John Paul II in Castel Gandolfo, a researcher at the Vatican Observatory and a member of the prestigious Pontifical Academy of Sciences

Jacek Slusarczyk<slusarczyk@tygodnik.com.pl>

TYGODNIK POWSZECHNY www.tygodnik.onet.pl Editor'sl office Krakow, Wislna 12, Poland, tel. 4812 - 422 2311, fax 4812 - 421 6731

DARWIN IN STAINED GLASS

A new debate over the theory of evolution

”Evolution in the sense of common ancestry might be true, but evolution in the neo-Darwinian sense - an unguided, unplanned process of random variation and natural selection - is not.“ This sentence from an op-ed article by Cardinal Christoph Schönborn in ”The New York Times“ caused a storm in scientific circles. We asked the Archbishop of Vienna what he meant to say.

Cardinal Schönborn has just returned from a prayer in the cathedral to the seminary situated at the foot of the Wawel Hill. He came to Cracow as a private person. The sixty year old Dominican priest is joking that in Vienna he had left his press spokesman Erich Leitenberger completely engulfed by work: since ”The New York Times“ published his article ”Finding Design in Nature“, the telephone won't stop ringing. The Cardinal, who is a theologian and philosopher by education, has been interested in the issues of creation and evolution for good thirty years. Many times he spoke on the subject at the Congregation for the Doctrine of the Faith. Now he does not hide his contentment that he managed to provoke a heated discussion: ”A good thing about the debate over evolution in America is that it is much more lively than in Europe“, he tells ”Tygodnik Powszechny“. He regrets, however, that Austrian newspapers - he did not follow other European media - limited themselves to emotional slogans: Kulturkampf, turning back to a time before the Enlightenment, the Church should not interfere with science.

”Today the Church's task is to defend reason“, explains Cardinal Schönborn. ”In principle I do not question that evolution has taken place. It is a scientifically open and in many respects also probable hypothesis. But the question is: is the evolution an unguided process? Perhaps it allows us to learn about design, intelligence, reason and order¿‘

Beetles and theology

Archbishop Józef yci ski, the author of the book ”God and Evolution“, claims that ”the Church did not fight the theory of evolution“. The metropolitan bishop of Lublin reminds us that Darwin had a Christian funeral ”in the Westminster Abbey, where there were even plans to immortalize him in one of the stained glass windows, as a man who contributed greatly to the progress of science.“ His family wanted him to become a priest, but during his studies ”he discovered that he is more interested in beetles than in theology; he changed his interests - and this proved to be good for science.“ The first disputes between Christians and Darwinists did not result from scientific premises, but from naive fears that the teaching on natural selection might become harmful for humanism. At the same time many theologians recognized that - as Father Marek S omka, the author of the book ”Christian Evolutionism on the Human Origin“, said - ”God manifests His creative powers in evolutionary transformations; there

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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

Haplotype configuration test

Dear Evoldir members, I want to apply the haplotype configuration test proposed by Innan et al. 2005 (Genetics 169:1763-1777) to a mitochondrial dataset using the software Haploconfig. I performed several simulations (10000) with the program but my observed haplotype configuration never appeared. Does it mean that my observed configuration in not probable under my null hypothesis? Is there some way to calculate directly the probabilities of all the possible configurations for my data? Ill appreciate if someone can give me some “tips” or recommend literature about this topic. Thank you very much to everyone! Kind regards, Romina

Impossible protein evolution

At the risk of starting things up again, I have let this one pass through since it is a request for help/comments on a specific article.

Please respond directly to Dan at dgraur@uh.edu.

Brian

The infamous creationist Michael Behe has published a paper on the impossibility of evolving new protein functions.

The paper was published in Protein Science (2004) 13:2651-2664.

I am compiling a list of errors in this article and I would greatly appreciate the contribution of the EvolDir members to this list.

If you do not have access to the article, please drop me a line and i’ll email you a pdf file.

Please send your comments to Dan Graur (dgraur@uh.edu).

Thank you

Dan

Dan Graur <dgraur@uh.edu>

Isolation distance altitude

Hey, I have got a question regarding isolation by distance: I am working with microsatellites and want to test, if genetic differentiation is correlated with altitude, but I have read that this might result in artificial outcomes, because there is no theoretical background for the relationship of Fst and altitude. Is this true and if yes, how can I deal with this problem in another way?

I would be thankful for suggestions and will post a summary of answers.

Thanks a lot in advance, Conny

– Cornelya Klütsch ZFMK- Zoologisches Forschungsinstitut und Museum Alexander Koenig Adenauerallee 160 53113 Bonn Germany Tel.: 49- 228-9122-242 Fax: 49- 228-9122-212 Mail: cornelya@freenet.de

Jesuit rebuttal

Brian, I am aware that the discussion following the NYT Op-Ed piece by Christoph Schönborn has been moved from evoldir. Nonetheless, I thought the recent response by George Coyne, SJ, Director of the Vatican Observatory, might be of general interest to the evoldir community. It reveals that Schönborn’s views should not be taken as representative for the church in general, and highlights the quite controversial discussion among leading representatives of the church. Feel free to direct this wherever deemed appropriate.

George Coyne, Gods chance creation. The Tablet 6 August 2005.

http://www.thetablet.co.uk/cgi-bin/register.cgi/-tablet-01063 – Markus Friedrich Associate Professor Department of Biological Sciences Department of Anatomy and Cell Biology Wayne State University 5047 Gullen Mall Detroit, MI 48202

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

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Kansas moves to limit evolteaching

This page was sent to you by: jkmckay@ucdavis.edu.

WASHINGTON | August 11, 2005 Kansas Moves to Stem Role of Evolution in Teaching By REUTERS OVERLAND PARK, (Reuters) - After months of debate over science and religion, the Kansas Board of Education has tentatively approved new state science standards that weaken the role evolution plays in teaching about the origin of life. http://www.nytimes.com/-reuters/politics/politics-life-evolution.html?ex=-1124424000&en=687798b59e1ed910&ei=5070&emc=-eta1

LeafDNAextraction answers

Dear colleagues, thank you to all that have contributed with suggestions to my email : "Oaks dry leaves DNA extraction".

The message was about how to optimize DNA extraction from dried oak leaves.

RESPONSES:

Dear Colleague, I have no particular experience with oak, but I have done some work on Sorbus aucuparia. One potential problem with dried material is that it has not been properly dried. I had this problem with sorbus leaves that were dried to slowly on silicagel (because the leaves were put in an envelope). If this is the case with your samples, it might well be that the DNA is degraded in the leave material. What exactly do you mean by poor results? Do you mean that you see little DNA on a control gel or that PCR yield is low, or both? To increase the purity of your DNA sample you can try the following: - repeat the chloroform protein extraction once before adding isopropanol. - skip the incubation at -20C for 90 minutes (DNA precipitation). Just mix gently 50 times and if necessary incubate 5 min on ice. DNA quantitavely precipitates at room temperature in a isopropanol/water solution. By incubating 90 minutes at -20C, you probably do not increase the yield of DNA but i! nstead increase coprecipitation of undesirable compounds that may inhibit further enzymatic reactions (PCR, restriction). If you are performing PCRs, you should add non-acetylated Bovine Serum Albumine to the PCR mix (final concentration: 200 μg/ml). It greatly imrpoved the yield and consistency of the PCRs I made on Sorbus. I hope these comments will be of help. Good luck and kind regards, Olivier Raspé

Dragos, you can get fairly large quantities of clean DNA from old oak leaves using several different protocols, including Qiagen's Plant DNeasy kit or Qiagen's DNA Mini Kit. However, I work on oaks and I have used a protocol from Keim et al. followed by a clean up using the Qiagen DNA Mini Kit and I am able to get large quantities of clean DNA. The Keim citation and adapted protocol is pasted below: Plant DNA Extraction Protocol (old leaves) (adapted from: Keim, P. et al. 1989. Genetic Analysis of an Interspecific Swarm of Populus: Occurrence of Unidirectional Introgression. Genetics 123: 557-565.)

