EvolDir

March 1, 2004

Month in Review

Forward

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

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

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

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Conferences

Auckland Bioinformatics Sep5-8

The 2004 International Conference on Bioinformatics (InCoB04) will be held in Auckland, New Zealand, from 5 - 8 September 2004. Oral and poster presentations are invited for the following symposia:

* Evolutionary Bioinformatics * Genome Bioinformatics * Biomedical Bioinformatics * Agricultural Bioinformatics * Microarrays and Proteomics * Applications and Platforms

In addition, there will be a DIMACS-sponsored symposium on Phylogenetics and Rapidly Evolving Pathogens (http://dimacs.rutgers.edu/Workshops/WGPhylogeneticTrees/)

There will also be a pre-conference workshop on Parallel Computing and Bioinformatics, from 2 - 3 September 2004.

Important information: Registration 30th June 2004 Late registration 31st July 2004 Receipt of abstracts 31st July 2004

For more details and to register please visit the InCoB04 website, http://www.incob.org . InCoB04 is hosted by New Zealand's Allan Wilson Centre for Molecular Ecology and Evolution (http://awcmee.massey.ac.nz), and the Bioinformatics Institute at the University of Auckland (http://awcmee.massey.ac.nz). InCoB is an international annual meeting of the Asia Pacific Bioinformatics Network (APBioNet, http://awcmee.massey.ac.nz)

Allen Rodrigo

Allen Rodrigo <a.rodrigo@auckland.ac.nz>

BridgesNY Evol Mar6

Building BRIDGES: Integrating Approaches to Evolutionary Biology http://www.nyu.edu/fas/dept/biology/bridges/ A NYC Area Student Symposium on Evolutionary Biology Saturday MARCH 6, 2004 9:00am-6:00pmJurow Auditorium and Silverstein LoungeSilver Center, New York University hosted by BRIDGES*, an integrative evolutionary biology graduate program at NYU-Biology We invite you to participate in a symposium to bring together NYC area students and postdocs interested in any aspect of evolutionary biology, from palaeontology to genomics. The aim is to provide a venue for intellectual exchange for young scientists working in the field of evolutionary biology, and affiliated with institutions in the Metropolitan area. The Symposium will feature a talk by a keynote speaker, oral presentations, and a refereed poster session. The winners will be awarded with a publication of their choice from several contributed by Sinauer Associates, an official sponsor of the symposium. Coffee and refreshments will be offered during the symposium; an evening reception will follow the presentations. The keynote speaker will be Greg Wray (Duke University), whose area of study encompasses a wide spectrum of evolutionary disciplines –from evolution of development in a phylogenetic framework, to evolution of regulatory networks in the context of a genome (http://www.biology.duke.edu/wraylab/). If you are interested in giving a talk or presenting a poster at the Building BRIDGES symposium, please submit an abstract of your presentation to jdl266@nyu.edu before Tuesday FEBRUARY 24, 2004 following these guidelines: 1. The Subject of the email should be "BRIDGES PRESENTATION"2. The body of the email must contain: - title of the talk - author(s) name(s), with presenting author underlined - academic affiliation3. Abstracts must contain no more than 250 words;4. Indicate whether your presentation should be considered for a talk or a poster. PLEASE FORWARD THIS CALL FOR PAPERS TO ANYONE WHO MIGHT BE INTERESTED IN ATTENDING or PRESENTING. For further details and updates on the BRIDGES symposium please refer to the symposium's website: http://www.nyu.edu/fas/dept/-biology/bridges/ Sincerely yours, Eduardo de la Torre (NYU/NYBG) Ilya Temkin (NYU/AMNH) BRIDGES graduate fellows and Symposium co-coordinators.

WE ACKNOWLEDGE AND THANK OUR SPONSORS: Sinauer Associates, New York University College of Arts and Science and Biology Department; The American Museum of Natural History, The New York Botanical Garden, and The World Conservation Society * BRIDGES, Biodiversity Research: Integrating Developmental genetics, Genomics, Evolution and Systematics a collaborative graduate studies track between New York University, The New York Botanical Garden, and the American Museum of Natural History. * BRIDGES, Biodiversity Research: Integrating Developmental genetics, Genomics, Evolution and Systematics a collaborative graduate studies track between New York University, The New York Botanical Garden, and the American Museum of Natural History.

Brisbane AncientDNA Jul12-17

Dear Colleagues,

Just a quick reminder that the 7th International ancient DNA and associated biomolecules conference is being held in Brisbane, Australia from the 12th to the 17th of July this year. Topics include population genetics, forensics, ancient disease, palaeomicrobiology, residues, new technologies, biomolecules, evolution and issues of preservation.

We are currently accepting abstracts for paper and poster sessions. The deadline for paper abstracts is the 30th of April so to avoid missing out submit you abstract today to abstracts.dna7@uq.edu.au

On-line registration is now available from the conference website at http://dna7.ansoc.uq.edu.au or for further information contact enquiries.dna7@uq.edu.au.

The DNA7 organising committee

Regards Tamara Brown DNA7 Organising Committee PhD Candidate Archaeological Science Laboratory School of Biomedical Sciences & School of Social Science University of Queensland

Lab: 3365 7252 Mobile: 0408 308 215 e-mail: tamara.brown@uqconnect.net

Tamara Brown <tamara.brown@uqconnect.net>

CornellU EGLME Apr24

CALL FOR PAPERS

EGLME VIII

Eighth Eastern Great Lakes Molecular Evolution Meeting

http://www.ars-grin.gov/gen/eglme Saturday, April 24, 2004 8:30am - 5:00pm

G10 Biotechnology Building Cornell University Ithaca, NY

The 2004 Eastern Great Lakes Molecular Evolution Meeting (EGLME VIII) will be held on Saturday, April 24, 2004 in room G10 of the Biotechnology Building at Cornell University in Ithaca, NY. Registration, coffee, and poster setup will begin at 8:30 A.M., the first talk at 9:30, with the meeting ending around 5 pm.

EGLME is a forum for faculty, postdocs, grad students, staff, and undergrads to share their work on molecular evolution (broadly defined, including studies of the molecular evolutionary biology or molecular population genetics of any trait in any organism). In the interest of stimulating interaction and discussion among all participants, there will not be concurrent sessions. (We anticipate 18 talks and 30-50 posters.)

There is a link to the abstract submission form at the EGLME VIII website (deadline: April 9, 2004).

Talks will be selected from submitted abstracts, and will be of 15 - 20 minutes duration. Selection will be made by the organizing committee based on the submitted abstract, with attention given to timeliness and general interest of the work. An effort will be made to have as many labs represented as possible. Individuals submitting requests to give talks will be informed by April 16, 2004 as to whether they have been selected to give a talk.

Those not chosen for talks will be strongly encouraged to present a poster on their work. Posters will be available all day, with a mid-day poster session set aside.

In addition, we are considering a computer software demonstration. If you have software relevant to the study of molecular evolution that you would like to demo, please email the organizers.

Registration: online at http://www.ars-grin.gov/gen/-eglme Registration Fee: None (and we anticipate lunch will be covered by sponsors as well)

Lunch (including a vegan option) will be available on site for all preregistered participants. There may or may not be a small fee for lunch, depending on sponsorship.

There is no charge for parking on the Cornell Ithaca campus on the weekend; however please do not park in service or handicap spots unless you have the necessary permit.

Whether you plan to attend the meeting or simply want to stay on the mailing list, please complete the online registration form at the EGLME VIII website no later than April 9, 2004 at 5:00pm, Eastern time.

Please feel free to duplicate and distribute copies of this notice to anyone interested in attending the meeting, particularly students and faculty who are new to these meetings or to the field of molecular evolution.

A schedule and additional details on the meeting will be available online no later than April 16th at the EGLME VIII website.

Links to information about travelling to Ithaca, maps of the Cornell campus, and links to descriptions of research and educational activities at the USDA-ARS Plant Genetic Resources Unit in Geneva, NY and Cornell University can also be found on the EGLME VIII website.

For general questions, please contact:

Sharon Walburn

swalburn@pgru.ars.usda.gov voice (315) 787-2244 or (607) 254-9244 fax (315) 787-2339 or (607) 254-9339

Organizing Committee: Chip Aquadro, Angela Baldo, Andy Clark, Steve Kresovich, Joanne Labate, Brian Lazzaro, Ross Macintyre, Heidi Schwaninger

– Angela M. Baldo Computational Biologist USDA, Agricultural Research Service Plant Genetic Resources Unit 630 W. North Street Geneva, NY 14456-0462 USA

voice 315 787-2413 or 607 254-9413 fax 315 787-2339 or 607 254-9339 abaldo@pgru.ars.usda.gov http://people.cornell.edu/pages/amb82

ECBB Aug28-31

Announcing, the

Second European Conference on Behavioural Biology (ECBB) August 28 - August 31 2004

www.biol.rug.nl/ecbb2004/ Thank you very much,

Greetings, Leon Steijvers

"l.j.steyvers" <l.j.steyvers@biol.rug.nl>

FortCollins SSBSSEASN Jun26-30 2

The web site for EVOLUTION04 is now accepting online registration and paper/poster submission at http://evolution04.biology.colostate.edu.

EVOLUTION04 is the joint meeting of the Society of Systematic Biologists, the Society for the Study of Evolution, and the American Society of Naturalists, to be held in Fort Collins, Colorado from 26th-30th June, 2004 hosted by Colorado State University. June 26th is the day of council meetings and an opening reception; June 30th is a full day of talks followed by the awards banquet.

Registration for Evolution 2004 is though the "Register" link at the bottom of the registration page. The deadline for early registration is June 1, 2004. Paper/poster submission is also online, and only may be done immediately after you have registered to attend. The link for paper/poster submission will appear when you complete online registration.

NOTE: The deadline for paper/poster submission is March 31, 2004.

Online forms for submission of posters and papers for the EVOLUTION04 conference are accessed through the registration page, and become available to conference registrants after registration is completed.

When you are ready to submit information for your papers and/or posters, please complete registration first.

Other information (also on the web site):

Air travel should be arranged to Denver International Airport. A regular shuttle service (Shamrock Airport Express) provides buses traveling from the airport to Fort Collins and the Colorado State University campus. For those driving to Fort Collins, free parking will be available on campus.

Inexpensive housing and meal plans are being offered through Colorado State University, although local hotels also offer reasonable prices (the University Park Holiday Inn and Best Western University Inn are immediately adjacent).

For additional information visit the conference web site, or contact the conference coordinator, Karen Weinbaum (weinbaum@cnr.colostate.edu). –

Michael F. Antolin

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Granada B-chromosomes Jun26-29

2nd B-CHROMOSOME CONFERENCE June 26-29, 2004 Bubión (Granada, Spain)

Second Announcement

Dear colleague,

The Evolutionary Genetics Group (Departamento de Genética, Universidad de=

Granada, Spain) is pleased to invite you to the Second B-Chromosome Conference, 26-29 June 2004. The Conference will be held at the Hotel Villa Turística de Bubión, in Bubión (Granada) (http://www.villabubion.com/), a small mountain village located in the Sierra Nevada mountains, the highest peaks of Iberia, 67 km south of Granada. The Local Organizing Committee will provide bus transport from Granada to the Conference venue on the afternoon of Saturday 26th, and from

the Conference venue back to Granada on the morning of Wednesday 30th (departing points and time will be announced in the conference web page: http://www.bchromosomes.org/). Scientific contributions will be mainly in Poster form to maximize

time devoted to discussion, but a small number of contributions will be selected by the chair of each session to be presented as short oral communications to form a basis for the discussions. There are two invited lectures. Robert Trivers (Rutgers University, USA) will give an opening lecture on Selfish Genetic Elements, and Hans de Jong (Wageningen University, The Netherlands) a= talk on "B-chromosomes and related cytogenetic hobbies - discussions about the B-chromosome concept". Registration should be performed before 29 February by filling in

the information requested in the conference web page (http://www.bchromosomes.org/). The FULLY INCLUSIVE registration fee of 360

is outstanding value, and will include: full board accommodation from Saturday afternoon (June 26) to Tuesday (June 29), entry to all scientific

sessions, abstract book, coffees, welcome reception, a special closing dinner, and the bus mentioned above. Late registration, after 29 February,

will be charged 60 extra. Please, be sure that your bank transfer does=

not include any cost to the Conference Local Organizing Committee, so that

we receive the full fee amount. Abstracts (max. 300 words) received before 31 March 2004 will appear in the Conference web page, and will be published in the abstract book. Please submit your abstract through the appropriate section in the Conference web page. Accommodation is limited, and for this reason reservations will be

made strictly in order of registration. The hotel consists of villas with one or two double rooms. There are also a limited number of single rooms which carry an additional charge of 92 . Some of you will recall that it will just over a decade since the

highly successful B1CC was held in Miraflores de la Sierra (Madrid) in September 1993, and we anticipate a lot of news of advances in knowledge and new ideas over this period of time, as well as many new and enthusiastic B-faces. It is also appropriate that B2CC will coincide with

the imminent publication of the “B Chromosomes in Eukaryote Genomes” as a special edition of the journal Cytogenetic and Genome Research. We very much look forward to seeing you in Granada in June.

Juan Pedro M. Camacho Secretary

Juan Pedro M. Camacho Departamento de Genética Universidad de Granada 18071 Granada Spain E-mail: jpmcamac@ugr.es web: http://www.ugr.es/˜cvi165/

JacksonLabMaine AntigenEvolution Sep16-19

4th International Workshop on Antigen Processing and Presentation

September 16 - 19, 2004 The Jackson Laboratory Bar Harbor, Maine

This meeting will emphasize the structural and biochemical basis for antigen processing and presentation, as well as the receptors involved in innate and adaptive immune recognition. A special session will be dedicated to interactions of the immune system and pathogens. In addition, two sessions will cover the topics of physiology of the antigen presenting cells with an emphasis on their function in vivo, and on the physiology of the T cell responses to antigen stimulation. The particular emphasis will be on the studies of the structural and biochemical basis for antigen processing and presentation as well as on the receptors involved in innate and adaptive immune recognition. To allow for intense discussions and exchange of ideas and results in the most informal setting, the meeting will be limited to 100-135 participants consisting of invited speakers, established investigators, post-doctoral fellows and graduate students. Postdoctoral and graduate students are encouraged to attend. This meeting has been held every two years since 1994 and continues to be unique and productive.

