
E v o l D i r

July 1, 2005

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

Forward

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

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

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Conferences

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BethesdaNIH EvolutionInfectiousDiseases Jul13-15

The National Institute of General Medical Sciences, NIH, DHHS, is hosting a symposium entitled Evolution of Infectious Disease, July 13-15, 2005, in Bethesda, MD at the Hyatt Regency Hotel in downtown Bethesda. The meeting will begin with a reception on the evening of July 13, and the scientific presentations will begin the morning of July 14. The meeting organizers, Dr. Howard Ochman and Dr. Holly Wichman, have scheduled outstanding presentations on new research in the field and made sure there is ample time throughout the meeting for conversation and discussion.

The meeting agenda focuses on understanding basic principles of evolution using infectious diseases as models and employing knowledge from computational sciences and mathematics in addition to infectious disease biology. This symposium will be an opportunity to share knowledge and resources and to define important questions for future interdisciplinary research in the field.

The meeting website is http://pub.nigms.nih.gov/generic_meeting/location.cfm?id=8 <http://pub.nigms.nih.gov/generic_meeting/location.cfm?id=8&lid=4> &lid=4

We are excited that the Burroughs-Wellcome Fund has offered \$500 travel scholarships to undergraduate and graduate students and postdoctoral fellows. The form for requesting these scholarships is on the meeting Web site.

Please check out the Web site, and if you still have questions, feel free to contact

Howard Ochman Meeting Organizer
(520) 626-8355 hochman@email.arizona.edu
<mailto:hochman@email.arizona.edu>

Holly Wichman Meeting Organizer
(208) 885-7805 hwichman@uidaho.edu
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Irene Anne Eckstrand NIGMS Meeting Li-
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<mailto:eckstrai@mail.nih.gov>

Saundra Bromberg Logistics Consultant (301) 468-
6004 , ext. 406 sbromberg@md.capconcorp.com
<mailto:sbromberg@md.capconcorp.com>

Irene Anne Eckstrand, Ph.D. Division of Genetics and
Developmental Biology Center for Bioinformatics and
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6200 20892-6200 Bethesda, MD

Tel: 301-594-0943 Email:
<mailto:eckstrai@mail.nih.gov> eckstrai@mail.nih.gov
Web: <<http://www.nigms.nih.gov>>
www.nigms.nih.gov

“Eckstrand, Irene (NIH/NIGMS)”
<ECKSTRAI@nigms.nih.gov>

ESEB GenomeEvol

This is to let people know that the timetable of talks for this symposium, and the selected talks, should now

(or soon) be on the meeting web site.

Our 'symposium' was heavily over-attended, but the organisers kindly gave us an extra allocation of time, so we now have two sessions planned, on both Friday (August 19th) and on the Saturday morning. However, there was still not enough time in the schedule to include the many very interesting talks that were offered. We apologise to those who are disappointed, but the good thing about this situation is that there is a large number of very interesting posters as well as talks, and there should be good opportunities for discussions of topics in genome evolution, so we do hope that people who had hoped to give a talk will still be willing to come and show a poster instead.

If anyone listed to give a talk does not wish to give a talk after all, we would be grateful if they would email me (DC, email below) as soon as possible, as we should like to offer their time slot to someone else.

Deborah and Brian Charlesworth

–

– Professor Deborah Charlesworth Institute of Evolutionary Biology, School of Biological Sciences, University of Edinburgh, Ashworth Lab., King's Buildings, West Mains Rd., Edinburgh EH9 3JT, UK

phone 131-650-5751 Fax: 131-650-6564 Deborah Charlesworth <deborah.charlesworth@ed.ac.uk>

Fribourg ParasiteResistance Oct3-4

SYMPOSIUM: EVOLUTIONARY ECOLOGY OF PARASITE RESISTANCE AND TOLERANCE IN PLANTS AND ANIMALS (3-4 October 2005, Fribourg/Switzerland)

Dear colleagues,

this is to remind you that the deadline for abstract submissions is July 8, 2005.

It is also possible to participate in the symposium without giving a talk (registration deadline: September 2).

See <http://www.unifr.ch/biol/ecology/resistevoeco> for more information.

In this symposium, we will discuss recent progress in the study of the evolution of resistance and tolerance to parasites (herbivores, fungal and bacterial pathogens, arthropods etc.) in both plants and animals.

Invited speakers: - Janis Antonovics (University of Virginia, USA) - Yannis Michalakis (CNRS, Montpellier, France) - Paul Schmid-Hempel (ETH Zurich, Switzerland) - Michael Siva-Jothy (University of Sheffield, UK) - Sharon Strauss (UC Davis, USA) - Peter Tiffin (University of Minnesota, USA)

Best regards,

Thomas Steinger (thomas.steinger@unifr.ch) Dieter Ebert (dieter.ebert@unibas.ch) Heinz Müller-Schärer (heinz.mueller@unifr.ch)

thomas.steinger@unifr.ch thomas.steinger@unifr.ch

Naples Malacology Oct10-14

Dear Colleagues, You are invited to attend the

IV International Congress of the European Malacological Societies Naples, Italy October 10-14 2005 Organized by the Italian Society of Malacology in synergy with the Zoological Museum of the University of Naples.

These are the topics:

- Molluscan Systematics - Molecular Systematics and Phylogeography of Molluscs - Molluscan Reproduction and Development - Molluscan Ecology, Biodiversity and Conservation - Molluscan Aquaculture and Exploitation - Molluscan Paleontology - Open session

There is also a special topic (posters and lectures) on: "Molecular Systematics and Phylogeography of Mollusks".

The deadline for submission registration form is 30 June 2005. Abstracts must be submitted up to 30 July 2005.

For detailed info and registration see the Congress website at <http://www.4cisme.org> If you have any questions, please contact us:

for the mollusks molecular session Francesco Paolo Patti fpatti@szn.it

for the other topics and for more general informations Paolo Crovato paolo.crovato@fastwebnet.it

Thank you! –

Dr. Francesco Paolo Patti, Ph.D.

Benthic Ecology Lab Zoological Station "A. Dohrn" Punta S. Pietro 1 80077 Ischia Porto, Naples, Italy +39 (081) 5833-507 phone +39 (081) 984201 fax E-

mail: fpatti@szn.it

Lecturer in Marine Biology University of Viterbo, Rome
Marine Genomics Europe EDD EG WP-2 coordinator

NaturalHistoryMusLondon Speciation Nov9

Half-day symposium on Speciation

9 November 2005

The Natural History Museum, Cromwell Road, London
Ralph Harbach and I are now organising a second Speciation Symposium, following the success of a meeting in 2003, to be held in the Flett Theatre on the afternoon of 9 November.

The programme this year will include an invited presentation by Dr Patrik Nosil, Simon Fraser University, on 'Divergent selection and gene flow interactions during the evolution of reproductive isolation between walking-stick populations' (provisional title).

The programme will also include talks by NHM scientists and there will be some space in the programme for contributed papers. If you are interested in making a presentation, please send me a provisional title as soon as possible, and certainly before 20 July.

If you would like to attend but not give a presentation, just make a note in your diary. Registration is not required but we will try to get an idea of numbers nearer the time.

Roger Butlin Professor of Evolutionary Biology

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

r.k.butlin@sheffield.ac.uk

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

Oslo HennigSociety July25-29 Deadline July1

24th MEETING of the WILLI HENNIG SOCIETY

**DEADLINE for REGISTRATION and ABSTRACT

SUBMISSION is 1 July 2005**

25-29 July 2005 in the mountains north of Oslo, Norway

- Oral and poster; can fit in topically with preliminary symposia, or be on other topics of phylogenetic interest. All effort will be made to include non-symposium oral presentations: first-come, first-served.

- Oral presentations: when registering (see below), please suggest amount of time requested, and every effort will be made to accommodate.

PRELIMINARY SYMPOSIUM PROGRAM

- Phylogenomics (organized by David Liberles and Jens Lagergren)

- Ancient DNA (organized by Lutz Bachmann)

- Lower-level Phylogenetics of Angiosperms (organized by Victor Albert)

The Willi Hennig Society strongly encourages participation from students and postdocs on their developing research, either theoretical or empirical. There are several cash student prizes that will be awarded.

REGISTRATION AND ABSTRACT SUBMISSION

http://folk.uio.no/victoraa/Frontpage_files/-slide0003htm

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

Oslo HennigSociety July25-29 LAST NOTICE

.....LAST NOTICE.....

24th MEETING of the WILLI HENNIG SOCIETY

DEADLINE for REGISTRATION and ABSTRACT SUBMISSION is 1 July 2005

SYMPOSIUM PROGRAM

- Phylogenomics (David Liberles, Jens Lagergren, Maria Anisimova, Victor A. Albert, Lars Arvestad, and Marie Skovgaard)

- Ancient DNA (Lutz Bachmann, Thomas Borge, Sangtae Kim)

- Lower-level Phylogenetics of Angiosperms (T.B.A.)

- Other papers and posters, T.B.A. on the site below after all submissions are registered

The Willi Hennig Society strongly encourages partici-

pation from students and postdocs on their developing research, either theoretical or empirical. There are several cash student prizes that will be awarded.

****REGISTRATION AND ABSTRACT SUBMISSION****

<http://folk.uio.no/victoraa/Frontpage.files/-slide0003htm> victor.albert@nhm.uio.no

<http://www.lirmm.fr/MEP05/> Moreover, based on survey papers presented at the first Mathematics of Evolution and Phylogeny conference (2003), this book is now available

<http://www.lirmm.fr/~w3ifa/MAAS/OUP-Book.html>
gascuel@lirmm.fr

Paris MathOfEvol Jun17-21

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

The subject is evolution, which is considered at different scales: sequences, genes, gene families, organelles, genomes, and species. The focus is on the mathematical and computational tools and concepts. There will be presentations by some of the leading experts in the field. The goal of the conference is to provide pedagogical presentations of the main subjects in the field, from basic principles to the cutting edge, with time for discussion and debate.

We still have room for a few attendees. Register online using the web site

Marseilles 7 EvolBiol Sep21-23 program

Dear Colleagues,

The preliminary program of the 9th Evolutionary Biology Meeting at Marseilles is available on our website www.up.univ-mrs.fr/evol/congres/.

The following topics will be discussed: -Genome evolution -Phylogeography -Evolution and adaptation -Phylogeny and bioinformatics

Few spots are available for oral presentations or posters.

We look forward to hearing from you soon.

Oumou Ba for the Evolutionary Biology Meeting at Marseilles.

egee@up.univ-mrs.fr

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Estonia ConservationGenetics

PhD Studentship in Agricultural Sciences (aquaculture conservation genetics), Estonian Agricultural University, Tartu, Estonia

Preliminary project title: Studies of genetic diversity in some artificially reproduced fish species in the Baltic Sea area: implications for conservation and sustainable management

A 4 year PhD-position is available within the research area Conservation Genetics. The project will focus on genetic structure and diversity of several endangered (migratory and resident brown trout, European grayling) or economically important (pikeperch, perch) fish species within and among different catchments in the Baltic Sea area which are artificially reproduced for stocking purposes. The aim is to reveal the appropriate units for sustainable management and conservation.

We seek a highly motivated individual with good communication abilities and with capabilities to work independently and in team with others. Candidates should possess an MSc degree or equivalent in evolutionary genetics, population genetics, molecular biology, fish biology or a related field, and should have a strong interest in using molecular methods to study key questions in conservation and population genetics.

This project will be supervised by Dr. Riho Gross, Department of Aquaculture, Institute of Veterinary Medicine and Animal Science, Estonian Agricultural University (<http://www.eau.ee/~lki/kalakasv/index.htm>). For additional information, please contact Dr. Riho Gross at rgross@eau.ee as soon as possible. Closing date for applications: 4 July 2005.

Tartu, with its population of 101,246 is the second largest city of Estonia, lying 185 kilometres south of Tallinn, the capital of Estonia. Tartu is the centre of Southern Estonia and carries the title of 'the city of students' as it hosts two universities, the University of Tartu and the Estonian Agricultural University. For more information, please visit http://www.tartu.ee/?lang_id=2 Riho.Gross@eau.ee Riho.Gross@eau.ee

FairchildGarden systematic anatomy

Graduate Student Assistantship in Plant Anatomy/Tropical Botany

Funding is expected for a Research Assistantship for a Master degree student in the Graduate Program in Tropical Plant Biology (<http://www.ftg.org/research/graduatestudies/gradstudies2.html>) at Fairchild Tropical Botanical Garden and Florida International University (FIU). We seek a student interested in tropical botany, plant anatomy, and systematics. The RA will prepare microscope slides and chose a project in systematic anatomy of palms that can serve as a MS thesis. This is part of a larger study of the systematic anatomy of the palm family (<http://www.virtualherbarium.org/palmresearch/>). Applicant must meet admission requirements for FIU (http://www.fiu.edu/gradadm/coas_biosc.ms.html). Position is available starting as early as January 2006 (August deadline) or delayed until September 2006 (February deadline). After checking above websites, applicant should first contact Dr. Jack Fisher (jfisher@fairchildgarden.org <<mailto:jfisher@fairchildgarden.org>>) before applying to FIU.

Pamela.Diggle@colorado.edu

HullU EvolGenetics

NERC-funded PhD studentship Evolutionary Genetics / Computational Biology

Applications are invited for a three-year NERC-funded studentship to be held in the Molecular & Evolutionary Ecology Group at Hull University, Hull, U.K.

The PhD project: The student will investigate the role of balancing selection and multigene evolution for the maintenance and generation of genetic variation at immunological genes of the Major Histocompatibility Complex (MHC). He/she will be writing software programs to model the evolution of sequence variation, as well as conduct data mining of DNA databases.

Research Group: The Molecular and Evolutionary Ecology team at Hull is a large, dynamic group, currently with a membership of 8 postdoctoral research assistants, 16 postgraduate students and 3 research technicians (see <http://www.hull.ac.uk/biosci/>). The student will receive training in the molecular and evolutionary theory and analysis, with many other training courses, tailored to the specific interests of the candidate, available within our established graduate school.

The NERC studentship covers University fees, and for UK students, pays a stipend of ca. £12,000 pa.

Profile: The successful candidate will have a strong interest in evolution, expertise in a programming language (e.g. C++, VBA), and ideally have some experience with data mining software. He/she will be supervised by Cock van Oosterhout (Molecular Ecology, University of Hull), John Greenman (Postgraduate Medical Institute, University of Hull) and Helen Wright (Computer Science Department, University of Hull).

Closing date for applications: 28 June 2005

Contact: For more information, please contact Cock van Oosterhout Email: c.van-oosterhout@hull.ac.uk Tel. 01482-465505

– Dr. Cock van Oosterhout University of Hull Hull HU6 7RX, UK Tel.: +44(0)1482 465505 Tel.: +44(0)1482 466434 Fax.: +44(0)1482 465458 <http://www.hull.ac.uk/biosci/staff/vanoosterhout.html> <http://www.microchecker.hull.ac.uk>

LausanneU EvolBioinformatics

Two graduate student positions will be available in October 2005 to join a new lab of Evolutionary Bioinformatics a Lausanne University (Switzerland).

The subjects a priori are functional evolution after genome duplication in fishes, and the evolution of nematode genomes. These subjects are open to discussion, according to the competences and interests of the students.

Although the ideal candidate will have a Master in Bioinformatics, I am open to any good CV from evolutionary biology, molecular biology, computer science, etc.

If you are interested, please send me by email you CV, email and phone contact information of two references, and explain briefly which subject interests you most (you are allowed to answer “both”).

More information here: <http://www.sdsc.edu/~marc/lausanne.html> Marc ____ Marc Robinson-Rechavi <http://www.sdsc.edu/~marc> Joint Center for Structural Genomics write to: Godzik lab, Burnham Institute, 10901 North Torrey Pines road, La Jolla, CA 92037, USA phone: +1 858 646 3100 x3553; fax: +1 858 713 9949

La liberte ne s'use que quand on ne s'en sert pas

marc@sdsc.edu marc@sdsc.edu

SaintLouisU BiologyGISposition

PhD Student Opportunity in Biology and GIS

Saint Louis University is seeking a PhD student for a Research Assistant (RA) position to begin this summer (1 July 2005) and continuing support for four to five years.

The prospective student will be working on a GIS database for Gulf Coast streams and fishes with Drs. Richard L. Mayden and Robert M. Wood in the GIS and Biodiversity laboratory. The ideal student should be familiar with topics in conservation, aquatic ecosystems, biodiversity and ArcGIS and GIS software.

If you are interested, please contact Dr. Richard Mayden at maydenrl@slu.edu or Peggy Gathard at (314) 977-3910.

St. Louis University is an equal opportunity institution and is particularly interested in increasing diversity with women, minorities, and cultural/international diversity.

With best wishes, Rick Mayden

Richard Mayden <maydenrl@slu.edu>

UEastAnglia phylogenetic theory

PhD-studentship at The University of East Anglia, Norwich, United Kingdom

Starting date: autumn 2005

Extending the theory behind phylogenetic inference

Drug resistant superbugs such as MSRA and novel virulent pathogens such as SARS or bird flu are just a few examples of potentially lethal organisms that have recently dominated the headlines. Although fundamentally different in nature a feature shared by all of them is that they have arisen relatively recently via complex evolutionary processes such as e.g. lateral gene transfer and recombination. An improved understanding of such processes may therefore hold the key for effective drug development strategies.

Traditionally, evolution has been assumed to be tree-like making a (graph theoretical) tree the model of choice. However, by its very nature, a tree cannot appropriately represent the intertwined evolutionary past of organisms such as the ones mentioned above. The need to better understand the netted character of evolution coupled with improved insight into the complex processes that drive evolution has led to the introduction of the novel concept of a phylogenetic network into phylogenetics – a young and flourishing area concerned with providing a theoretical framework for studying evolution. Recently, these structures have received a considerable amount of attention in the literature from mathematicians, computer scientists and biologists alike.

The main thrust of this interdisciplinary project is to take on some of the challenges involved in extending the theory behind phylogenetic inference. It will draw on the supervisor's expertise and is expected to result in novel approaches plus software for constructing phylogenetic networks. In close collaboration with biologists the resulting methods will be assessed and compared with other phylogenetic inference techniques.

The project will be supervised by Dr. Katharina Huber (www.cmp.uea.ac.uk/people/faculty/kth), School of Computing Sciences, University of East Anglia, Norwich, United Kingdom.

Students interested in this PhD-studentship should have excellent programming skills, a good background in theoretical computer sciences and/or mathematics and an interest in biology.

Application forms are available on: www.cmp.uea.ac.uk/admissions/researchdegrees.jsp
Dr. Katharina Huber, School of Computing Sciences, University of East Anglia, Norwich, NR4 7TJ, United Kingdom. phone: +44 (0) 1603 593211, FAX: +44 (0) 1603 593345, email: katharina.huber@cmp.uea.ac.uk
www: <http://www.cmp.uea.ac.uk/people/kth>

UGoettingen EvoDevo

Prof. Dr. Ernst A. Wimmer Department of Developmental Biology, GZMB Institute of Zoology, Anthropology and Developmental Biology Georg-August-University Goettingen Justus-von-Liebig-Weg 11 37077 Goettingen Germany Email: ewimmer@gwdg.de

Marie Curie Research Training Network "Zoonet" De-

velopment and evolution of animal form: Training modern comparative zoologists

A Ph.D studentship is available for 36 months from October/December, 2005, funded by the Marie Curie Research Training Network "ZOONET" (<http://www.zoonet.eu.com/>), to study arthropod head development. The project will involve cloning and functional characterization of candidate head genes in diverse arthropod species.

Applicants should have a relevant M.Sc. or equivalent and some experience in molecular biology as well as zoology. Training will be given in the full range of approaches relevant to Evolutionary Developmental Biology (e.g. identification and isolation of homologous developmental genes from diverse arthropod species, in situ hybridization, and gene knock down by RNA-interference), and may require exchanges between laboratories in the ZOONET Network, as well as participation in network meetings.