1. Grind approximately 0.5g leaf material to a fine powder with a mortar and pestle with liquid nitrogen. Make sure to keep leaf material frozen at -70 degrees C until ready to use. 2.Warm extraction buffer to 650C. 3.Immediately add 1mL extraction buffer and 20 microliters of 20mg/mL proteinase K to leaf powder. Mix well and incubate at 650C for 1 to 1 $\frac{1}{2}$ hours or overnight while shaking constantly (on a shaker). 4.After incubation, add 100 microliters of 5M potassium acetate and incubate on ice for 1 hour. 5.Centrifuge to pellet debris. 6.Place supernatant in a new, clean 1.5mL tube and add 0.65 volume ice-cold isopropanol. Discard pelleted debris. 7.Incubate tubes at -80 degrees C for 15 minutes followed by incubation at 4 degrees C overnight. 8.Centrifuge at high speed for 15 minutes to pellet DNA 9.Wash pellet in 70% ethanol and air dry overnight. 10.Resuspend in sterile ddH2O or TE buffer. 11.For very clean DNA, follow with Qiagen's DNA Mini Kit clean-up using the "crude lysates" protocol. You can also try 2 phenol-chloroform cleanups depending on how clean ou need the DNA to be. Extraction Buffer: 0.005 M 1,10 phenanthroline 0.05 M Tris (pH8.0) 0.02 M EDTA (sodium EDTA) 0.25

M NaCl 1% SDS)wt/vol) 1% PVP-40 (vol/vol) Good luck, Kathy, University of Illinois at Chicago.

Hi, I suggest a similar protocol (attached as well as the paper where it is from). The sorbitol extraction might help to get rid of some secondary compunds which are more abundant in old leaves. Additionally, you may add a bit of PVP to the extraction steps which has a similar effect. (Forget about the CTAB conservation - we use the protocol a lot for a wide range of plant and fungal material and also for herbarium samples) Of course, the quality and yield of the DNA will depend on the speed and way the leaves were dried. If the DNA is degraded already, you can't help it. But this can be checked by running an aliquot of the isolated DNA on a gel first.

Good luck, Judith

Dr. Judith Fehrer Institute of Botany CZ-25243 Pruhonice, Czech Republic.

Protocol: DNA Isolation from plant tissue (this Protocol is attached in FILES on http://groups.yahoo.com/group/ForestBiodiversityEurope/)

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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

Likelihood Bayesian Clocks

Dear Colleagues,

I am interesting in hearing advice or comments from anyone who has used either Mike Sanderson's R8's or Jeff Thorne's MULTIDIVTIME to estimate divergence times from DNA sequence data.

I am especially interested in hearing advice on how treat analyses of multiple data sets. Is there a way to combine information from multiple genes with different mutation rates in R8's?

Similarly, I am interested in the effect of model parameters on the behavior of MULTIDIVTIME. The release notes suggest that the most complicated model that can be implemented is F84+gamma. Does anyone have experience using this program for data sets where more complicated models - say, GTR+I+G for example - are justified? What are the consequences of using the simpler model if the data depart significantly from the expectations of F84+gamma?

Thanks,

Chris Smith

Christopher Irwin Smith, Ph.D.

Post Doctoral Research Fellow University of Idaho Department of Biological Sciences Moscow, Idaho 83844

ph: (lab) 208 885.8860 (office) 208 885 4229

http://www.webpages.uidaho.edu/ ˜ csmith/ChrisSmith.htm

Lynch on Behe

For those interested – I have produced a response to the BS (Behe and Snoke) model, which should appear in Protein Science within the next few weeks. As the first (and perhaps only) peer-reviewed paper published in a quality sicience journal by an IDer, it should come as no surprise that their paper is viewed as a major coup by the ID community. Mike Lynch

Michael Lynch milynch@indiana.edu Distinguished Professor Dept. of Biology Phone: 812-855-7384

Indiana University FAX: 812-855-6705 Bloomington, IN 47405

Lab Research: http://www.bio.indiana.edu/facultyresearch/faculty/Lynch.html IU Biology: http://www.bio.indiana.edu/ NSF Training Grant in Evolution, Development, and Genomics: http://evodevo.uoregon.edu/ Daphnia Genomics Consortium: http://daphnia.cgb.indiana.edu/ Michael Lynch <milynch@indiana.edu>

Micro polymorphisms

Dear colleagues, I work on a Ranunculaceae, a rare and endangered plant species found in the parisian region. I designed microsatellites markers from it and found absolutely no polymorphism for all analyzed individuals, even for individuals collected in other regions. Nevertheless, polymorphism was found in a closely-related species using these markers. I am a little bit confused with these results and I am looking for people who had similar experience. I thank you in advance for your answers! Please, respond to fnoel@mnhn.fr Best wishes Florence Noel pHD student

Florence NOEL doctorante UMR 5173 CNRS MNHN Conservation des espèces, restauration et suivi des populations et USM 2699 Inventaire et suivi de la biodiversité Conservatoire Botanique National du Bassin Parisien Muséum National d'Histoire Naturelle 61, rue Buffon, 75005 Paris Tel 01 40 79 35 57 Fax 01 40 79 35 53

NOEL Florence <fnoel@mnhn.fr>

Micro polymorphisms answers

Hi all,

Here is the summary of responses that I received to my question: Do you have experience with lack of polymorphism using microsatellites? for those that were interested.

Thanks a lot again to those that responded!!

Florence NOEL

1- The species could be apomictic 2- Generally [XY]n less than ten are not very informative. I also tend to steer clear of interrupted or complex microsatellites. 3- Microsatellites which have interrupted repeats (for example, GAGAGATGAGAGA where there's a T interrupting the GA repeat motif) are often less ploymorphic than microsatellites with uninterrupted repeat motifs. The reason is probably that a substitution in the repeat motif changes the mutation process (from slippage- to point mutations) and that this lowers the mutation rate and hence the level of polymorphism. 4- The mean of reproduction and the size of the populations could also explain the lack of genetic diversity.

MultiplexPCR primer design answers

Hi all,

Here are the suggestions I received to my query on "Multiplex PCR primer design" for those that were interested.

Thanks a lot again to those that responded!!

MuPlex http://nar.oxfordjournals.org/cgi/content/-abstract/33/suppl_2/W544 Vector Nti http://-www.biocenter.helsinki.fi/bi/Programs/fastpcr.htm Primer Express http://www.molbio.princeton.edu/-facility/synseq/services.html Margarita Ramos mramos@princeton.edu

NYT Intelligent Design

August 5, 2005 Design for Confusion By PAUL KRUGMAN I'd like to nominate Irving Kristol, the neoconservative former editor of The Public Interest, as the father of "intelligent design." No, he didn't play any role in developing the doctrine. But he is the father of the political strategy that lies behind the intelligent design movement - a strategy that has been used with great success by the economic right and has now been adopted by the religious right.

Back in 1978 Mr. Kristol urged corporations to make "philanthropic contributions to scholars and institutions who are likely to advocate preservation of a strong private sector." That was delicately worded, but the clear implication was that corporations that didn't like the results of academic research, however valid, should support people willing to say something more to their liking.

Mr. Kristol led by example, using The Public Interest to promote supply-side economics, a doctrine whose central claim - that tax cuts have such miraculous positive effects on the economy that they pay for themselves - has never been backed by evidence. He would later concede, or perhaps boast, that he had a "cavalier attitude toward the budget deficit."

"Political effectiveness was the priority," he wrote in 1995, "not the accounting deficiencies of government."

Corporations followed his lead, pouring a steady stream of money into think tanks that created a sort of parallel intellectual universe, a world of "scholars" whose careers are based on toeing an ideological line, rather than on doing research that stands up to scrutiny by their peers.

You might have thought that a strategy of creating doubt about inconvenient research results could work only in soft fields like economics. But it turns out that the strategy works equally well when deployed against the hard sciences.

The most spectacular example is the campaign to discredit research on global warming. Despite an overwhelming scientific consensus, many people have the impression that the issue is still unresolved. This impression reflects the assiduous work of conservative think tanks, which produce and promote skeptical reports that look like peer-reviewed research, but aren't. And behind it all lies lavish financing from the energy industry, especially ExxonMobil.

There are several reasons why fake research is so effective. One is that nonscientists sometimes find it hard to tell the difference between research and advocacy - if it's got numbers and charts in it, doesn't that make it science?

Even when reporters do know the difference, the conventions of he-said-she-said journalism get in the way of conveying that knowledge to readers. I once joked that if President Bush said that the Earth was flat, the headlines of news articles would read, "Opinions Differ on Shape of the Earth." The headlines on many articles about the intelligent design controversy come pretty close.

Finally, the self-policing nature of science - scientific truth is determined by peer review, not public opinion - can be exploited by skilled purveyors of cultural resentment. Do virtually all biologists agree that Darwin was right? Well, that just shows that they're elitists who think they're smarter than the rest of us.