Topics include: Structure and function of molecules involved in immune recognition Assembly of MHC molecules and generation of MHC ligands Antigen presentation in vivo and APC Pathogen recognition by immune system MHC/TCR interactions in T cell physiology

Scientific Organizers:

Alexander Chervonsky, Ph.D., The Jackson Laboratory Peter Cresswell, Ph.D., Yale Univ. School of Medicine John Macauley, Ph.D., The Jackson Laboratory Diane Mathis, Ph.D., Harvard University Elizabeth Mellins, M.D., Stanford Univ. School of Medicine. Ruslan Medzhitov, Ph.D., Yale University Ira Mellman, Ph.D., Yale Univ. School of Medicine Hidde Ploegh, Ph.D., Harvard Medical School Kenneth Rock, M.D., Univ. of Massachusetts Alexander Rudensky, Ph.D., University of Washington Colin Watts, Ph.D., University of Dundee Ian Wilson, Ph.D., Scrippe Research Institute

For additional information, please access the web page at: http://www.jax.org/courses/events/coursedetails.do?id=3D5

Karen Grant Course Coordinator The Jackson Laboratory 600 Main Street Bar Harbor, Maine 04609-1500 Phone: 207-288-6263 Fax: 207-288-6080 E-mail: kgk@jax.org web address: http://www.jax.org/courses Office Hours: 7:00 am - 3:00 pm Monday - Friday Office Hours: 7:00 am - 3:00 pm Monday - Friday

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JacksonLabMaine ComplexTraits Jul6-9

Complex Trait Consortium 2004, 3rd Annual Conference July 6 - 9, 2004 The Jackson Laboratory Bar Harbor, Maine

The goal of the Complex Trait Consortium (CTC) conference is to bring together investigators who have common interest in the development and use of the laboratory mouse as a genetic tool for understanding human health and disease.

Our specific goals are to increase the visibility of complex traits in contemporary biomedical research through: 1) Improved awareness and appreciation for the natural variation that exists within species and is responsible for significant phenotypic variation. 2) Recognition by the broader community of scientists that the vast majority of human phenotypes have complex multigenic components whose contributions need to be understood to obtain comprehensive understanding of relevant human phenotypes. 3) Acceptance that the environment, through complex interactions with genetic variation, is a critical determinant of phenotypic diversity. 4)Development of community-wide resources that enable efficient experimental dissection of the causes of phenotypic diversity. Postdoctoral and graduate students are encouraged to attend.

Scientific Organizers:

Molly Bogue, Ph.D., The Jackson Laboratory Gary Churchill, Ph.D., The Jackson Laboratory William Dietrich, Ph.D., Harvard Medical School Robert Hitzemann, Ph.D., Oregon Health Sciences University Kent Hunter, Ph.D., National Cancer Institute Joseph Nadeau, Ph.D., Case Western Reserve University David Threadgill, Ph.D., University of North Carolina at Chapel Hill Robert Williams, Ph.D., University of Tennessee

For additional information, please access the web page at: http://www.jax.org/courses/events/-coursedetails.do?id=30

Karen Grant Course Coordinator The Jackson Laboratory 600 Main Street Bar Harbor, Maine 04609-1500 Phone: 207-288-6263 Fax: 207-288-6080 E-mail: kgk@jax.org web address: http://www.jax.org/courses Office Hours: 7:00 am - 3:00 pm Monday - Friday Office Hours: 7:00 am - 3:00 pm Monday - Friday

JyvaskylaFinland ISBE Jul10-15

ISBE 2004 10-15 July 2004 Jyväskylä, Finland. http://www.isbe2004.com/ We welcome you to the 10th Congress of International Society for Behavioral Ecology. The congress will cover a wide variety of topics, as illustrated by our choice of plenary and Hamilton lecture speakers.

Hamilton lecture: Mary Jane West-Eberhard. Plenary speakers include: Manfred Milinski, Josephine Pemberton, Vladimir Pravosudov, Barry Sinervo, Liselotte Sundström, William Sutherland, Fritz Vollrath, Christer Wiklund.

The goal of the ISBE meetings has always been to allow the latest developments and results to be presented in a minimally formal context. Thus, we do not have any specific symposia for talks, rather we expect researchers to come with their latest ideas and results that can be fitted as oral and poster presentations into the program.

Registration to the congress is now open, and we invite abstracts for posters and talks. Deadline for abstract submission is 29th February 2004.

For registeration and further information, go to the congress website at http://www.isbe2004.com/ ISBE 2004 organizing committee

“M.Puurtinen” <hemipu@cc.jyu.fi>

LeidenU AncientDNA Mar9

Dear friends,

The Leiden University community will be host to an ancient DNA symposium next month that will take place in the Auditorium of the Naturalis National Natural History Museum at Darwinweg 2 in Leiden, The Netherlands, on the 9th of March.

For this event we have brought together some of the best researchers in this rapidly growing field from all over Europe to present their research on DNA isolated from museum collections and discuss potential applications.

The presentations will cover a wide variety of disciplines that incorporate ancient DNA techniques, including archaeology, botany, paleoecology, human and animal migration, evolution, and crop origins. Admission is free. More information can be found at: http://www.naturalis.nl Dr. B. Gravendeel Nationaal Herbarium Nederland Universiteit Leiden Einsteinweg 2 Postbus 9514 2300 RA LEIDEN The Netherlands tel. +31 (0)71-5273578/5127 fax +31 (0)71-5273511 email: Gravendeel@nhn.leidenuniv.nl http://www.nationaalherbarium.nl

London PlantPhylogeny Mar15-16

What? Plant phylogeny and the origin of major biomes When? 15/16 March 2004 Where? At the Royal Society, London Cost? Free to all, but registration required How? Register on-line at www.royalsoc.ac.uk/events Meeting Summary Continental biomes are the world’s most biodiverse areas, but little is known about their history. Molecular phylogenies offer a new means of dating the origin of plant taxa that form the structural framework of these ecosystems. This meeting will discuss the theoretical background to dating phylogenies and place insights from calibrated plant phylogenies in a palaeobotanical and ecological context. Organised by Dr Toby Pennington, Dr Quentin Cronk and Dr James Richardson Speakers include: Mike Sanderson, University of California, Davis, Ian Woodward, University of Sheffield, Jonathan Davies, Royal Botanic Gardens, Kew, James Richardson, University of California, Robyn Burnham and Kirk R Johnson,University of Michigan and Denver Museum of Natural History, Denver, Toby Pennington, Royal Botanic Garden, Edinburgh, Matt Lavin, Montana State University, Bob Hill, University of Adelaide, Mike Crisp, Australian National University, Barbara Gravendeel, Nationaal Herbarium Nederland, Leiden, Quentin Cronk, University of British Columbia, Vancouver, Canada, Bonnie Jacobs, Southern Methodist University, Peter Linder, Institute of Systematic Botany, Vanessa Plana, Royal Botanic Garden, Edinburgh, Suzanne Renner, Systematische Botanik and Michael Donoghue, University of Yale. Posters are invited for this scientific discussion meeting. Those wishing to submit a poster should contact Suzi White using the contact us form </contact/intro.htm> and selecting the 'events' drop down flag. Spaces will be limited

Public Lecture

Amazonian rainforests: thriving or surviving in a 21st century atmosphere?

Monday 15 March 2003 at 6:30pm

When not writing up his research, Royal Society Fellow Yadvinder Malhi spends much of his time trekking through the rainforests of South America in search of answers to some of the most important issues affecting our environment: Will trees grow faster and absorb some of the extra carbon dioxide human industries are generating, for example, and how will this affect biodiversity? In this talk Yadvinder will describe his research and its importance in helping us to better understand global climate change.

Admission Free - no ticket or advance booking required. Further information and registration details can be found on the Royal Society website www.royalsoc.ac.uk/events. Or contact Suzi White Events Officer tel +44 (0)20 7451 2581 fax +44 (0)20 7451 2693 web http://www.royalsoc.ac.uk The Royal Society 6-9 Carlton House Terrace London SW1Y 5AG Registered Charity No 207043 The Royal Society - excellence in science

Suzi White Events Officer

tel +44 (0)20 7451 2581 fax +44 (0)20 7451 2692 web http://www.royalsoc.ac.uk The Royal Society 6-9 Carlton House Terrace London SW1Y 5AG

Registered Charity No 207043 The Royal Society - excellence in science

"White, Suzi" <Suzi.White@royalsoc.ac.uk>

Marseille EvolBiol Sep22-24 2

The next evolutionary biology meeting at Marseille will take place this year from September 22 to September 24.

The program should be similar to the one proposed the former years the following topics will be discuss: systematic, biodiversity, comparative genomics and postgenomics (at all the taxonomic levels), gene duplication and evolution, functional phylogenies, amphioxus genomics and biology, concept of evolution

You can submit and register on line on the meeting web site

http://www.up.univ-mrs.fr/evol/congres/

The early registration dead line is the first of May

best regards

– Pierre Pontarotti

evolutionary biology Laboratory

Université d'Aix Marseille I Centre St Charles 3 Place Victor Hugo 13331 Marseille Cedex 3 33491106489 http://www.up.univ-mrs.fr/evol

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PennStateU GenomeEvol Jun17-20

INTERNATIONAL MEETING Genomes and Evolution 2004 http://www.outreach.psu.edu/C&I/-genomes/ Highlighting research at the interface of molecular biology, evolution, and genomics

Location: The Pennsylvania State University University Park, Pennsylvania, USA

Dates: June 17-20, 2004

Annual Meeting of the Society for Molecular Biology and Evolution Annual Meeting of the American Genetic Association

Keynote and Plenary talks by: -Sydney Brenner -Leroy Hood -John Avise -Walter Gehring

And international leaders in genomics and evolution speaking in nine diverse symposia: Early Evolution of Life: Doolittle, Ochman, Koonin, Baldauf Genome Evolution: Andersson, Green, Palmer, Wessler, Wolfe Molecular Phylogeny and Clocks: Cracraft, Kumar, O'Brien, Vilgalys Development and Evolution: Carroll, Theissen, Sinha, Levine Genome Evolution in Primates: Paabo, Eichler, Varki, Saitou Origins and Evolution of Genetic Systems: Gojobori, Parham, Klein, Firestein Molecular Polymorphisms and Evolution: Hartl, Batzer, Nachman, Clark Molecules and Biodiversity: Cheng, Mathews, Real, Rieseberg Adaptive Evolution: Zhang, O'Neill, Kocher, Jeffery

**Additional symposium speakers selected from abstract submissions

Plan ahead to attend this key event, and register early to assure a place. Affordable registration fees, including a special rate for graduate students. See the website (URL above) now for details.

Regensburg PopBio2004 May19-23 2

Dear members of the POPBIO meeting in Regensburg (19 - 23 May 2004),

We recommended you to make your reservation for the hotel rooms as soon as possible. As other events are taking place during the time of the POPBIO meeting, hotel rooms are very scarce in Regensburg. There is a limited contingent for the members of the POPBIO meeting 2004 in the following hotels until the end of February 2004:

http://www.hotel-am-peterstor.de/index_englisch.html

http://www.hotel-straubinger-hof.de/

Afterwards it will be difficult to get an accommodation.

Sincerely yours

Wioletta Moggert

University of Regensburg Institute of Botany Prof. Dr. Peter Poschlod

D-93040 Regensburg

Phone 0941 943 3107 Fax 0941 943 3106

wioletta.moggert@biologie.uni-regensburg.de

POP BIO <pop.bio@biologie.uni-regensburg.de>

Shropshire PhDstudents Aug29-Sep3

To all of EvolDir: THE 10TH MEETING OF PHD STUDENTS IN EVOLUTIONARY BIOLOGY

The meeting will bring together PhD students from all over Europe to discuss current topics in evolutionary biology. The meeting will take place from the 29th August to the 3rd of September 2004, at the Preston Montford Field Centre, Shropshire, UK. The conference is open to 100 PhD students and registration will begin on the 23rd February at 10am (UK time).

Topic sessions will include: Experimental and Microbial Evolution, Population Genetics and Genomics, Phylogenetics, Coevolution, Palaeobiology, Life-history Evolution, Behavioural Ecology, and Ecology and Conservation.

Please see our website <<http://students.bath.ac.uk/bspght/>> for further details.

Toronto GeneticsSocietyCanada Jun17-20

GSC CONFERENCE 2004 The 47th Annual Conference of The Genetics Society of Canada University of Toronto June 17 to 20, 2004 http://www.thesnidersweb.com/gsc2004/

The Genetics Society of Canada's annual meeting will be held this year in Toronto. Plenary sessions will include a tribute to Professor Margaret Thompson on Medical Genetics, a session on genetically modified organisms and one on functional genomics. There will be workshops, platform and poster sessions, award winner lectures and a dinner at the Kortwright Centre.

Register before April 7th for early booking discounts.

For more details and registration forms visit the meeting web site at http://www.thesnidersweb.com/gsc2004/

For further information contact Doreen Ostrowski at Tel. 416-465-8756 or e-mail at doreen.gsc2004@sympatico.ca

Doreen <doreen.gsc2004@sympatico.ca>

UGranada Bchromosome Feb18-23

Dear colleague,

The Internet service in the University of Granada will have some problems during 18-23 February, so that the web page for the Second B Chromosome Conference (http://www.bchromosomes.org) might not be accessible during this period. For this reason, we have decided to extend the registration deadline till 8 march. The remaining deadlines are not modified.

Best regards, Juan Pedro M. Camacho

Juan Pedro M. Camacho Departamento de Genética Universidad de Granada 18071 Granada Spain E-mail: jpmcamac@ugr.es web: http://www.ugr.es/~cvi165/

UPuertoRico Lepidoptera Apr16-19

A meeting will be held at the University of Puerto Rico, San Juan, Puerto Rico from April 16-19, focusing on the Evolution and Development in the Lepidoptera. Most of the emphasis will be on wing pattern evolution and/or development, but other talks will focus on evo-devo of other morphological characters or life histories.

We are expecting a small and intimate meeting that will provide plenty of opportunity for interactions outside of a formal talk schedule. A visit to a natural park with plenty of butterflies, south of San Juan, is also being planned. Accommodations will be in a single or shared room in downtown San Juan and will cost around $100 per night. We are currently looking into reserving a block of rooms close to the University. In addition there will be a small registration fee (approximately $50) to cover transportation and entertainment.

If you want to attend the meeting please send us a title for your talk.

We encourage meeting participants to arrive on Friday, April 16 before dinner. Talks will be held the whole day Saturday and Sunday morning, and the visit to the natural park will be scheduled for Sunday afternoon. Plan your return for Monday, or stay a few extra days to enjoy San Juan or the surroundings.