In the selection process, the sponsor stipulates that:

Candidates must have no more than four years (full time equivalent) of graduate research experience; They must not be a national of the state within which the appointment will be held (Germany in this case); At the start of their fellowship, researchers may not have resided or carried out their main activity (work, studies, etc.) in Germany for more than 12 months in the 3 years immediately prior to the appointment.

The Georg-August-University aims to increase the number of female scientific staff and expressly requests applications from qualified women. In the framework of the legal requirements and in the case of equal qualifications, women will be considered preferentially in all areas in which they are under-represented.

Disabled persons will also be considered preferentially in the case of equal aptitude.

The stipend will be approximately 15.000 (brutto) per annum.

Researchers will also be eligible for an annual travel allowance as well as a monthly mobility allowance of approximately 500 per month (approximately 900 per month for married candidates). Additionally there is a one-off Career exploration allowance of 2000.

Applicants should send to the address mentioned above: their CV together with a brief letter of intent explaining motivation and project interests and the contact details of at least two referees (address, email, telephone number).

– Dr Max Telford Department of Biology, University College London, Darwin Building, Gower Street, Lon-

don WC1E 6BT, UK. Tel: +44 (0)20 7679 2554 Fax: +44 (0)20 7679 7096

<http://www.ucl.ac.uk/biology/new/admin/-staffpages/telford/telford.html> Zoonet website:
<http://www.zoonet.eu.com> m.telford@ucl.ac.uk
 m.telford@ucl.ac.uk

UHelsinki MetacommunityDynamics

POST GRADUATE FELLOWSHIP IN METACOMMUNITY DYNAMICS IN HELSINKI, FINLAND

Ever wanted to know how interspecific interactions are affected by the spatial setting? If so, you are invited to apply for a three-year post graduate fellowship, available from August 2005 onwards in the Metapopulation Research Group (www.helsinki.fi/science/metapop), Department of Biological and Environmental Sciences, 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 local communities of insects on oak (*Quercus robur*) are affected by host tree genotype and the spatial location of the host tree. You will combine large-scale field experiments with repeated surveys of local insect communities. The project has a strong empirical focus, but allows for interaction with several theoretically-minded members of a broader research group. A demonstrated record of coping with strenuous field work and good skills in statistical analysis (generalized linear models in particular) are counted as major advantages.

Applications including a short CV and two letters of recommendation should be submitted by 25 June 2005 to Dr. Tomas Roslin by email, tomas.roslin@helsinki.fi.

Further information: 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

UHelsinki Sticklebacks

PhD position in Evolutionary Ecology The effects of eutrophication on sexual selection and viability of stickleback populations

A 3-year PhD project is available in the research group of Ulrika Candolin in the Department of Biology and Environmental Sciences of the University of Helsinki, Finland.

Environmental heterogeneity can cause the intensity and direction of selection to vary in time and space. Yet, the effects of human-induced environmental changes on selection and evolution are poorly known. Currently, the breeding habitats of the three-spine stickleback *Gasterosteus aculeatus* are changing in the Baltic Sea due to eutrophication and increased growth of filamentous algae and phytoplankton. The aim of the project is to investigate the effects of increased algae growth and water turbidity on sexual signalling, mate preferences and the intensity and direction of selection on different traits in sticklebacks. The work will be realised through field and laboratory experiments, both at a field station by the sea (Tvärminne Zoological Station) and in the lab in the city. Molecular genetic techniques will be applied to determine the paternity of eggs. For further information, see <http://www.mv.helsinki.fi/home/ucandoli/> or contact ulrika.candolin@helsinki.fi.

Starting date would be August 1st at the earliest. The salary is approximately 1900 EUR/month. Experience of working with fish as experimental animals and of molecular techniques is an advantage, but not necessary. Interested candidates should send a curriculum vitae, a brief summary of research experience and interests, and contact details of two referees to ulrika.candolin@helsinki.fi, or Ulrika Candolin, Dept of Biological & Environmental Sciences, PO Box 65, FI-00014 University of Helsinki, Finland. The review of applicants will start on June 24th.

Ulrika Candolin Div of Ecology and Evolutionary Biology Dept of Biological & Environmental Sciences PO Box 65 (Biocenter 3, Viikinkaari 1) FI-00014 University of Helsinki Finland

Phone: +358-(0)9-191 57815 Fax: +358-(0)9-191 57694 Mobile: +358-(0)40-767 7072 Email: ulrika.candolin@helsinki.fi <http://www.mv.helsinki.fi/home/ucandoli/>

UHertfordshire bioalgorithms

Dear Colleagues,

We are offering PhD opportunities and studentships in the areas of Computer Science and Informatics below, many of which involve bioalgorithms and/or evolution in adaptive systems (esp. areas 7, 6, 4, 5 and 9).

Please forward this to excellent candidates with suitable backgrounds.

Chrystopher L. Nehaniv

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PhD Studentships in Adaptive Systems, Algorithms, and other Areas University of Hertfordshire, UK Research PhD Studentships in Computer Science & Informatics Science and Technology Research Institute

The STRI produced the largest FTE staff Computer Science submission to be graded at 4 in the UK 2001 Universities Research Assessment Exercise.

Applications are invited from candidates with good first degrees in computer science, computing, information technology, electronic engineering or other suitable backgrounds to join projects as research students for a three year period in the following areas:

1. Algebraic Engineering
2. Automatic Differentiation
3. Behavioural Analysis and Motivational Modeling of Autonomous Agents
4. BioComputation
5. Biologically-Inspired Affect-Based Regulatory Systems for Robots
6. Developmental Genetic Regulatory Networks
7. Evolution of Sensors and the Perception-Action Loop
8. High Performance Processor Design, Array and Distributed Computing
9. Neural Computation Biological and Cognitive Modelling
10. Optical Fibre Communication Systems/Networks
11. Requirements Engineering and HCI
12. Security and Integrity in Distributed Systems
13. Social Robotics and Human-Robot Interaction
14. Software Evolution and Maintenance
15. Software Quality/Processes/Measurement

Successful candidates may be eligible for a research studentship award from the University in some of these areas (equivalent to about 9000 per annum bursary plus the payment of the standard UK student fees).

For further information and an application form, contact

Mrs Lorraine Nicholls, Research Student Administrator, STRI, Faculty of Engineering and Information Sciences, University of Hertfordshire, College Lane, Hatfield, Herts, AL10 9AB.

Tel: +44-1707 286083 Fax: +44-1707 284185 or email: L.Nicholls@herts.ac.uk.

The shortlisting process will begin shortly and search will continue until suitable candidates are found.

<http://www.jobs.ac.uk/jobfiles/PS831.html>

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

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

Director, EPSRC Network on Evolvability in Biological & Software Systems Associate Editor, BioSystems Associate Editor, Interaction Studies

c.l.nehaniv@herts.ac.uk

UHull Evolution of Pheromones

NERC Studentship: Sensory and Chemical Ecology Group

Department of Biological Sciences

Closing date for applications: 28 June 2005

Applications are invited for a three-year NERC-funded CASE studentship to be held in the Sensory & Chemical Ecology Group at the University of Hull. The studentship will be supported by the CASE partner English Nature.

Background: Pheromones are key players in the regulation of social interactions of almost all animals. The identification of pheromones can give great insight into the physiology, behavioural ecology and evolution of a species and it facilitates research into the physiological and genetic basis of olfactory receptors, as well as into the function of the brain. In freshwater crayfish chemical signals are involved in aggressive as well as sexual behaviour. They are crucial for the maintenance of dominance hierarchies and appear to be important for the assessment of sexual receptivity. Yet, the specific function and chemical nature of crayfish pheromones is not known. Environmental organisations have a strong interest to enrich pheromones in order to use them as lures to trap invasive crayfish species.

The PhD project: The PhD student will perform a complement of behavioural and chemical studies into the nature of sex and dominance pheromones in two invasive crayfish species *Pacifastacus leniusculus* and

Procambarus clarkii. The NERC studentship covers University fees, and for UK students, pays a stipend of ca. £12,000 pa

Research Group: The Sensory and Chemical Ecology group at Hull is an expanding team with 2 lecturers, 2 TAs, 5 PhDs and 3 Masters students working on the chemical ecology, behaviour and ecotoxicology of marine and freshwater crustaceans, polychaetes and fish. We are well equipped with aquatic facilities, behavioural analysis tools (video tools, analysis software) and chemical analytical facilities (HPLC, GC-MS, access to LC-MS).

Profile: Applicants should have an appropriate degree in the life science disciplines (biology, biochemistry, zoology, behavioural ecology) and a broad interest in chemical ecology, behaviour and evolution. Some experiences in behavioural and chemical techniques or with crustaceans would be advantageous but the candidate will receive good training in all relevant techniques. He/she will be supervised by Drs. Thomas Breithaupt and Joerg Hardege (Department of Biology, Hull) and David Fraser (English Nature).

Contact: For further information please contact Thomas Breithaupt Email: t.breithaupt@hull.ac.uk Tel. 01482-465924

C.Van-Oosterhout@hull.ac.uk

UKansas EvoGenetics

Graduate Research Assistantship:

Graduate Research Assistantship in Animal Behavior / Evolutionary Genetics

A graduate research assistantship will be available in the Department of Ecology & Evolutionary Biology at the University of Kansas to examine the evolutionary genetics of sexually-selected behavior in acoustic insects. The work will involve behavioral and molecular genetic studies of *Achroia grisella* (lesser waxmoth), a species in which males attract females with an ultrasonic mating song. *A. grisella* is a symbiont of honeybees, and some emphasis will be placed on behavioral studies at bee colonies in the field. The laboratories are well-equipped for research focused on or involving acoustic communication, signal processing, and molecular techniques, including quantitative trait loci (QTL) mapping.

Contacts: Dr. Michael Greenfield or Dr. Jennifer Gleason,

Dept. of Ecology & Evolutionary Biology, Univ. of Kansas, 100 Sunnyside Road, Lawrence, KS 66045, or via email at greenfie@ku.edu or jgleason@ku.edu. Phone: 785-864-7366 (M. Greenfield); 785-864-5858 (J. Gleason).

Michael D. Greenfield Professor Department of Ecology & Evolutionary Biology University of Kansas Lawrence, Kansas 66045

tel. 785-864-7366 fax 785-864-5321 email greenfie@ku.edu

“Michael D. Greenfield” <greenfie@ku.edu>

ULausanne ConservationBiol

Available:

Two PhD positions (3 years),

In the Conservation Biology Group, Department of Ecology and Evolution, University of Lausanne, Switzerland.

Start: Sept 2005 or later Salary: according to the guidelines of the Swiss National Science Foundation

We study the selective forces that currently act on fish and mammal populations, i.e. the effects of human activities in interaction with natural and sexual selection. We are also exploring the link between cooperation theory and conservation issues. We aim at predicting the consequences of different management options for the long-term survival of populations.

We are seeking candidates with a strong interest in conservation genetics, life-history, evolution, and/or game theory.

Please send your application by email (all material in one attached file) to Prof. Claus Wedekind (wedekind@fas.harvard.edu). Include your Curriculum vitae, a short description of your research interests and research experience, and names and email addresses of one or two references who could be contacted. Please do not send any letter post (we are not yet in Lausanne). Review of applications will begin July 20, 2005. Applications will be accepted until the positions are filled. See www.unil.ch/dee/ for further information.

– Claus Wedekind Hrdy Visiting Professor for Conservation Biology Harvard University One Brattle Square, 6th Floor Cambridge MA 02138; USA phone: 617-496-5543; fax: 617-496-

4629 http://www.unil.ch/dee/page21538_en.html
<http://www.conservation.unibe.ch/>
 wedekind@fas.harvard.edu

UNewcastle PlantMolEvol

I need all the help I can get with finding a PhD student!

A NERC PhD studentship has become available in the research group of Dr Kirsten Wolff at the University of Newcastle, UK

Title: Genetical Ecology and Molecular Evolution in plants.

Eligibility: Applicants must be eligible according to NERC criteria which can be found at <http://www.nerc.ac.uk/students/eligible/> (UK students only, sorry)

Genetic diversity and adaptation are important issues when we want to understand biodiversity and maintenance of diversity in plant species, wild as well as cultivated. With the development of molecular markers we can now get much deeper insights in the evolution-

ary and population genetic processes that contribute to this. In this studentship there is a range of questions that could be answered depending on the interest of the student.

There are opportunities for developing the project in a number of directions depending on the interests of the student appointed.

You will join an active research group, interested in a broad range of aspects of population genetics and evolutionary biology, in both animals and plants. The group is housed in a well equipped molecular laboratory, including DNA sequencer. Newcastle is a great and exciting place to live, with wonderful countryside within reach. For further information on the project, requirements and how to apply: <http://www.ncl.ac.uk/biol/postgrad/kw.phd.htm> Best wishes, Kirsten

Dr. Kirsten Wolff Reader in Evolutionary Genetics University of Newcastle, School of Biology Ridley Building, room 461, Newcastle NE1 7RU, UK phone: (+44) 0191 222 5626 fax: (+44) 0191 222 5229 Plants have fingerprints too! Check it out: <http://www.ncl.ac.uk/biol/about/news.htm?type=3D1&id=-3D2782> <http://www.staff.ncl.ac.uk/kirsten.wolff/> <http://www.bioprofiles.co.uk/> <http://www.ncl.ac.uk/biol/> Kirsten.Wolff@newcastle.ac.uk

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Bogota VertebrateEvol

El Departamento de Ciencias Biológicas, Universidad de los Andes (Bogotá, Colombia) busca aplicaciones para una posición de profesor investigador de tiempo completo en el área de Biología de Vertebrados con énfasis en sistemática y conservación de fauna neotropical. El candidato seleccionado deberá poseer título de Ph.D., y deberá liderar investigación, supervisar estudiantes de pre- y posgrado, y realizar docencia. Son especialmente bienvenidos candidatos con especialidad en mamíferos y/o aves.

Enviar hoja de vida, copias de publicaciones recientes, una breve descripción del programa de investigación y docencia, y dos cartas de recomendación antes del 31 de julio, 2005 a:

Comité de Contrataciones Profesorales Atención: Alicia Ortega <aortega@uniandes.edu.co> Departamento de Ciencias Biológica Universidad de Los Andes Carrera 1 No. 18A-70 Bogotá, Colombia

The Department of Biological Sciences, Universidad de los Andes (Bogotá, Colombia) seeks applications for a full time teaching/research position in Biology of Vertebrates with emphasis in systematics and conservation of neotropical fauna. The successful candidate should have a Ph.D., and will be expected to lead research, supervise undergraduate and graduate students, and carry out teaching. Candidates specializing in mammals and/or birds are specially welcomed.

Send curriculum vitae, copies of recent publications, a brief description of research and teaching program, and two letters of recommendation before July 31, 2005 to:

Faculty Search Committee Attention: Alicia Ortega <aortega@uniandes.edu.co> Departamento de Ciencias Biológicas Universidad de Los Andes Carrera 1 No. 18A-70 Bogotá, Colombia

samadrin@uniandes.edu.co

Cemagref France SturgeonGenetics

Dear colleagues Please find enclosed the description of a post doctoral training period (12-18 months) offered by Cemagref. Undoubtedly, the work should be realised with your cooperation. May I ask you to encourage the spreading of the proposal.

Applicants are requested to provide a: i) Motivation letter ii) Working schedule giving methods and means that should be used to reach the objective iii)

Curriculum vitae Applications should be sent to Paul Gonthier (paul.gonthier@cemagref.fr) with copies to Eric Rochard (eric.rochard@cemagref.fr) and Patrick Williot

Collected applications will be sent to Cemagref's ad-hoc commission which hold a get-together every two months. Best regards Patrick Williot

Patrick Williot Cemagref, Directeur de Recherche, Ph D, HDR Unité de Recherche Ecosystèmes Estuariens et Poissons Migrateurs 50, Avenue de Verdun - Gazinet 33612 Cestas cedex Tel: 05 57 89 08 15; From abroad: 33 5 57 89 08 15 Fax: 05 57 89 08 01; From abroad 33 5 57 89 08 01 Web: <<http://cemagref.fr>>[http://-cemagref.fr](http://cemagref.fr) <<MatingSturio2005A.doc>>

berrebi@univ-montp2.fr

NewYorkU GeneticAnalysisFacilityManager

WANTED: GENETICS ANALYSIS FACILITY MANAGER

We seek a dedicated, highly motivated individual to run and manage a new DNA analysis facility for the Department of Biology, New York University. Responsibilities include running an ABI 3100 sequencing machine for departmental and outside clients, managing overall service to produce efficient turnaround, manage the accounting, and interface with service personnel and scientists. Additional future duties may include supervision of microarray reader and quantitative PCR machines. In particular, we seek applicants experienced in DNA sequencing and PCR, who have demonstrated organizational skills, ability to troubleshoot, and a strong dedication to building a quality service. Salary will start at \$30-35K with a competitive fringe benefits package. In-service training on all equipment will be included. Significant opportunity for increasing the salary exists with annual reappointment.

Send CV and 3 Reference Letters (with contact information) to:

Prof. David Fitch Center for Comparative Functional Genomics Department of Biology Silver Center, Room 1009 New York University 100 Washington Square East New York, NY 10003 (212) 998-8254 david.fitch@nyu.edu

~ ~ David H. A. Fitch ~ \ / / / ~ Associate Professor

Department of Biology New York University
Main Building, Room 1009
100 Washington Square East New York, NY 10003
U S A Tel.: (212) 998-8254
Fax: (212) 995-4015 e-mail: david.fitch@nyu.edu

<http://www.nyu.edu/projects/fitch/>
david.fitch@nyu.edu david.fitch@nyu.edu

NorthCarolinaStateU ResearchTech MolGenet

NorthCarolinaResearchTechnician/MolecularGenetics

Job description:

Our laboratory uses genetic markers to map genes that code for differences between two moth species in ecological traits, mating behavior, and resistance to pest control methods.

We are seeking a bright, motivated researcher who will

- 1) Conduct genetic analyses of differences between the moths, *Heliothis virescens* and *Heliothis subflexa*, using hybrid crosses followed by Quantitative Trait Locus (QTL) analysis via AFLP markers.
- 2) Develop co-dominant PCR markers for specific QTL.
- 3) Sequence candidate genes.
- 4) Use BAC library screening and cDNA-AFLP methods to examine candidate genes.
- 5) Train and supervise undergraduate and graduate students to work in a molecular lab setting.
- 6) Order supplies and maintain cost control for the molecular portion of the lab.
- 7) Maintain equipment.
- 8) Train new users in a Licor sequencing facility shared by faculty members in the College of Agricultural and Life Sciences and administered by our laboratory.
- 9) Assist in writing research articles.

We do not expect candidates to have experience in each of these areas. We do expect the person who takes this job to be interested in learning, to be careful with details, to be good at handling many tasks within a day, and to work well with others. We need to fill this position as soon as possible.

See lab web page for more details about lab. <http://www4.ncsu.edu:8030/%7Efgould/> North Carolina State University is a leading research institution with a strong commitment to the study of quantitative and molecular genetics. The University is situated in Raleigh, NC and is within 30 miles of Duke University, UNC-Chapel Hill, NIEHS, an EPA research unit, and

the Research Triangle Park. NC State University is an equal opportunity and affirmative action employer.

Minimum qualifications:

MS in entomology, biochemistry, genetics, or molecular biology. Also considered- BS in biology plus rigorous research experience.