Which brings us, finally, to intelligent design. Some of America's most powerful politicians have a deep hatred for Darwinism. Tom DeLay, the House majority leader, blamed the theory of evolution for the Columbine school shootings. But sheer political power hasn't been enough to get creationism into the school curriculum. The theory of evolution has overwhelming scientific support, and the country isn't ready - yet - to teach religious doctrine in public schools.

But what if creationists do to evolutionary theory what corporate interests did to global warming: create a widespread impression that the scientific consensus has shaky foundations?

Creationists failed when they pretended to be engaged in science, not religious indoctrination: "creation science" was too crude to fool anyone. But intelligent design, which spreads doubt about evolution without being too overtly religious, may succeed where creation science failed.

The important thing to remember is that like supply-side economics or global-warming skepticism, intelligent design doesn't have to attract significant support from actual researchers to be effective. All it has to do is create confusion, to make it seem as if there really is a controversy about the validity of evolutionary theory. That, together with the political muscle of the religious right, may be enough to start a process that ends with banishing Darwin from the classroom.

E-mail: krugman@nytimes.com

Perciformes divergence

Dear all:

I am looking for a decent figure (whether journal or book) showing dated nodes with estimates of divergence times of major lineages (suborders, families) within the Perciformes. Any suggestions?

Thank you, JL

seareef@gmail.com

Pigeon phylogeny

Hi,

I am in search of persons working with the phylogeny of pigeons (Columbidae).

Please, do not hesitate in sending e-mail addresses so that I can get in touch directly.

Many thanks in advance,

Pierre-Yves

Pierre-Yves HENRY Département Ecologie et Gestion de la Biodiversité UMR 5173 - Conservation des Espèces, Restauration et Suivi des Populations Muséum National d'Histoire Naturelle 55 rue Buffon 75005 Paris, France

Tél: +33 (0)1 40 76 30 81 Fax: +33 (0)1 40 76 38 35

pierreyveshenry@yahoo.fr

Recomb rates

Hi All,

I am collecting data on genome-wide estimates (as well as more detailed estimates) of recombination rates (i.e. recombinational genome size relative to physical genome size) in higher eukaryotes.

I would greatly appreciate published or unpublished estimates that you have or know of, along with information how recombination and physical size were estimated.

Thank you,

Olav Rueppell (olav_rueppell@uncg.edu)

Shipping specimens

Can anyone provide suggestions on shipping museum samples that are normally stored in ethanol (e.g. frogs, fish, crustaceans)? Best I can tell it is virtually impossible to do this anymore legally. Does anyone have suggestions for alternative methods of shipment (different storage solutions, etc). Certainly museums must deal with this issue on a regular basis.

Thanks Paul

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

Software LAMARC 2 0 2

LAMARC version 2.0.2 is now available for download at

http://evolution.genetics.washington.edu/lamarc/-lamarc.download.html This release fixes a problem with v2.0 runs with multiple replicates in likelihood analyses, and problems with v2.0 runs with multiple genomic regions in Bayesian and (in one case) likelihood analyses. You will need to download and run the new version if you:

- Ran a likelihood analysis with replication. - Ran a Bayesian analysis with multiple genomic regions. - Ran a likelihood analysis with multiple genomic regions and specified different effective population sizes (e.g., for nuclear and mtDNA) for the different genomic regions.

Versions of LAMARC prior to 2.0 and analyses that did not fall into one of the three above categories are unaffected by this bug.

If you were a student at the Workshop on Molecular Evolution at Woods Hole, you might have LAMARC version 2.0.1a, which this version also supercedes.

Replication, as you might recall, is a feature added in v2.0 that estimated parameters from a single region multiple times. Since no new data is included in these anlyses, the likelihood curves need to be averaged, but instead were being multiplied, resulting in similar estimates, but too-narrow confidence intervals.

Parameter estimates from different genomic regions, however, each come from unique data, so the probability curves need to be multiplied. In Bayesian runs, these curves were being averaged, resulting in similar estimates, but too-wide confidence intervals. (Good news if your confidence intervals were disappointing.)

Version 2.0 has only been out for a couple of months, but if you've already analyzed a lot of data and are loathe to repeat it, there may be hope for you yet.

If you have done a likelihood run with multiple replicates and/or with different specified effective population sizes and have saved a 'summary file' from this run (by default, the name of this file is 'outsumfile'), this summary file can be read in by version 2.0.2 to redo the analysis on the same set of trees, saving you the time spent generating the trees.

If you have done a Bayesian run with multiple genomic regions, you can multiply the 'curvefiles' from the individual regions by hand to produce accurate estimates over all regions. In brief, you take the files labelled 'curvefile_reg1_*', 'curvefile_reg2_*', (etc.) for the appropriate parameter, line them up, multiply the values for the same points by each other, integrate over the result, then divide by the result of the integration (so the resulting curve will integrate to 1.0). The peak of this curve is your Most Probable Estimate (MPE), and you can integrate over sections of the curve to get your confidence intervals. Don't forget that by default, many of these curvefiles will be on the log scale!

As a reward for reading this far, we have also included an enhancement with the new code: you can now read and write summary files from a Bayesian run. In addition, these summaries are now written as they are generated, so a run that is terminated halfway through now can be (partially) recovered.

Please don't hesitate to e-mail the LAMARC team (lamarc@gs.washington.edu) if you have any questions about the new code, or for more details on how to perform the recovery steps outlined above.

-The LAMARC Development Team lamarc@gs.washington.edu

Lamarc-announce mailing list Lamarc-announce@evolution.gs.washington.edu http://evolution.gs.washington.edu/mailman/listinfo/lamarc-announce http://evolution.gs.washington.edu/lamarc.html "Mary K. Kuhner" <mkkuhner@gs.washington.edu>

Software PaupUp

Dear Evoldir members, The ones here interested in phylogenetics probably know the PAUP* software from D. Swofford. It is indeed a very useful package for phylogenetics analysis and probably one of the most widely used nowadays. Unfortunately, there is no user-friendly interface for PC versions (both DOS and Windows are essentially line input command based). This makes PAUP* a difficult software to use both for research but also for education purposes on PC computers. That is why we provide today PaupUp, a user-friendly interface to PAUP* DOS version available for free at http://www.agro-montpellier.fr/sppe/Recherche/JFM/PaupUp/ This interface is a frontend and therefore DOES NOT include PAUP* that needs to be purchased. It includes around 80% of the available commands, representing in our opinion the most commonly used ones, and the rest can still be entered in a command line interface as usual. PaupUp also includes links with treeview software for drawing trees and Modeltest. We hope that PaupUp will prove as useful to you as it has proven for educational purpose here.

Sincerely,

Jean-Francois Martin and Frederic Calendini.

Software phyloXML specifications

ANNOUNCING VERSION 0.3 OF PROPOSED SPECIFICATIONS FOR phyloXML

This message is to announce the release of version 0.3 for the specifications of phyloXML level 1.

The specifications can be found at: http://www.phyloxml.org/ Please feel free to comment on it.

Please consider joining our phyloXML Yahoo Group in order to receive further updates/comments and for discussion with other interested scientists: http://groups.yahoo.com/group/phyloxml/ Our current plans are to translate these specification into an XML Schema (XSL) and then complete the phyloXML parser/writer classes in the FORESTER Java package (based on which ATV is built).

We really appreciate all the insightful comments and suggestions we got for phyloXML version 0.2 and we tried to incorporate as many of them as we could, without changing the intentions of phyloXML.

In short, the major changes from version 0.2 to version 0.3 are as follows:

dropped <parent> tag and replaced with <branch> tags which can reference clades outside its nested structure. # Removed all style attributes except color for branches # The <length> child tag of <branch>is now a <distance> tag and can have associated attributes, for example, unit. # The <name> child tag of <clade> changed to <label>. # Dropped two child tags from <sequence>: <pathway_name> and <pathway_id>. # Dropped <expression> tag. All non-phylogenetic data associated with sequences and clades will have to be represented as <custom> tags.

(The specification document itself is more comprehensive.)

Thank you,

Ethalinda Cannon Christian Zmasek

czmasek@gnf.org

Subtraction cDNA kits

Hi,

I'll have to use a subtraction cDNA kit (supression subtractive hybridization or SSH) next semester and I need feedback from people who used one; if it worked well, which company was it from, what to be carefull with and what kind of results you have obtained.

As for now, I was considering the Clontech PCR-Select cDNA subtraction kit.