Our preliminary group of speakers and talk titles are:

Patricia Beldade, University of California at Irvine, Generating phenotypic variation: evolution, development, and genetics of butterfly wing patterns

Margarida Beltran, Smithsonian Tropical Research Institute, Panama, Phylogeny and evolution of color pattern in Heliconius butterflies

Richard ffrench-Constant, Bath University, 'Melanism and mimicry in swallowtails'

Marian Goldsmith, University of Rhode Island, Title to be announced

Chris Jiggins, University of Edinburgh, Linkage mapping in Heliconious melpomene

Durrell Kapan, University of Puerto Rico, “Qualitative & quantitative analysis of Heliconius erato wing patterns”

Marcus Kronforst, University of Texas at Austin, “The Evolutionary History of Candidate Wing Patterning and Pigmentation Genes in Heliconius.”

Anthony Long, University of California at Irvine, “Association Studies in Drosophila as a Model for Dissecting the Genetic Architecture of Butterfly Eyespots”

James Mallet, University College London, “Evolution of mimicry genes in Heliconius butterflies at the population and genetic level”

Owen McMillan,University of Puerto Rico, Towards a comparative map of Müllerian mimicry

Antonia Monteiro, University at Buffalo, Using germ line transformations to test the function of candidate genes in color patterning the butterfly wing

Diane Ramos, University at Buffalo, Using the heat-shock response element, and biophotonics to targeting ectopic gene expression on butterfly wings

Robert Reed, Duke University, “Microarray analysis of Heliconius wing pattern development and polymorphism”

Kendra Robertson, University at Buffalo, The functional significance of the eyespot central pupils in mate choice

Mike Serfas, University of Wisconsin, Madison, Pharmacologic manipulation of Junonia wing pattern elements

Bas Zwaan, University of Leiden, The Netherlands, Life history evolution in seasonal environments

For more information, or to submit a title please contact the meeting organizers:

Owen McMillan University of Puerto Rico- Rio Piedras P.O. Box 23360 San Juan, PR 00931-3360 Tel: + 1 787-764-0000 [(1)2909] e-mail: wmcmilla@rrpac.upr.clu.edu

or

Antonia Monteiro Dept. Biological Sciences University at Buffalo Buffalo, NY 14228 Tel: + 1 716 6452363 ext:135 e-mail: monteiro@buffalo.edu

GradStudentPositions

Australia 2 Bioinformatics

Dear all,

Can I please ask you to draw to the attention of potential candidates the following two Australian PhD Scholarships?

All the best,

Lars

—— Two PhD Scholarships in Bioinformatics (one in Comparative Genomics and one in Evolutionary Biology)

Two PhD scholarships are available for suitably qualified candidates with good Honours degrees in biology, mathematics, statistics, computer science, computational science or physics to undertake full-time research leading to PhDs in Comparative Genomics and Evolutionary Biology. The aim of the research is to retrace the early evolution of animals through development and use of new phylogenetic tools and data. The successful applicants will be part of a research team from the University of Sydney and the University of Adelaide, but will be affiliated with only one of these institutions (i.e., one in Adelaide and the other in Sydney).

The Sydney-based student will be developing bioinformatics tools for phylogenetic analyses of whole genomes and will be analysing data from completely sequenced mitochondrial genomes of animals within an evolutionary context. S/he must have a good grasp on computer science and/or statistics, and a keen interest in developing maximum-likelihood programs that employ the latest techniques in high-performance (or grid) computing. Programming skills are essential and a broad knowledge of evolutionary biology is desirable.

The Adelaide-based student will be collecting and analysing morphological and developmental data from previous broad-scaled phylogenetic studies, as well as generating new observations and data. S/he must have a good grasp of animal morphology and systematics, and a keen interest in using computers to study morphological and developmental information obtained from animals. Experience in various microscopy techniques will be an advantage.

The PhD scholarships are funded via a grant from the

Australian Research Council, and are valued at $18,484 per annum (tax exempt, and indexed annually); they may be renewed for up to three (3) years, subject to satisfactory progress. In addition, relocation allowance may be provided in certain circumstances. Applicants must be citizens or permanent residents of Australia, or citizens of New Zealand. International students can also apply but they will be expected to cover their own tuition fees.

Further information can be obtained from Dr Lars S Jermiin, School of Biological Sciences (A08), The University of Sydney, NSW 2006, Australia (Phone: +61-2-9351-3717; Fax: +61-2-9351-4119 E-mail: lsj@bio.usyd.edu.au) or Dr Greg W Rouse, The South Australian Museum, North Terrace, Adelaide, SA 5000, Australia (Ph: +61-8-8207-7498; Fax: +61-8-8207-7222; E-mail: rouse.greg@saugov.sa.gov.au. Applications for the position at The University of Sydney should be sent directly to Dr Jermiin at the above address and should include a Curriculum Vitae, a copy of an academic transcript, and the names and contact details of at least two referees. Applications for the position at The University of Adelaide should be sent directly to Dr Rouse at the above address and should include a Curriculum Vitae, a copy of an academic transcript, and the names and contact details of at least two referees.

Closing Date: March 1, 2004

This data gives us time to go through the applications and call for referee reports - we aim at making offers on March 12, to give the students time to enrol (deadline is March 31, 2004).

– Dr Lars S Jermiin, Senior Lecturer Acting Director, SUBIT Chair, Bioinformatics Degree Program Committee School of Biological Sciences Heydon-Laurence Building A08 University of Sydney New South Wales 2006, Australia

Phone +61 (02) 9351 3717 Fax +61 (02) 9351 4119 E-mail lsj@bio.usyd.edu.au WWW page http://www.bio.usyd.edu.au/~jermiin

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Barcelona TrainingPositions MolEvol

Short Predoctoral Marie Curie Training Positions

One Vacancy !!!

http://www.ub.es/molevol/MarieCurieAnuncio.html The Molecular Evolutionary Genetics Group at Universitat de Barcelona http://www.ub.es/molevol has been selected as a Marie Curie Training Site in Molecular Population Genetics and Evolution by the EU Commission (Contract No. HPMT-2000-00108). A short training fellowship of 6 months is available to non-Spanish EU registered predoctoral students. Fellows will receive an allowance of 1200 euros per month.

Within the area of Molecular Population Genetics and Evolution, the host group studies nucleotide variation at both the intraspecific and interspecific levels in different species of Drosophila and of Cruciferae. This work aims to establish the role of natural selection in shaping nucleotide variation, and also to infer the evolutionary history of populations and/or species.

Further details of the research programme of the group, and the job description for the present vacancies are available from the group's web site: http://www.ub.es/molevol/MarieCurieAnuncio.html http://www.ub.es/molevol

Main Marie Curie Requirements:

Nationality All fellows must be nationals of an EU Member or Associated State, or have resided in the EU for at least five years immediately prior to their selection.

Mobility They must not undertake their fellowship in the country of their nationality or recent centre of activity.

Age At the time of selection the fellow must be 35 years old or less.

Research Experience The scheme is directed to postgraduate researchers pursuing doctoral studies in a subject area similar to that of the Training Site. Applicants should be affiliated to a University as PhD students both at the time of application and during the Marie Curie training fellowship.

Montserrat Aguadé Departament de Genètica, Facultat de Biologia, Universitat de Barcelona Diagonal 645, 08028 Barcelona Spain E-mail: aguade@bio.ub.es

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LavalU SalmonidEvolEcol

We are seeking to recruit a Ph.D. student to undertake studies on the alternative reproductive tactics of Atlantic salmon. The successful candidate will conduct experiments in the field and in the laboratory to document the spatial and temporal variability of early male maturity among different genetic populations of salmon, to estimate the heritability of morphological and behavioural characteristics associated with early maturity and anadromy and to examine the nature of gene-environment interactions in the expression of alternative life history tactics. The successful candidate will be part of a team working in the context of an NSERC funded strategic research grant aimed at the elucidation of the functional genomic basis of local adaptation in Atlantic salmon. The successful candidate will receive a scholarship of 16, 000.00$ CAN annually and enjoy additional student benefits as members of CIRSA (Centre Interuniversitaire de Recherche sur le Saumon Atlantique) and Québec-Océan. The candidate will be co-directed by Professors Julian J. Dodson and Louis Bernatchez at Laval University, Québec City, Canada. The candidate may start the project as early as May 2004.

Please send enquiries to Julian Dodson julian.dodson@bio.ulaval.ca.

Interested candidates are invited to consult the following web pages for further information. http://www.bio.ulaval.ca/ http://www.bio.ulaval.ca/CIRSA http://www.quebec-ocean.ulaval.ca/ Nous recherchons un ou une candidate aux études doctorales pour entreprendre un projet de recherche portant sur les stratégies= alternatives de reproduction chez le saumon Atlantique. Le ou la candidat(e) choisi(e) mènera des études sur le terrain et au laboratoire afin de documenter la variabilité spatiale et temporale de la maturité hâtive chez les mâles parmi différentes populations de saumon, destimer lhéritabilité des traits morphologiques et comportementales associés avec la maturité hâtive et lanadromie et dexaminer les interactions gène environnement dans lexpression des tactiques de reproduction. Le ou la candidat(e) choisi(e) fera partie dune équipe détudiants et de chercheurs, subventionn ée par le programme stratégique du CRSNG, travaillant sur les bases génomiques fonctionnelles de ladaptation locale chez le saumon Atlantique. Le ou la candidat(e) recevra une bourse de 16, 000$ annuellement et aura accès aux bénéfices additionnels comme membre étudiant de CIRSA (Centre Interuniversitaire de recherche sur le saumon Atlantique) et de Québec-Océan. Le ou la candidat(e) sera codirigé(e) par les professeurs Julian J. Dodson et Louis Bernatchez, Université Laval, Québec. Le ou la candidat(e) choisi(e) pourra commencer dès mai 2004.

Les intéressé(e)s sont prié(e)s de communiquer avec Julian Dodson à julian.dodson@bio.ulaval.ca.

Vous pouvez également consulter les pages web suivantes; http://www.bio.ulaval.ca/ http://www.bio.ulaval.ca/CIRSA http://www.quebec-ocean.ulaval.ca/

Louis Bernatchez, Titulaire de la Chaire de recherche du Canada en conservation génétique des ressources aquatiques

Département de biologie, Pavillon Vachon Université Laval Ste-Foy, QC G1K 7P4 Canada

Tél: 418 656-3402 Télécopie: 418 656-2043 Couriel: Louis.Bernatchez@bio.ulaval.ca Toile: http://www.bio.ulaval.ca/index-alt.html

Chaires de recherche du Canada: www.chaires.gc.ca

LundU AnimalMigration

Dear All,

We would like to advertise an international PhD student course on the topic “The Ecology of Animal Migration” which will be held at the Department of Animal Ecology, Lund University, in Sweden 14-23 April 2004. The tentative program of the course is exposed at the Bird Migration Group home page (see address below), and include a large number of lectures of international experts in the fields Locomotion, Orientation and Navigation, Ecophysiology, Genetics of migration, Migration patterns and Modelling migration. There will be ample time for discussions, presentations of own work, excursion and own projects trying various methods used to study migration during the course. To cover part of the costs for the course we will have to take a course fee of 2000 SEK, which will be paid upon arrival. The logistics and food will have to be paid by the students, but we can help to arrange for low cost rooms with kitchen available.

If you are interested to attend the course, please contact Rachel Muheim (Email: Rachel.Muheim@zooekol.lu.se).

We would be most grateful if you, please, could spread the word to your students or other interested persons. We very much hope the course will be as successful as it has been the previous two times we have given it here in Lund, when students from 9 and 11 countries participated.

Very Welcome to Lund!

With best wishes,

Susanne Åkesson and Thomas Alerstam

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

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

Nuenster PopGenetics

PhD in population genetics in Muenster, Germany

We invite applications for 1 PhD position at the Institute for Animal Evolution and Ecology in Muenster, Germany, financed through the German Science Foundation.

Subject: Population genetic analysis of parasite-host interactions in the common earthworm Lumbricus terrestris. Analysis of earthworm population structure and dynamics in relation to parasite load and immunocompetence. Molecular markers will include microsatellites and immunity genes. Furthermore, analysis of inter- and intra-specific diversity of the main parasite taxon, gregarine protists of the genus Monocystis. Techniques include DNA-/RNA-isolation, PCR, RT-PCR, DNA sequencing, microsatellite genotyping, Single strand conformation polymorphism (SSCP) analysis.

Requirements: Degree in Biology (BA, BSc, MA, MSc, or equivalent degree); good knowledge of molecular techniques (PCR, DNA Sequencing, etc.) and statistics; ideally already knowledge concerning work with C. elegans, analysis of microarrays or mathematical models to characterise parasite-host co-evolution.

Check our homepage at http://www.uni-muenster.de/biologie.evoeco/evolbio/ .

Deadline: 15 April 2004. Start: as soon as possible. The position is available for 2 years, and can be extended for another year.

In case of equivalent qualifications, disabled people are preferentially employed. We also specifically encourage women to apply.

Application: Send CV, 1-2 pdfs of publications (if available), and email details of 2 referees by email to Nico Michiels (Prof.), michiels@uni-muenster.de

Prof. Dr. Nico K. Michiels Institute of Animal Evolution and Ecology Westphalian Wilhelms-University Muenster Huefferstrasse 1, D-48149 Muenster, Germany

Tel. +49 (0)251 83 24661 Mobile +49 (0)170 4758003 Fax. +49 (0)251 83 24668

michiels@uni-muenster.de http://www.uni-muenster.de/Biologie.EvoEco/Evolbio/ Nico Michiels <michiels@uni-muenster.de>

UAlaska PlantEvol

GRADUATE STUDIES Plant evolutionary ecology and genetics University of Alaska, Fairbanks

Experience science in the last frontier, Alaska!

The graduate program in Biology at the University of Alaska, Fairbanks (UAF) has openings for highly motivated graduate students with research interests in the evolution, ecology and genetics of plants and the organisms with which they interact. Faculty research interests include population & ecological genetics, breeding system evolution, molecular evolution & genomics, theoretical population genetics, and plant-insect/plant-microbial interactions. Successful applicants to the program are invited to work on projects currently underway, or to design a project of their own.