Salary: \$32,000+ depending on experience

Contact: Send resume and letter of intent to Fred Gould via email: Fred_Gould@ncsu.edu

fred_gould@ncsu.edu

PennStateU ComparativeGenomics

The Center for Comparative Genomics and Bioinformatics seeks an individual with experience and enthusiasm in the field of high through-put sequencing. Located on the 3rd floor of Wartik Laboratories a facility is currently being created for automated sample preparation and massive parallel sequencing using a novel bead-based sequencing technology. The position will require an understanding of various molecular biological techniques, as well as the technical aspects of the robotic pipetting and sequencing machinery. Extensive training will be given into all aspects of the applied technologies. Ideal candidates will have experience in at least one of the fields of DNA-sequencing, microarray technology, quantitative PCR, or general laboratory automation. Application will be considered from individuals with degrees ranging from B.A. to doctoral degrees.

For further information please contact:

Stephan C. Schuster 310 Wartik Laboratory Pennsylvania State University University Park, 16803

Phone: 814-863-9278 Email: scs@bx.psu.edu

Or

John Carlson 405C Life Sciences Building University Park, PA 16802 Phone: (814) 863-9164 Email: jec16@psu.edu

Edward Holmes <ech15@psu.edu>

UAlaskaFairbanks HerbariumCurator

The application deadline for the following position has been extended to 1 September 2005. We welcome inquiries during the forthcoming Evolution 2005 meeting, although no interviews will be conducted until after 1 September.

CURATOR-FACULTY POSITION BOTANY UNIVERSITY OF ALASKA FAIRBANKS

World-class Outdoor Opportunities!

The University of Alaska Museum of the North and the Department of Biology & Wildlife at the University of Alaska Fairbanks seek qualified applicants for a tenure-track, Assistant-Professor position as Curator of the Herbarium. Successful candidates are expected to: establish a vigorous, extramurally funded research program complementing the University's programs; curate the herbarium; teach one course per year (Systematic Botany or a specialized course); and advise undergraduate and graduate students. The position will also be associated with the Institute of Arctic Biology. A newly expanded museum and laboratory, greenhouse, core laboratory for nucleic acid research, and super-computer facilities are available. Opportunities exist to use field areas such as the Bonanza Creek/Poker Creek and Toolik LTER sites. Preferred applicants will have a strong background in developing, managing, and using museum collections and in a specialized research area (which is flexible). An earned Ph.D. is mandatory, and postdoctoral experience is preferred. Applicants who can successfully implement their vision for how traditional collections can be used on the leading edges of science are especially encouraged to apply. Laboratory space and startup funds are included. Further information about the University and Museum is available at www.uaf.edu/museum, mercury.bio.uaf.edu, and mercury.bio.uaf.edu/iab. Applications should include: a completed applicant form (www.alaska.edu/hr/forms/hr_employmentforms); curriculum vitae; three letters of reference; and separate summaries of interests and experience in research, curation, and teaching. Please send complete application package by 1 September 2005 to Curator of the Herbarium Search, c/o UAF Human Resources, P.O. Box 757860, Fairbanks, Alaska 99775-7860. Questions about this announcement can be addressed to Molly Lee (ffmcl@uaf.edu).

The University of Alaska is an Affirmative Action/Equal Opportunity Employer. Women and minorities are encouraged to apply.

Kevin Winker <ffksw@uaf.edu>

UCapeTown ResAssist BirdBreeding

RESEARCH ASSISTANTS IN SOUTH AFRICA (3) for projects run by the Percy FitzPatrick Institute (University of Cape Town) examining co-operative breeding and nesting ecology of several bird species in Koeberg Nature Reserve, on the west coast north of Cape Town. Responsibilities will include nest-searching and monitoring, mist-netting and colour-ringing birds, resighting and monitoring post-fledging survival, and a variety of experimental manipulations. Positions available from early Aug through 31 Oct 2005. Accommodation will be provided in a rented house in a coastal village close to the study site. We are not permitted to pay a stipend, but all your subsistence (food) costs will be covered. To apply, please send a cover letter, resume, and e-mail addresses for three referees to PENN LLOYD (plloyd@botzoo.uct.ac.za). See <http://www.fitzpatrick.uct.ac.za/coe/docs/koeberg.html> for background on the research program.

CEISING@BOTZOO.uct.ac.za
CEISING@BOTZOO.uct.ac.za

CEIS-

UCincinnati FieldDirector

INTERIM DIRECTOR: Cincinnati Center for Field Studies

Duration: 7/1/05-6/30/06 Status: Full time Salary Range: \$40-52,000 per annum based upon qualifications Reports To: Associate Dean for Research, McMicken College of Arts and Science, University of Cincinnati

The Cincinnati Center for Field Studies (CCFS) is a new field station being formed in eastern Cincinnati, Ohio as a collaboration between the Cincinnati Nature Center (CNC - www.cincynature.org/) and the University of Cincinnati (UC - www.uc.edu). The Interim Director will work with the Steering Committee to sup-

port, guide and direct the development of a comprehensive plan for the center and will coordinate the planning process.

Essential Job Responsibilities: - Drive the planning process by working closely with the Executive Committee and with a facilitator - Provide vision and maintain a timeline for the planning process - Synthesize ideas and construct reports to reflect the work of various committees - Facilitate communication between all parties involved in the development of CCFS - Attend meetings of Executive Committee, full Steering Committee, subcommittees and task forces - Meet individually with stakeholders in planning process as needed - Obtain information on issues/questions brought up during planning - Serve as liaison between UC & CNC to establish research projects (manage current and upcoming projects at CNC in terms of logistics, site placement, timelines), educational offerings (contact prospective instructors, handle logistics, arrange supplies and facilities), land management zones on CNC property, and to develop outreach opportunities with potential collaborators (e.g., area colleges and universities, environmental agencies, municipalities).

Qualifications: - M.S. or higher degree in related scientific field - Working knowledge of field stations - Collaborative leadership style - Excellent oral and written communication skills - Can synthesize others' thoughts coherently - Good listener - Highly organized, ability to manage many tasks simultaneously - Ability to anticipate potential problems/conflicts as planning evolves - Readily engages other people - Shows initiative, self-starter - Computer skills word processing, spreadsheets, email, Blackboard (see <http://blackboard.com>)

Applications should include a statement outlining qualifications, a current resume, and names of three professional references [including phone numbers and email addresses]. Applications are due by 1 July 2005 and should be submitted to: Dr. Guy N. Cameron, Department of Biological Sciences, University of Cincinnati, Cincinnati, OH 45221-0006: Applications may be submitted electronically to g.cameron@uc.edu.

theresa.culley@UC.Edu

UMaryland ConsGenetics

Conservation Genetics of Oysters in Chesapeake Bay
A research assistant position is opening in the conser-

vation genetics laboratory of Dr. Matthew Hare in the Department of Biology of the University of Maryland, College Park. Research in the Hare lab focuses on conservation and evolutionary genetics and uses genetic markers as indicators of dispersal, gene flow, selection, hybridization and speciation in marine organisms. The open position is funded by NOAA-SeaGrant to measure the recruitment patterns of disease-resistant oyster strains used for restoration in Chesapeake Bay. More information on the Hare lab can be found at <http://www.life.umd.edu/biology/-faculty/hare/index.html> The successful candidate will conduct microsatellite genotyping and DNA sequencing in support of laboratory goals. In addition to having research responsibilities, the candidate will interact closely with graduate students and postdocs and help in the training and supervision of undergraduate students in the laboratory. The successful candidate will also be asked to help manage the day to day operation of the laboratory. Minimum of 1 year laboratory research experience is required. Successful candidates must have experience using standard techniques in population genetics research, with priority given to experience with microsatellite genotyping. Pay scale is commensurate with experience, starting at 24K.

Applicants should send (electronic preferred) a brief letter describing their prior research experience and current interests, a curriculum vitae, and the names and contact information of three references to Matthew Hare, Biology Department, Bio/Psych Bldg. #144, University of Maryland, College Park, MD 20742 (FAX: 301-314-9358; e-mail: matthare@umd.edu). Starting dates in July or August of 2005 are desired. Applications will be reviewed as soon as they are received.

The University of Maryland is located in a suburb of Washington D.C. with easy access to a number of research institutions in the Baltimore/D.C. area including the Smithsonian, Johns Hopkins University, and the Center of Marine Biotechnology. More information about the Biology Department and the Behavior, Ecology, Evolution, and Systematics (BEES) program at UMCP is available at <http://www.life.umd.edu/-biology/> and <http://www.life.umd.edu/grad/BEES/>

The University of Maryland is an equal opportunity/affirmative action employer.

*****Please note new email address*****
Dr. Matthew Hare
Biology Department
University of Maryland College Park, MD 20742
voice: 301-405-7264 fax: 301-314-9358
email: matthare@umd.edu

UMassachusettsAmherst ComputBiol

In addition to the position below we are also actively searching for a Department Head (see <http://www.bio.umass.edu/micro/news/deptheadad.htm>)

The Department of Microbiology at the University of Massachusetts, Amherst invites applications for a tenure-track position at the Assistant Professor level. The Department is seeking outstanding candidates in the area of Computational Biology, Bioinformatics and or Systems Biology to investigate biological problems in medical or environmental microbiology involving prokaryotes, eukaryotes and or viruses. Candidates must have a strong commitment to excellence in undergraduate and graduate education. The successful candidate will be expected to establish a strong independent, extramurally funded research program and participate in the teaching of undergraduate and graduate courses. Research facilities and competitive salary and start-up funds will be provided. Opportunities exist to develop strong collaborations with faculty in the Five College Consortium and at Bay State Medical Center. Ph.D. in Biochemistry, Molecular Genetics, Computer Science or a related field is required. Review of applications will begin August 5, 2005 and continue until the position is filled. Applicants should send a letter of application, curriculum vitae, a summary of research interests and future plans, teaching interests and representative publications electronically as PDF files to the following address: microbiodept@microbio.umass.edu. Arrange to have three letters of recommendation sent to: Microbiology Search Committee Chair, Department of Microbiology, 203 Morrill Science Center IV North, 639 North Pleasant Street, University of Massachusetts, Amherst, MA 01003. The University of Massachusetts is an Affirmative Action/Equal Opportunity Employer. Women and members of minority groups are encouraged to apply.

Jeffrey L. Blanchard Assistant Professor Department of Microbiology University of Massachusetts Amherst, MA 01003 Office and Lab: Morrill I N330 Tel: 413-577-2130 Fax: 413-545-1578 http://www.bio.umass.edu/micro/blanchard/Lab_About.html Jeffrey Blanchard <blanchard@microbio.umass.edu>

UMelbourne ConservationBiol

ECOLOGIST (terrestrial or aquatic) Lecturer, level B University of Melbourne, Australia

The Department of Zoology at the University of Melbourne invites applications for an ECOLOGIST. This is a full-time (continuing) position at the level of Lecturer level B, equivalent to Assistant Professor in the United States. High quality applicants will be considered regardless of their research speciality within terrestrial or freshwater animal ecology, but applicants must possess good quantitative skills and be able to teach within the Conservation/Wildlife and Ecology programs.

Full description of the position and the university, and advice on how to apply, are available at: <http://www.hr.unimelb.edu.au/pds/Y9400551.pdf> Applications should be sent by 15 July 2005 to: Vice-Principal (Human Resources) The University of Melbourne VIC 3010, Australia Email hr-applications@unimelb.edu.au or fax +61 3 8344 6080.

Further questions should be directed to Prof David Macmillan, telephone +61 3 8344 6259, email d.macmillan@unimelb.edu.au

UNebraska PopBiol

POPULATION BIOLOGY and COMMUNITY ECOLOGY FACULTY POST-DOCTORAL FELLOWSHIPS in POPULATION BIOLOGY UNIVERSITY of NEBRASKA

The School of Biological Sciences of the University of Nebraska-Lincoln invites applications for two tenure-track faculty positions and two postdoctoral fellowships. 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

The University of Nebraska Program of Excellence in Population Biology announces two two-year Postdoctoral fellowships in Population Biology. Candidates will develop a research project with a faculty member associated with the Program. These positions will provide recent graduates the opportunity for independent research associated with a faculty sponsor (in Biological Sciences, Mathematics, Natural Resources, or Entomology). The Program of Excellence in Population Biology is an integrative, cross-disciplinary program and fellows will, therefore be expected to teach a cross-disciplinary graduate seminar each year. Review of applications will begin August 1, 2005. A Ph.D. and expertise in any aspect of population biology is required. To apply, send a CV, a 5-page research proposal, and description of potential graduate seminars and arrange for three letters of reference, one of which must be from the proposed faculty sponsor, to the Population Biology Post-doctoral Fellowship Selection Committee, School of Biological Sciences, University of Nebraska-Lincoln, 348 Manter Hall, Lincoln, NE 68588-0118. Program details are available at (<http://popbio.unl.edu>). Fellowship positions will remain open until suitable candidates are selected.

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

Diana Pilson <dpilson1@unl.edu>

UNevadaReno EvolPhysiology

Postdoctoral Position(s) in Evolutionary Physiology
University of Nevada, Reno.

An NSF-funded postdoctoral position is available in the laboratory of Jack Hayes to conduct artificial selection experiments on the basal and maximal metabolic rates of mice. The ultimate goal of these experiments is to test the aerobic capacity model for the evolution of endothermy. Applicants should have a Ph.D. and an interest in evolutionary physiology. Strong quantitative and computer skills are desirable as is the capacity to bring new perspectives to this project and the laboratory. Reno, Nevada, is located on the eastern slope of the Sierra Nevada and was recently rated the 9th best city to live in the United States. The Department of Biology has a strong group of ecologists and evolutionary biologists with whom to interact. To apply, send a letter of interest, a cv, and email addresses for three references to jhayes@unr.edu. A second post-doctoral position to work on this project may become available soon. Benefits include health insurance and defined contribution retirement plan.

Mike Sears <msears@unr.edu>

UTuebingen TheoreticalBiol

Theoretical biologist (2 + 4 years).

We have a research associate position (German pay scale W1) for 2 years with a possible prolongation of another 4 years.

We are looking for an expert in the use of bio-mathematical tools in research and teaching, in particular in the analysis of evolutionary principles using analytical and simulation approaches on a widely accepted platform (e.g. C++, MatLab, Mathematica). We are specifically looking for a candidate with a background or willingness to integrate himself/herself in our current research fields which deal with sexual conflict, sex ratio or sex allocation, sex determination and gender expression.

Prerequisites for application are a Ph.D., international experience and papers in peer-reviewed journals in evolutionary biology. Teaching load is 9 hours per week during term (15 + 12 weeks). Fluency in English is a necessity. Good knowledge of German is an advantage. Teaching will be (largely) in English.

Disabled candidates will be given preference when qualifications are equivalent. The University Tuebingen would like to increase the proportion of women in academic science and teaching and therefore strongly encourages qualified female scientists to apply.

Send your application by Email to Prof. Dr. Nico Michiels nico.michiels@uni-tuebingen.de. Screening will start from 15 July 2005 onwards and continues until a suitable candidate is found.

The appointment will be made by the university administration.

Tuebingen, by the way, is a great place to be. It is one of the oldest University towns in Europe, will much of its historical flair preserved. With 80.000 inhabitants and 20.000 students it is a very cosmopolitan and academic town in a beautiful natural setting.

Prof. Dr. Nico Michiels Animal Evolutionary Ecology Zoological Institute, Faculty of Biology University Tuebingen Auf der Morgenstelle 28 E 72076 Tuebingen Germany

Tel. +49 7071 29 74649 Mobile +49 170 4758003 Fax 07071 29 5634

<http://www.uni-tuebingen.de/evoeco> Nico Michiels <nico.michiels@uni-tuebingen.de>

UWyoming MolEvol

POSITIONS AVAILABLE

From December, 2005, the Liberles Research Group will have moved from University of Bergen (Norway) to University of Wyoming (USA). The research group works on detecting and characterizing lineage-specific evolution using a combination of experimental and computational approaches. The computational approaches include modeling, comparative sequence analysis, methods development, and database generation. Several positions are available. A postdoctoral position is available for someone interested in computational evolutionary comparative genomics (broadly defined). If you are interested, please send me a cover letter, your c.v., con-

tact information for two references, and your two favorite papers that you have published. A systems administrator/scientific programmer position is available. Experience with linux, cluster maintenance, database maintenance, and programming is necessary. Work is expected to involve 25% systems and other administrative work and 75% contribution to ongoing scientific projects (which can be their own depending upon experience level). If interested, please send me a cover letter, your c.v., and contact information for two references. Ph.D. student positions are also available through formal application. Please first contact me informally if you are interested in this, and include a cover letter, your c.v. and contact information for two references.

Please send all materials by email to liberles@cbu.uib.no or by post to: David Liberles Computational Biology Unit BCCS University of Bergen 5020 Bergen Norway

David Liberles <David.Liberles@bccs.uib.no>

WDFW OlympiaWA EvolFishGenetics

Fish Geneticist - DNA

Washington Department of Fish & Wildlife (WDFW), Olympia, Washington USA

WDFW anticipates filling one or two biologist positions (Bio-3 or Bio-4) in the next few months. These positions will provide opportunities for qualified individuals to make significant contributions at the interface of applied science (genetics) and fish management and conservation while working for one of the major resource management agencies in the Pacific Northwest.

Responsibilities: lead (and work as a member of) team-based projects collecting and analyzing DNA data to address management and conservation issues for Pacific salmon, steelhead, trout, and selected marine fish and invertebrates. Current and future studies include: analysis of population structure, stock & species ID, mixture analysis (mixed-stock fisheries & stock-of-origin assignments), pedigree/parentage assignment analysis, and genetic evaluation & monitoring of hatchery and recovery programs.

Qualifications: General qualifications for Fish and Wildlife Biologist positions can be found at: <http://hr.dop.wa.gov> (select Current Job Openings, Natural Resources & Parks, Fish & Wildlife Biologists, Fish &

Wildlife Biologist 1-4 Eligibility Pool; see Announcement # 1-0-061-OC). Applicants must be U.S. citizens or currently hold a valid U.S. work visa that would allow them to complete at least the first year of the 2-yr appointment.

Salary: Salary ranges: Bio-3 (range 53) \$40,756 - \$52,211 and Bio-4 (range 55) \$42,849 - \$54,836 per year, plus benefits. The positions will be 2-yr project positions. Renewal/extension beyond the second year is dependent on performance and funding.

Closing Date: when filled

Contact: To be considered for the position(s), individuals must be registered on the FISH AND WILDLIFE BIOLOGIST 1-4 ELIGIBILITY POOL. On the Internet, go to <http://hr.dop.wa.gov/statejobs/jobs.htm> to find the relevant Recruitment Announcement (under Current State Job Openings, Search by Job Category, Natural Resources & Parks, Fish and Wildlife, Fish and Wildlife Biologists [#1-0-061-OC]) and State Job Application Form (under Application Form, State Job Application Form Word format or PDF format). Applicants should complete a Washington State Job Application Form after consulting the relevant Announcement mentioned above; and complete the Specialty Fields Supplemental Form (download from link at bottom of the Fish and Wildlife Biologists Eligibility Pool Announcement). Applicants need to obtain a copy of the knowledge, skills, and experience (KSE) exam from Jim Shaklee (email address: shakljbs@dfw.wa.gov) and use it to complete the "exam" answer portion (part 9) of the State Job Application Form. Candidates should FAX or mail the completed, signed Application with KSE "exam" answers and the Specialty Fields Supplemental Form to: James B. Shaklee, Washington Department of Fish and Wildlife, 600 Capitol Way N, Olympia, WA 98501 (FAX: 360-902-2943). For more information about this position, contact Jim Shaklee by email or by telephone (360-902-2752) or Sewall Young (email: youngsfy@dfw.wa.gov; phone: 360-902-2773).

If you want more information about the application process, please contact Joe Vidales at 360-902-2624. WDFW is an Equal Opportunity/Affirmative Action/Equal Access Employer.