Thanks in advance

Eric Normandeau

SymmeTREE Div rates

Dear Colleagues,

Has anyone had difficulties initiating the diversification rates software, SymmeTREE (Chan & Moore, 2004), in Terminal from the Home Directory on a Mac iBook using OSX? The example files provided do not seem to work.

Any advice would be awesome.

Michael McLeish School of Biological Sciences Flinders University Bedford Park South Australia, 5042

Ph: 61-8-8201 5112 Fax: 61-8-8201 3015

michael.mcleish@flinders.edu.au

PostDocs

AMNatHist Bioinformatics

The American Museum of Natural History seeks candidates with expertise in computational science/bioinformatics for two 2 year postdoctoral positions. These positions are part of a larger federally funded project with the main goal of using genomic, phyloinformatic and biodiversity informatic approaches to develop retrospective and predictive hypotheses of the emergence of infections disease.

Algorithm Scientist: Ph.D. in computational science to perform research and implementation of algorithms for full-genome phylogenetic and biogeographic analysis. Experience in algorithm design , especially combinatorial optimization problems crucial. Experience in string and parallel algorithms, and computational biology, desired. Programming skills for prototyping necessary.

Systems Scientist: Ph.D. in computational science to perform R&D of a computational system to integrate results of whole genome phylogenetic analysis with geographic and phenotypic data. Experience in data modeling and development of middleware and user interfaces for large-scale data management across diverse research sites is crucial. Experience in geographic information systems important, programming skills in Java preferred. Contact: wheeler@amnh.org Very competitive salary and benefits.

Position available Fall 2005.

Send cover letter, CV, representative publications and names, addresses, phone numbers/e-mail addresses of 3 references to:

Dr. Ward Wheeler Division of Invertebrate Zoology American Museum of Natural History Central Park West at 79th Street New York, New York 10024 Ph: 212.759.5754 wheeler@amnh.org

Susan Perkins <perkins@amnh.org>

AMNatHist GenomicsGIS

The American Museum of Natural History seeks candidates with expertise in biogeographic analysis, Geographic Information Systems, and an interest in the evolution of viral pathogenecity for a 2 year postdoctoral position. The position is part of a larger federally funded project with the main goal of using genomic, phyloinformatic and biodiversity informatic approaches to develop retrospective and predictive hypotheses of the emergence of infections disease. This position entails some paid travel to coordinate with collaborators at the University of Colorado at Boulder.

Desired attributes: Ph.D. in biology Strong background and demonstrated ability in systematic and biogeographic theory Interest in genomic data of viruses in a biogeographical context Experience using Geographic Information Systems Excellent communication skills Ability to work independently and in team settings

Some programming knowledge, especially using Java or Python, is also desired but not necessary. Very competitive salary and benefits.

Position available Fall 2005.

Send cover letter, CV, representative publications and names, addresses, phone numbers/e-mail addresses of 3 references to:

Susan L. Perkins, Ph.D. Asisistant Curator, Microbial Systematics and Genomics Division of Invertebrate Zoology American Museum of Natural History Central Park West at 79th Street New York, New York 10024 Ph: 212.313.7646 Web: http://research.amnh.org/~perkins Susan Perkins <perkins@amnh.org>

AMNatHist ViralGenomics

The American Museum of Natural History seeks candidates with expertise in virology, particularly viral genomics, phylogenetics and evolutionary biology for a 2 year postdoctoral position. The position is part of a larger federally funded project with the main goal of using genomic, phyloinformatic and biodiversity informatic approaches to develop retrospective and predictive hypotheses of the emergence of infections disease.

Desired attributes: Ph.D. in biology Strong background and demonstrated ability in viral genetics/genome sequencing Interest in analysis of genomic data of viruses Experience in phylogenetic methods Excellent communication skills Ability to work independently and in team settings

Competitive salary and benefits.

Position available Fall 2005.

Send cover letter, CV, representative publications and names, addresses, phone numbers/e-mail addresses of 3 references to:

Susan L. Perkins, Ph.D. Asisistant Curator, Microbial Systematics and Genomics Division of Invertebrate Zoology American Museum of Natural History Central Park West at 79th Street New York, New York 10024 Ph: 212.313.7646 Web: http://research.amnh.org/~perkins Susan Perkins <perkins@amnh.org>

Bergen EvolEcol

*** 1 Post doc position in evolutionary ecology in Bergen, Norway ***

Position is available at the Institute of Marine Research in Bergen, Norway, to develop and analyse eco-genetic models of fisheries-induced adaptive change. This modelling framework aims at combining a realistic description of the ecological setting as well as population structure with a description of genetic detail at a level that would still allow predictions on rate of evolutionary change. Potential empirical interfaces include applications to cod, plaice, salmon and oysters.

The post is funded as part of a EU Marie Curie Research Training Network FishACE (Fisheries-induced Adaptive Change in Exploited Stocks). According to fellowship rules (see http://www.iiasa.ac.at/Research/ADN/FishACE/Positions.html), applicants must be of non-Norwegian nationality and must not have resided in Norway for more than 12 months in the last three years [notice that Norwegian citizens and residents can apply for positions in other teams in this network.] Skills in life history theory, ecological and evolutionary modelling and an interest in fisheries would be an advantage. The work will be carried out in collaboration with other teams in the network, facilitated by short research visits.

FishACE (http://www.iiasa.ac.at/Research/ADN/FishACE/) is an EU Marie Curie Research Training Network set up to investigate the prevalence and consequences of fisheries-induced adaptive changes in exploited aquatic systems in European waters. The network is coordinated by International Institute for Applied Systems Analysis in Laxenburg, Austria. There are altogether 11 network teams in 8 European countries. Besides training through research, the network provides tailored training courses on relevant methods and skills.

Institute of Marine Research (http://www.imr.no) is a national research centre affiliated with the Norwegian Ministry of Coast and Fisheries. The institute conducts research in the fields of marine environment, marine resources, and aquaculture. IMR, in its area, is one of the largest research institutes in the world, focusing on both applied and fundamental marine research. The main office of IMR is located in Bergen on the west coast of Norway. Bergen is a lively town with rich cultural life, and the surroundings offer excellent opportunities for all sorts of outdoor pursuits.

The postdoctoral position is initially for 18 months, with a possibility of an extension with 12 more months. Salary, which include travel and mobility allowances, follows the rates prescribed by EC and are competitive. Preferred starting date is in autumn 2005. The review of applications will start September 1 and continue until the positions are filled.

For more information, please contact Mikko Heino (http://www.imr.no/research/heino), preferably via e-mail (mikko@imr.no). An application, consisting of an application letter, curriculum vitae and two references, should be sent to the Personnel Section, Institute of Marine Research, P.O. Box 1870 Nordnes, NO-5817 Bergen, Norway. Mark the application with the reference number “34-05”. Please also submit an electronic copy of the application to Mikko Heino by email.

mikko.heino@imr.no mikko.heino@imr.no

CSIRO Canberra CitrusPhylogeny

We are seeking candidates to apply to work on the following project:

Title: A multilocus linkage group phylogeny of Citrus (Rutaceae: Limonioideae).

Project Background: The Citrus industry is one of the largest horticultural industries in the world and the breeding of new, high quality Citrus cultivars for the industry depends on reliable information about the relationships among the cultivated and wild Citrus species. Wild Citrus species are of interest to Citrus breeders as they possess genes that may provide a number of beneficial traits (e.g., disease resistance and new fruit characteristics). Although, Citrus fruits are the most widely cultivated tree fruit in the world, the evolutionary origins of many of the commercial classes of cultivars, i.e. lemons, oranges, limes, grapefruits, are unknown. As a consequence it has been exceedingly difficult to produce new cultivars by traditional hybridization/selection techniques, and it is therefore important to understand the relationships among the different species of the tribe for advancing breeding techniques and developing better conservation strategies for wild germplasm. Our current understanding of the group suggest that few of the cultivated species are true biological species [e.g., C. maxima (pummelo), C. medica (citron) and C. reticulata (mandarin / tangerine)], while many of the more widely known Citrus types [e.g., sweet oranges (C. sinensis), grapefruits (C. paradisi), lemons (C. limon), sour oranges (C. aurantium) and limes (C. aurantifolia)] are fixed hybrid biotypes derived from the “true” species that are maintained by vegetative reproduction. The chimeric nature of these hybrid Citrus genomes makes it impossible to apply standard phylogenetic strategies for determining historical genetic relationships.