Faculty members working in this area include:

Pat Doak (Insect-plant interactions) http://mercury.bio.uaf.edu/~pat_doak/ Christa Mulder (Plant-animal, plant-disease interactions) http://mercury.bio.uaf.edu/~christa_mulder/cv.htm/ Matt Olson (Plant ecological genetics) http://mercury.bio.uaf.edu/~matt_olson/ Kent Schwaegerle (Plant quantitative genetics) http://mercury.bio.uaf.edu/~kent_schwaegerle/ Lee Taylor (Plant-microbial associations) http://mercury.bio.uaf.edu/~lee_taylor/ Naoki Takebayashi (Theoretical population genetics) http://www.faculty.uaf.edu/ffnt/ Diane Wagner (Insect-plant interactions) http://mercury.bio.uaf.edu/~diane_wagner/ Diana Wolf (Plant evolutionary genetics) http://www.faculty.uaf.edu/ffdew2/ There are also opportunities to interact with a diverse array of faculty with interests in plant ecology and the evolutionary biology of birds and mammals http://mercury.bio.uaf.edu/iab/index.html . The Department of Biology and Wildlife http://mercury.bio.uaf.edu/

biolwild/index.htm) and the Institute of Arctic Biology (http://mercury.bio.uaf.edu/iab/index.html) at UAF provide a dynamic setting in which to pursue a graduate degree. Our program is highly collaborative, and offers a diverse array of graduate student course offerings in evolutionary biology. The 43 faculty and >100 graduate students offer a vital intellectual community with interests in biological systems. Facilities include a state of the art greenhouse (http://www.uaf.edu/grnhouse/), herbarium collections at University of Alaska Museum (http://www.uaf.edu/museum/index2.html), the Alaska Geobotany Center (http://www.geobotany.uaf.edu/), and a newly modernized DNA CORE lab with high throughput sequencing and SNP detection capabilities (http://mercury.bio.uaf.edu/core/index.html). Regional study areas include Toolik Field station (http://www.uaf.edu/toolik/) and Bonanza Creek LTER (http://www.lter.alaska.edu/).

The location of the University offers unparalleled opportunities for research in understudied natural communities (the storied 365 million acre classroom) and the climate offers a great opportunity to enjoy winter sports and long summer days. The campus is situated on a sunny hill, overlooking the town of Fairbanks, with a view of the Alaska Range. Fairbanks is an extremely welcoming community, with many opportunities for outdoor sports. Groomed cross country ski trails start just outside the building, downhill skiing less than 15 minutes from campus, and many places for hiking, bird watching and snow machining. Denali National Park is just 2 hours from campus. Your graduate-student life will be an unforgettable life-time experience in this beautiful subarctic region.

Currently, financial support is available through research and teaching assistantships, and we anticipate funding for a competitive graduate fellowship program will be available soon. In addition, students are encouraged to apply for nationally competitive fellowships. Start time is negotiable, and we do not have a set application deadline.

Please don't hesitate to contact faculty member(s) that share your interests.

For more information on research and graduate study in Plant Ecology and Evolution at The University of Alaska, Fairbanks, see

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

UBath EvolGenomics

BBSRC-funded Ph.D. studentship -with 2000GBP enhancement- in evolutionary genomics / bioinformatics at the University of Bath, UK

Supervisors: Dr. Martin Lercher, Prof. Laurence Hurst

RECOMBINATION-INDUCED MUTATIONAL EVENTS AND THEIR IMPACT ON GENOMIC EVOLUTION

Meiotic recombination is one of the major forces shaping genomic evolution. Recombination can break up linkage disequilibrium, thereby allowing selection to act on small genomic regions rather than on whole chromosomes. What has received comparatively little attention is the mechanistic impact recombination has on chromosomes.

There is accumulating evidence that recombination can cause a range of mutational events. In addition, recombination is implicated in the expansion of repetitive sequences, and it is possible that it also plays a role in the generation of gene duplications. Finally, it appears likely that recombination-associated double strand breaks may also induce inversions.

Except for some studies that examined the distribution of single-nucleotide polymorphisms, no systematic analyses of these issues have been performed to date. In particular, it is currently unclear how much recombination contributes to the genomic incidence of regional duplications and inversions. A range of genomic patterns (e.g., nucleotide diversity, codon usage bias, or the clustering of essential genes) have been associated with recombination. These have mostly been interpreted within the framework of Hill-Robertson effects. Can they alternatively be explained by recombination-induced mutational effects?

The Ph.D. candidate will examine these issues, using publicly available data and a combination of computational and theoretical methods. The results will contribute substantially to our understanding of the processes that have shaped the evolution of eukaryotic genomes.

This project is funded by the BBSRC, including a 2000 GBP studentship enhancement. Fees-only support will also be available to EU citizens; unfortunately, no support can be offered to anyone outside Europe.

*=graduate student

Papp, B*., Pál, C., and Hurst, L.D. (2003) Dosage sensitivity and the evolution of gene families in yeast. Nature 424 194-197

Pál, C. and Hurst, L.D. (2003) Evidence for co-evolution of gene order and recombination rate. Nature Genetics 33 392 - 395

Pál, C., Papp, B*. and Hurst, L.D. (2003) Rate of evolution and gene dispensability. Nature 421 496-497

Urrutia, A.O*. and Hurst, L.D. (2003) The signature of selection mediated by expression on human genes. Genome Research (in press)

Lercher, M.J., Urrutia, A.O.* Pavlicek, A. and Hurst, L.D. (2003) A unification of mosaic structures in the human genome. Human Molecular Genetics 12: 2411-2415

Lercher, M.J., Blumenthal, T. and Hurst, L.D. (2003) Co-expression of neighbouring genes in Caenorhabditis elegans is mostly due to operons and duplicate genes. Genome Research 13 238-243

Lercher, M.J., Urrutia, A.O.* and Hurst, L.D. (2002) Clustering of house keeping genes provides a unified model of gene order in the human genome. Nature Genetics 31 180-183

Hurst, L.D., Williams, E.J.B*. and Pál, C. (2002) Natural selection promotes the conservation of linkage of co-expressed genes. Trends in Genetics 18 604-606

Eyre-Walker, A and Hurst, L.D. (2001) The evolution of isochores. Nature Reviews Genetics 2 549-555 (Review)

Williams, E.J.B*. and Hurst, L.D. (2000) The proteins of linked genes evolve at similar rates. Nature 407 900-903

Department of Biology and Biochemistry University of Bath Claverton Down Bath BA2 7AY UK

Dr Martin Lercher: m.j.lercher@bath.ac.uk www.bath.ac.uk/bio-sci/lercher Prof Laurence Hurst: l.d.hurst@bath.ac.uk www.bath.ac.uk/bio-sci/hurst

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UCollegeLondon SexulSelection

Phd University College London to start October 2004

Sexual selection in stalk-eyed flies BBSRC funded PhD Studentship in Evolutionary Biology Supervisor: Professor Andrew Pomiankowski

Male stalk-eyed flies have greatly exaggerated eyespans which are sexually attractive to females. We are using stalk-eyed flies to investigate: a) the genetic and developmental basis of male eyespan and its use as a signal of male genetic quality and as a signal of male reproductive ability, b) the molecular genetic basis of male ejaculate proteins, their role in sexual conflict at reproduction and the evolutionary consequences of increases and decreases in sexual conflicts, c) the expression patterns of key regulators of head development in males and females, and across a range of species varying in eyespan exaggeration and sexual dimorphism.

The Studentship holder will be trained in modern molecular genetic and developmental techniques applied to evolutionary questions. The Phd student will join the stalk-eyed fly research group, a large and diverse group of research scientists, working on various aspects of stalk-eyed fly biology. This research is supported by grants from the BBSRC. For further details: http://www.ucl.ac.uk/%7Eucbhkof/new%20phd/ohPhD2004.html Expressions of interest should be sent as soon as possible, and definitely before the end of February. E-mail applications to a.pomiankowski@ucl.ac.uk Please enclose a CV with the names, addresses and telephone numbers of two referees. Applicants should have a strong interest in evolutionary biology and preferably have some experience in molecular techniques, expect to obtain at least a 2i degree in a relevant subject

Please note that you must fulfill standard Research Council residency requirements: http://www.bbsrc.ac.uk/funding/training/Welcome.html ucbhpom@ucl.ac.uk ucbhpom@ucl.ac.uk

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UEdinburgh LanguageEvol 2

MSc in the EVOLUTION OF LANGUAGE & COGNITION One year taught Masters

University of Edinburgh, UK

REMINDER - Applications should be sent before March 31st (although applicants *may* be considered after this date).

What is it that makes us human? How did our brains evolve? What are the origins of human language? Why do we think the way we do? What are the mechanisms of biological, cultural and linguistic evolution?

The University of Edinburgh is introducing a new MSc taught course as part of its postgraduate programme in the Evolution of Language and Cognition. Students will tackle the key questions that are at the heart of the recent renaissance in the scientific study of the origins and evolution of human language and cognition.

Human evolution is a topic for cognitive scientists, psychologists, linguists, archaeologists, anthropologists, biologists, and computer scientists. Because of this, the postgraduate programme will suit students from a wide range of backgrounds. If you are interested in learning more about the evolution of human cognition and language, and about the many disciplines that contribute to its study, we'd like to hear from you.

We are now accepting applications for entry to the MSc in September 2004. Applicants should aim to submit applications by March 31st.

To find out more about the course, and what it will be like to live and work in Edinburgh, go to our website. Here you will also find full details about how to apply.

http://www.ling.ed.ac.uk/lec/elc

[Please feel free to pass on this email to anyone who might be interested.]

– Simon Kirby Language Evolution & Computation Research Unit School of Philosophy, Psychology & Language Sciences University of Edinburgh www.ling.ed.ac.uk/~simon

Simon Kirby <simon@ling.ed.ac.uk>

UGlasgow AvianEvol

BBSRC Industrial CASE Ph. D. studentship, University of Glasgow The role of maternal antioxidants in mediating offspring fitness

In birds, bright plumage ornaments are often attractive to the opposite sex and can be honest signals of quality. This project will manipulate the diet of breeding birds in order to determine the evolutionary links between nutrition and immune function, reproduction and behaviour.

This project will be jointly supervised by Dr. K. Arnold at the University of Glasgow, (<http://www.gla.ac.uk:443/ibls/staff/staff.php?who0816>http://www.gla.ac.uk:443/ibls/staff/staff.php?who0816) where the student will be based, and Dr. A. Stevenson of the Waltham Centre for Pet Nutrition. (www.Waltham.com).

For further details on the project please contact K. Arnold, Division of Environmental and Evolutionary Biology, Graham Kerr Building, University of Glasgow G12 8QQ (K.Arnold@bio.gla.ac.uk). See also the University of Glasgow studentship website http://www.gla.ac.uk/ibls/GradSchool/2004/. The closing date for applications is 12. March 2004 and interviews will take place soon afterwards.

The start date is 1st October 2004 and the duration of the project is 3 years. The maintenance grant in the first year (2004/5) will be £13,500.

Dr. Kathryn Arnold

Division of Environmental & Evolutionary Biology, Graham Kerr Building, University of Glasgow, Glasgow G12 8QQ

Tel. + 44 141 3302898 Fax. + 44 141 3305971 http://www.gla.ac.uk:559/staff/staff.php?who=190816

Kathryn Arnold <K.Arnold@bio.gla.ac.uk>

UGroningen 3 EvolBiol

3 PhD positions in Theoretical Biology at the University of Groningen, the Netherlands

Project 1. Self-organization of social behaviour in animal societies

In models of artificial societies it has been shown that complex social behaviour may arise from simple interactions between individuals and their environment by self-organization. The PhD project addresses all kinds of social behaviour in animal societies (in particular of primates) ranging from coalition strategies, reconciliation behaviour, exchange strategies, maternal styles to migratory behaviour. The aim is to study whether we can explain such complex social phenomena by self-organization. The primary methods are simulation models in which artificial individuals are supplied with behavioural rules and social phenomena are studied at the level of relationships and of the group. Behavioural rules of various degrees of complexity will be implemented to examine their relation to patterns at a group level. Using this procedure it will also be investigated to what extend such social phenomena may arise as emergent properties from the interactions among the individuals and environmental characteristics, such as the distribution of food, the degree of predator pressure, and the competitive regime.

We are looking for a foreign (non-Dutch) student with: - MSc in biology or other relevant discipline - experience with computer programming - knowledge about, and interest in self-organization - knowledge of social behaviour of animals (preferably primates) - ambition to obtain a PhD degree within 4 years

If you are interested in this position, please submit your application with curriculum vitae, list of publications, summary of research interests and two letters of reference by March 10, 2004 to:

Dr. Charlotte K. Hemelrijk, Tel. 0031-50-3638084, Email c.hemelrijk@biol.rug.nl, Theoretical Biology, Biological Centre, Kerklaan 30, 9751 NN Haren, The Netherlands (for more information www.rug.nl/-biologie/theobio)

Project 2. Theoretical Evolutionary Ecology

I am looking for students interested in theoretical evolutionary ecology. Successful applicants will be free to do research for 4 years in any area they like in this field. Potential projects include kin selection, sex allocation, life history theory, genetic conflict. Applicants must send a short research proposal (no more than 3 pages) containing their favorite research questions and an outline of their modeling approach to tackle the questions.

Only non-Dutch students can apply and they must posses an MSc in biology or mathematics or physics or any other relevant field. Please send your application plus CV, proposal and 2 letters of recommendation before March 10th to Dr Ido Pen, Theoretical Biology, Centre for Ecological and Evolutionary Studies, University of Groningen, P.O. Box 14, 9750 AA Haren, The Netherlands or email the complete application to i.r.pen@biol.rug.nl.

For more info, you can check out http://www.rug.nl/-biologie/theobio

Project 3. Causes and consequences of environmental sex determination.

This is a combined theoretical and experimental project. In the theoretical part of the project population genetic models will be developed to gain insight in the evolutionary causes and consequences of environmental sex determination. The experimental part investigates the dynamics of sex determining mechanisms in laboratory and wild populations of the housefly, a species in which several mechanisms of sex determination co-exist.

We are looking for students with experience in mathematical/computer modeling as well as modern molecular genetic methods. Note: ONLY German students can apply. Applicants must have an MSc in biology or any other relevant field. Please send your application plus CV and 2 letters of recommendation before March 1st to Dr Ido Pen, Theoretical Biology, Centre for Ecological and Evolutionary Studies, University of Groningen, P.O. Box 14, 9750 AA Haren, The Netherlands or email the complete application to i.r.pen@biol.rug.nl.