SHAKLJBS@DFW.WA.GOV
SHAKLJBS@DFW.WA.GOV

WoodsHoleMA ResAssistant

POSITION: RESEARCH ASSISTANT I/II, Woods Hole, MA

Date: 06/16/2005

Description: The Marine Biological Laboratory is seeking applicants for a full-time year round Research Assistant I or II position in the Global Infectious Disease program within the Josephine Bay Paul Center for Comparative Molecular Biology and Evolution. This position is part of the Center's Global Infectious Disease Program and will involve interconnections among parasitology, evolutionary genomics and virology. The successful candidate could start as early as July 2005. The exact position will depend upon previous education and experience.

Duties: Duties include but are not limited to: Wolbachia are a genus of obligate intracellular bacteria that span the spectrum of symbiotic associations from parasitism in arthropods, mutualism in nematodes and pathogenesis in humans. One unique aspect of the biology of the Wolbachia parasites is a bacteriophage that represents one of the only elements that may laterally transfer among obligate intracellular bacteria. The successful candidate will study the molecular evolution and life cycle of this bacteriophage. Techniques may include genomic, molecular biology and microscopy approaches to understand structure, function and evolutionary pattern. Questions regarding the exact duties and responsibilities may be addressed to sbordenstein@mbi.edu. Additional information about the Center and the Bordenstein Lab may be found at <http://jbpc.mbl.edu/-bordenstein>. Conditions: This position is available as early as July 2005. The exact position will depend upon previous education and experience. Continuation is contingent on performance and available funds.

Education: EDUCATIONAL/EXPERIENCE/SKILLS: A BA or MS in biology or related field. Candidates with interest and experience in Molecular Biology, Virology, Evolution, Genetics or Comparative Genomics may find this position particularly rewarding. Training in some genomics or microscopy techniques required, including DNA extraction, high-throughput sequencing, cloning, genome assembly, population genetics or electron microscopy. A demonstrated familiarity with computational skills (Mac OS, Windows and Linux/Unix, PERL) is a plus. The successful candidate is expected to have good team skills, but work with a high level of independence under broad supervision.

Instructions: To apply: Applicants should submit a cover letter, curriculum vitae or resume, transcripts and a list of three or more references including telephone numbers and email addresses to: Marine Bio-

logical Laboratory, Attn: Human Resources, reference code [RA GID SB], 7 MBL Street, Woods Hole, MA 02543; telephone 508 289-7422; email materials with RA GID SB reference code to: resume@mbl.edu. An Equal Opportunity/Affirmative Action Employer/Non-smoking workplace

Deadline: Until a suitable candidate is identified.

– Seth Bordenstein Assistant Research Scientist Josephine Bay Paul Center for Comparative Molecular Biology and Evolution The Marine Biological Laboratory 7 MBL Street Woods Hole, MA 02543

phone: 1-508-289-7220 fax: 1-508-457-4727 email: sbordenstein@mbl.edu <http://jbpc.mbl.edu/~bordenstein>

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Advice on Phylogenetic Software

Hi,

my name is Marc Hoepfner and I am a student at the University Of Muenster, Germany, currently working on my Diploma thesis (MSc). Part of my work is the phylogenetic analysis of a certain domain-class. Right now I have my final protein-dataset, containing approx.

630 Sequences, and I need to decide which program to use. What I need is a software, that is able to compute a heuristic tree search (ML) using the WAG-I-G model for over 600 Sequences (~130 AAs in length). I first thought of using something like TreePuzzle, but it seems ot be limited to less then 300 Sequences/dataset. My second idea was MrBayes but tests I performed to-day showed that no computer I have access to is able to deal with this amount of data in MrBayes (out of Memory).

In case someone has a good advice on which programm

to test next I would really appreciate a short notice (hoepner AT uni-muenster.de).

Best wishes

Marc Hoepner

Marc Hoepner <marc.hoepner@web.de>

Anthro Forum

Dear colleagues,

The Istituto Italiano di Antropologia (ISItA) www.isita-org.com is launching the Journal of Anthropological Sciences (JASs) forum http://www.isita-org.com/jass_index.htm, an online publication, designed to stimulate interdisciplinary discussion regarding anthropological issues for and with an international audience.

The topic for the JASs 2005 forum is: Anthropology and Reductivism

Everyone may participate to the forum by discussing the subject and the relative commentary. All interventions in the JASs forum will be also published in the JASs printed version. Visit the site http://www.isita-org.com/jass_index.htm for further info.

giovanni destro-bisol <destrobisol@uniroma1.it>

Arlequin AFLP answers

Thank you to the many people who responded to my question regarding Arlequin, AMOVA, and AFLP data input files. Below I have summarized what I found so far to be the four most helpful solutions, including my feedback in capital letters and annotated versions of selected email responses. Cheers, Molly

Molly Stephens Graduate Group in Ecology Genomic Variation Lab University of California, Davis mrstephens@ucdavis.edu <http://genome-lab.ucdavis.edu> 530-752-6351

Solution #1: Use Transformer-3b.01 software to create Arlequin file. THIS WAS THE BEST SOLUTION FOR MY PARTICULAR DATA SET,

AND I EXPECT WOULD BE VERY USEFUL FOR ANYONE. VERY VERY EASY TO USE - CUT AND PASTE INTO SIMPLE EXCEL FORMAT. I HAD MY WORKING ARLEQUIN FILE IN LESS THAN 1 MINUTE(!). EVEN HAS A FUNCTION TO CREATE THE GROUP "STRUCTURE" SECTION OF THE ARLEQUIN FILE. THIS IS A GREAT SOLUTION FOR THOSE WHO ARE ALREADY COMFORTABLE USING ARLEQUIN AND JUST HAVING PROBLEMS GETTING THEIR INPUT FILE TO WORK. HANDLES DOMINANT AND CODOMINANT DATA. REQUEST PROGRAM FROM AUTHORS.

> The correct way to cite this beta version is: > Caujapé-Castells J and Baccarani-Rosas M (2005). Transformer-3b.01: a program for the population genetic analysis of > dominant and codominant molecular data. Jardín Botánico Canario "Viera y Clavijo". Cabildo de Gran Canaria. (Test > version, distributed by the authors).

> email me [Juli] in order to obtain a free beta version. As I mentioned to you, the final version will Transform into > many formats for dominant and codominant data, and will be announced in the evoldir directory in due time. By the way, > were you interested in the version for codominant data only (Transformer-2), it can be downloaded free of charge from > <http://www.step.es/jardcan/trnsformer.html> along with a manual and two example files. > Best regards, > Juli > > Dr. Juli Caujapé Castells > Molecular Biodiversity labs & DNA bank > Jardin Botanico Canario "Viera y Clavijo" > Ap. de Correos 14 de Tafira Alta 35017 Las Palmas de Gran Canaria Spain > email: julicaujape@grancanaria.com > phone: ##34 928219421 ext. 4770 > fax: ##34 219581 > <http://www.step.es/jardcan/> >

Solution #2: Use GenAIEx to create your Arlequin file and/or do your actual analyses in GenAIEx. GENAIEX VER.6.0 DOESN'T CURRENTLY CONVERT DOMINANT DATA TO ARLEQUIN FORMAT (ONLY CODOMINANT DATA); HOWEVER, YOU CAN DO THE AMOVA IN GENAIEX WITHOUT CONVERTING TO ARLEQUIN. CAVEATS: MISSING DATA NOT ALLOWED; AMOVA ANALYSIS WILL NOT PROCEED IF ANY POPULATION HAS ONLY ONE INDIVIDUAL. OVERALL, VERY EASY TO USE AND COULD BE A VERY GOOD SOLUTION FOR MOST USERS. Peakall R and Smouse PE (2005) GenAIEx 6: Genetic Analysis in Excel. Population genetic software for teaching and research. The Australian National University, Canberra, Australia. <http://www.anu.edu.au/BoZo/GenAIEx/> You can try

another program to run your analysis. I recommend GenAlEx (by Smouse and Peakall). The input file and use of the program is user friendly. You can also use GenAlEx to format your input file for Arlequin (and other programs). GenAlEx version 6.0 has just been release a few weeks ago and it is freely available for PCs and Macs. Good luck, eva Eva Gonzales, PhD Department of Plant Biology University of Georgia (706) 542-0281 (lab) <http://www.plantbio.uga.edu/~egonz/>

Solution #3. Use AMOVA server software (Rodney Dyer). ALSO VERY EASY TO USE. SERVER-DRIVEN; ONLY SINGLE-LEVEL ANALYSIS CURRENTLY AVAILABLE, BUT NESTED ANALYSIS FORTHCOMING.

> You may want to check out the software section of my web server >(<http://dyerlab.bio.vcu.edu> <<http://dyerlab.bio.vcu.edu>). I have an AMOVA analysis that is web >based that handles zymes/sats/binary markers. The input format is a tab >delimited text file (as you would export from Excel or some other >spreadsheet). It does pair-wise and significance testing for a single >level of nesting. There are some example data sets and some general >instruction available for download at the top of the page. I haven't >announced it yet as it is just coming on line with some other analyses. >Rodney J. Dyer >Professor of Population Genetics >Department of Biology >Virginia Commonwealth University >Richmond, Virginia 23284 ><http://dyerlab.bio.vcu.edu> <<http://dyerlab.bio.vcu.edu>

— / —

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>

Basommatophorans Mollusca samples

Dear all,

I am looking for specimens of three species of Basommatophorans (Mollusca) from all over Europe for phylogeographic analysis: *Ancylus fluviatilis*, *Acroloxus lacustris* and *Radix auricularia*.

Please contact me:

Mathilde Cordellier

m.cordellier@zoology.uni-frankfurt.de Abteilung Ökologie und Evolution Zoologisches Institut JWGU-Universität 60054 Frankfurt am Main Germany

Tel: +49-069-798-24721 Fax: +49-069-798-24910

Mathilde Cordellier <m.cordellier@zoology.uni-frankfurt.de>

Bovine faecal preservation

Hi,

I'm looking for ways of preserving bovine faecal samples for subsequent DNA analysis that don't involve a freezer! Ethanol or silica-based drying methods appear to be commonly used for ungulates, however most of the studies I've encountered so far involve the preservation of "pellets" rather than "pats". Can anyone recommend an alternative method that may be better than ethanol or silica, which avoids the usual problems of transporting flammable liquids and trying to dry faeces in the field?

Thanks in advance, Bill

Dr Bill Hutchinson Genome Analysis Suite Manager Molecular Ecology & Fisheries Genetics, Biological Sciences, Hull University, HULL HU6 7RX United Kingdom

Tel:- 01482 465804 office 01482 465536 lab Fax:- 01482 465458 <http://www.hull.ac.uk/biosci/-staff/hutchinson.html> <http://www.hull.ac.uk/-GAS/> <http://www.microchecker.hull.ac.uk/> w.f.hutchinson@hull.ac.uk

Calculating TD

Dear Evoldir members, did anyone hear about any available software that implements the statistics TD as described in Zhivotovsky 2001 "Estimating divergence time with the use of microsatellite genetic distances: impacts of population growth and gene flow". Mol. Biol. Evol. 18(5):700-709? thanks

Gabriele

Gabriele Gentile, Ph.D. Department of Biology Tor Vergata University Via della Ricerca Scientifica 00133 Rome, Italy

phone: +39 06 72 59 59 77 fax: +39 06 72 59 59 65
email: gabriele.gentile@uniroma2.it

Cloning mystery

Hello,

I would be grateful if anyone would be able to help me in construction of clone libraries .

I use to clone PCR fragments but since one month I try without success to clone a 2.3Kb DNA fragment. I cloned a 2.3 KB fragment (16S-23S rDNA) from environmental samples with TOPO TA kit. I checked by PCR the transformants: I had with success 40 clones. I sent them for sequencing and surprise: the cloned fragment was a piece of the vector TOPO.

I tried again to clone my fragment in pGMT Easy, previously isolated in agarose gel. I had white colonies, but when I checked by digestion with Eco RI all the transformants were without the right fragment.

If you know of anyone that might be able to help, I would also appreciate your help. Please contact me to the address given below.

Thank you very much for your help!

Estelle

Estelle Masseret, PhD Assistant-Professor University of Montpellier II UMR-CNRS 5119, cc93 Place Eugene Bataillon 34095 Montpellier Cedex 05 France Tel: 33 4 67 14 47 62 Fax: 33 4 67 14 37 19 mailto:masseret@univ-montp2.fr

masseret@univ-montp2.fr

ContigEditors answers

Dear Colleagues,

I received many responses to my query about contig editors. In particular, I am seeking one that will 1) align contigs (to each other, across individuals), 2) al-

low access to chromatograms with a simple mouse click (so that data can be compared quickly and easily both between primer reads from one individual and between multiple individuals in a data set), 3) work with Beckman sequencer data, 4) be economical for evolutionary biologists without huge grants, and 5) be relatively easy to use and bug-free.

In brief, no one wrote and said that they know of a package that meets all these criteria. But hope is (hopefully) on the horizon. Peter Richterich of Codoncode informed me that he has received several requests for the contig alignment feature with easy access to chromatograms, and he hopes to incorporate this feature into Codoncode Aligner (<http://www.codoncode.com/>) by the end of this year. For non-profits, this program costs US \$960 for the first copy and \$480 for subsequent copies (and the prices are easily found on their website, unlike some companies). I use this program in my lab and am very happy with it (except for the lack of the nested contig feature). It meets criteria 3, 4, and 5, and is easy to use. It also can do base calling and assembly with PC versions of PHRED and PHRAP. The programmers at Codoncode are very accessible (responses to emails within the hour, and answering their own phones) and even have a webpage for suggestions. Based on responses I received to my query, many of you will be anxious to have the contig alignment feature as well.

Several people recommended Staden, and Bioedit (<http://www.mbio.ncsu.edu/BioEdit/bioedit.htm>), which are free. I don't know these programs, but Tom Hall, the author of Bioedit told me that it doesn't do contig assembly (see below). A user disagrees and sent me a screenshot to prove it. Does it use an accessory program to do this? In any case, it sounds like a versatile and useful program, and you can't beat the price.

Biolign is by Tom Hall as well, and Kristen Shepard (below) says that it does many things I asked about.

I received several recommendations for Seqman II. I have checked this program out and it was expensive and didn't align contigs.

At any rate, I plan to sit tight and hope that Codoncode gets it right, and soon. In the meantime, a lot of us are feeling pretty frustrated with the options available (many responses NOT included below).

Thanks,

Steve

Responses, in reverse order received and excluding many expressing dismay at the current state of affairs:

***** Hi Steve,

Have you tried Staden?

Staden is sufficiently powerful to do (very) large assemblies (I have assembled several BAC clones). It also has a mutation/heterozygous indels detection component (originally designed for clinical mutation scans, but is easily adapted for SNP/population genetics and other evolutionary analyses).

It is fast, free, has good graphics and trace viewing facilities and has an excellent manual/online help. Staden runs on any UNIX platform with X windows. There is also a PC/MSWindows port, but it is somewhat buggy and no longer supported, however, for some purposes it will do just fine - I wouldn't recommend the Windows version for large assemblies, though.

<http://staden.sourceforge.net/> It takes some time to learn to make best use of its large number of features. If you choose to give it a try and need any pointers, feel free to contact me.

Best wishes

Anette Becher ***** Hi Steve,

BioEdit is freely available at <http://www.mbio.ncsu.edu/BioEdit/bioedit.html> It does not do contig assemblies and was never published in a peer-reviewed journal.

BioLign is an editor that sits on top of multiple short phrap assemblies. It is not freely available at this time. It does not do contig assembly itself, but requires legal copies of phred and phrap and uses phrap output. I think those are legally free to academic users. It is unsuitable for genome-size assemblies, and is not well suited for assemblies that contain more than about 20 traces passing through any one region of an assembly, because of the way that trace viewing was implemented. It was primarily designed for doing automated alignments of multiple assemblies of alleles of the same gene or very close homologs that align well at the nucleotide level. The interface provides a multiple alignment of sequence assemblies, with each assembly expandable into a synchronized alignment of the sequence traces for manual inspection of the data. It can be useful for a narrow range of uses, but is not the most versatile program for sequence assemblies.

Best regards,

-Tom Hall ***** Steve,

— / —

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

DNA extraction techniques

Message:

Does anyone know of a cheap 96 well DNA extraction protocol that has worked on Penaeids? I have previously had difficulty with inhibitors that I assume coprecipitate with DNA in precipitation based extractions. A colleague suggested that these may be glycoproteins found in the exoskeleton of the prawns, but I encounter the problem when extracting from muscle tissue with no traces of exoskeleton. I have had good success with Qiagen DNeasy columns in both single and plate format but they are cost prohibitive given the large number of samples I have. Any advice on other plate format extraction techniques would be appreciated.

Thanks

Jason Bartlett

Jason Bartlett Fisheries Biologist Department of Primary Industries and Fisheries

Telephone 0421 930 785 Facsimile 07 3408 3535
Email jason.bartlett@dpi.qld.gov.au Website
www.dpi.qld.gov.au Call Centre 13 25 23

“Bartlett, Jason” <Jason.Bartlett@dpi.qld.gov.au>

DNA sequence editing software

We are planning to obtain new software for DNA sequence editing (including e.g. proofreading options of raw sequences, sequence aligning, primer design, etc.). We have experience with the freeware BioEdit and Sequencher. Do you have suggestions for other suitable program packages (freeware or commercial)? I will pool the answers and post it to EvolDir.

Regards,

PhD Håvard Kauserud haavarka@bio.uio.no

Drosophila RedBook

Greetings EvolDir community-

I'm looking to obtain a copy of Lindsley & Zimm 1992 (the *Drosophila* "red book"), preferably for less than the \$150 price for a new copy. It can be old and battered!

thank you.

Brian Bettencourt Brian.Bettencourt@uml.edu

Electrofishing methods

Dear all,

I am looking for literature about electro-fishing efficiency (regarding fish species, fish size, water current, water depth, etc, etc) and (statistically based) recommendations for better electro-fishing assessment methodologies.

Furthermore, the book "Fishing with electricity, applications in freshwater fisheries management" (by Cowx and Lamarque) appears to be unavailable nowadays (it already dates from 1990). If you are aware of a more recent must-have electro-fishery handbook, please pass the word.

Thanks, Dieter

– Dieter Anseeuw Katholieke Universiteit Leuven
Campus Kortrijk Subfaculteit Wetenschappen Etienne
Sabbelaan 53 B-8500 Kortrijk Belgium

Direct phone: +32.(0)56.24.61.72 Fax:
+32.(0)56.24.69.99 <http://www.kulak.be/~danseeuw>

Fairbanks housing

Last moment ad: On-campus housing at Fairbanks, roommate needed .

Hello All,

Sorry for a late posting. We have one opening for a female participant for on-campus housing at Evolution Meeting in Fairbanks. On-campus housing is much cheaper than hotels (\$32 per night, \$160 total) and has been booked since March. If you know any female who would like to save a few dollars on housing, please let em know ASAP. She will be a roommate of a student of mine, Jennifer Whittington.

Thanks!

–

Lev Yampolsky

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

Lev Yampolsky <yampolsk@etsu.edu>

Hermatipic coral tissue preservation

Dear EvolDir

I am new to coral genetics and I wonder if someone has a ambient temperature preservation method for hermatipic coral tissue samples that works well with subsequent specific DNA extraction protocols required for these organisms. Any help will be appreciated, as usual, I will post a summary of the information received. (BTW, any pointers to a Coral Reef science bulletin board will also be appreciated).