Proposed Research: We propose to produce phylogenies based on sequences representing each arm of the nine chromosomes in the Citrus genome. The resulting phylogenies will help us determine the phylogenetic origin of each of the chromosomes arms of the of the various cultivar groups. >From this information we will be able to establish the origin of each linkage group in each of the cultivar groups, i.e., oranges, grapefruits, lemons, and limes. Rudimentary genetic linkage maps exist for Citrus. To date, 19 linkage maps have been constructed from a series of ten studies. These maps will form the basis for selecting appropriate sequences from each linkage group for sequencing and phylogenetic reconstruction.

Tenure: 3 years

Salary: $58K to $64K (Australian dollars)

Eligibility: International applicants welcome. To be eligible for a Postdoctoral Fellowship you will have received your Ph.D. after the 1st Jan 2003.

Closing Date for Application: 1 September 2005

For more information on application procedures contact: Dr. Randall Bayer, CSIRO, Plant Industry, Canberra, Australia. randy.bayer@csiro.au

Web link: http://recruitment.csiro.au/asp/job_details.asp?RefNo=2005/784

GaterslebenGermany StJohnsWort

A one-year post doctoral position is being funded by the DAAD (www.daad.de) to work in my laboratory on apomixis evolution in St John's wort (Hypericum perforatum).

St John's wort populations are composed of diploid sexual and/or tetraploid facultative apomictic (asexual reproduction through seed) forms. We are interested in understanding how and why apomixis has evolved in Hypericum, and how the expression of apomixis may be correlated with polyploidy and/or interspecific hybridization.

We have a large number of wild accessions growing in our greenhouses, in addition to a number of crosses between sexual and apomictic genotypes. We are furthermore generating a genetic map using AFLP and microsatellite markers, and are quantifying variation in the apomictic phenotype using flow cytometric seed screens. The post doctoral position would involve the analysis of microsatellite and SNP markers in the wild and crossing populations.

My lab is found at the IPK in Gatersleben (www.ipk-gatersleben.de), which is about 2 hours southwest of Berlin near the beautiful Harz mountains (http://www.nationalpark-harz.de/) where you can do lots of hiking, mountain biking and skiing. The IPK is a very well funded institute which is composed of a broad spectrum of research groups working on many different aspects of plant genetics.

The position is scheduled to start in May 2006.

If you are interested in the position, please don't hesitate to contact me for more information.

Best wishes from Germany! Tim

Dr. Tim Sharbel Apomixis Research Group Dept. of Cytogenetics Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK) Corrensstraße 3, D-06466 Gatersleben Germany

Apomixis Group Webpage http://www.ipk-gatersleben.de/en/02/04/05/index.html IPKWebpage www.ipk-gatersleben.de tel: +049 (0)3948 25608 fax: +049 (0)3948 25137

IndianaU EvolGenomicsHornedBeetles

Department of Biology Indiana University, Bloomington IN

Postdoctoral / Research Associate Position in Evolutionary Developmental Genomics of Horned Beetles

We are seeking a motivated individual for a new project applying functional genomics to study the evolutionary developmental genetics of horned beetles in the genus Onthophagus. We study beetle horns as an example of an evolutionary novelty that has undergone a tremendous amount of morphological diversification. We are developing the first genomic resources to explore the genomic basis of this diversification, which so far has only been studied using a target-gene approach. This project is an interdisciplinary collaboration between the labs of Justen Andrews (http://www.bio.indiana.edu/facultyresearch/faculty/Andrews.html) and Armin Moczek (http://www.bio.indiana.edu/facultyresearch/faculty/Moczek.html) and provides an outstanding opportunity to train across disciplines.

The immediate aims include developing a comprehensive EST library and microarrays to screen for differential gene expression in the context of horn development in alternative male morphs, sexual dimorphisms, and interspecfic differences in the type and location of horn growth. Consequently, the position suits candidates with a strong background in molecular biology and/or biochemistry, and a background in bioinformatics would also be advantageous. Additionally, since the project focuses on non-model organisms it will require a creative and independent researcher. We will provide substantial technical and conceptual support, however, the successful candidate will be expected to conduct significant amounts of work independently.

The research environment at IUB is outstanding and it is expected the successful candidate will participate in the scholarly activities of the Department as well as attending conferences, preparing manuscripts and contributing to grant applications. It should be noted that the campus is well equipped with the infrastructure required for the project (<http://cgb.indiana.edu/->http://cgb.indiana.edu/). Additionally the project will benefit from the concentration of arthropod genomics at IU including The Drosophila Genomics Resource Center (<http://dgrc.cgb.indiana.edu/>http://-/dgrc.cgb.indiana.edu/), the Daphnia Genomics Consortium <http://daphnia.cgb.indiana.edu/->http://daphnia.cgb.indiana.edu/), and the Center for Insect Genomics (<http://cgb.indiana.edu/-genomics/projects/18>http://cgb.indiana.edu/-genomics/projects/18).

The position is available immediately for 1-2 years contingent upon progress, and may possibly be extended to include a third year. Candidates must have a Masters or PhD degree in a suitable field and appropriate experience. Salary is $35-$40K (plus benefits) commensurate with experience. If you are interested, please email the Personnel Manager (malockha@indiana.edu) with a CV, statement of research interests, and the names, phone numbers and email addresses of three references. Please direct all inquiries about the position to Armin Moczek (<mailto:armin@indiana.edu>armin@indiana.edu). Women and minorities are particularly encouraged to apply. We will begin reviewing applications as soon as they are received and will continue to do so until the position is filled.

Indiana University is an Equal Opportunity / Affirmative Action Employer.

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

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

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

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MaynoothIreland ProkaryoticEvol

There is a position available for a post-doc to start immediately in James McInerney's research group at the National University of Ireland Maynooth. The research project centres on the analysis of horizontal gene transfer in prokaryotes and will run for a total of 23 months.

The laboratory is exclusively engaged in computational analysis of molecular data and the development of algorithms and software. More information can be found at: http://bioinf.nuim.ie/. Prospective candidates should have completed or be in the final stages of completing a PhD in bioinformatics and should have worked in the area of molecular evolution. The position will require the development of software and methods of analysis. Competence in a programming language is desired, although for exceptional candidates with little programming experience, there is the opportunity to take programming classes.

Salary: The position carries a salary of 36,506 Euro per annum, with an additional 8,980 Euro per annum being paid into a pension scheme, 3,924 Euro per annum being paid into national insurance and 1,825 Euro per annum being paid into other statutory schemes, including redundancy. The total remuneration comes to 51,236 Euro per annum.

Further details concerning the research project will be made available on application. Deadline for applications is August 19th. If interested, send a CV and covering letter to james.o.mcinerney@nuim.ie.

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

NESC Durham SabbaticalsWorkshops

Postdoctoral Fellows, Sabbaticals, and Workshops at the National Evolutionary Synthesis Center

The National Evolutionary Synthesis Center (NESCent) is a new NSF-funded center in Durham, North Carolina. Our Center represents a collaborative effort by three Universities in North Carolina's Research Triangle: Duke, NC State, and UNC-Chapel Hill. Our goal is to help foster a grand synthesis of the biological disciplines through the unifying principle of descent with modification.

NESCent announces a call for proposals for Postdoctoral Fellows, Sabbaticals, and two kinds of workshops (Catalysis Meetings and Working Groups). NESCent will be targeting 7 postdocs, 5 sabbatical faculty, and 4 groups. Proposals are welcome from scientists of all nationalities and successful applicants will join our onsite community of scientists as well as interacting with many visiting working groups. The range of activities supported by the center will include ambitious efforts to synthesize existing data from a wide range of disciplines, database development and exploitation, and theoretical research of all kinds.

Postdoctoral Fellows will be supported for two years at a salary of $36 K per year plus research expenses. Sabbatical fellowships fall under two categories: "traditional" half-salary fellowships; and our novel "targeted sabbatical" program. Targeted full-salary fellowships will support individuals committed to increasing the number of applicants to evolutionary biology programs from Minority Serving Institutions. Each researcher will have a primary project of their own design, but as a whole the group will have a great deal of "free energy" to take advantage of new opportunities for synthesis and collaboration as they arise.

Cross-Disciplinary Network Catalysis Meetings are one-time meetings to bring together ˜ 30 scientists from diverse disciplines to focus on a major question or research area. These meetings are intended to identify avenues for synthesis, and classes of primary data that must be collected before grand-scale synthesis is possible. These meetings are intended to increase the scale and ambition of our scientific vision.