For more information, check out http://www.rug.nl/-biologie/theobio or http://www.rug.nl/biologie/-onderzoek/onderzoekinstituten/cees/jprog/unitemp/

UHawaii EvolEntomology

ENTOMOLOGY GRADUATE STUDENT TEACHING ASSISTANTSHIP

The University of Hawaii at Manoa, Department of Plant and Environmental Protection Sciences seeks applicants for a graduate student teaching assistantship.

Duties: Assist with courses taught by faculty in the Entomology Graduate Program, and other departmental instructional support as needed. Research and instructional areas in the Entomology graduate program include biological control, conservation, ecology, evolution, genetics, IPM, systematics, molecular biology, urban entomology, and vector entomology.

Minimum

Qualifications: Bachelor's degree in biological sciences, and admission to the MS or PhD program in Entomology.

Desirable

Qualifications: Course work in entomology, prior teaching experience.

Salary: $1108.00 / month for MS student, $1198.50 / month for PhD student. Includes benefits and tuition waver.

Contact: Dr. Stephen H. Saul, Entomology Graduate Chair, saul@hawaii.edu. Contact Dr. Saul to indicate your interest in the position, and for information on applying to the Graduate Program.

Submit a full application for admission to the Entomology Graduate Program as described by the Graduate Division of the University of Hawaii at Manoa at http://www.hawaii.edu/graduate/admissions/html/apply.htm . Closing Date: March 31, 2004, or until a qualified applicant is found.

Department of Plant and Environmental Protection Sciences College of Tropical Agriculture and Human Resources University of Hawaii at Manoa 3050 Maile Way, Room 310 Honolulu, Hawaii 96822-2271 http://www.ctahr.hawaii.edu/peps rubinoff@hawaii.edu

UKonstanz EvoDevo

Graduate Student (Ph.D.) Research Opportunities at the University of Konstanz, Germany

We are seeking highly motivated students interested in pursuing graduate study (3 years) at the Ph.D. level in the fields of Evolutionary Developmental Biology or Developmental Biology in the Department of Evolutionary Biology (Prof. A. Meyer) at the University of Konstanz, Germany

We are working with zebrafish and poeciliid fish (swordtails/platies) to study, in an ongoing molecular screen, the genetic basis of a sexually selected trait in swordtail fishes (1,2), and to understand the role of retinoid signaling during zebrafish fin development (3). Putative Ph.D. projects will be broadly based around one of these themes. (References: (1) Zauner et al. (2003) Evolution & Development 5: pp.466, and comment in (2) Wilkins (2004) BioEssays 26: pp.116; (3) Begemann et al. (2001) Development 128: pp.3081)

Successful applicants should ideally have good practical skills in molecular biology (PCR, cloning) and should be highly interested in evolutionary and/or developmental biology.

We have an international group and the everyday working language is English. The Department is excellently equipped for molecular genetic and developmental analyses and houses large zebrafish, as well as poeciliid and cichlid, aquarium facilities. For more information, see: http://www.evolutionsbiologie.uni-konstanz.de/begemann-lab.htm Funding at the German BAT2a/2 level is available, but candidates are also encouraged to apply for their own funding. Expected starting date is before the end of 2004.

Applications should include CV, 1-2 reprints of publications (if available), and names and emails of 2 referees. They should be sent preferentially by email to gerrit.begemann@uni-konstanz.de, or to:

Dr. Gerrit Begemann Department of Evolutionary Biology University of Konstanz, Fach M617 D-78457 Konstanz, Germany Tel: +49 7531 882881 Fax: +49 7531 883018

Gerrit.Begemann@uni-konstanz.de

ULausanne PrimateGeneEvol

A PhD position is available beginning April 1, 2004 in the group of Henrik Kaessmann at the recently founded Center for Integrative Genomics, University of Lausanne, Switzerland.

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

For more information on the group and our institute more generally, see the website: http://www.unil.ch/cig/ I am seeking highly qualified and motivated applicants with experience and a strong interest in one or several of the following fields: computational biology (bioinformatics/data mining), molecular evolution, and/or population genetics. Note that the candidate is expected to also pursue some experimental work, and thus wet lab experience/interest is required.

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

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

Applications including a CV, statement of research interest, copies of relevant publications, and two letters of recommendation should be emailed or mailed to me at the address below. Review of applications will begin immediately. Starting dates after April 1, 2004 are flexible.

Henrik Kaessmann, Ph.D. Assistant Professor Center for Integrative Genomics BEP University of Lausanne CH-1015 Lausanne Switzerland Phone: +41-(0)21-692-3907 Fax: +41-(0)21-692-3907 E-mail: Henrik.Kaessmann@cig.unil.ch www: http://www.unil.ch/cig/page6396_en.html

UNewOrleans EvolEcol

Graduate Studies in Evolutionary Ecology and Conservation Genetics

Positions are available at the Ph.D. level in the laboratory of Steve Johnson (sgjohnso@uno.edu) in the Department of Biological Sciences at the University of New Orleans for students interested in evolutionary ecology, conservation genetics, and coevolution. Two areas of current research are the maintenance of sexual and parthenogenetic reproduction in freshwater snails, and the conservation genetics of hydrobiid snails in Cuatro Cienegas Mexico. Students must apply for admission to the Ph.D. program in Conservation Biology. Interested students should consult the Biological Sciences web page at http://biology.uno.edu/ for application instructions and contact me about their interests. Nationally competitive stipends are available through Louisiana State Board of Regents Doctoral Fellowships, as well as through teaching and research assistantships. For more information on research in the Johnson lab, go to <http://www.uno.edu/%7Esgjohnso/sgjwebpa.html> http://www.uno.edu/%7Esgjohnso/sgjwebpa.html

STeve Johnson Associate Professor & Chair Department of Biological Sciences University of New Orleans New Orleans, LA 504-280-7040 (Office) 504-280-6121 (Fax) Web Page: http://www.uno.edu/%7Esgjohnso/sgjwebpa.html Conservation Biology Ph.D. website: http://biology.uno.edu/phdhome.html

Steven G Johnson <SGJohnso@uno.edu>

UOslo EvolBiol

POSITION AS RESEARCH FELLOW (STIPENDIAT) in biology (evolutionary biology)

available at the DEPARTMENT OF BIOLOGY

A research fellowship (stipendiat) is available at the Department of Biology, University of Oslo from July 1, 2004 for three years (the starting date is negotiable). The position is financed by The Research Council of Norway (NFR) and is administrated by the Faculty of Mathematics and Natural Sciences. We seek candidates for a position based at the Centre for Ecological and Evolutionary Synthesis, Department of Biology University of Oslo, Norway. The position is attached to a recently funded project entitled Integrated ecological and genetic approach to infer the spatio-temporal population-structure dynamics in small salmonid populations. Eligible candidates must have a master of science degree (or equivalent) in a discipline that is closely related to the projects subject area, with specialization(s) in one or more of the following: population genetics, ecology, evolutionary biology. Previous experience with microsatellite DNA analyses would be a major asset. The study includes extensive field- and laboratory work. The successful candidate will also spend 1 year in Canada (Quebec) under the supervision of Louis Bernatchez (http://www.bio.ulaval.ca/louisbernatchez/). For more information about the project, see the following web page: http://folk.uio.no/avollest/trout%20project . The purpose of the fellowship is research training leading to the successful completion of a PhD degree. The fellowship requires admission to the research training programme at the Faculty of Mathematics and Natural Sciences. Firstly applicants must have obtained undergraduate (Cand.mag., i.e. B.Sc. level) and postgraduate (cand.scient. or Siv.ing., i.e. M.Sc. level) qualifications. Together this should represent approximately five years of full time study after completion of European Upper Secondary School/International Baccalaureate. For more information see: http://www.matnat.uio.no/english/research/research_edu/education.html . Appointment to a research fellowship is conditional upon admission to the research training programme. An approved plan for the research training must be submitted no later than six month after taking up the position, and admission approved within the duration of the probationary period of three months. For more information see: http://www.uio.no/admhb/reglhb/personal/tilsettingvitenskapelig/appointresea rchfellow.html.

The University of Oslo wishes to achieve a more equal distribution of scientific employees between the sexes. Female applicants are encouraged to apply.

For further information please contact: professor A. V, tlf. +47= 22 85 46 40, e-mail: avollest@bio.uio.no Deadline for applications: March 23, 2004. REF. NO.: 04/2124 Applicants should submit a letter of application, with 3 copies of CV, a list of published and unpublished works and published papers. One set of certified copies of certificates should also be submitted. The application may be written in Norwegian or English. Applications (marked with the REF. NO.) should be sent to the Faculty of Mathematics and Natural Sciences, att. Senior Executive Officer Bente Schjoldager, P. O. Box 1032, 0315 OSLO The position is available from May 1, 2004 for a period of three years.

UPuertoRico 2 EvolBiol

GRADUATE STUDENT FELLOWSHIPS- UNIVERSITY OF PUERTO RICO

Two Graduate Student Fellowships (Ph.D. or M.S.) are available to work in the lab of W. Owen McMillan at the University of Puerto Rico Rio-Piedras. Fellowships are sponsored by the Center for Applied Tropical Ecology and Conservation (CATEC). Potential projects include:

Evolutionary Genomics: The student will join an international research team focusing on the genetic and developmental basis of wing pattern variation in the Neotropical butterfly Heliconius erato. Heliconius erato has undergone a rapid and extensive adaptive radiation in wing patterns. The vivid wing patterns of this species are adaptations that warn potential predators of the butterflies' unpalatability. Ongoing research is utilizing genomic technologies (high-resolution genetic mapping and gene expression data) to study the developmental and genetic architecture of this extraordinary evolutionary radiation.

Conservation and Population Biology: The student will join an active conservation genetics group that utilizes powerful molecular genetic techniques to address questions about the ecology of endangered or threatened tropical organisms. Ongoing projects include genetic and ecological research on i) reproductive and population biology of hawksbill turtles ii) territoriality and reproductive behavior of the Mona rock iguana, and iii) population persistence, reproductive success, and gene flow in a riparian orchid metapopulation. Student research is not restricted to ongoing projects and there are ample opportunities to develop independent projects, particularly relating to the management and conservation of coral reef organisms.

About the University: Located in San Juan, the University of Puerto Rico-Rio Piedras (UPR-RP) is the oldest and largest campus of the UPR system. UPR-RP has a rich history of teaching and research excellence. The University possesses all essential core infrastructure for state-of-the-art genetic/genomic research. This fact, coupled with the University's proximity to tropical marine and terrestrial habitat and strong links with Central and South America means that UPR-RP is positioned to become a prominent research center in tropical ecology and evolution. Spanish is the major language of the island, but English is also widely spoken. Students are encouraged to become fluent in both languages. Please see http://zephyr.hpcf.upr.edu/˜mcmi-lab/ for additional details about the University and my laboratory. E-mail inquiries to wmcmilla@rrpac.upr.clu.edu.

–

W. Owen McMillan Associate Professor Department of Biology University of Puerto Rico- Rio Piedras P.O. Box 23360 San Juan, PR 00931-3360

wmcmilla@rrpac.upr.clu.edu http://zephyr.hpcf.upr.edu/ ˜ mcmi-lab/ phone (office): 787-764-0000 [(1)2909] phone (lab): 787-764-0000 [(1)2902, (1)2853] phone (home): 787-764-3564 fax: 787-764-3875

Owen McMillan <wmcmilla@rrpac.upr.clu.edu>

UStAndrews EvolGenet

The evolutionary genetics of song in flies; from QTL to candidate gene.

ONLY AVAILABLE FOR UK CITIZENS, I'M AFRAID.

A PhD studentship is available at the University of St Andrews for a joint project between the laboratories of Prof. M. G. Ritchie (St Andrews) and Dr Stephen Goodwin (University of Glasgow). The aims of the project are to combine an evolutionary approach to the evolution of song differences amongst species of Drosophila with molecular and neurogenetic approaches to behaviour genetics. Quantitative Trait Loci approaches have identified chromosomal regions implicated in the evolution of species-specific song traits important to speciation. Candidate genes previously known to influence song are implicated in some of these regions. The student will assess the role of candidate genes directly using modern behaviour genetic techniques such as gene knockout or transfer between species and the molecular evolution of the genes will be analysed by sequence analysis. This project has the potential to provide breakthroughs in the understanding of the genetics of species differences in behaviour. Further details available by e-mailing mgr@st-and.ac.uk or s.goodwin@bio.gla.ac.uk

Formal application materials are available from: The Postgraduate Secretary, Jane Williamson, Gatty Marine Laboratory, University of St. Andrews, St. Andrews Fife KY16 8LB Scotland e-mail: pgbiology@st-and.ac.uk

Mike Ritchie Phone 0 (44 outside UK) 1334 463495 Environmental & Evolutionary Biology Fax 0 (44 outside UK) 1334 463366 Dyers Brae House University of St Andrews E-mail mgr@st-andrews.ac.uk St Andrews, Fife Scotland KY16 9TH

Research group website: http://www.st-and.ac.uk/~bugs Treasurer of the Association for the Study of Animal Behaviour ASAB information: http://www.societies.ncl.ac.uk/asab/

UWindsor FishConservation

3 Graduate student positions available.

I am looking for students to start work on three funded projects at the MSc and PhD levels. The projects include;

1) Darter conservation genetics (MSc or PhD): Develop and apply microsatellite markers to a system of fragmented and introduced populations of the greenside darter in Southwestern Ontario. The analysis will concentrate on metapopulation dynamics in the fragmented populations, and on founder effects in the introduced populations. The student will work with the Canadian Dept. of Fisheries & Oceans in the field, and do the lab work at the Great Lakes Institute for Environmental Research (U Windsor, ON). Applications of the technique will also be possible in the threatened Eastern Sand Darter.

2) Population structure in hybridizing marine mussels (MSc or PhD): Mussels in the 3 sibling species in the genus Mytilus hybridize widely. Hybrid zones have been described on both the west and east coasts of Canada. Recently developed microsatellite markers, combined with diagnostic species markers, will be used to determine the effect of hybridization on population structure and dynamics. Molecular methods will be used to estimate the role of selection against hybrids in both hybrid zones. The student will use archived samples, as well as travel to one or both coasts to perform in situ experiments and collect samples.

3) Adaptation at the gene transcription level in walleye and Chinook salmon (PhD): Both walleye and Chinook salmon are known to exhibit extreme life history variation among populations. This project will address the genetic basis of this variation using neutral genetic markers to estimate additive genetic variance for life history traits, as well as RT-PCR and DNA microarray techniques to assess differences in gene transcription levels in feral populations exhibiting life history trait variation..