Best regards,

Axayacatl Rocha-Olivares, Ph.D. Chair Biological
Oceanography Department CICESE P. O. Box 434844
San Diego, CA, 92143-4844

DOMESTIC: Apartado Postal 2732 Ensenada, Baja
California, CP 22830 Mexico

COURIER: Km 107 Carretera Tijuana-Ensenada En-
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Email: arocha@cicese.mx <http://dob.cicese.mx/pag/-arocha.htm>

Axayacatl Rocha <arocha@cicese.mx>

IntelligentDesign film at Smithsonian

To the evolution community:

Many of you may be aware from recent newspaper articles (for example, the New York Times article available at <http://www.nytimes.com/2005/05/28/national/28smithsonian>), that the NationalMuseum of Natural History at the Smithsonian Institution is about to show a film that was co-written and co-produced by members of the creationist Discovery Institute. (The showing is on June 23.) This film, called "The Privileged Planet", the Search for Purpose in the Universe". It is an attempt to use geology, climatology, and physics to show that the earth was designed by an intelligent designer, and of course is part of the latest strategy of "intelligent design" creationists to worm their way into the public consciousness and school curriculum. You can read about the film at its website <http://www.privilegedplanet.com/>, and see the Discovery Institute's announcement of the co-sponsorship at <http://www.discovery.org/scripts/viewDB/index.php?command=view&id=-133&program=CSC&isEvent=true>

Although the Smithsonian must give non-profit organizations (of which the Discovery Institute is apparently one) the right to present films in its facilities, it seems wrong for the Smithsonian to also co-sponsor such films. The Smithsonian has a history of supporting the fact of evolution, and in fact has a wonderful Hall of Evolution in the NMNH to present the data. Why, then, is it co-sponsoring this film? The effect of this is to give a U.S. government imprimatur to the activities of the Discovery Institute. The Discovery Institute is of course playing up this co-sponsorship on its website.

The director of the National Museum of Natual History, which is co-sponsoring the film, is Christian Samper, whose email address is SamperC@si.edu . I would urge you to consider emailing him and expressing your feelings about this event.

I am sure that Dr. Samper is not very happy with this event (apparently the Discovery Institute sneaked in the film under the Museum's radar), but perhaps a series of emails from evolutionists could get the Smithsonian re-examine its policy of cosponsoring events like this. Needless to say, we should all be polite in our emails.

Thanks. Jerry Coyne

Jerry Coyne <j-coyne@uchicago.edu>

Magnisphere beads

Dear members,

I have to questions concerning the use of magnisphere beads and a mix of oligos for the enrichment step of a microsat library protocol 1) We have promega magnisphere beads Z5481. Unfortunately, the leaflets that come with the beads are lost. I looked up the protocol on Promegas website, but it describes RNA purification. Can I use the same protocol for the enrichment step of my genomic DNA or are there maybe other (better) protocols out there?

2) We have GA15B, CA15B, GATA5B. Could I use a mix of those three bitynilated probes or would I get better results if I used them one by one in the hybridization step?

Thanks,

Eva etoth@vims.edu

Multiple Outgroups

I performed a PAUP run with two outgroup taxa specified indicating that the ingroup should be made monophyletic and this message came up: "tree can not be rooted such that specified ingroup is monophyletic". The resultant tree emerged with one of the outgroup taxa (the second in my MacClade list) pairing up with one of the ingroup taxa. When I reversed the order of the outgroup taxa in MacClade and reran, the outgroups reversed positions in the tree. The second outgroup always seems to pair up with an ingroup taxon. Is there an explanation? Many thanks. Bill Chapco.

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

William.Chapco@uregina.ca

Tel.: 0045 35281639 Fax.: 0045 3528 1511
dsa@kvl.dk

New SSE Website

Dear SSE members,

I am delighted to announce that the Society for the Study of Evolution now has a new (stunning and highly informative!) web site online, at: www.evolutionandsociety.org Take a look! There's a lot to see—for example, check out the link for the White Paper—the electronic version is gorgeous.

I wanted to get it up and functioning asap, but keep in mind that it will be undergoing both short term and long term refinements (and some parts are still incomplete). This is just a start, although I think it's a very good one, and puts SSE onto the internet with a strong new presence.

The site was designed by Chris Gates, a professional web site designer with a background in evolutionary biology, me, and Patrick Phillips. It is being refined and run by our new webmaster, Mark Jonas.

We sincerely hope that you like it, enjoy it, and especially, that you use it.

Jessica Gurevitch

Executive Vice President

Scott Starr <ssstarr@allenpress.com>

Parentage analysis SSR

Dear Colleagues,

could anyone mention existing softwares for parentage analysis that take into account microsatellite size also accounting for possible mistyping errors? I would like to use a method that can assign a higher probability of identity to alleles with very similar size, not a merely qualitative assignment.

I will be thankful for your help

Daniela Salvini

PhD student Center for Forest and Landscape (Arboretum) Royal Veterinary and Agricultural University HKongvej 11 2970 HDENMARK

Population tree

Does anyone know a program that will calculate a population tree based on sequence data AND generate support indices, ideally using a maximum likelihood approach? Thanks - Vicki

friesenv@biology.queensu.ca

Pratylenchus Meloidogyne samples

Dear All,

Hopefully someone is able to help me in my quest for *Pratylenchus vulnus* & *Meloidogyne* hapla DNA (or biomass).

Since I have no experience working with nematodes I am initially interested in trying to isolate some genes by PCR. For this I would need some biomass (dead nematodes in EtOH) or preferentially DNA.

I appreciate any help in this matter.

Best wishes, Mark

– Dr. Mark van der Giezen Lecturer in Microbiology School of Biological Sciences Queen Mary, University of London Mile End Road, London E1 4NS, UK tel.: +44 207 8823057/fax: +44 208 9830973 e-mail: m.vandergiezen@qmul.ac.uk <http://web.onetel.com/~vandergiezen> m.vandergiezen@qmul.ac.uk

PygmyPipehorse samples

Dear all,

I am trying to get hold of a single sample of a pygmy pipehorse for a phylogenetic study on the evolution of seahorses.

Description: There are three genera of pygmy pipehorses, namely *Idiotropiscis* (Australia), *Acentronura* (Indo-Pacific) and *Amphelikturus* (Caribbean). Any one of these will be suitable for the study. Please see the following websites for details: *Idiotropiscis*: www.amonline.net.au/fishes/fish-facts/fish/ilumnitzi.htm *Acentronura*: <http://www.seahorse.org/gallery/Pipehorses> (*Amphelikturus* looks similar)

Reward: Anyone who can send a good-quality sample (ideally preserved in ethanol and not dried or formaldehyde-fixed) will receive co-authorship. We already have a large data-base of nuclear and mitochondrial seahorse and pipefish sequences, and the pygmy pipehorse will be crucial in understanding how and when seahorses derived from their pipefish ancestors. This is likely to get published in a very high-ranking journal!!

Legislation: Pygmy pipehorses are not CITES listed, but any local regulations should be adhered to (this applies particularly to Australia).

For manuscripts of some similar studies, please see the following website: http://www.ru.ac.za/academic/departments/botany_research/peter/ – Dr. Peter R. Teske Postdoctoral Researcher Molecular Ecology and Systematics Group Department of Botany Rhodes University 6041 Grahamstown South Africa P.Teske@ru.ac.za http://www.ru.ac.za/academic/departments/botany_research/Peter/

Qst computation

I am writing a simulation program for a quantitative trait in a structured population and I have a question about how one computes Q_{st} (the population differentiation in a quantitative trait; similar to F_{st}). It is defined as the ratio of the mean additive genetic variation within demes to the sum of two times the mean additive genetic variation within demes and that for between deme variance. I have been computing the within and between deme components of variance using ANOVA logic (sum of squares over degrees of freedom) but this does not appear to be the same as the terms that make up the Q_{st} ratio as both the sum of squares and degrees of freedom are partitioned additively but not the actual total variance. Any help or optimally a 'toy' example of an actual computation (given some simple structured population with individ-

uals having some given quantitatively determined phenotypes) would be greatly appreciated. Thank you very much, Bryan.

Bryan Patrick Wood <bpw5@georgetown.edu>

Rate Constancy

Dear EvolDir members,

I have intraspecific COI data in which certain populations (group A) appear to have about twice larger substitution rate than others (group B). This assumption is based on the mean number of pairwise differences within each group and on terminal branch lengths in a neighbour-joining tree.

Could you suggest me an appropriate method to test this assumption, i.e. particularly that the group A has faster substitution rate than the group B. Is it possible to evaluate how much faster?

The data set consists of 55 haplotypes (22 in group A) and there is little support for the nodes in the NJ tree. Groups A and B are not monophyletic as well, therefore tests based on a well defined topology do not seem suitable to me.

thanks in advance, Asta
<asta.audzijonyte@helsinki.fi>

Asta Audzijonyte <asta.audzijonyte@helsinki.fi>

Reducing ABI costs answers

QUESTION: What companies make inexpensive reliable reagents for ABI machines genotyping microsatellites? Please provide contact info (email/phone) for company; I will post a summary on evolDir. Thanks.

AEM Baker 101 Morgan Bio University of KY Lexington KY 40506 0225 mouse@lamar.colostate.edu

RESPONSES:

Friday, May 27, 2005 "Giraldo, Martha Cecilia (CIAT)" <m.c.giraldo@cgiar.org> Hi you can try with the gel company the web pag is gelcompany.com, they bring prices so low and alphadna.com for primers. Be successful, Marthace

reerd@fiu.edu> I've just completed some major microsat work using ABI 3100 capillary machines. I found that for labelled primers, those from Integrated DNA Technologies (www.idtdna.com) seem to be equal to ABI's in performance, and cost a fraction as much for a comparable amount. You have to order a larger quantity at once, but it's still significantly cheaper than a minimum-quantity order from ABI. I've used IDT primers with HEX and 6-FAM labels - I can't say first-hand how other labels work.

I don't know of a commercial alternative for ABI's labelled size standards. I found that I could use 1/2 or even 1/4 of the recommended amount of ABI's ROX-350 or ROX-500 per sample and still get perfectly good results most of the time - a few samples would fail here and there, but I came out way ahead in the long run. Since then, our DNA core lab has developed its own ROX-labelled size standard (there are protocols for this in the literature), which works fine, but probably isn't practical for a single Good luck, Doug Creer

June 01, 2005 8:59 AM Lee Timms <leetimms@gmail.com> The ladders are reliable. I have been using the 1000bp ladder for a long time. We have never had a problem with it.

The ABI 1000 bp ladder only works for non denaturing gels. The Bioventures ladder and maybe the ladders supplied by The Gel Company, are to be used in denaturing conditions. The capillary ABI machines use a polymer (it acts like the 'gel') - your fragments run through this polymer. The polymer is denaturing so you have to make sure you use a ladder that is reliable and accurate under denaturing conditions.

Lee

> Lee, > 1. Thanks for continuing to help and let the "tail" accumulate" (our > past emails). I talked with the gel company: their bp ladder is about > 100bucks less than ABI. I am sorry to keep imposing on your time, but > I am in the steep learning curve phase still. > 2. Are all these ladders equally reliable (precision)/ accurate? > 3. My microsat amplified regions are ca. 90 to 300 bp, though I > consider using more microsats of higher bp so I can maximize > the loci per well. > 4. I don't know enough details about the capillary ABI to know > denatured or not, so some of these questions should be tabled until > I learn more; since no gel is used, I assume denatured is moot. > 5. The mapmarker 1000 is only used for nondenatured gels (w/o urea, > formamide)? > 6. I don't know what you mean by polymer? > 7. I want to use the ABI capillary machine (no gel. > Respectfully, > Ann > > ===== Original Message From Lee Timms <leetimms@gmail.com> ===== >

>I thought you were asking for ABI reagents in general - not > >specifically those used for genotyping, sorry didn't read the question > >properly. You can use the 10X buffer from the gel company, formamide > >and the 96 well plates. Bioventures offers cheaper ladders, the > >MapMarker 1000 (good for fragments less than 1000bp), this is not > >offered through ABI, their 1000 bp ladder is only used in > >nondenaturing conditions and cannot be used with their polymers. I > >think that Bioventures also has a ladder for smaller fragments, maybe > >400bp and less. > > > >On 5/31/05, mouse <mouse@lamar.colostate.edu> wrote: > > > Lee, > > > I am missing the point: > > > (1) I hope to do microsat genotyping in the ABI > > > (2) I am unsure what costs at one place 4bucks/well for ABI microsats: > > > - taq > > > - primers > > > - dNTP > > > - 10X with Mg > > > - bp ladder within each well > > > (3) How can I use what you said to help me to learn how to decrease > > > ABI microsat genotyping costs? > > > Respectfully,

— / —

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>

Rodent population cycling

Dear Biologists of Rodent Population Cycling,

I have been involved in a project with Bo Niklasson in Stockholm demonstrating the determinative impact of a newly discovered picornavirus on the population cycles of rodents in northern Sweden (see Niklasson et al. 1999. A new picornavirus isolated from bank voles. Virology 255:89-93). Interacting with stress, the virus causes diabetes, heart and reproductive diseases in rodents. Additionally, this work suggests a determinative impact on human diseases. We would like to extend the rodent studies to North America, where the virus has also been found in native rodents.

Please let me know if you might be interesting in collaborating on this work by making available field-caught rodents (voles are of particular interest) for diabetes testing. We envision that we would come to your locale to perform glucose tolerance tests on the animals, and retain tissue samples to test for the virus.

Bill Klitz klitz@berkeley.edu

Bill Klitz <klitz@socrates.berkeley.edu>

Sciurus vulgaris samples

Dear Evoldir readers

We recently found that Dutch *Sciurus vulgaris* (Eurasian red squirrel) has a deviating prion gene sequences probably associated with a relatively recent gene duplication. We would like to track down this duplication event and are therefore looking for non-Dutch *S. vulgaris* genomic DNA, enough for a few PCR reactions (some 200ng-400ng).

If you can help, please contact: o.madsen@ncmls.ru.nl

Thanks, Ole Madsen

Ole Madsen University of Nijmegen 161 Department of Biochemistry P.O.Box 9101 NL-6500 HB Nijmegen The Netherlands Phone: +31-24-3616676 Fax: +31-24-3540525 e-mail: o.madsen@ncmls.ru.nl

O.Madsen@ncmls.ru.nl

tems. He also demonstrated that high species diversity among competitors – as observed, for example, in rocky inter-tidal communities, or in tropical rain forests – can be maintained by recurrent disturbance. Professor Levin has actively collaborated with economists and environmental scientists to propose methods for dealing with environmental problems. His work has shown that ecosystems and the biosphere are not super-organisms, as previously suggested, but complex adaptive systems with apparent regularity emerging from self-organization processes. Among his primary concerns are the staggering losses in biodiversity worldwide that have resulted in the recent past from the mass production, consumption and waste disposal practices of human populations. His 1999 book, “Fragile Dominion,” illustrates how the loss of biodiversity has created direct threats to human survival, and identifies a series of actions urgently necessary for maintaining biodiversity. In proposing many methods of biological conservation and ecosystem management, Professor Levin has made fundamental contributions to environmental science.

Simon Levin served as SMB President from 1987 to 1989. Congratulations Simon!

Golding@McMaster.ca Golding@McMaster.ca

SimonLevin wins KyotoPrize

>From - The Bulletin of Mathematical Biology -

Inamori Foundation Announces 21st Annual Kyoto Prize Laureates for Lifetime Achievements in Technology, Science, and the Arts

http://www.kyotoprize.org/pressrel_061005.htm The announcement for the Basic Science Prize reads as follows:

The 2005 Kyoto Prize in Basic Sciences focuses on the field of Biological Sciences. Professor Simon A. Levin will receive the award for establishing the field of “spatial ecology” and expanding scientific understanding of the biosphere as a “complex adaptive system.”

Professor Levin’s use of mathematical models to understand the complex patterns of the biosphere has made a substantial impact on environmental sciences and led to new methods of environmental protection. In 1974, with Dr. Robert T. Paine, he proposed the “patch dynamics model” that forms the basis of many current ecological models for marine and terrestrial ecosys-

Smithsonian ThankYou

Dear Evoldir members,

As you may know, the Smithsonian Institution’s National Museum of Natural History has withdrawn its support of the ID-creationist movie “The Privileged Planet” and has returned the \$16,000 “donation” to the Discovery Institute. I want to thank the many of you who wrote in to the NMNH’s director, Christian Samper, and to share with you the response he wrote in to everyone who emailed him:

Dear -----,

“Thank you for your mail and for sharing your views. Enclosed please find a statement issued by the Museum on June 1. National Museum of Natural History, Smithsonian Institution The Smithsonian’s National Museum of Natural History recently approved a request by the Discovery Institute to hold a private, invitation-only screening and reception at the Museum on June 23 for the film ”The Privileged Planet.“ Upon further review we have determined that the content of the film is not

consistent with the mission of the Smithsonian Institution's scientific research. Neither the Smithsonian Institution nor the National Museum of Natural History supports or endorses the views of the Discovery Institute or the film "The Privileged Planet." Given that the Discovery Institute has already issued invitations, we will honor the commitment made to provide space for the event, but will not participate or accept a donation for it."

When one of you wrote in thanking Samper for his actions, Samper wrote the following response:

>My pleasure, I can further assure you we are taking steps to make sure this >does not happen again.
Cristián Samper

So it looks as if we have won a small skirmish in the continuing battle against ID. I suggest that it might be nice if we sent one more email to Dr. Samper, thanking him for his action, which really is a courageous one in today's political climate.

His email address at the Smithsonian is: Samper.Cristian@nmnh.si.edu

Jerry Coyne

Jerry Coyne <j-coyne@uchicago.edu>

Smithsonian withdraws sponsorship of creationist film

Good news for the evolution community: after initially agreeing to co-sponsor and screen a creationist film by the Discovery Institute (as I announced last week), the Smithsonian's National Museum of Natural History has withdrawn its co-sponsorship and returned the donation from the Discovery Institute. I do not know whether the film might be screened at another Smithsonian museum as a cultural document, but this is clearly a victory for evolutionists (and all scientists!). Thanks to all of you who wrote into the Museum's director protesting sponsorship of the film; I'm sure those emails played a role in this.

Jerry Coyne

Museum Quits as Film Sponsor

By THE NEW YORK TIMES Published: June 3, 2005

The Smithsonian Institution's National Museum of Natural History has withdrawn its co-sponsorship of a showing later this month of a film that supports the

theory of "intelligent design."

The museum said it would not cancel the screening of the film, "The Privileged Planet," but would return the \$16,000 that the Discovery Institute, an organization that promotes a skeptical view of the Darwinian theory of evolution, had paid it.

Proposals for events at the National Museum of Natural History are reviewed by members of the staff, and it shares sponsorship of all events. After the news of the showing caused controversy, however, officials of the museum screened "Privileged Planet" for themselves.

"The major problem with the film is the wrap-up," said Randall Kremer, a museum spokesman.

"It takes a philosophical bent rather than a clear statement of the science, and that's where we part ways with them

Jerry Coyne <j-coyne@uchicago.edu>

Software Lamarc 2 0

Aloha SMBE attendees,

I am looking for someone (or a couple people) to share a cab from the Auckland airport to the conference center area. I'm staying at the carlton and someone there told me the cab fare is ~\$NZ50 from the airport. I will be arriving sunday morning ~7am. Anyone else arriving around the same time?

Many thanks Cam

- Cam Muir Ph.D. Assistant Professor Biology Department University of Hawai'i - Hilo 200 W. Kawili St. Hilo, HI, 96720 cmuir@hawaii.edu 808-933-3154 (office)

It is more fun to talk with someone who doesn't use long, difficult words but rather short, easy words like "What about lunch?" Winnie the Pooh (AA Milne)

Cedric C Muir <cmuir@hawaii.edu>

Software Lamarc2 0

We have just released version 2.0 of the LAMARC program (part of the LAMARC package).

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

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

A serious bug existed in previous versions of Lamarc (not including Recombine) that could lead to failure to adequately deal with DNA or SNP markers of unknown phase. Please disregard any earlier results with DNA or SNP markers of unknown phase and re-run the analysis.

Version 2.0 adds:

Bayesian Analysis. LAMARC can now run a Bayesian analysis instead of performing a Frequentist one. LAMARC supports both linear and logarithmic priors with arbitrary boundaries. Users are strongly encouraged to set the prior boundaries appropriately for their datasets.