Working Group Meetings involve small groups of scientists (10-12 participants) collaborating intensively on the analysis or synthesis of data, models or both, to address a major question in evolutionary biology, or to solve a particular analytical problem. NESCent will not fund collection of new data or field research, but encourages the mining of public and private databases.

The deadline is October 15 for positions and groups beginning in the Summer or Fall of 2006. For complete application instructions and other details, please visit our website at www.nescent.org. Duke University is an Equal Opportunity Employer.

Karen Henry Assistant Director of Research Administration National Evolutionary Synthesis Center 605 Broad Street Durham, NC 27705

email: khenry@duke.edu telephone: 919-286-5706 fax: 919-286-5753

Karen Henry <khenry@duke.edu>

OhioStateU EvolMath

The Mathematical Biosciences Institute (MBI) at The Ohio State University is accepting applications for postdoctoral positions to start September, 2006, which are renewable for up to 3 years. Some positions are cosponsored by industry or academic bioscience labs. The deadline for applications is January 18, 2006. Short- and long-term visitors may apply at any time. To access the application form or for more information, visit the MBI website at http://mbi.osu.edu or call (614) 292-3648.

Kimberly Ann Holle, MSW, MS, LSW, LCDC-III Program Specialist Mathematical Biosciences Institute The Ohio State University 231 West 18th Avenue, #250-A Columbus, Ohio 43210-1174 (614) 292-5755 - phone (614) 247-6643 - FAX E-mail: kimberly@mbi.osu.edu http://mbi.osu.edu Kimberly Holle <kimberly@mbi.ohio-state.edu>

SantaBarbara BeetlePhylogeography

[This is a final posting for this position, which was originally posted without an application deadline.]

Postdoc: Comparative phylogeography and faunistics of California beetles

The Santa Barbara Museum of Natural History is seeking a postdoctoral researcher to participate in an NSF-funded survey of beetles in southern California. The project includes field inventory, databasing, and comparative phylogeography. The postdoc will have primary responsibility for phylogeographic study, and will play an active role in field surveys and project outreach.

The ideal candidate will have a strong background in molecular phylogenetics, with some experience in intraspecific studies. A candidate with taxonomic expertise in a beetle group found in the region will be preferred, though specialists in other terrestrial arthropod taxa will be considered. Experience with collections based research is also desireable. The candidate's Ph. D. must have been completed prior to start date. The position is available for up to two years.

Mail or fax CV, description of interests/qualifications, and names and contact details for two references to: Human Resources EntPD, Santa Barbara Museum of Natural History, 2559 Puesta del Sol Rd., Santa Barbara, CA 93105; FAX (805) 569-3170. A more detailed job description is posted at www.sbnature.org/-visitors/hr.php. For additional information email Dr. Michael Caterino at mcaterino@sbnature2.org. Applications must be received by September 1, 2005. EOE

– Michael S. Caterino Curator of Entomology Santa Barbara Museum of Natural History 2559 Puesta del Sol Rd. Santa Barbara, CA 93105-2998 USA Phone (805) 682-4711 Ext. 151 FAX (805) 563-0574 http://www.sbnature.org/collections/invert/entom/-cbphomepage.php mcaterino@SBNATURE2.ORG

mcaterino@SBNATURE2.ORG

UAlbany PhageLifeHistory

Postdoc: Evolution of bacteriophage life history traits

A postdoctoral position is available to work on an NIH funded project on the evolution of bacteriophage life history traits.

This project includes: (1) investigation of bacteriophage life history traits using phage competition experiment in tube culture and continuous cellstat culture, (2) molecular population genetics of phage lysis cassettes, and (3) experimental protein evolution of bacteriophage holin protein.

This project will be performed in the newly constructed Life Science Research Building, with fully equipped research core facilities, including molecular (sequencing, real-time PCR), cell biology (various imaging facilities), fermentation, computation, NMR, and tissue culture.

Individuals interested in using bacteriophage as an experimental system to study ecological and evolutionary questions and would like to obtain diverse training opportunities are welcomed to apply. To apply, please send a CV, a short statement of research interests, and three recommendation letters to:

Ing-Nang Wang Assistant Professor Dept. of Biological Sciences University at Albany State University of New York 1400 Washington Ave. Albany, NY 12222

Phone: (518) 437-3704 (O) (518) 442-4382 (L) Fax: (518) 442-4767 email: ingnang@albany.edu

UAmsterdam PlantEvolGenetics

The Experimental Plant Systematics group of the University of Amsterdam is hiring a plant evolutionary geneticist to work on genetic variation and adaptation in Draba and Rorippa species (postdoc, 2.5 years).

You can read the details at: http://www.uva.nl/-vacatures/object.cfm/objectID=C88CBE53-B962-401F-8A8F223460399834

Regards, Peter van Tienderen Institute for Biodiversity and Ecosystem Dynamics Univerrsity of Amsterdam

tiendere@science.uva.nl

UArizona InsectEvol

Postdoc: Center for Insect Science University of Arizona Postdoctoral Fellowships–Review of applications will begin on August 17, 2005 for positions beginning fall, 2005 and spring, 2006.

Postdoctoral Excellence in Research and Teaching (PERT) offers up to three years of support to outstanding candidates seeking advanced research training in insect science and preparation for the additional demands of an academic career. Trainees may receive up to three years of support. Each trainee will participate in several PERT program components designed to prepare trainees to be successful in tenure track academic positions. Because the demands of an academic career include research productivity, teaching, and service, the following activities will be required of all trainees:

*RESEARCH training is available under the supervision of one or more participating CIS faculty members in a wide range of academic units. Detailed descriptions of CIS faculty research can be obtained from individual web pages for participating faculty listed at the bottom of this announcement. Collaborative, interdisciplinary research is encouraged. Applicants are encouraged to contact prospective research mentors as early as possible in the application process. Each trainee will receive $6,000 in research funds, $1500 for travel, and use of a laptop computer. The Center for Insect Science provides a rich environment for research training through regular seminars, data blitzes, Visiting Distinguished Scientist series and Hexapodium events.

*TEACHING skills will be developed through participation in a two semester science pedagogy program simultaneously with trainee research. Flexibility exists with respect to which two semesters will be the pedagogy semesters for each trainee. During one semester, each trainee will attend a three credit hour course in science pedagogy at the University of Arizona. The pedagogy course involves the development of a single original undergraduate laboratory exercise using insects and feedback on teaching proficiency. In a subsequent semester, the trainee will teach one undergraduate course and laboratory section at Pima Community College (PCC), near the University of Arizona, under the direction of a PCC teaching mentor.

*MENTORING skills will be developed through the supervision of a research project by a minority undergraduate student from PCC. Undergraduate research projects may be subcomponents of the trainee's own research.

*SERVICE to the CIS community will involve the PERT seminar series in which trainees select, invite and host a distinguished insect scientist to deliver a special seminar each semester at the University of Arizona.

*SURVIVAL SKILLS will be shared with trainees through special workshops dealing with grant writing, the job application process, promotion and tenure strategies and the integration of research, teaching, and service in an academic career. Workshops will utilize the strengths of the CIS faculty, including members of the National Academy of Sciences, MacArthur Fellows, Regents' Professors and other distinguished scientists.

*SALARIES for postdoctoral trainees begin at $31,092/year. Trainees will be eligible for full university benefits including medical and dental insurance.

Applicants must have a Ph.D. in a related field and must be U.S. citizens or permanent residents. Applicants must have less than two years of previous postdoctoral experience.

Apply electronically through the University of Arizona Career Track website at: https://www.uacareertrack.com, citing job #32236. All applications should include the following:

1. A letter of application that includes a statement as to how the PERT program will assist the applicant in attaining her/his career goals 2. C.V. 3. Three letters of reference 4. A three to six page research proposal, developed with the intended PERT research mentor describing the project to be undertaken during the training period 5. A letter of support from the intended PERT research mentor

The 3 letters of reference and letter of support from the intended research mentor should be mailed to: PERT Program Center for Insect Science 1007 E. Lowell Street P.O. Box 210106 University of Arizona Tucson, Arizona 85721-0106

All other materials above should be submitted electronically.

Review of applications will begin on August 17, 2005 for positions beginning fall, 2005 and spring, 2006.

For more information, please contact Teresa Kudrna, tkudrna@email.arizona.edu, 520-621-4923.