Information on the lab, or the Great Lakes Institute can be viewed at;

http://cronus.uwindsor.ca/units/glier/genetics/lab.nsf/2c282f7e3e232d1c052568b1007351c3/2ebc9caf173fb356852569d900583436!OpenDocument or

http://athena.uwindsor.ca/units/glier/main.nsf/c571b39ad1991eb98525694b005101c3/54cf892a73bcaca38525694b0061bbad!OpenDocument

Daniel Heath Great Lakes Institute for Environmental Research University of Windsor Windsor, Ont, Canada N9B 3P4

Phone: (519) 253-3000; Ext 3762 Fax: 971-3616

dheath@uwindsor.ca

Jobs

ChicagoBotanicGarden 2 internships

TWO POSITIONS IN PLANT CONSERVATION RESEARCH

–Ideal positions for graduates and soon-to-be-graduates interested in plant genetics, conservation ecology, or regional floristics–

Two 12-month paid internships are available for individuals with a bachelor's degree in biology, botany, ecology, or a related major and a commitment to the study and practice of native plant conservation and restoration. If you are graduated or a soon-to-graduate student with a background in biology and want to start a career in ecology, botany, environmental science or if you have a strong background and interest in flora of the upper Midwest, we encourage you to apply.

Position 1. As a conservation science intern, you will contribute to ongoing research on the reproductive biology, demography, and conservation genetics of the prairie plant Echinacea angustifolia. You will design and implement your own research project. Summer fieldwork occurs in western Minnesota and greenhouse and lab activities are at the CBG. For more information visit http://www.cbs.umn.edu/~wagenius/jobs/index.html or contact Dr. Stuart Wagenius (swagenius@chicagobotanic.org).

Position 2. As a regional floristics intern, you will assist with all aspects of Plants of Concern, a regional rare plant monitoring program that works with volunteers: monitoring of plants throughout northeast Illinois, training of volunteers, data entry and analysis and program planning. You will also assist with the management of the Herbarium, including collection of plant specimens. You will have the opportunity to work independently as well as in a team context. For more information visit http://www.chicagobotanic.org/internship/Intern_sm.html or contact Susanne Masi (smasi@chicagobotanic.org).

As an intern, you will participate in a variety of conservation-related activities, attend seminars, participate in meetings, and interact closely with botanists, researchers, and conservation scientists.

The Institute for Plant Conservation at the Chicago Botanic Garden is dedicated to applied research about the preservation of rare plants in the upper Midwest and to the restoration of plants lost from natural landscapes. Research focuses on understanding the genetic, ecological, and management factors that influence the reproductive success and population stability of plants in both natural and reintroduced settings.

Applications will be reviewed starting 15 March 2004. The salary is $8/h with added allowances for extended summer fieldwork (position 1).

For further information and application materials please see the Chicago Botanic Garden Internship Program website: http://www.chicagobotanic.org/internship/index.html —– Stuart Wagenius, Ph.D. Institute for Plant Conservation Chicago Botanic Garden 1000 Lake Cook Road Glencoe, IL 60022

phone: 847 835 6978 fax: 847 835 5484

email: swagenius@chicagobotanic.org

ChicagoBotanicGarden SummerResearch

Summer Field Research for undergrads or recent graduates

Are you interested in gaining field research experience and learning about the ecology and evolution of plant-pollinator and plant-herbivore interactions? We are looking for field assistants (two undergraduates and one recent grad) for an NSF-funded research project on habitat fragmentation of the tallgrass prairie. We are investigating how small plant population sizes influence inbreeding, pollination, and herbivory in the purple coneflower (Echinacea angustifolia).

No experience is necessary, but you must be enthusiastic and hard-working. You will survey natural plant populations, measure fitness and floral traits in experimental plots, hand-pollinate plants, observe insects, and assist in all aspects of research. Housing is included and there is a stipend. There are opportunities for doing an independent project.

If you want more information or wish to apply, please look here http://www.cbs.umn.edu/˜wagenius/jobs/index.html or contact Stuart Wagenius. Applications due 26 March 2002.

—– Stuart Wagenius, Ph.D. Institute for Plant Conservation Chicago Botanic Garden 1000 Lake Cook Road Glencoe, IL 60022

phone: 847 835 6978 fax: 847 835 5484

email: swagenius@chicagobotanic.org

GeorgiaInstTech Bioinformatics

BIOINFORMATICS FACULTY POSITION The Georgia Institute of Technology

The School of Biology invites applications for a faculty position in bioinformatics at the level of ASSISTANT PROFESSOR. The successful candidate is expected to pursue innovative research in an area of bioinformatics such as developing methods for nucleic acid and protein sequence analysis, particularly DNA and protein function prediction, protein folding, and biomolecular evolution modeling, and have a commitment to and talent for teaching at both the undergraduate and graduate levels. Georgia Tech has established a graduate program in bioinformatics and plans to expand its activities through the Center for Bioinformatics and Computational Biology (website: http://www.biology.gatech.edu/gt_bioinfo). Curriculum vitae, research interest statement, and three reference letters should be mailed to: Chair of Bioinformatics Search Committee, School of Biology, Georgia Institute of Technology, Atlanta, GA 30332-0230.

Michael A D Goodisman

Assistant Professor School of Biology The Georgia Institute of Technology Cherry Emerson Bldg A110 310 Ferst Drive Atlanta, GA 30332-0230 United States

webpage: http://www.biology.gatech.edu/professors/goodisman.html email: michael.goodisman@biology.gatech.edu office: 404-385-6311 lab: 404-385-6312 fax: 404-894-0519

McGillU Bioinformatics

Bioinformatics. The Biology Department at McGill University seeks candidates to fill a tenure-track position from individuals applying and developing informatics and computational approaches to ecology, systematics, or evolution. While we anticipate that this hiring will be at the Assistant Professor level, more senior candidates may be considered for recruitment at a higher rank. The appointee will be expected to teach at the undergraduate and graduate levels, supervise graduate students, develop a strong, externally funded research program, and interact with members of the McGill Bioinformatics Centre. This position is part a Faculty of Science initiative in Bioinformatics. Consult for information on staff and facilities in the Biology Department. Send letter of application, curriculum vitae, and statements of teaching and research interests, and arrange for three letters of reference all to be received no later than 30 April 2004 to Louise Sabaz, Biology Department, McGill University, 1205 Dr. Penfield, Montreal, Quebec, CANADA H3A 1B1. All qualified applicants are encouraged to apply; however, in accordance with Canadian immigration requirements, Canadian citizens and permanent residents of Canada will be given priority. McGill University is committed to equity in employment.

daniel.schoen@mcgill.ca

NatlMusNatHist SystZool

The National Marine Fisheries Service National Systematics Laboratory has an opening for an invertebrate systematic zoologist based in the National Museum of Natural History. See Feb. 6 issue of Science, p. 896. Closing date is Feb. 27. Access Commerce On-Line site: http://www.jobs.doc.gov

Bruce B. Collette, Ph. D. National Marine Fisheries Service Systematics Laboratory Smithsonian Institution, PO Box 37012 NMNH Rm. WC-57, MRC 0153 Washington DC, 20013-7012 e-mail: collette.bruce@nmnh.si.edu phone (202)-357-2524 FAX (202) 357-1896

For UPS and FedEx, please use my old address:

NMFS Systematics Lab. MRC 153 National Museum of Natural History Washington DC, 20560-0153

Collette Bruce <Collette.Bruce@NMNH.SI.EDU>

PanamaCity Wasp FieldAssist

Field assistant required for tropical wasp study.

A field assistant is required for the period May through July 2004 to aid research on caste determination systems in social paper wasps (Polistes). The study area is on a beach near Panama City. Work involves marking and monitoring wasps, observing behaviour, conducting manipulation experiments. The position would be ideal for a biology graduate/undergraduate. A substantial contribution to travel and living expenses will be offered to applicants who can commit to the full 3-month period.

Interested applicants can obtain information about the project and job description at http://www.zoo.cam.ac.uk/ioz/jobs.htm. The deadline for applications is 23rd February.

Dr. Seirian Sumner Institute of Zoology Zoological Society of London

http://www.zoo.cam.ac.uk/ioz/people/sumner.htm –

Seirian Sumner Postdoctoral Fellow in Molecular Evolution

Smithsonian Tropical Research Institute Att: Seirian Sumner - Gamboa Unit 0948 APO AA 34002 USA

Email: sumners@naos.si.edu or Seirian.Sumner@ioz.ac.uk http://www.zoo.cam.ac.uk/ioz/people/sumner.htm

Current contact address:

Institute of Zoology Zoological Society of London Regent's Park London NW1 4RY UK

tel: (44) 020 7449 6640 fax: (44) 020 7586 2870 http://www.seirian.co.uk

Seirian Sumner <seirian.sumner@ioz.ac.uk>

Perth PlantConservation

3 POSITIONS AVAILABLE

NATIVE PLANT CONSERVATION AND RESTORATION

1. CONSERVATION RESEARCH SCIENTIST 2. RESEARCH ASSOCIATE (POST-DOCTORAL EQUIVALENT) 3. RESEARCH ASSISTANT

1. CONSERVATION RESEARCH SCIENTIST

The Botanic Gardens and Parks Authority (Kings Park and Botanic Garden, =

Perth, Western Australia) is seeking to appoint a Conservation Research =

Scientist on the project "Integrated conservation and restoration biology of the DRF Tetratheca paynterae (Tremandraceae)"

The DRF T. paynterae is to be impacted by the expansion of iron ore mining activities by Portman Iron Ore Pty Ltd, north of the Koolyanobbing mine, near Southern Cross, Western Australia. Tetratheca =

paynterae is restricted to a single ironstone peak with approximately 5000 individuals. As a key component of the management of this DRF species, Portman have commissioned an integrated research program focused on practical outcomes for the on- and off-site conservation, restoration and translocation of T. paynterae. Key research areas include conservation genetics, the genetic analysis of mating system and dispersal, population ecology and viability, propagation, off-site =

storage of germplasm, and restoration and translocation.

We seek an experienced research scientist for a 3-year appointment, with a possibility of extension dependent on funding. Minimum requirements are a PhD in the biological sciences (preferably molecular =

ecology or restoration ecology), experience with molecular markers and =

an automated sequencer, an understanding of genetic issues associated with small populations, a demonstrated ability or interest to undertake =

restoration ecology, and a strong publication record. Experience with =

one or more of plant propagation, off-site storage of germplasm, seed biology, and translocation of native plants, is desirable, as is a track record of student supervision, project management and grant success.

While this position will be predominantly based at Kings Park and Botanic Gardens, Perth, Western Australia, an ability to work in isolated areas is essential, as is an ability to work both independently and as part of a team. The successful applicant will have excellent communication skills, and will be required to present research results in the usual academic forums, as well as to prepare reports for, and liaise regularly with, industry partner representatives.

Salary: GOSACC Level 4-5 ($46,640 $57,338)

For further details, contact either Dr Siegy Krauss (08 9480 3673 skrauss@kpbg.wa.gov.au) or Dr Kingsley Dixon (08 9480 3637 kdixon@kpbg.wa.gov.au). Details about the position, including selection criteria and application packs, are available at http://www.bgpa.wa.gov.au/ Closing date: Friday 5th March 2004

2. RESEARCH ASSOCIATE (POST-DOCTORAL EQUIVALENT) 3. RESEARCH ASSISTANT

The Botanic Gardens and Parks Authority (Kings Park and Botanic Garden, =

Perth, Western Australia) and Murdoch University are seeking to appoint =

a Research Associate (Post-doctoral equivalent) and a Research Assistant on the project "Rapid genetic delineation of local provenance =

for effective restoration of urban bushland remnants" for 2.5 year fixed term appointments.

This ARC Linkage grant funded project seeks to generate urgently needed =

genetic provenance guidelines and principles for the native plant restoration industry nationally, as well as provenance data for key species for urban bushland rehabilitation in south-west Australia. Key =

components of this project include the generation of genetic provenance =

data using molecular markers such as AFLP and SSRs, liaison with rehabilitation practitioners to achieve practical restoration outcomes =

and to plan, conduct and analyze field-based experiments to assess the =

consequences of genetic mixing. Our objective is ultimately to generate a "provenance atlas" for the industry and to develop the principles and guidelines of provenance.

Minimum requirements for the Research Associate position include a PhD =

in a relevant discipline, experience with AFLP or SSRs, an understanding of genetic issues associated with native plant community =

restoration and excellent written and verbal communication and project =

management skills. The Research Assistant position will work with the =

Research Associate, be predominantly genetics laboratory based, focused =

on generating genetic provenance data for targeted species. Minimum requirements include demonstrated experience with genetic laboratory procedures such as AFLP and/or SSRs and the use of an automated sequencer.

The successful applicants will join the large dynamic research teams based at Murdoch University (with Prof Richard Hobbs) and Kings Park & =

— / —

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

SanFranciscoStateU EnvStudies

DIRECTOR ENVIRONMENTAL STUDIES SAN FRANCISCO STATE UNIVERSITY

San Francisco State University and the College of Behavioral and Social Sciences invite applications for an energetic Director (Associate Professor to Professor rank with tenure) for our innovative, rapidly growing, four-year-old interdisciplinary Environmental Studies Program. The ENVS Program at San Francisco State University currently has about 150 majors taking courses in six of the eight University colleges. The Program awards five degrees: two BS degrees in Earth Systems Science and Natural Resource Management and Conservation, and three BA degrees in Environmental Sustainability and Justice, Humanities and the Environment, and Urban Environment. For more details on the ENVS Program, please visit our website at http://bss.sfsu.edu/envstudies . The successful applicant must have a doctoral degree or equivalent in Environmental Studies or relevant field and be a committed teacher and researcher, show clear potential for being an articulate spokesperson for the Program and for securing external Program funding, and be able to collaborate with faculty from Arts, Humanities, Science, and Social Science disciplines. Rank and salary will be negotiated and commensurate with experience.

San Francisco State University, a member of the California State University system, seeks to promote an appreciation of scholarship, freedom, and human diversity through excellence in instruction and intellectual accomplishment. We are particularly interested in attracting women, ethnic minorities, and persons with disabilities. San Francisco State University is an Affirmative Action/Equal Opportunity Employer.