Converter Graphical User Interface. A GUI that replaces the current text menu converter is now available for all supported platforms. The GUI is a beta-test release which works poorly on X11 windowing environments. The text-based file converter is still available.

Constrained Parameters. LAMARC can now combine subsets of parameters for a particular force into groups. Each group can either be held constant at a given value or constrained to all be equal to each other. Runs which estimate fewer independent parameters will use their search time more efficiently, but incorrectly constraining a parameter may bias the estimate of all other parameters.

Relative Mu and Ne. LAMARC now handles analysis of data with known differing rates of mutation or population size: for example, a run can correctly incorporate both mtDNA and nuclear DNA. It does not currently allow for the specification of a distribution of rates or sizes.

Performance improvements. Maximization of the likelihood surface now succeeds on a wider range of surfaces. A new arranger is available for use that just lengthens and shrinks all the branches in the tree; this may increase the effectiveness of the search, particularly in Bayesian runs.

Interface Cleanup. Models of marker evolution may

now be set/changed in the menu.

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

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

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

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

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

mkkuhner <mkkuhner@kingman.gs.washington.edu>

Software SQUINT 1 0

We have released a new multiple sequence alignment editor called SQUINT. SQUINT is written in Java and requires that a Java Virtual Machine (JVM) is installed. The program can be downloaded without a JVM from <http://www.bioinformatics.org.nz> under the Software Link, and is available for Windows, MacOS, and Linux.

SQUINT has the following features:

- o- Read and export files in FASTA, PHYLIP and NEXUS formats
- o- Nucleotide sequences can be viewed as amino acids or codons, with codon boundaries indicated
- o- Display sequences in split windows, with different windows showing different views (e.g., nucleotides and amino acids)
- o- View changes to alignment scores in real time as alignment is edited
- o- Versatile editing features, including block selection, point selection, left and right insertion of gaps

In addition to its editing features, SQUINT is also a multiple alignment program. SQUINT can align all sequences in the alignment, selected sequences, or even selected blocks within an existing alignment. SQUINT can align the translated amino acids of nucleotide sequences, and back-translate the alignment to the original nucleotide sequences, a feature that we consider to be particularly useful.

Documentation is embedded within the program within the Help menu option, and the context-specific Help

buttons.

SQUINT is available at no charge. Please contact us with your comments, good and bad, and reports of bugs.

Matthew Goode (mailto:m.goode@auckland.ac.nz)
Allen Rodrigo (mailto:a.rodrigo@auckland.ac.nz)

Bioinformatics Institute and The Allan Wilson Centre for Molecular Ecology and Evolution University of Auckland

a.rodrigo@auckland.ac.nz

Stationarity tests answers

Stationarity of nucleotide frequencies is an important assumption of most sequence evolution models. Although ML tree reconstruction is to some extent robust against the violation of underlying assumptions, one never knows how much violation is actually tolerated before the method produces wrong results. It is therefore good practice to exclude sequences from the analysis whose base compositions deviate too much from the average.

A popular method to facilitate this decision is a simple chi-square test which compares the nucleotide distribution of each sequence with that of the whole data set: It rejects a sequence if it becomes improbable that the two distributions are equal. Many people have been using this test over years and I too have implemented it in my own software - without thinking too much about it.

The problem is that p-values produced by this method depend strongly on the sequence lengths. Any naturally evolving sequence which is to some extent off the equilibrium will pass the test if it is only short enough, and any sequence that is long enough will fail - no matter how good or bad it is. Especially the punishment of long sequences is bad because ML tree reconstruction is known to become more and more reliable the longer the sequences are.

Take a small sequence alignment whose sequences have passed the chi-square test and concatenate it several times with itself. You will be surprised that very likely some of the sequences are being rejected now, though the phylogenetic information can not have changed.

I am looking for alternatives. Any ideas? Is there a simple way to check that the base composition in a data

set is or was suitable for tree reconstruction?

Gangolf

Hi Gangolf

Perhaps one way to do this is to use parametric bootstrapping, as follows:

1. Estimate the best (i.e., ML) model of evolution, stationary frequencies, and tree for a given dataset.
2. Use the estimated model, frequencies and tree to generate simulated datasets.
3. Now estimate the distribution of your Chi-squared statistics using the simulated sequences.

You can now assess how each sequence fits against this distribution.

Of course, this approach is predicated on your choice of the model that best describes the evolution of the sequences. The ML rate/tree/frequency estimates of a less-than-satisfactory model will give an inappropriate chi-squared distribution.

Be interested to know how this works. Cheers

Allen Rodrigo

Dear Jobb

We developed a Disparity Index test that is more powerful than the Chi-square test for this purpose. This method can also be used to compute the disparity index per site, as well. It is implemented in the software MEGA (www.megasoftware.net) for DNA and protein sequences and it has been used for analysis of mammalian DNA and proteins. Relevant references are given below (note that all pdfs are available at www.kumarlab.net/publications):

Kumar S & Gadagkar SR (2001) Disparity Index: A Simple Statistic to Measure and Test the Homogeneity of Substitution Pattern Between Molecular Sequences. *Genetics* 158:1321-1327.

Tamura K & Kumar S (2002) Evolutionary Distance Estimation Under Heterogeneous Substitution Pattern Among Lineages *Molecular Biology and Evolution* 19:1727-1736.

I hope this is helpful.

Sudhir Kumar www.biodesign.org/efg
www.kumarlab.net

Dear Gandolf,

We recently published a paper (*Systematic Biology* 53, 638-643 [2004]) in which we reviewed methods for assessing compositional heterogeneity.

All the best,

Lars

Hi,

My view on how to think about this is as a model selection problem: We have to choose between a model M0 under which all sequences have the same base composition, and models M1,... under which some sequences have different base compositions.

It is well known that many classical (p-value/likelihood/LRT/AIC) model selection methods are asymptotically inconsistent, meaning that as the number of i.i.d. observations goes to infinity the probability of selecting the the right model does not go to one. In contrast, the Bayes factor and BIC (a.k.a. Schwarz criterion) are asymptotically consistent. Note that consistency is an entirely classical concept, referring to probabilities in repeated sampling under the same true model. In this sense, Bayesian methods perform better by a classical criterion.

The BIC is like a LRT/AIC model selection criterion, but is

$$\text{BIC} = 2 \times (\ln L(M1) - \ln L(M0)) - k \ln(n)$$

where k is the difference in degrees of freedom of the two models, and n is the number of i.i.d. observations. Thus as n gets large we

— / —

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>

Stationarity tests answers2

Dear Brian,

here are some collected late answers to my queries, and one answer to an answer. The first is about my I+Gamma question, the other two about stationarity tests.

Best wishes, Gangolf

Dear Gangolf,

Concerning the I+G questions and the interesting discussion that followed ? given the high increase in

sequence-data availability it certainly looks like the I+G model is problematic. We have recently developed a novel evolutionary model that is based on a mixture of gamma density functions. This model generalizes the traditional gamma distribution model and the I+G model by assuming the existence of a number of gamma distributions (components), each characterized by its own set of parameters (alpha and beta). This mixture-model further defines the a priori probability for each gamma component. The resulting model can accommodate a multi-modal rate distribution, where the number of modes depends on the number of gamma components and how different each component is from another. We showed that the Gamma-mixture model can better describe the among-site-rate-heterogeneity of sequence evolution using both simulations and real data examples. This model also improves the inference of site-specific evolutionary rates.

The paper describing the Gamma-mixture model will be presented in the upcoming ECCB meetings and will appear in Bioinformatics (attached please find the latest draft).

Best,

Itay Mayrose and Tal Pupko

Gangolf:

You have initiated a great discussion on the evoldir.

I am about to submit a ms for publication in which I use ANOVA to compare the principal components of the nucleotide frequencies across the eutherian tree. I presented the results at the 2004 evolution meetings in Colorado. This tree is a great example of the homogeneity test failing to reveal serious base composition bias across the tree. This happens for several related reasons.

Negative results for the homogeneity test do not suggest that the sequences are homogeneous but rather suggests that they contain insufficient evidence to reject homogeneity in favor of heterogeneity. In short, compared to the mean base frequencies, the standard errors are too large to reveal heterogeneity. And that is because so much of the variance (within that standard error) among sequences is explained by differences across the clades. The among-clade differences inflate the standard error so and these go undetected by the homogeneity test.

Note that Swofford warns of this problem at the end of the output for his test in PAUP. The test ignores tree structure. So a test that accounts specifically for the variance among the clades is needed too.

Principal components analysis looks at the full multivariate correlation structure of the four nucleotide frequencies across the sequences and transforms them to uncorrelated variables (the principal components that are appropriate for ANOVA. ANOVA on the PCs separates the within-clade variance from the among-clade variance to demonstrate the serious departure from base composition homogeneity demanded by current models of sequence evolution.

Hope that makes some sense.

Cheers, Pat

Hi,

Be careful about using the BIC. It is known to be too conservative for model selection, even in quite simple experimental situations. Work is currently being undertaken to improve it. BIC is an asymptotic approximation to the Bayes factor which ASSUMES A UNIT REFERENCE PRIOR. ie a prior whose information content is equal to the average information content of one observation. This may or may not be appropriate for your analysis. BIC will not approximate the Bayes factor calculated under different priors. If you are willing to make the standard Bayesian assumptions, direct specification of priors and calculation of Bayes factors is the way to go for Bayesian model selection, in my humble opinion. Of course, in many circumstances this can be difficult.

See Sociological Methods Research Vol. 33 (2004) and Vol. 27 (1999) for a thorough discussion on the use and abuse of the BIC for model selection.

Cheers,

Simon.

Gangolf Jobb <gangolf@treefinder.de>

d'Endoume MarineStation

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structure. So a test that accounts specifically for the variance among the clades is needed too.

Principal components analysis looks at the full multivariate correlation structure of the four nucleotide frequencies across the sequences and transforms them to uncorrelated variables (the principal components that are appropriate for ANOVA. ANOVA on the PCs separates the within-clade variance from the among-clade variance to demonstrate the serious departure from base composition homogeneity demanded by current models of sequence evolution.

Hope that makes some sense.

Cheers, Pat

Hi,

Be careful about using the BIC. It is known to be too conservative for model selection, even in quite simple experimental situations. Work is currently being undertaken to improve it. BIC is an asymptotic approximation to the Bayes factor which ASSUMES A UNIT REFERENCE PRIOR. ie a prior whose information content is equal to the average information content of one observation. This may or may not be appropriate for your analysis. BIC will not approximate the Bayes factor calculated under different priors. If you are willing to make the standard Bayesian assumptions, direct specification of priors and calculation of Bayes factors is the way to go for Bayesian model selection, in my humble opinion. Of course, in many circumstances this can be difficult.

See Sociological Methods Research Vol. 33 (2004) and Vol. 27 (1999) for a thorough discussion on the use and abuse of the BIC for model selection.

Cheers,

Simon.

Gangolf Jobb <gangolf@treefinder.de>

d'Endoume MarineStation 2

Dear Brian,

here are some collected late answers to my queries, and one answer to an answer. The first is about my I+Gamma question, the other two about stationarity tests.

Best wishes, Gangolf

Dear Gangolf,

Concerning the I+G questions and the interesting discussion that followed ? given the high increase in sequence-data availability it certainly looks like the I+G model is problematic. We have recently developed a novel evolutionary model that is based on a mixture of gamma density functions. This model generalizes the traditional gamma distribution model and the I+G model by assuming the existence of a number of gamma distributions (components), each characterized by its own set of parameters (alpha and beta). This mixture-model further defines the a priori probability for each gamma component. The resulting model can accommodate a multi-modal rate distribution, where the number of modes depends on the number of gamma components and how different each component is from another. We showed that the Gamma-mixture model can better describe the among-site-rate-heterogeneity of sequence evolution using both simulations and real data examples. This model also improves the inference of site-specific evolutionary rates.

The paper describing the Gamma-mixture model will be presented in the upcoming ECCB meetings and will appear in Bioinformatics (attached please find the latest draft).

Best,

Itay Mayrose and Tal Pupko

Gangolf:

You have initiated a great discussion on the evolDir.

I am about to submit a ms for publication in which I use ANOVA to compare the principal components of the nucleotide frequencies across the eutherian tree. I presented the results at the 2004 evolution meetings in Colorado. This tree is a great example of the homogeneity test failing to reveal serious base composition bias across the tree. This happens for several related reasons.

Negative results for the homogeneity test do not suggest that the sequences are homogeneous but rather suggests that they contain insufficient evidence to reject homogeneity in favor of heterogeneity. In short, compared to the mean base frequencies, the standard errors are too large to reveal heterogeneity. And that is because so much of the variance (within that standard error) among sequences is explained by differences across the clades. The among-clade differences inflate the standard error so and these go undetected by the homogeneity test.

Note that Swofford warns of this problem at the end of the output for his test in PAUP. The test ignores tree structure. So a test that accounts specifically for the variance among the clades is needed too.

Principal components analysis looks at the full multivariate correlation structure of the four nucleotide frequencies across the sequences and transforms them to uncorrelated variables (the principal components that are appropriate for ANOVA. ANOVA on the PCs separates the within-clade variance from the among-clade variance to demonstrate the serious departure from base composition homogeneity demanded by current models of sequence evolution.

Hope that makes some sense.

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Hi,

Be careful about using the BIC. It is known to be too conservative for model selection, even in quite simple

experimental situations. Work is currently being undertaken to improve it. BIC is an asymptotic approximation to the Bayes factor which ASSUMES A UNIT REFERENCE PRIOR. ie a prior whose information content is equal to the average information content of one observation. This may or may not be appropriate for your analysis. BIC will not approximate the Bayes factor calculated under different priors. If you are willing to make the standard Bayesian assumptions, direct specification of priors and calculation of Bayes factors is the way to go for Bayesian model selection, in my humble opinion. Of course, in many circumstances this can be difficult.

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Cheers,

Simon.

Gangolf Jobb <gangolf@treefinder.de>

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Comparative phylogeography

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 pri-

mary 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 desirable. The candidate's Ph. D. must have been completed prior to start date of September 1, 2005. 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. Review of applications will begin July 1, 2005, and will continue until position is filled. 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

FairchildGarden anatomical survey

Postdoctoral Position in Plant Systematics and Anatomy

Expected funding for a postdoc researcher starts September 2005 or later, if need be. Applicant should be well versed in modern phylogenetic techniques and have a strong interest (if not experience) in plant anatomy. The project features an anatomical survey of the palm family (Arecaceae/Palmae) in collaboration with Dr. Jack Fisher (Fairchild Tropical Botanic Garden) and Dr. P. Barry Tomlinson (National Tropical Botanical Garden). For the Project description, see: <http://www.virtualherbarium.org/palmresearch/>. For other activities in palms and systematics at Fairchild, see: <http://www.ftg.org/research/palmbiology.html>. Research will be based on living collections in Florida and Hawaii. Responsibilities include: supervising

technical assistant, collecting palm specimens and anatomical data, phylogenetic analysis, and manuscript and website preparation. Applicants should send resume, brief statement of botanical interests, and names and e-mail addresses of three potential references to Jack Fisher (jfisher@fairchildgarden.org <<mailto:jfisher@fairchildgarden.org>>). Fairchild Tropical Botanical Garden is an Equal Opportunity Employer.

Pamela.Diggle@colorado.edu

HebrewU InvasiveBirds

Post-doc position available: Invasive Birds in Europe

A post-doctoral position is available immediately for a study on invasive birds in Europe. The post-doc will be part of the European Commission Sixth Framework multi-country consortium DAISIE (Delivering Alien Species Inventories for Europe). The post-doc will work together with Dr. Salit Kark and the Biodiversity Research Group and will be based at the Hebrew University of Jerusalem, Israel. There may also be a possibility to spend part of the period at the University of Bern, Switzerland to work on the project. The post-doc will also take part in workshops of the consortium members in Europe several times a year. The study includes the generation of a database on invasive birds in Europe, analysis of spatial and temporal patterns and processes of invasion using the database, research on impacts and detailed work on the worst avian invaders. More details in: <http://www.DAISIE.ceh.ac.uk/>. Requirements: Experience with avian ecology (preference will be given to those experienced with invasion biology), experience with database generation and analysis, and experience with GIS. Knowledge of several European languages is an advantage, as this study will collate data from diverse resources. The position is available immediately for one year. There may be a possibility to extend the position for a second year. For more details and to apply, please send an e-mail with a cover letter, your CV and publication list, names and contact info (address and e-mail) of three references to:

Dr. Salit Kark The Biodiversity Research Group Dept. of Evolution, Systematics and Ecology, The Institute of Life Sciences, The Hebrew University of Jerusalem, Jerusalem 91904, Israel E-mail: salit@cc.huji.ac.il Web page: <http://shum.huji.ac.il/~salit/> salit@cc.huji.ac.il

INRA Bordeaux OakEvolPopGenet

Post-doctoral proposition at Mixed Unit Research BioGEco-Bordeaux (INRA forestry department) P21: Differential molecular and physiological response of pedunculate and sessile oaks to hypoxia

The genetic group of UMR BIOGECO is conducting research activities in three main areas 1- Evolutionary biology and population genetics 2- Genomics 3- Tree improvement

Since several years, this group is working on molecular differentiation between pedunculate and sessile oaks. These two species are sympatric although they occupy ecological different niches: pedunculate oak grows on humid and rich soils and is tolerant to waterlogging but is sensitive to drought and sessile oak needs acid and dry soil. Hybridization is observed between the two species. Several genetic studies using neutral molecular markers showed similar genetic diversity between the two species with a very low interspecific differentiation. Only allelic frequency differences were obtained. However, morphological and physiological differences were observed. For instance, pedunculate oak is more tolerant to waterlogging than sessile oak. Although genomes of both species exhibit high molecular similarity, genomic regions involved in species differentiation do exist. It seems particularly interesting to focus our work on the detection of these regions. A genetic map has been developed on a full sib family of pedunculate oak and has been completed for QTL analysis of bud burst, growth and hypoxia. Experimental trials are developed in Nancy and hypoxic stress will be applied this summer on the same full sib family.

The recruited person will work at the BioGEco unit in INRA Bordeaux with a close cooperation with EEF unit in INRA Nancy. He/She will be in charge on the identification of molecular markers differentially expressed between the two species on stressed or non stressed conditions by using SSH libraries and proteomic analysis. He/She will assess the expression level of differentially expressed genes (hybridization, quantitative PCR) and will compare transcriptomic and proteomic results. He/She will realise co-locations analysis of QTL/candidate genes.

Required knowledges: molecular biology, molecular genetic, bioinformatic knowledge and population genetics. Langage: English, French

This project has been selected by INRA. The net salary will be about 2000 .

Administrative conditions: The candidate should possess his PhD should be less than 40 years old should not have work at INRA Bordeaux should be free in october or november or december 2005.

If you need more informations, please contact Catherine Bodénès catherine.bodenes@pierroton.inra.fr Antoine Kremer antoine.kremer@pierroton.inra.fr Or go on the EFPA web site <http://www.inra.fr/efpa/internet/post-docs.htm> To submit your candidature, please go to this site http://w3.inra.fr/les_hommes_et_les_femmes/rejoignez_nous/completer_sa_formation/le_recrutement_de_post_doctorants The number project is P21. You should send your candidature file by electronic way to EFPA/INRA web site before the 31th of july 2005. Thank to send a copy to catherine.bodenes@pierroton.inra.fr.

Catherine Bodénès <Catherine.Bodenes@pierroton.inra.fr>

LausanneU EvolBioinformatics

A post-doctoral fellowship will be available in October 2005 to join a new lab of Evolutionary Bioinformatics a Lausanne University (Switzerland).

There is no predefined subject, but the post-doc should fit in the general topics of the lab, namely the evolution of gene and genome function in animals. The work can be more biological or more methodological. I am open to any good CV from biology, bioinformatics or computer science, but some knowledge of programming and some knowledge of biology is a prerequisite.