– Nancy A. Moran

Regents' Professor Department of Ecology and Evolutionary Biology University of Arizona Tucson Arizona 85721

nmoran@email.arizona.edu

tel 520-621-3581 fax 520-621-9190

nmoran@u.arizona.edu nmoran@u.arizona.edu

UCBerkeley IslandSpiders

Postdoctoral Position

Evolution and adaptive radiation of Pacific island spiders

A postdoctoral position is available to study diversification patterns of various different spider groups in the islands of the Pacific (including the Hawaiian Islands, French Polynesia, Micronesia, and Fiji).

Specific objectives of the project are to understand patterns of diversification within and between island systems, and to assess the role of factors such as priority/ exclusion, immigration/ speciation, shifts in ecology/ morphology, and interactions of species over space and time. We are looking for a postdoctoral researcher to participate in all aspects of the project, including field and laboratory work. Applicants should have familiarity with molecular techniques (DNA amplification and sequencing, microsatellites, etc), an aptitude for fieldwork in remote locations, and an interest in island biology. The islands on which we are currently focusing include Hawaii, Societies, Marquesas, Australs, Fiji, Tonga, Samoa, Pohnpei, Kosrae, Chuuk, and Palau. Some familiarity with spiders is preferred but not required.

The person will be based in the joint laboratory of Professors Rosemary Gillespie and George Roderick (see http://nature.berkeley.edu/evolab/) and in the Berkeley Natural History Museums (http://bnhm.berkeley.edu/).

Funding is available for two years, beginning September 2005. Please send inquiries and applications to Rosemary Gillespie at gillespi@nature.berkeley.edu. Applications should include a cover letter describing your research interests, a CV, and names of three references.

– Rosemary G. Gillespie, Director, Essig Museum of Entomology, Professor, Insect Biology, University of California Berkeley, 201 Wellman Hall, Berkeley, CA 94720-3112. Tel 510-642-3445 Fax 510-642-7428 email: gillespi@nature.berkeley.edu http://nature.berkeley.edu/˜gillespi/ http://essig.berkeley.edu/ gillespi@nature.berkeley.edu gillespi@nature.berkeley.edu

UCD Dublin FishGenetics

Post-Doctoral Position in Marine Fisheries Genetics - UCD Dublin, Ireland

Applications are invited for a 2-year postdoctoral position in the School of Biological & Environmental Science at UCD Dublin, working with Dr Stefano Mariani in a newly-established group focusing on the evolutionary ecology and fisheries genetics of marine animals. The research is funded by BIM, the Irish Marine Fisheries Board, and is aimed at understanding the patterns of stock structure of the common whelk (Buccinum undatum) in Irish waters, using molecular genetic markers. The project will also look at the factors underlying the marked variation in shell morphology observed among whelk populations, by rearing wild-caught animals under "common garden" conditions. The ideal candidate should possess a PhD in empirical population genetics or evolutionary biology, though we welcome applicants from other disciplines such as ecology or marine biology. Proficiency in molecular laboratory techniques would be very advantageous, as would some experience of morphological analyses. A strong commitment to timely publication and interdisciplinary research is critical. The appointee will join the Marine Biodiversity, Ecology & Evolution Group and the Molecular Genetics Lab, which together comprise 11 PhD students, one Post-doctoral fellow and three academic staff, working on a broad range of topics from comparative genomics, molecular phylogenetics and population genetics, to fisheries science, community ecology and ecosystem management.

Application procedure: Please send a 1-page covering letter and a CV no longer than 3 pages, plus names and emails of three people who can be contacted for references, to: stefano.mariani@ucd.ie Closing date for applications: 30th September (interviews in mid october). Project start date: 1st December. Salary: in excess of 36,000 per annum. Committed to Equal Opportunities.

Feel free to contact me for any further information about the project and related issues.

Best,

Stefano Mariani

Dr Stefano Mariani MARine Biodiversity, Ecology & Evolution School of Biological & Environmental Science University College Dublin Belfield Dublin 4 Republic of Ireland tel. +353.1.716.2347 fax. +353.1.716.1152 http://www.ucd.ie/zoology/mariani/ stefano.mariani@ucd.ie

UEdinburgh WaspPopGenetics

A 2-year NERC-funded post-doc is available at the Institute of Evolutionary Biology of the University of Edinburgh (Salary scale: £19,640 - £29,128 pa)

START DATE JANUARY 1 2006

The successful applicant will work on the population genetic structure of natural populations of parasitoid wasps. The project will focus on the chalcid communities associated with oak cynipid galls, and use mtDNA sequences and microsatellites (1) to assess the extent to which parasitoid populations are structured by host gall traits, and (2) to infer the mechanisms by which parasitoids recruit to invading gallwasp hosts. The project will make use of existing samples, but there will also be opportunities for involvement in fieldwork. The project will be supported by a full time technician, and will use new lab and automated ABI genotyping facilities at IEB. Applicants must have a Ph.D. in a relevant field, with experience in the use of automated genotyping and in the analysis of population genetic datasets. The applicant will be expected to have considerable experience in the screening of microsatellite markers and their analysis, and to have project management skills. Interest in entomology is an advantage.

This project is in collaboration with Dr. Karsten Schönrogge at the NERC Centre for Ecology and Hydrology, Winfrith, Dorset U.K.

Fixed term: up to 2 years Salary scale: £19,640 - £29,128 pa Please quote Ref: 3004856 Closing date: 15 September 2005

For more information and to apply please follow this link: https://www.jobs.ed.ac.uk/jobs/-index.cfm?action=jobdet&jobid=3004856 And for more information about my research see http://www.homepages.ed.ac.uk/amegilla/home

All formal applications must be made via the Edinburgh jobs website above, but feel free to contact me directly for further details or if you have any questions.

PLEASE IGNORE the incorrect start date, if still present, of September 1st 2005 on the Edinburgh jobs web page! The start date for the post is Jan 1st 2006.

Graham Stone Institute of Evolutionary Biology School of Biology University of Edinburgh Edinburgh EH9 3JT Scotland UK Tel: (+44)(0)131 650 7194 Fax: (+44)(0)131 650 6564 http://-www.homepages.ed.ac.uk/amegilla/home

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UIdaho SpottedKnapweed

Postdoctoral position, to investigate the ecology and systematics of endophytes in Centauria maculosa, spotted knapweed, in its native and introduced ranges, and to play a leading role in collaborative study. Controlled greenhouse experiments to determine interactions among plants, endophytes, and insects will be conducted. Molecular systematics of endophytic fungi in the introduced and host ranges will be examined. On line application required, at www.hr.uidaho.edu. See Announcement #12508005483. Review of applications will continue until the position is filled. For further information, contact Dr. George Newcombe, email: georgen@uidaho.edu ; tel : 208 885 5289.

The University of Idaho does not discriminate against an individual with a disability in regard to job application procedures, the hiring or discharge of employees, employee compensation, advancement, job training, and other terms, conditions, and privileges of employment.

Cort L. Anderson Laboratory for Ecological and Conservation Genetics College of Natural Resources P.O. Box 441136 University of Idaho Moscow, ID 83844

tel: 208 885 8914 fax 208 885 9080 email: cla@uidaho.edu

“Cort L. Anderson” <cla@uidaho.edu>

UManchester ArabidopsisAdaptation

A 3 year position as Post-doctoral researcher is available at the University of Manchester (UK) to study the molecular basis of adaptation in Arabidopsis thaliana.

This NERC funded project will involve performing selection for early flowering on an outbred population of A. thaliana. Molecular response will be monitored genomewise using SNPs ; and correlated responses at the phenotypic level will be evaluated by measuring a number of life-history traits. This project is collaboration with Drs. Barbara Schaal, Jim Cheverud and Michael Purugganan

The ideal candidate will have previous experience in quantitative genetics and/or population genetics. Demonstrated skills in writing and analyzing data needed, Experience with molecular genetics would be a plus. Start date is somewhat flexible, but no later than Jan 15th 2006.

The University of Manchester has a strong group in

Evolution and bioinformatics. The city of Manchester offers both a lively urban life and easy access to and from the countryside.

Interested candidates should send CV, relevant publications, and the names of two people that can write letters of references by email to : kover@manchester.ac.uk

Feel free to contact me if any further information is required,

Dr. Paula X. Kover University of Manchester School of Biological Sciences Stopford Building 3.614 Oxford Road, Manchester M13 9PT - UK Tel.: 44-(0)161-2751550 Fax: 44-(0)161- 2753938

“Paula X. kover” <paula.X.Kover@manchester.ac.uk>

UStellenboschSA EvolGenetics

Post Doctoral position available in the Department of Genetics, University Stellenbosch, South Africa (23 Aug 2005)

A Post Doctoral position in molecular genetics is available in the Aquaculture Division, Department of Genetics, Stellenbosch University with the project title “Genetic improvement of the abalone, Haliotis midae.”