Please send letter of application, curriculum vitae, three letters of reference, and statement of philosophy of academic leadership to:

Dr. Trish Foschi Chair, ENVS Search Committee Department of Geography and HES San Francisco State University 1600 Holloway Avenue San Francisco, CA 94132

Email: tfoschi@sfsu.edu Fax: 415-338-6243 Tel: 415-338-7508

Applicant screening will begin March 8, 2004, and continue until the position is filled. Appointment starts August 2004.

tfoschi <tfoschi@sfsu.edu>

StKilda Five FieldAssist

Soay sheep RESEARCH Spring 2004

Fieldwork Assistants

We are currently looking for 5 volunteers for this year's Soay sheep lambing expedition to St. Kilda, a group of islands 180 km off the coast of north-west Scotland. The expedition runs from mid-March to late-May during which time there are fieldwork assistant posts available within two teams:

Activity: Detailed behavioural observations on ewe-lamb interactions; measuring parasitism in ewes throughout lambing Timing: Early April to End May Contact: Louisa Tempest Email: ljt1@stir.ac.uk <mailto:ljt1@stir.ac.uk>

Activity: Censusing sheep with telescopes and hand-held computers; mortality searches; lamb tagging Timing: Mid-March to Early May & Late March to Early May Contact: Jill Pilkington Email: j.pilkington@ed.ac.uk

Requirements: * Must be available for the full period stated * Must be reasonably fit, St Kilda has a very demanding terrain * A background in Biological Sciences * An interest in animal behaviour

Travel to the island will be by helicopter from Benbecula (Outer Hebrides) and the team will stay in cottages built by the original inhabitants of St. Kilda (since restored by the National Trust for Scotland). Expenses incurred whilst travelling will be reimbursed and food/accommodation on island are provided. This is an ideal opportunity to gain field experience in behavioural research and to visit St. Kilda, the remotest of British islands.

If you wish to apply for this work then please send a CV with covering letter and details of two referees to the relevant contact named above.

Louisa-Jayne Tempest Department of Biological Sciences University of Stirling STIRLING FK9 4LA

(01786) 467818 ext 7818 Email: ljt1@stir.ac.uk

StonyBrookU EvolMorphology

Opening for Assistant Professor

The Department of Anatomical Sciences, Stony Brook University, invites applications for a tenure-track Assistant Professor position, with primary teaching responsibilities in human gross anatomy to healthcare professional students. Applicants must hold a Ph.D. and have taken, and preferably taught, a dissection-based human gross anatomy course. In addition to teaching, the successful applicant will be expected to demonstrate research expertise and the ability to develop a program of funded research that augments or complements the department's existing research strengths in evolutionary and functional morphology (see http://www.informatics .sunysb.edu/anatomy/). Appropriate research specializations include biomechanics, bone biology, developmental biology, physical anthropology, systematics (including molecular systematics) and vertebrate paleontology. Deadline for receipt of applications is March 2, 2004. Please send a letter of application, curriculum vitae, statement of research interests, and the names, addresses, telephone numbers, and e-mail addresses of at least three references to Search Committee, Department of Anatomical Sciences, Stony Brook University, Stony Brook, NY 11794-8081.

cjohnson@notes.cc.sunysb.edu

UCBerkeley PlantEvol

The Department of Integrative Biology at the University of California, Berkeley is seeking an outstanding scientist for a tenure track position (Assistant Professor) with a focus on plant structure, function and/or development. This position provides the opportunity to interface with the strong plant genomics, systematics, and whole plant ecology/evolution programs at Berkeley. In addition, the University and Jepson Herbaria and the UC Botanical Garden collections have a broad range of resources available for research.

Candidates must also have a strong interest in undergraduate and graduate teaching, and the successful candidate will be responsible for the development of undergraduate and graduate courses in plant structure, function and/or development, as well as contributing to ongoing instruction in plant biology, ecology and evolution.

Interested applicants should send a CV, bibliography, brief description of research accomplishments and objectives, statement of teaching interests and selected reprints to the address below, and should arrange to have three letters of reference sent to the same address.

All applicants with a Ph.D. and an exceptional research record will be given serious consideration; postdoctoral experience is desirable.

Applications should be sent to:

Plant Biology Search Committee Department of Integrative Biology 3060 Valley Life Sciences Building University of California Berkeley, CA 94720-3140

Application deadline: February 17, 2004

The University of California is an Affirmative Action/Equal Opportunity Employer

esimms@socrates.Berkeley.EDU

UCBerkeley ResAssoc

Staff Research Associate II - (SRA II)

The Museum of Vertebrate Zoology (MVZ) (http://www.mip.berkeley.edu/mvz) and the new Center for Integrative Genomics (CIG) (http://mcb.berkeley.edu/cig) on the University of California, Berkeley campus are jointly hiring a research associate to work in the Evolutionary Genetics Laboratory of the MVZ. The MVZ has a long history in molecular evolution and systematics, and is only just moving into applying new information and tools from comparative genomics to problems in evolutionary biology, population genetics and systematics.

The new hire will help to build connections between the computational and experimental genomics group in CIG and the vertebrate evolution group in the MVZ. Initial priorities are to advance expertise in genomic and cDNA library construction, screening (standard vectors, BACs, fosmids etc.), and sequence analysis and assembly, as well as to help optimize high-throughput sequencing genotyping, etc. Experience in the application of SNP or haplotype analysis, and colony probing would be an advantage. The appointee will work directly on selected projects, train and supervise students and others working in the labs, and optimize and write up protocols for use throughout the lab group.

Qualifications: Minimum MSc or equivalent lab and research experience required; Laboratory experience in molecular biology is essential, plus some relevant background in computational genomics, molecular evolution, etc. would be an advantage. Ability to supervise and train researchers in the relevant methods.

The Salary Range for this position is $34,500 - 54,876, including benefits. The review of resumes will begin on March 1, 2004

Please apply online http://jobs.berkeley.edu, indicating job number 001015. Additional information can be found at http://hrweb,berkeley.edu/jobs/apply.htm. EOE

If more information is needed please let me know.

Thank you, Dina Sanders

– Dina Sanders Museum of Vertebrate Zoology 3101 VLSB #3160 UC Berkeley, CA 94720-3160 Phone: (510) 642-7869 Fax: (510) 643-8238

UCollegeLondon ResTech

Genetics, Endocrinology and Evolution of Ageing

Two Positions Currently Available in Gems Lab, University College London

(1) Senior Research Technician/Laboratory Manager (level I)

Applicants are invited for a Wellcome Trust funded high level technician post (3 years) to investigate the biology of ageing in C. elegans. Position currently open. Seeking exceptional individual with strong research track record to take lead role in research project. Suitable for experienced technician or ex-post-doc. Experience with C. elegans an advantage. Starting salary, £29,073 [US $53,000] (subject to age, experience). For further description of this project see http://-www.ucl.ac.uk/˜ucbtdag/AdvertWTFG.html (2) BBSRC funded Ph.D. Studentship

Available immediately, but (unfortunately) only to UK nationals/long-term residents. Subject area: biology of ageing in C. elegans. Join a growing research team working as part of a well-funded collaborative network based at UCL investigating the biology of ageing in C. elegans, Drosophila and rodents. See http://-www.ucl.ac.uk/ ˜ ucbtdag/advert03.html for details of project.

Inquiries, or applications with CV and 3 referees to Dr David Gems (david.gems@ucl.ac.uk, Tel: 020 7679 4381), Department Biology, UCL, Gower St., London WC1E 6BT, UK.

See http://www.ucl.ac.uk/˜ucbtdag/ for details of research in Gems laboratory.

David Gems <david.gems@ucl.ac.uk>

UHouston SummerRes

Undergraduate Research Assistants

We are looking for four positions for the summer of 2004 (June 1 to August 15) to aid in research on foraging behavior and reproductive allocation of Pogonomyrmex harvester ants. The study area is located approximately 20 miles northwest of Grand Junction, Colorado on the Colorado plateau. Students will monitor daily activity patterns, measure food intake and help with estimating reproductive output. In addition to salary, student housing costs will be covered. Applicants should be willing to work in desert conditions and have their own car.

Interested individuals should send a CV or resume, including relevant course work, to Drs. Blaine J. Cole or Diane C. Wiernasz, Department of Biology, University of Houston, Houston TX 77204-5001, or by email to bcole@uh.edu or dwiernasz@uh.edu. A description of the study site and study projects can be found at: http://www.bchs.uh.edu/˜bcole/pogo/

– Blaine J. Cole Department of Biology and Biochemistry University of Houston Houston, TX 77204-5001 http://www.bchs.uh.edu/ ˜ bcole/pogo/ Phone:713-743-2679 Fax: 713-743-2636

Blaine Cole <bcole@uh.edu>

ULausanne ConservationBiol

University of Lausanne (Switzerland) Faculty of Biology and Medicine

Professorship in Conservation Biology

at the Department of Ecology and Evolution (http://www2.unil.ch/ie/). The domain of expertise is open, including functional aspects of biodiversity as well as population- or community ecology. The candidate's strong and independent research program should complement local fields of expertise. The position involves some teaching in Conservation Biology. The successful candidate will be appointed at the level of associate Professor or Assistant Professor (tenure track) depending on previous experience,

A complete CV, including a publication list, a list of references, as well as a detailed research program, should be sent to Prof. Patrice Mangin, Dean of the Faculty, University of Lausanne, rue du Bugnon 21, 1005 Lausanne (Switzerland), no later than March 31, 2004.

Further information : Prof. N.Perrin, nicolas.perrin@ie-zea.unil.ch

Context : http://www2.unil.ch/fbm http://www.lausanne.ch/ Nicolas Perrin <Nicolas.Perrin@ie-zea.unil.ch>

UMaryland ChairBiol

Chair, Department of Biology

NOTE: APPLICATIONS SHOULD BE RECEIVED BY MARCH 12 FOR PRIMARY CONSIDERATION, ALTHOUGH WE WILL CONTINUE TO ACCEPT APPLICATIONS AFTER THAT DATE UNTIL THE POSITION IS FILLED

We seek a distinguished senior scientist with the broad vision, experience, and energy to lead major growth and enhancement of the department as part of an ambitious campus drive for advancement in the life sciences. Biology is already a diverse and excellent department, with 35 tenure-track faculty, 150 graduate and postdoctoral students, and research programs ranging from the molecular to the ecosystem level. Building from its current focal areas in neurobiology/biophysics, ecology/evolution, and evolutionary developmental biology, the department will co-lead College of Life Sciences initiatives in comparative and functional genomics, sensory neurobiology, and host-pathogen interactions. This targeted expansion will coincide with construction of a new Bioscience Research Building and seeks to leverage our proximity to the wealth of research institutions in the Washington, D.C., area. For more information about the department, the college, and the university, visit our web site at www.life.umd.edu/ biology.

Applicants: Email curriculum vitae; statement of research interests, academic vision, and administrative style; and names and addresses of four references to Charles Mitter, Search Chair, at cmitter@umd.edu (301-405-3912). Review of credentials is ongoing and will continue until the position is filled.

The University of Maryland, College Park is the flagship campus of the University System of Maryland and one of the most rapidly

advancing public research universities in the country. Our close proximity to Washington, Baltimore, and the Maryland Biotechnology Corridor facilitates interactions with an extraordinary range of major research institutions, including the NIH, FDA, Smithsonian Institution, USDA, and TIGR.

University of Maryland is an equal opportunity affirmative action employer. Minorities and women are encouraged to apply.

tishkoff@umd.edu

UMaryland SeniorEvolBiol

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Senior Faculty Positions, Biology

We are searching for faculty to be appointed at the Associate or Full Professor level. We seek applicants using comparative or functional genomic approaches to address significant problems in our research target areas, with preference given to those who integrate across them. The three areas are: Cellular Biophysics/Neurobiology, Evolution and Ecology, Evolutionary Developmental Biology. Successful candidates will have already developed an outstanding research program and have a record of extensive research funding. We will provide generous startup packages and laboratory space in our new 155,000 sq. ft. state-of-the-art interdepartmental Bioscience Research Building. Growth in the life sciences is the top priority for the campus, and the department expects to make numerous faculty hires over the next five years. Emphases for expansion in the College of Life Sciences include comparative and functional genomics, sensory neuroscience, and host-pathogen interactions.

Applicants: Mail curriculum vitae, statement of recent research accomplishments and future plans, copies of three significant publications, and names and addresses (mail and email) of three references. Applications will be entertained at any time, although those received by March 1, 2004, will receive the best consideration during the current academic year. Mail materials to: Senior Faculty Search, Department of Biology, University of Maryland, College Park, MD 20742.

The University of Maryland, College Park is the flagship campus of the University System of Maryland and one of the most rapidly advancing public research universities in the country. Our close proximity to Washington, Baltimore, and the Maryland Biotechnology Corridor facilitates interactions with an extraordinary range of major research institutions, including the NIH, FDA, Smithsonian Institution, USDA, and TIGR.

University of Maryland is an equal opportunity affirmative action employer. Minorities and women are encouraged to apply.

tishkoff@umd.edu

UMarylandCollegePark Chair

University of Maryland, College Park Chair, Department of Biology

We seek a distinguished senior scientist with the broad vision, experience, and energy to lead major growth and enhancement of the department as part of an ambitious campus drive for advancement in the life sciences. Biology is already a diverse and excellent department, with 35 tenure-track faculty, 150 graduate and postdoctoral students, and research programs ranging from the molecular to the ecosystem level. Building from its current focal areas in neurobiology/biophysics, ecology/evolution, and evolutionary developmental biology, the department will co-lead College of Life Sciences initiatives in comparative and functional genomics, sensory neurobiology, and host-pathogen interactions. This targeted expansion will coincide with construction of a new Bioscience Research Building and seeks to leverage our proximity to the wealth of research institutions in the Washington, D.C., area. For more information about the department, the college, and the university, visit our web site at www.life.umd.edu/ biology.

Applicants: Email curriculum vitae; statement of research interests, academic vision, and administrative style; and names and addresses of four references to Charles Mitter, Search Chair, at cmitter@umd.edu (301-405-3912). Review of credentials is ongoing and will continue until the position is filled.

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Applicants: Mail curriculum vitae, statement of recent research accomplishments and future plans, copies of three significant publications, and names and addresses (mail and email) of three references. Applications will be entertained at any time, although those received by March 1, 2004, will receive the best consideration during the current academic year. Mail materials to: Senior Faculty Search, Department of Biology, University of Maryland, College Park, MD 20742.

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advancing public research universities in the country. Our close proximity to Washington, Baltimore, and the Maryland Biotechnology Corridor facilitates interactions with an extraordinary range of major research institutions, including the NIH, FDA, Smithsonian Institution, USDA, and TIGR.