If you are interested, please send me by email you CV, email and phone contact information of two references, and a one page research project.

More information here: <http://www.sdsc.edu/~marc/-lausanne.html> Marc ____ Marc Robinson-Rechavi <http://www.sdsc.edu/~marc> Joint Center for Structural Genomics write to: Godzik lab, Burnham Institute, 10901 North Torrey Pines road, La Jolla, CA 92037, USA phone: +1 858 646 3100 x3553; fax: +1 858 713 9949

La liberte ne s'use que quand on ne s'en sert pas
marc@sdsc.edu marc@sdsc.edu

NorthCarolinaStateU EvolMolGenetics

NorthCarolinaEvolutionaryMolecularGenetics/ChemicalEcology

We just received three years of NSF funding to study “Evolution of moth sexual communication systems”. Our approach involves combining Quantitative Trait Locus analysis and candidate gene approaches with field tests of mating success to determine the number of genes and identity of genes that code for species specific mating. We are especially interested in understanding evolutionary mechanisms involved in diversification of complex traits that appear to be under stabilizing selection. We are looking for a postdoc who wants to conduct molecular genetic analyses to identify genes that control sexual communication, and who also wants to do some field work. Candidates must have a background in molecular/quantitative genetics. Experience in chemical ecology and the use of GC equipment would be very helpful. The successful applicant will work in the labs of Fred Gould and Coby Schal.

MORE BACKGROUND: Most night-flying moth species locate mates through production of, and response to, a very precise blend of two or more volatile chemical compounds. Within a population, females with atypical blends have been shown to be less attractive to males than females with the population’s common blend. Similarly, rare males that respond to atypical blends have been found to be at a disadvantage in finding mates. The genes that control pheromone blend ratios have never been found to be linked to, or affect male response, so mutations that cause changes in each of the two components of communication are expected to arise independently. On a simple theoretical level, this type of sexual communication system is expected to be evolutionarily constrained because an individual with a mutation leading to an altered blend or response will be selected against, when rare. Even if the selective disadvantage to rare individuals with alleles for novel signals or responses is minimal, mass selection is not expected to increase their frequency in the population. Based on these assumptions it is difficult to account for the great diversification of chemical mixtures used in mate communication by over 10,000 moth species. By dissecting the genetic underpinnings of selective mating in moths we are investigating a number of potential evolutionary mechanisms that could have resulted in this diversification . We are working with two sympatric

moth species that have very distinct sex pheromone blends, do not mate in the wild, but can be induced to mate in the lab. We have used segregating backcross families to map a number of QTL that control production of specific female sex pheromone components and male response to these components. We have moved one specific QTL between species and tested its impact on mating in the field. There are a lot more experiments waiting for the right postdoc!

North Carolina State University is a leading research institution with a strong commitment to the study of quantitative, molecular, and population genetics. The University is situated in Raleigh, NC and is within 30 miles of Duke University, UNC-Chapel Hill, NIEHS, an EPA research unit, and the Research Triangle Park. NC State University is an equal opportunity and affirmative action employer. For more details on our labs see: <http://www4.ncsu.edu:8030/%7Efgould/> and <http://www.cals.ncsu.edu/entomology/schal/> The successful applicant will participate in the inter-departmental Keck Program in Behavior Biology—<http://www.cals.ncsu.edu/beh.bio/index.html> To apply: Send to Fred.Gould@NCSU.edu 1) A one or two page letter of intent. 2) CV, and 3) Names of 3-4 references. Closing date for applications is July 20, 2005, or until a suitable candidate is found. For further information call Fred Gould at 919-515-1647 or email to above email address.

fred_gould@ncsu.edu

NorthCarolinaStateU VectorGeneticModels

Postdoc:

North Carolina State University –Vector/disease genetic models

Posdoctoral Fellowship

Vector/disease genetic models: We need an evolutionary biologist with experience in computer simulation modeling (C++ preferred) to work on an NIH-funded project. The project is aimed at building simulation models that link insect population dynamics and population genetics in a way that can contribute to improving strategies for releasing transgenic mosquitoes to reduce the incidence of human disease. Once the insect modeling is complete, disease epidemiology models will be built and linked to the insect models. The

fellowship is for 2-3 years. In addition to working on model development and testing, the person in this position will collaborate in an interdisciplinary group composed of mosquito ecologists, disease epidemiologists, molecular biologists, biomathematicians, ethicists, and scientists from disease-endemic countries, in efforts to develop novel transgenic strategies for disease reduction. The person in this position will work with the PI and at least one other postdoc in organizing a workshop to teach other researchers how to use the models. There will be an opportunity for some empirical research (if desired), and for interactions with other members of the lab who are working on other evolutionary and modeling research. We also anticipate interaction with the newly established National Evolutionary Synthesis Center in Durham, NC.

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

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

To apply: Send to Fred.Gould@NCSU.edu 1) A one or two page letter of intent. 2) CV, and 3) Names of 3-4 references. Closing date for applications is July 15, 2005, or until a suitable candidate is found. For further information call Fred Gould at 919-515-1647 or email to above email address. candidate is found. For further information call Fred Gould at 919-515-1647 or email to above email address.

OregonStateU AquaticPopBio

POSTDOCTORAL RESEARCH ASSOCIATE: The Department of Zoology, Oregon State University seeks candidates for a postdoctoral position in Aquatic Population Biology and Genetics. Start date is approximately 15 September 2005 (negotiable). As part of an NSF-funded project (<http://www.science.oregonstate.edu/lytlelab/projects.htm>), the appointee will use molecular methods to under-

stand patterns of adaptive evolution in populations of desert aquatic insects. The molecular work will complement other projects in the research group pertaining to behavioral evolution, evolutionary theory, and conservation biology, and so an interest in cross-disciplinary collaboration is desirable. Although based at Oregon State, the project may include fieldwork in the Southwestern U.S. and Mexico. Required qualifications include a Ph.D. in evolutionary biology, ecology, genetics, or a related discipline, as well as experience with relevant statistical and computational methods. Candidates with experience in microsatellite development and data analysis are especially encouraged to apply. Complete job description available at <http://oregonstate.edu/jobs>. For full consideration apply by 15 June 2005. Email a letter of application, CV, statement of research interests and qualifications, and contact information for three references to: Dr. David A. Lytle, lytle@science.oregonstate.edu (Dept. of Zoology, OSU, Corvallis OR 97331). OSU is an AA/EOE.

lytle@science.oregonstate.edu
lytle@science.oregonstate.edu

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RutgersU ShellfishGenetics

Postdoctoral Position In Shellfish Genetics

A postdoctoral associate position is available at the Haskin Shellfish Research Laboratory, Rutgers University. The position is funded by grants from NOAA Sea Grant and New Jersey Commission on Science and Technology. Research will focus on the identification and mapping of genes and quantitative trait loci related to disease resistance in the eastern oyster. Applicants should have a Ph.D. and background in genetics and molecular biology. Prior experience in cloning, sequencing and genotyping is preferred. The appointment starts on July 1, 2005 or soon after, and is for one year with possible renewal. Search will continue until the position is filled. Interested individuals should submit a CV, a brief statement of interest, and three references to: Dr. Ximing Guo, Haskin Shellfish Research Laboratory, Institute of Marine and Coastal Sciences, Rutgers University, 6959 Miller Avenue, Port Norris, NJ 08349. Phone: (856) 785-0074 x4324; Fax: (856) 785-1544; Email: xguo@hsrl.rutgers.edu. Web: <http://www.hsrl.rutgers.edu>. Affirmative Action/Equal Opportunity Employer.

Ximing Guo <xguo@vertigo.hsrl.rutgers.edu>

TexasStateU EvolBiol

Postdoctoral Teaching Fellowship

The Graduate Program in Biology at Texas State University announces a one-year POSTDOCTORAL FELLOWSHIP/LECTURESHIP. Our program offers unique training and research opportunities in the fields of ecology and evolutionary biology. Our research/lecture position provides recent Ph.D.s with an opportunity for independent research with a faculty sponsor as well as experience developing and teaching new courses. Teaching is anticipated to be an introductory majors biology course in Organismal Biology (Evolution and Ecology) for undergraduates and a non-majors biology course entitled Organisms, Evolution and Environment each semester. Preference is given to candidates identifying collaborative work with a faculty member of the department. This position is available starting fall 2005 and requires a year commitment. Salary is \$34,578.

To apply, email your curriculum vitae, three letters of reference, statements of research and teaching interests, and letter of interest to your potential faculty sponsor. Then have your faculty sponsor forward your application to Joe Koke (jkoke@txstate.edu). The department chair will select from the applicant pool. Review of applications is ongoing and will continue until a successful candidate is found. Please visit <http://www.bio.txstate.edu> for a full description of the Department's Programs and Faculty.

—

Caitlin R. Gabor, Ph. D. Assistant Professor Texas State University (Formerly SWT) Department of Biology, Science Building Room 384 San Marcos, TX 78666-4615 Work: (512) 245-3387; Fax: (512) 245-8713 E-mail: gabor@txstate.edu

<http://www.bio.txstate.edu/~gabor/gabor.htm>

**UCaliforniaIrvine Viral
Phylogenetics**

Department of Ecology and Evolutionary Biology

Open Position: POSTDOCTORAL SCHOLAR

A postdoctoral scholar position in the Lab of Dr. Walter M. Fitch is available at U.C. Irvine. The laboratory studies the conclusions one can derive from viral phylogenetic analysis. These include new methods for determining the migrations around the world of the human influenza virus. We also study how to predict the future evolution of the human influenza virus.

The successful candidate will have had several courses in Biology and know several programming languages. Funding for this position is available for two years. Review of applicants will begin July 1, 2005 and position will remain open until filled. Salary to be commensurate with experience. To apply, send your name, CV, address, and phone numbers to the address below along with the names and addresses of two referees along with their phone numbers.

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

URL: ecoevo.bio.uci.edu/Faculty/Fitch/Fitch.html

The Department of Ecology and Evolutionary Biology at UC Irvine houses a dynamic group of faculty in evolutionary genetics, including Professors Long, Clegg, Bush, Ayala, Wallace, and Fitch, among others. Information about the department and the campus is available at ecoevo.bio.uci.edu

Applications due by: 07/01/05

Contact information:

Dr. Walter M. Fitch Department of Ecology and Evolutionary Biology 321 Steinhaus Hall University of California, Irvine Irvine, CA 92697-2525 e-mail: wfitch@uci.edu

The University of California, Irvine has an active career partner program, is an equal opportunity employer committed to excellence through diversity, and has a National Science Foundation Advance Gender Equity Program. Posted: May 24, 2005

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wfitch <wfitch@uci.edu>

UCollegeLondon SexualConflict

NERC-funded Post-Doctoral Research Fellow, Department of Biology, University College London

Determining the genetic basis of sexual conflict in *Drosophila melanogaster*: the role of the sex peptide.

A full-time NERC funded post-doctoral position is available for up to 36 months in the fruit-fly laboratory of Dr Tracey Chapman (<http://www.ucl.ac.uk/~ucbhctoc/tc1.html>). Sexual conflict exists when the evolutionary interests of the sexes diverge over reproductive decisions. In *D. melanogaster*, seminal fluid proteins such as the sex peptide (SP) are implicated in mediating such conflicts of interests (e.g. Chapman et al. 1995 *Nature* 373, 241-244; Wigby & Chapman 2005 *Current Biology* 15, 316-321). In this project we will study the function of the SP, using males in which the SP is over or under expressed (e.g. Chapman et al. 2003 *PNAS*, 100, 9923-9928) to conduct life history assays. We will investigate important questions in three areas.

- (1) What is the extent to which SP underlies conflict?
- (2) In terms of the life history, how does the sex peptide exert its harm on females?
- (3) What is the extent to which SP-induced harm to females and SP-derived benefit to males interact with the environment?

The candidate should have experience in general molecular biology and flywork. Starting salary is 21,640 GBP per annum pro-rata (23,970 GBP including London Allowance) and the preferred starting date is January or February 2006.

To apply and for further information, please send a covering letter and a CV with the names and contact details of 3 referees to Tracey Chapman (t.chapman@ucl.ac.uk) Department of Biology, University College London, Darwin Building, Gower Street, London WC1E 6BT. Tel:020 7679 4393 Fax:020 7679 7096. Applications by email are preferred. The closing date is 25th July 2005.

Tracey Chapman Department of Biology University College London Darwin Building Gower Street London WC1E 6BT

Phone: 00 44 (0) 20 7679 4393 FAX: 00 44 (0) 20 7679 7096 <http://www.ucl.ac.uk/~ucbhctoc/tc1.html>

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

UGoettingen **EvoDevo**

N.B. Reply to Ernst Wimmer!!

Prof. Dr. Ernst A. Wimmer Department of Developmental Biology, GZMB Institute of Zoology, Anthropology and Developmental Biology Georg-August-University Goettingen Justus-von-Liebig-Weg 11 37077 Goettingen Germany Email: ewimmer@gwdg.de

Marie Curie Research Training Network "Zoonet" Development and evolution of animal form: Training modern comparative zoologists

A postdoctoral position is available for 30 months funded by the Marie Curie Research Training Network "ZOONET" (<http://www.zoonet.eu.com/>), to study arthropod development in a comparative way. The project will involve participation in an ongoing transposon mutagenesis and enhancer trap screen to identify developmental mutants in the red flour beetle *Tribolium castaneum*. Moreover, the postdoc will be encouraged to transfer these technologies to other arthropod species.

Applicants should have a doctorate and relevant experience in molecular biology as well as raising arthropods. Training will be given in the full range of approaches relevant to Evolutionary Developmental Biology (e.g. identification and isolation of gene functions from diverse arthropod species by the transgenic approaches of insertional mutagenesis and enhancer analysis), and may require exchanges between laboratories in the ZOONET Network, as well as participation in network meetings.

In the selection process, the sponsor stipulates that:

Candidates must have at least four and no more than ten years (full time equivalent) of graduate research experience; They must not be a national of the state within which the appointment will be held (Germany in this case); At the start of their fellowship, researchers may not have resided or carried out their main activity (work, studies, etc.) in Germany for more than 12 months in the 3 years immediately prior to the appointment.

The Georg-August-University aims to increase the number of female scientific staff employed and expressly requests applications from qualified women. In the framework of the legal requirements and in the case of equal qualifications, women will be considered preferentially in all areas in which they are under-represented.

Disabled persons will also be considered preferentially in the case of equal aptitude. Part-time employment may be possible under certain conditions.

The salary will be based on a German BAT IIa position. Researchers will also be eligible for an annual travel

allowance as well as a monthly mobility allowance of approximately 500 per month (approximately 900 per month for married candidates). Additionally there is a one-off Career exploration allowance of 2000.

Applicants should send to the address mentioned above: their CV and publication list together with a brief letter of intent explaining motivation and project interests and the contact details of at least two referees (address, email, telephone number).

– Dr Max Telford Department of Biology, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel: +44 (0)20 7679 2554 Fax: +44 (0)20 7679 7096

<http://www.ucl.ac.uk/biology/new/admin/-staffpages/telford/telford.html> Zoonet website: <http://www.zoonet.eu.com> – Dr Max Telford Department of Biology, University College London, Darwin Building, Gower Street, London WC1E 6BT, UK. Tel: +44 (0)20 7679 2554 Fax: +44 (0)20 7679 7096

<http://www.ucl.ac.uk/biology/new/admin/-staffpages/telford/telford.html> Zoonet website: <http://www.zoonet.eu.com> m.telford@ucl.ac.uk m.telford@ucl.ac.uk

ready in our database, including red-tailed chipmunks, Idaho giant salamanders, Coeur d'Alene salamanders, Rocky mountain tailed frogs, Columbian ground squirrels, a polydesmid millipede, dusky willows, white-bark pines, and Constance's bittercress.

As part of the CRISSP mission, the postdoc will also be involved in 100 hours of outreach per year which may involve public education, and/or workshops with land managers.

Please contact Steve Brunsfeld (sbruns@uidaho.edu), Jack Sullivan (jacks@uidaho.edu), or Lisette Waits (lwaits@uidaho.edu) for more information and apply via the website <http://www.hr.uidaho.edu/> announcement number 12508090943. Review of applications will begin on July 15, and continue until the position is filled. The starting date is flexible and funding may begin as soon as the position is filled. To enrich education through diversity, the University of Idaho is an equal opportunity/affirmative action employer.

– Jack Sullivan Department of Biological Sciences Box 443051 University of Idaho Moscow, ID 83844-3051 jacks@uidaho.edu <http://www.webpages.uidaho.edu/~jacks/> (208) 885-9049

jacks@uidaho.edu jacks@uidaho.edu

UIIdaho ConservationGenetics

Postdoctoral Fellowship University of Idaho Center for Research on Invasive Species & Small Populations (CRISSP)

We are seeking a postdoctoral fellow to join a collaborative effort to examine the genetic diversity and structure of mesic forest ecosystems in the Inland Northwest. Two full years of funding are available and the successful candidate will collaborate with Steven Brunsfeld, Jack Sullivan, & Lisette Waits (see CRISSP website <http://www.cnrhome.uidaho.edu/crissp>). This project entails fieldwork, labwork and computationally intensive data analysis using the Beowulf clusters of our computational biology facility. The taxonomic focus is broad, including plants and animals that are endemic to the inland mesic forest ecosystem, but we will focus specifically on amphibian and tree species. Markers to be employed include organellar DNA sequences, SNP data, and microsatellite data, so candidates with experience with one or more of those markers will be preferred. Genetic analysis will include and integrate phylogeography, population genetics and landscape genetics. There are genetic data for several endemic taxa al-

UKansas SexuallySelectedBehavior

Postdoctoral Research Associate:

Post-doctoral Position in Animal Behavior / Evolutionary Genetics

A post-doctoral research associate position is available to examine the evolutionary genetics of sexually-selected behavior in acoustic insects. The work will involve behavioral and molecular genetic studies of *Achroia grisella* (lesser waxmoth), a species in which males attract females with an ultrasonic mating song. *A. grisella* is a symbiont of honeybees, and some emphasis will be placed on behavioral studies at bee colonies in the field. The laboratories are well-equipped for research focused on or involving acoustic communication, signal processing, and molecular techniques, including quantitative trait loci (QTL) mapping. Required qualifications are: 1) A Ph.D. in Biology or a related field by the start of the appointment; 2) Experience in at least two of the following areas: a) animal behavior, preferably with invertebrates, b) quantitative or population genetics, c) molecular biology; 3) Good organizational

and statistical skills; 4) Demonstrated verbal and written communication skills; 5) An ability to work independently, as well as to collaborate productively with other scientists. A complete application will include a letter of application stating the research and career interests of the applicant, a curriculum vita, and three letters of reference.

Application materials should be sent to Dr. Michael Greenfield or Dr. Jennifer Gleason, Dept. of Ecology & Evolutionary Biology, Univ. of Kansas, 100 Sunnyside Road, Lawrence, KS 66045, or (preferably) via email at greenfie@ku.edu or jgleason@ku.edu. Phone: 785-864-7366 (M. Greenfield); 785-864-5858 (J. Gleason). You may also apply directly to the Univ. of Kansas personnel site:

<https://jobs.ku.edu/applicants/jsp/shared/frameSet/Frameset.jsp?name=19886231619>

Review of applications begins 15 July 2005 and will continue until the position is filled.

Lawrence is a fun and historic university town located approx. 40 miles west of Kansas City. The town offers museums, a performing arts center, restaurants and clubs, bookstores, an excellent public school system, and a variety of recreational activities; areas for hiking, fishing, and boating are found nearby. The University of Kansas is a comprehensive research institution with a superior library and laboratory facilities. Within the Division of Biological Sciences are several dynamic and collegial groups studying behavior and evolution that meet regularly for seminars and discussions. The project is funded by the U.S. National Science Foundation grant 'Genotype x environment interactions and the evolution of sexually-selected traits'. The University of Kansas is an EO/AA employer.