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

The successful candidate will be primarily responsible for developing EST and SNP markers in the abalone species, Haliotis midae. Only a few ESTs are available for Haliotis and other mollusk species; therefore this project will be the first large-scale development of ESTs in a Haliotis species. SNPs identified within the ESTs will be used to generate a genetic map of Haliotis midae together with other markers such as AFLPs and microsatellites. Novel genes identified could also be applied in future gene-transfer technology in Haliotis midae. Candidate should have a strong background in molecular genetics with applicable knowledge in cDNA technology. Practical experience in RNA isolation, reverse transcription-PCR, cDNA library construction and automated sequencing is a prerequisite. A sound knowledge of sequence analysis or related biostatistical software is advisable. The position is available for 2 years

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

Closing date: 30 September 2005.

Dr. Rouvay Roodt-Wilding Aquaculture Division Department of Genetics JC Smuts Building Room 213 University of Stellenbosch Private Bag X1 Matieland SOUTH AFRICA 7602 Tel: +27 (0) 21 808 5831 Fax: +27 (0) 21 808 5833

I'm not afraid of storms, for I'm learning to sail my ship. Louisa May Alcott

WoodsHole EvolGenomics

The Marine Biological Laboratory in Woods Hole, Mass. is seeking applicants for a full-time POSTDOC POSITION in the Josephine Bay Paul Center in Comparative Molecular Biology and Evolution. This position is available immediately as part of the Center?s Global Infectious Disease Program. Project will explore comparative genomics, molecular diversity, and evolution of virulence in host-associated bacteria.

For more information, please see:

http://www.mbl.edu/inside/what/human_resources/-job_search.php?func=detail&par=job_id=424

Jennifer Wernegreen <jwernegreen@mbl.edu>

WorkshopsCourses

CamarinoItaly microarray workshop Sept19-21

THere are still places available for the microarray and molecular ecology workshop to be held 19-21 Sept in Camarino Italy register at this website http://-web.unicam.it/micropad/public/workshop.asp – thank you for your consideration

Dr. Linda Medlin Alfred Wegener Institute Am Handelshafen 12 D-27570 Bremerhaven Germany New Telephone Number and Fax Number below

Tel. 49-471-4831-1443 Fax. 49-471-4831-1425 see my homepage for latest trees etc. http://www.awi-bremerhaven.de/Biomeer/molecular-genetics-e.html Wise words of the day "Those who do not stop asking silly questions become scientists." -Leon Ledermen, physicist

"A 'No' uttered from deepest conviction is better and greater than a 'Yes' merely uttered to please, or what is worse, to avoid trouble." - Mahatma Gandhi

linda medlin <lkmedlin@awi-bremerhaven.de>

East Asia Summer Institutes

Course: Graduate Students: 2006 East Asia Summer Institutes Program (EAPSI)

The EAPSI provide U.S. graduate students in science and engineering first-hand research experience in Australia, China, Japan, Korea, or Taiwan, an introduction to the science and science policy infrastructure of the respective location, and orientation to the culture and language. The primary goals of EAPSI are to introduce students to East Asia and Pacific science and engineering in the context of a research laboratory, and to initiate personal relationships that will better enable them to collaborate with foreign counterparts in the future. The institutes last approximately eight weeks from June to August and are administered in the United States by the National Science Foundation (NSF). The National Institutes of Health (NIH) co-sponsor the Summer Institute in Japan.

Please note that the new EAPSI website www.nsf.gov/-eapsi is now a portal for all information regarding the EAPSI. The help desk for all questions and concerns is (eapinfo@nsf.gov) but the new website should better serve potential applicants and hosts.

The deadline for applying to the 2006 EAPSI program is December 13, 2005.

Contact for more information:

Tony Teolis Program Specialist Office of International Science and Engineering National Science Foundation Tel: 703-292-7343 ateolis@nsf.gov

"Courtney, Mark W." <mcourtne@nsf.gov>

OnlineCourse EvolutionaryComputation

On-line course offering: ICS 682: Evolutionary Computation (Numerical Methods), Faculty: Prof. Lee Altenberg Department of Information and Computer Sciences, University of Hawaii at Manoa.

There are a number of seats available through the Outreach College at the University of Hawaii at Manoa for the on-line graduate level course in evolutionary computation that I am offering for this semester. This course will be an introduction to the field of evolutionary computation (genetic algorithms, evolution strategies, evolutionary programming, genetic programming, artificial life), geared to getting the student involved in research in the field as quickly as possible. This is a condensed 10 week course running September 12 to November 19, 2005. So, students will be done in time to focus on finishing up their local campus courses.

Course work will consist of a research project, class discussions, and readings from the texts:

Evolutionary Computation 1: Basic Algorithms and Operators, ed. T. Back, D. B. Fogel and T. Michalewicz, Institute of Physics Publishing, Bristol and Philadelphia. ISBN 0-7503-0664-5. 2000.

How To Solve It: Modern Heuristics, by Zbigniew Michalewicz and David B. Fogel, Springer, ISBN 3-540-66061-5. 2000.

Research projects can be on applications, theory, history, or empirical studies of evolutionary algorithms. The goal is that the student's project be published in one of the many proceedings or journals on evolutionary computation. The course is entirely Web- based, using the WebCT system, and asynchronous, except for deadlines on submissions.

This fall's introductory course will be followed in the Spring 2006 semester by an in-depth course on Genetic Programming, which is the application of evolutionary approaches to the engineering of executable programs.

The listing is at:

http://myuh.hawaii.edu/pls/uhdad/avail.class?i=-MAN&t=200613&c=1103

and the catalog of online courses is at:

http://myuh.hawaii.edu/pls/uhdad/avail.classes?i=-MAN&t=200613&s=ICS

A guide to registration is at:

http://www.outreach.hawaii.edu/myuh/-quick_guide.asp Additional information is available at my Web site,

http://dynamics.org/UH_ICS/ The course runs 10 weeks from September 12 to November 19. Questions about the course can be e-mailed to me directly.

Best regards, Dr. Lee Altenberg

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Lee Altenberg, Ph.D. Associate Professor, Information and Computer Sciences University of Hawai'i at Manoa Phone: (808) 875-0745, Fax: call to arrange E-mail: altenber@hawaii.edu, altenber@santafe.edu Web: http://dynamics.org/Altenberg/ Lee Altenberg <altenber@santafe.edu>

WesterheverGermany PhDstudents EvolofBiodiversity Sep19-21

Workshop: Evolution and Ecology of Biodiversity

PhD workshop Lighthouse of Westerhever, Germany Sept. 19 ? 21. 2005

PhD students working on evolutionary or ecological aspects of biodiversity are invited to apply for participation in a workshop on ?Evolution and Ecology of Biodiversity?.

Focusing on recent, ongoing projects and even plans, the workshop will give ample opportunity for discussion in a small group, together with Andy Purvis (London, UK) and Sarah Jackson (Sheffield, UK), two experts in this field of research. We will stay directly at a beautiful lighthouse at the North Sea. The program will also comprise a guided tour into the wadden sea. See http://www.uni-kiel.de/ zoologie/institut/limnologie/evolecol.htm for further information and a flyer for download.

The workshop will begin Monday morning (Sept. 19.) and end Wednesday evening (Sept. 21.). Westerhever is in the very north of Germany. We will organize travel from Kiel, so it is most convenient if you travel to Kiel on Sunday (Sept. 18). 100 Euro per person are requested as a contribution to food and accommodation.

Please send applications, including title and abstract (< 200 words) of your presentation, until Aug. 22. to mzimmer@zoologie.uni-kiel.de

Martin Zimmer (Uni Kiel) & Joachim Kurtz (ETH Zurich)

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Dr. Joachim Kurtz

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Phone: + 41 44 633 6032 Fax: + 41 44 632 1271

E-mail: joachim.kurtz@env.ethz.ch

WWW: http://www.eco.ethz.ch http://www.mpil-ploen.mpg.de/english/evoleco/staff/ kurtz.htm

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Joachim Kurtz <joachim.kurtz@env.ethz.ch>

Instructions

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

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

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

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

Afterward

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