Michael D. Greenfield Professor Department of Ecology & Evolutionary Biology University of Kansas Lawrence, Kansas 66045

tel. 785-864-7366 fax 785-864-5321 email greenfie@ku.edu

"Michael D. Greenfield" <greenfie@ku.edu>

ULausanne ConservationBiol

Available:

One postdoc position (1 year, elongation possible)

In the Conservation Biology Group, Department of Ecology and Evolution, University of Lausanne,

Switzerland.

Start: Sept 2005 or later Salary: according to the guidelines of the Swiss National Science Foundation

We study the selective forces that currently act on fish and mammal populations, i.e. the effects of human activities in interaction with natural and sexual selection. We are also exploring the link between cooperation theory and conservation issues. We aim at predicting the consequences of different management options for the long-term survival of populations.

We are seeking candidates with a strong interest in conservation genetics, life-history, evolution, and/or game theory.

Please send your application by email (all material in one attached file) to Prof. Claus Wedekind (wedekind@fas.harvard.edu). Include your Curriculum vitae, a short description of your research interests and research experience, and names and email addresses of one or two references who could be contacted. Please do not send any letter post (we are not yet in Lausanne). Review of applications will begin July 20, 2005. Applications will be accepted until the positions are filled. See www.unil.ch/dee/ for further information.

– Claus Wedekind Hrdy Visiting Professor for Conservation Biology Harvard University One Brattle Square, 6th Floor Cambridge MA 02138; USA phone: 617-496-5543; fax: 617-496-4629 http://www.unil.ch/dee/page21538_en.html <http://www.conservation.unibe.ch/> wedekind@fas.harvard.edu

UNebraska TermiteEvol

Post Doctorate Associate-Termite Research (Molecular Biology/Insect Biochemistry/Toxicology) Postdoc position: One year and renewable depending upon progress and funding availability. Available: ASAP or until suitable candidate is found. Research will be focused on one or more areas as follows: 1) Uptake termiticides, Secondary toxicity (through trophalaxis) of bait products to subterranean termites, 2) Effect of soil eco-factors on performance of termiticides including bait products, 3) Growth regulators affecting termite physiology, and 4) Molecular characterization of subterranean termites. Techniques include: Gel electrophoresis, DNA isolation, DNA amplification and sequencing, PCR, genomic DNA library construction,

and other molecular techniques. Qualification: Ph.D. in Entomology with training in toxicology, biochemistry and/or molecular biology. Desired experience with GC, HPLC, insecticide extraction and analysis or molecular techniques. Writing and publishing data in peer reviewed journals will be required. Salary: Negotiable based upon training and experience. Send CV, publications and names of three references to: Dr. Shripat T. Kamble, Department of Entomology, University of Nebraska, Lincoln, NE 68583-0816. Phone: (402) 472-6857, Email: skamble1@unl.edu

Position: Ph.D. Research Assistantship - Subterranean Termites. The Urban Entomology Program at the University of Nebraska has one opening for a graduate assistantship to pursue Ph.D. The assistantship will include research on: "Effect of New Generation Termiticides on Feeding Behavior of Subterranean Termites" OR "Biochemical characterization proteins/fatty acids in Subterranean Termites". The successful candidate should have background in insect physiology, insect toxicology, biochemistry and molecular techniques. Since, student will be assisting in field projects, a valid driver license will be required. The research assistantship is \$17,160/year. In addition, approximately \$4,799 will be paid to the University for your tuition remission. The total cost is \$21,959. Publications are required from dissertation research in peer-reviewed scientific journals. It is the policy of the University of Nebraska that student who holds assistantship may not work more than halftime, or 20 hours per week, all jobs considered, including assistantship. Please contact: Dr. Shripat T. Kamble, Professor of Entomology, Department of Entomology University of Nebraska, Lincoln, NE 68583-0816, USA, Phone: (402) 472-6857, Email: skamble1@unl.unl.edu

I would appreciate your help in informing other researcher on your list serve.

Thank you for your help.

Shripat T. Kamble, Ph.D. Professor of Urban Entomology Department of Entomology University of Nebraska Lincoln, NE 68583-0816

skamble1@unl.edu

UNorthCarolinaCH Speciation

Postdoctoral Position at the University of North Carolina, Chapel Hill

A position is available for a Postdoctoral Research Associate in the lab of Maria Servedio at the University of North Carolina, Chapel Hill. The successful applicant should have an interest in speciation, sexual selection, behavioral ecology, and evolution, as well as a desire to study these questions using theoretical techniques. The applicant will be expected to develop an independent research project (theoretical or empirical) in addition to collaborating with the PI on theoretical projects. Examples of prior projects in the lab are described in brief on the webpage <http://www.bio.unc.edu/faculty/servedio/Lab/index.htm>. Prior experience with theoretical techniques, a strong mathematical background, and/or programming skills is preferred. A Ph.D. and a strong background in evolution is required. The appointment is for 1-2 years starting preferably in January 2006 (start date somewhat flexible). Send applications including a CV, description of research experience and interests, description of background in theory and related skills, and names and addresses of three references to

Maria Servedio Department of Biology University of North Carolina CB# 3280, Coker Hall Chapel Hill, NC 27599 or by e-mail to: servedio@email.unc.edu

Informal inquiries welcome by e-mail. Review of applications will begin on July 15 and continue until the position is filled.

***** Dr. Maria Servedio Department of Biology University of North Carolina CB# 3280, Coker Hall Chapel Hill, NC 27599 Phone: 919-843-2692 Fax: 919-962-1625 e-mail: servedio@email.unc.edu <http://www.bio.unc.edu/faculty/servedio/Lab/index.htm>

UReading PlantConservation

A three-year position is available, funded by the Darwin Initiative, to develop DNA technologies to support the conservation of Mexican desert cacti. We are seeking candidates with laboratory experience in microsatellite development and the use of molecular marker data to address questions in evolution/ecology. The main responsibility of the successful candidate will be to develop microsatellite markers for Cactaceae which will be used to determine whether plants in trade are the ex-situ progeny of parents collected under permit. As well as being used to for certification of plants in trade the markers will be used to address ecological questions re-

lating to the reproductive and dispersal biology of cacti. Mexican project members will pilot DNA sequencing strategies for species identification. The successful candidate will play a role in the development of this scheme through supervision of visiting Mexican scientists; an interest in DNA bar-coding technologies would therefore be desirable. The successful candidate will be an employee of The University of Reading, working with Dr Julie Hawkins in the School of Plant Sciences. There will be close collaboration with Dr Rolando Bárcenas Luna at the Universidad Autonoma de Querétaro in Mexico. Short periods will be spent in the field, and the successful candidate will contribute to a three-day training workshop in molecular marker technologies in Mexico. Informal enquiries and requests for further particulars to Julie Hawkins (j.a.hawkins@reading.ac.uk, or 0118 378 6546).

Application form and further particulars available from the Personnel Office, The University of Reading, Reading, RG6 6AH, telephone 0118 378 6771 or email Personnel@reading.ac.uk giving full name and address. Application Forms also available from www.reading.ac.uk/Jobs. Closing date for applications 24 June 2005. Interviews will be held on Thursday 7th July. Ideally the start date would be 1st September 2005.

Salary on the RA1A scale, spine point 6, £21, 640 p.a.

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

USDA EvolMolBiol

I have a job opening for a molecular biologist/molecular geneticist that I would greatly appreciate posting on your site:

The USDA National Wildlife Research Center has an opening for an APHIS Science Fellow - a 2 year renewable (4 year total) appointment for a molecular biologist/molecular populations geneticist in Fort Collins, CO. The individual selected for this position will apply molecular genetic techniques to improve the selectivity of wildlife management activities including predation control, wildlife disease management and invasive species control. The successful applicant will be hired at the GS-11 or GS-12 level (stating salary = \$53,409 or \$64,013). Full promotion potential = GS-13. Application period closes on June 13, 2005. For additional information, please see:

<http://www.aphis.usda.gov/ws/nwrc/employment/-index.html> or apply for position 2497-2005-0086 at <http://www.usajobs.opm.gov/> for additional information, email: john.j.johnston@aphis.usda.gov

John.J.Johnston@aphis.usda.gov

UTennessee EvolBioinformatics

This is a second announcement for this position. Please note I will be attending the SSE/Am. Nat meetings in Fairbanks, AK this month and would be happy to talk to any interested candidates.

Also, note that applicants interested in the evolution of diseases are also encouraged to apply.

Please contact me if you have any questions.

Mike

Postdoctoral Research Position: Evolutionary Bioinformatics Department of Ecology & Evolutionary Biology University of Tennessee Knoxville

Applications are currently being accepted for an 18-month postdoctoral position in the laboratory of Michael A. Gilchrist in the Department of Ecology & Evolutionary Biology at the University of Tennessee, Knoxville. The position is to help develop, integrate and test mechanistic models of intra-cellular processes with large scale databases on the yeast proteome, genome, and transcriptome within an evolutionary framework.

The emphasis of the laboratory is focused on using relatively simple deterministic and stochastic models to analyze complex, heterogeneous datasets to answer biologically motivated questions. The research associated with this position draws upon a wide range of scientific disciplines including: cellular biology, evolutionary theory, differential equations, and probability/likelihood. Consequently, the ideal candidate would have a Ph.D. in biology with a solid background in, mathematics and/or statistics. The researcher is expected to collaborate closely with the PI (Michael Gilchrist) in on-going lab projects as well as initiate new areas of research based on their own interest.

Additional areas of research conducted by the lab include: host, parasite, and saprophytic fungal life-history evolution as well as macro-ecology. The laboratory itself is part of a dynamic and growing Department, located in a medium sized city with relatively

mild weather and many opportunities for cultural and outdoor recreation.

Review of applications begins immediately and will continue until the position is filled. The start date is flexible but the position is available immediately. The position employment period is 18 months, but may be extended if additional funding becomes available.

To apply, please submit curriculum vitae, brief statement of research interests, up to 3 relevant manuscripts and 3 professional references either via email or postal mail to:

Michael A. Gilchrist, Ph.D. Department of Ecology & Evolutionary Biology 569 Dabney Hall University of Tennessee Knoxville, TN 37996-1610

email:mikeg@utk.edu

Additional information can be found at <http://eeb.bio.utk.edu/gilchrist.asp> The University of Tennessee is an Equal Opportunity/Affirmative Action Employer. Men and women of diverse racial/ethnic backgrounds and cultures are encouraged to apply.

mikeg@utk.edu

UppsalaU BacterialGenomeEvol

POSTDOCTORAL POSITION IN COMPARATIVE GENOMICS/MOLECULAR EVOLUTION

The Linnaeus Centre for Bioinformatics, Uppsala University, Uppsala, Sweden

A postdoctoral position is available funded privately by

Carl Tryggers Stiftelse. The position is guaranteed for one year with possible extensions of an additional year and is available immediately. Work must begin before January 1, 2006. Salary level is 192,000 SEK per year tax-free.

The project involves analysis of the structure, function and evolution of bacterial tRNA and rRNA operons in their full genomic context. Initial work on this topic appears this week in the inaugural issue of PLoS Computational Biology (Ardell and Kirsebom 2005). The genomic pattern of tDNA operon expression in *E. coli*.)

The successful candidate will have experience or strong interest in the following: bacterial genomes and their evolution, tRNA and rRNA biology, molecular phylogenetics, tests of selection and statistics. Applicants should have a Ph.D. in biology, genetics, biostatistics, bioinformatics or allied field.

These projects provide opportunities to collaborate with experimental groups at the Biomedical Center in Uppsala, particularly the lab of Professor Leif A. Kirsebom. (<http://www.icm.uu.se>).

Applications should be sent by email to tRNA@lcb.uu.se or by mail to: David Ardell, Linnaeus Centre for Bioinformatics Box 598, Biomedical Center, SE- 751 24 Uppsala, Sweden.

Please include CV, cover letter with research interests, relevant reprints, and contact information for at least two, preferably three, references in all applications.

For more information about the project or the position please see <http://www.lcb.uu.se/~dave> and contact me by email at tRNA@lcb.uu.se or by telephone at +46 (0)18 471 6694.

dave.ardell@lcb.uu.se dave.ardell@lcb.uu.se

WorkshopsCourses

GrubGermany ConservationGenet Nov20-Dec2 50	Switzerland FragmentedPops Sep14-17 51
LilleFrance RegulatoryNetworks Sep3-7 50	
Spain ConservationGenetics Nov17-19 50	

GrubGermany ConservationGenet Nov20-Dec2

Course announcement - International PhD-course

Conservation genetics of animals

November 20th - December 2nd, 2005, in Grub, Germany

Rapid decline in the number of livestock breeds and reduction of genetic variability within breeds has initiated growing interest for the conservation of farm animal genetic resources. We are offering a course covering important aspects and topics in conservation genetics to raise the competence in this field.

The course will consist of lectures, computer exercises (using a variety of software packages), written exercises (pen and paper), paper discussion with presentations (landmark papers) as well as demonstration of particular case studies and group work on given projects.

Main topics covered in the course are: definitions, glossary and basic knowledge; variation within populations; variation between populations; detrimental effects and extinction; assignment problems; criteria for choosing units for conservation priority and conservation strategies. Although targeted to the conservation of farm animal genetic resources, the subject covered will also be relevant and applicable to a large number of zoo and wildlife populations.

Participants are awarded 5 ECTS credits.

For course details see <http://www.nas.boku.ac.at> Follow the link "courses and workshops".

– Prof. Johann (Hans) Sölkner BOKU - University of Natural Resources and Applied Life Sciences Vienna Department of Sustainable Agricultural Systems Section Livestock Sciences Gregor Mendel Str. 33, A-1180 Vienna, Austria Tel: +43 1 47654 3271 Fax: +43 1 47654 3254 e-mail: soelkner@boku.ac.at Url: <http://nas.boku.ac.at> johann.soelkner@boku.ac.at

LilleFrance RegulatoryNetworks Sep3-7

Subject : an interdisciplinary school on Noise and ro-

bustness in transcriptional regulatory networks

Between September 3 and September 7 2005 we organize an interdisciplinary school on 'Noise and robustness in transcriptional regulatory networks' in Coquelles (France). The aim of this school is to bring together biologists, physicists, computer scientists and mathematicians to investigate how cells tolerate, control and use fluctuations in transcriptional regulatory networks. The interplay between computational and experimental approaches, between in vivo and in vitro studies in conditions mimicking the cellular nanoenvironment will be emphasized. Ralf Blossey, Bahram Houchmandzadeh and Stanislas Leibler are co-organizers of this school. Further informations can be found at the following address: (<http://www.ibl.fr/noisitransnet/>). We invite contributions for poster or oral presentations. Priority will be given to papers associating experimental and theoretical approaches in the field of single molecule studies or in single (eukaryotic) cell expression studies. The dead line for the submission of the papers is June 15 and the notification of acceptance will be on July 1st.

Bernard Vandembunder, PhD

Interdisciplinary Research Institut <http://iri.ibl.fr> IRI @ Institut de Biologie de Lille 1 rue du professeur Calmette BP447, 59021 Lille Cedex, France. tel : 33 3 20 87 10 90 fax : 33 3 20 87 11 11

Bernard
<bernard.vandembunder@ibl.fr>

Vandembunder

Spain ConservationGenetics Nov17-19

ESF CONSERVATION GENETICS WORKSHOP 17-19 November 2005, Santiago de Compostela, Spain
CALL FOR PARTICIPANTS (DEADLINE 24 June 2005)

The European Science Foundation is funding a series of workshops under the ConGen programme (Integrating population genetics and conservation biology: merging theoretical, experimental and applied approaches). The three-day meeting (arrival Wednesday 16, departure Sunday 20 November) in Santiago de Compostela will focus on approaches to studying genetic sources of extinction, responses to environmental stress (in the broadest sense) and the maintenance of adaptive diversity in small and subdivided populations.

We plan to host 40-44 participants, of which 14 have already been invited. We are now selecting a further 30 participants (funding restricted to European Union residents). If you would like to attend, send a brief description of your research activity in conservation genetics together with a title and abstract of a presentation or poster (Deadline 24 June) to Ilik Saccheri (saccheri@liv.ac.uk).

There is no registration fee and we are able to cover local costs (full board) for all participants, but for travel costs are limited to a contribution of 150 EUR.

Current list of speakers - Richard Frankham (Macquarie University, Australia) Genetics and extinction - Joop Ouburg (University of Nijmegen, The Netherlands) The rough edges of the conservation genetics paradigm - Lukas Keller (University of Zurich, Switzerland) Inbreeding depression in the wild - Carlos García (University of Santiago de Compostela, Spain) Genetic sources of extinction: a field experiment - Carlos López-Fanjul (University of Madrid, Spain) Changes in the components of the genetic variance/covariance matrix after bottlenecks - Outi Savolainen (University of Oulu, Finland) Genetics of adaptation and constraints in relation to environmental change - Kuke Bijlsma (University of Groningen, The Netherlands) Environmental dependence of inbreeding depression - Juha Merilä (University of Helsinki, Finland) Local adaptation and genetics of acid-stress tolerance in the moor frog - Richard Nichols (University of London, UK) Selection, genetic load and N_e - Aurora García-Dorado (University of Madrid, Spain) The fitness consequences of reduced population size under different mutational parameters - Jinliang Wang (Institute of Zoology, UK) Effects of population structure on purging - Ilik Saccheri (University of Liverpool, UK) Constraints to purging - Armando Caballero (University of Vigo, Spain) Genetic management strategies - Miguel Toro (INIA, Spain) Estimating coancestry using molecular markers

Further details on ESF ConGen and Santiago workshop can be found at <http://www.usc.es/congresos/esf05/-index.html> - School of Biological Sciences University of Liverpool The Biosciences Building Crown Street Liverpool L69 7ZB UK

Tel. (+44) 0151 7954522

I.J.Saccheri@liverpool.ac.uk

Switzerland FragmentedPops Sep14-17

Meeting / workshop Demogenetics in fragmented populations

Dates: 14-17. Sept. 2005 Site: La Fouly (VS, Switzerland) <http://www.dolent.ch/> Small and fragmented populations incur large viability risks in terms of dynamics (demographic stochasticity, Allee effects) and genetics (genetic drift, inbreeding load). Up to now, analytical models were developed mostly under simple geographic (island or lattice) and demographic (patch occupancy) conditions. But the non-equilibrium dynamics of metapopulations is obviously important, for both practitioners and theoreticians. Recent approaches have succeeded in introducing more realistic features of landscape and demography to investigate their effects on population genetics (e.g. effective population size), population viability (e.g. metapopulation capacity), and their interactions.

We have invited the 6 following people who will present their research and lead discussion groups: Otso Ovaskainen (Helsinki), Denis Couvet (Paris), Oscar Gaggiotti (Grenoble), Xavier Lambin (Aberdeen), Andrew Young (Sidney) and Etienne Rampal (Haren)

Participants will have the opportunity to present their own research. Ample time will be allowed for discussions.

Registration and further info at: <http://www.unil.ch/dee/page11644.html> Attendance limited to 30 participants Registration fees (including food and accommodation) are CHF 250.-, except for students from the Swiss universities affiliated to the CUSO (Genève, Lausanne, Neuchâtel, Fribourg and Bern), who will be given priority. Deadline for registration 30th June 2005.

Organizers: Jerome Goudet (Lausanne) Nicolas Perrin (Lausanne) Laurent Excoffier (Bern)

Nicolas Perrin Dept. Ecology & Evolution University of Lausanne (Switzerland) http://www.unil.ch/dee/-page5090_en.html Tel (0041) 21 692 41 84 new mail: nicolas.perrin@unil.ch

Nicolas Perrin <Nicolas.Perrin@unil.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 notification of the availability of a monthly review pdf file.

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

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

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

Afterward

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