University of Maryland is an equal opportunity affirmative action employer. Minorities and women are encouraged to apply.

tishkoff@umd.edu

UOttawa Bioinformatics

Le département de biologie de l'Université d'Ottawa cherche à combler un poste à temps-plein menant à la permanence en bioinformatique. Les postes sont normalement au rang de professeur adjoint, mais les demandes provenant de candidats avec plus d'expérience seront considérées. Les candidats choisis participeront aux programmes de premier, deuxième et troisième cycle en sciences biopharmaceutiques, en biologie ainsi qu'en et/ou en sciences de l'environnement. Ceux qui désirent postuler doivent détenir un doctorat et doivent mener un programme de recherche indépendant de haut calibre. Puisque l'Université d'Ottawa est une institution bilingue, ce poste est destiné à une personne capable d'enseigner en franais ainsi qu'en anglais. Le département a obtenu une subvention importante de la Fondation Canadienne pour I'innovation pour établir un Centre de Recherches Avancées en Génomique Environnementale; la personne choisie pour ce poste sera encouragé à participer aux activités du Centre. Nous avons des laboratoires équipés pour la fabrication de puces d'ADNc, et la bioinformatique. De plus, nous avons des lieux de travail conus pour plusieurs types d'analyses environnementales. Les candidat(e)s intéressé(e)s doivent faire parvenir une description de leurs intérêts en recherche et en enseignement, un curriculum vitae, ainsi que les noms et les coordonnées de quatre personnes pouvant fournir des lettres d'appréciation avant le 1 mars, 2004. Veuillez envoyer les demandes au: Comité de sélection en bioinformatique, Département de biologie, Université d'Ottawa, C.P. 450 Succursale A, Ottawa, Ontario K1N 6N5 Canada. Télécopieur: 613-562-5486. L'équité en matière d'emploi est une politique de l'université; nous encourageons fortement les candidatures provenant de femmes, de membres d'une minorité visible, d'autochtones, ainsi que de personnes handicapées. En accord avec les règlements d'immigration, la priorité sera donnée aux citoyen(ne)s canadien(ne)s et aux résident(e)s permanent(e)s du Canada.

The Department of Biology of the University of Ottawa invites applications for a tenure-track position in bioinformatics. Appointments will normally be at the Assistant Professor level, but applications from candidates at higher ranks may be considered. The successful candidates will participate in undergraduate and graduate teaching in programs in Biopharmaceutical Sciences, in Biology and/or Environmental Sciences. Candidates must have a PhD and a strong, independent research program. The University is a bilingual institution; the successful candidate must be able to teach in both French and English. The department has recently received major funding from the Canada Foundation for Innovation to establish a Centre for Advanced Research in Environmental Genomics; the incumbents will be encouraged to participate in the activities of the Centre. We have excellent laboratory facilities for cDNA microarray analysis and bioinformatics, as well as facilities for many types of environmental analyses. Applicants should send a description of their teaching interests and (for the bioinformatics position) their proposed research program, as well as a curriculum vitae, and the names of four referees before March1, 2004 to: Bioinformatics Search Committee, Department of Biology, University of Ottawa, Box 450 Station A, Ottawa K1N 6N5 Canada. Fax: 613-562-5486. Equity is a University policy; the University strongly encourages applications from women, members of visible minorities, native peoples, and persons with disabilities. In accordance with Canadian immigration requirements, priority will be given to Canadian citizens and permanent residents of Canada.

– Dr. Guy Drouin Département de biologie Université d'Ottawa 150, rue Louis Pasteur C.P. 450 Succursale A Ottawa, Ontario Canada K1N 6N5

tel: (613) 562-5800 ext. 6052 FAX: (613) 562-5486 E-Mail: gdrouin@science.uottawa.ca Web: http://www.science.uottawa.ca/BIO/eng/prof/drouin/

USDA PlantGenetics

Research Plant Geneticist. The U. S. Department of Agriculture (USDA), Agricultural Research Service (ARS), Plant Science Research Unit, Raleigh, NC is seeking a permanent full-time Research Plant Geneticist (GS12/13) to understand the molecular basis of complex traits in maize. Research will be conducted independently and in collaboration with other scientists. The major objective of this research is to understand, identify and manipulate the genetic factors responsible for quantitative variation. Specifically, the objectives include understanding the genetic basis of complex traits in maize; understanding quantitative variation as it relates to the use of ancestral and landrace genes in maize and other cereal crops; and the development of methodologies that will enable improved marker-assisted selection of key quantitative traits in cereals. Salary range of $57,556 to $88,973. For program information, contact Dr. David Marshall at david_marshall@ncsu.edu <mailto:david_marshall@ncsu.edu> or 919-515-6819. For application information see <http://www.afm.ars.usda.gov/jobs/announcement-number.htm> and select vacancy number ARS-X4S-0114. To have a printed copy mailed, call 301-504-1482. U.S. citizenship is required. Announcement closes 03/19/2004. USDA/ARS is an equal opportunity employer and provider.

Julie Douglas Pederson, Ph.D. Assistant Dept. Head Department of Genetics, Box 7614 North Carolina State University Raleigh, NC 27695-7614 julie_pederson@ncsu.edu

Julie Pederson <jdpeders@unity.ncsu.edu>

USFishWildlife FishGenetics

Fishery Biologist (Genetics). TWO positions are currently available in the U.S. Fish and Wildlife Service Region 5 Conservation Genetics Lab at the Northeast Fishery Center in Lamar, Pennsylvania. To view the full announcements, and for application and contact requirements, please visit: www.usajobs.opm.gov, and search for the position title FWS5-04-012 and/or FWS5-04-013. Please note differences in closing dates.

-Announcement number FWS5-04-012 is a GS-7/9 TERM appointment

-Announcement number FWS5-04-013 is a GS-9/11 PERMANENT appointment

The incumbents for both positions perform a variety of duties and investigations integral to the U.S. Fish and Wildlife Service, Region 5, Conservation Genetics Laboratory at the Northeast Fishery Center. The Region 5, Conservation Genetics Laboratory provides applied genetics research capabilities to the region, with the focus being on the integration of genetics research to management and conservation of species of interest for the Service. To perform such work, the laboratory relies on having and using the necessary equipment, facilities, and human resources to address the region-wide research needs. The incumbents will perform a variety of routine laboratory and analytical tasks associated with molecular genetic studies, and ensure that laboratory practices adhere to safety and operating protocols. The incumbents will be members of the Population Ecology/Biometrics Branch of the Northeast Fishery Center.

We invite interested applicants to contact NEFC for further information. Please call or email Dr. Mike Millard (570) 726-4247 (ext 28)/ Mike_Millard@fws.gov or Dr. Meredith Bartron (570) 726-4995 / Meredith_Bartron@fws.gov

Meredith Bartron U.S. Fish and Wildlife Service Northeast Fishery Center P.O. Box 75 227 Washington Ave. Lamar, PA, 16848 ph: (570) 726-4995 fax: (570) 726-3255 Meredith_Bartron@fws.gov

USGeologicalSurvey Genomics

The U.S. Geological Survey, Leetown Science Center (LSC), Aquatic Ecology Branch (Kearneysville, West Virginia), has advertised the permanent position of Research Geneticist (GS-12). The ideal candidate would specialize in functional genomics and its applications to ecological issues (i.e., ecological genomics). The scientist will perform laboratory and field research in genomics to expand current genetics and ecological expertise at LSC. The successful applicant is expected to identify and investigate the function and expression of ecologically important genes in species in need of conservation. The scientist will apply genomics investigations to ongoing studies in population genetics, phylogeography, and molecular systematics currently conducted by the branch. The scientist will also interact with ecologists in the Aquatic Ecology Branch, and with microbial geneticists, molecular biologists, and others at LSC. This interaction is expected to shed light on the relationship between genotypes and phenotypes by understanding the associated genetic and environmental interactions that affect individual fitness. Another line of productive research could extrapolate organismal biology to population and species evolution to test how regulatory gene networks evolve and how they differ among populations of closely related species.

To learn more about the position and to apply on-line: 1) Go to the USAJobs website: www.usajobs.opm.gov ; 2) Select Basic Search ; 3) Select Keyword Search ; 4) enter Geneticist ; 5) Scroll to bottom of screen and select: Search for Jobs ; 6) Scroll down to: Research Geneticist, ER-04-001 ; and 7) Click on Research Geneticist.

Please note that this position is limited to U.S. citizens.

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

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

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

UTours ForeignAssociate

Opening for foreign associate researcher : Applications are now being accepted for a foreign associate researcher position in a project on European termites at the Institut de Recherche sur la Biologie de l’Insecte in Tours, France. The selected applicant will work with Dr. A-G. Bagnères who heads a group devoted to social insects including termites. The appointment is for one year with a possibility of extension for 12 months. The starting date will be determined in agreement with the selected applicant who should propose his/her preferences, end of 2004 would be a favored period. Applicants must hold a PhD with additional years of research experience and publications. Applicants must be familiar with social insects and molecular biology but the overall qualifications will be most decisive. A good knowledge on subterranean termites would be welcome. French scientists and PhDs without experience will not be considered. Remuneration and housing will be covered by a grant from the STUDIUM, a scientific agency of the Region Centre in France. An announcement including a summary of the scientific project can be found on the Studium web site (lestudium.cnrs-orleans.fr) . Exact project details are open to discussion but must involve behavior, genetics and chemical ecology (the exact proportion of each factor can be discussed) on the European subterranean termite Reticulitermes. To obtain further information on the Institut de Recherche sur la Biologie de l’Insecte in Tours, please visit the institution’s web site (univ-tours.fr/irbi/). Applicants should submit a C.V., cover letter and recommendations to Dr. A-G. Bagnères (email: bagneres@univ-tours.fr).

Anne Geneviève Bagnères <bagneres@univ-tours.fr>

WestWashingtonU MinorityIntern

Minority Opportunities for Research on Evolution (MORE):

Funded by the National Science Foundation, this summer internship provides research opportunities for sophomores and juniors who are members of racial and/or ethnic groups that are typically underrepresented in the biological sciences. Groups targeted by this program are Native Americans, Alaskan Natives, African Americans, Latinos/Hispanics, and Pacific Islanders.

Selected students will spend 12 weeks (starting in early June; exact dates negotiable) at Western Washington University, in Bellingham, Washington, to participate in NSF- funded research on hybridizing beetles. MORE participants will work in the field and in the laboratory, studying beetle behavior and molecular population genetics. Participants will be trained in basic research skills, including data analysis, graphing, and interpretation, and in the preparation of a poster to be presented at a regional or national scientific meeting.

Financial support for students selected to participate in MORE will include a stipend and round-trip airfare between the students residence and Bellingham, WA.

Applications are due April 10, 2004, and selections will be announced by April 30, 2004. For a downloadable application form, or for more information about this research project, Western Washington University, and Bellingham, WA, see the MORE web page (http://www.biol.wwu.edu/peterson/MORE.html). WWU is an AA/EO employer. For disability accommodation call (360) 650-3771 (V) or 650-7696 (TTY).

For further information, contact Merrill Peterson, Biology Department, Western Washington University, via email: peterson@biol.wwu.edu.

“peterson@biol.wwu.edu” <peterson@biol.wwu.edu>

WoodsHole MolEvol

REU POSITION IN MOLECULAR EVOLUTION OF ENDOSYMBIONTS WOODS HOLE, MASS. SUMMER 2004

Description: The Marine Biological Laboratory in Woods Hole, Mass. seeks a highly motivated undergraduate student for an NSF-supported REU (Research Experience for Undergraduates) position in molecular evolution. The student will work within Jennifer Wernegreen’s lab at the MBL, where (s)he will pursue an independent project focusing on the evolution of bacterial endosymbionts associated with insects. This position will provide exposure to DNA sequence analysis, bioinformatics, phylogenetics, and other molecular evolutionary approaches. The 10-week position will include support for housing at the MBL, travel, and a summer stipend.

Qualifications: Applicants must be highly motivated, eager to learn new approaches, and able to work both independently and collaboratively. Strong interests in evolutionary genetics, molecular evolution and phylogenetics, population genetics, entomology, and/or molecular ecology are desired. Prior exposure to molecular lab techniques in a course or research setting is also preferred. REU positions are funded by the NSF and are only open to U.S. citizens or permanent residents who are currently enrolled in an undergraduate institution and have not graduated prior to starting the position.

Additional information: Please see http://jbpc.mbl.edu/Pages/werneg.descrip.html for more information about the lab and relevant publications. Contact Jennifer Wernegreen (jwernegreen@mbl.edu) with any questions about projects or the position.

To Apply: Applications should include the following: (i) a statement describing your interests and any prior research experience; (ii) CV, (iii) a copy of your transcript, and (iv) the names and contact info of three references who are well acquainted with your abilities. Mailing instructions and a position reference code will be posted by early March on the following site: http://www.mbl.edu/inside/what/human_resources/job_search.php Before that time, you may email materials to jwernegreen@mbl.edu. Review of applications will continue until a suitable candidate is identified.

– Jennifer Wernegreen Associate Scientist Josephine Bay Paul Center for Comparative Molecular Biology and Evolution Marine Biological Lab 7 MBL Street Woods Hole, MA 02543 email: jwernegreen@mbl.edu

YorkU Bioinformatics

BIOINFORMATICS – FACULTY OF PURE AND APPLIED SCIENCE, YORK UNIVERSITY

The Department of Mathematics and Statistics invites applications for a tenure stream appointment at the Assistant Professor level in the area of Bioinformatics to commence July 1, 2004.

We are searching for an outstanding bioinformaticist who will help us launch an innovative program that will involve biologists and computer scientists as well as mathematicians and statisticians. The successful candidate will have a PhD, a proven record of research excellence, and promise of superior teaching ability. The successful candidate will be expected to develop a strong, externally-funded research program and to contribute to teaching at the undergraduate and graduate levels in an interdisciplinary context.

All positions at York University are subject to budgetary approval.

York University is an Affirmative Action Employer. The Affirmative Action Program can be found on

York's website at www.yorku.ca/acadjobs or a copy can be obtained by calling the affirmative action office at 416-736-5713. All qualified candidates are encouraged to apply; however, Canadian citizens and Permanent Residents will be given priority.

Please mail curriculum vitae, an outline of research plans, summary of research publications and three letters of recommendation (one of which should address teaching) to

Bioinformatics Search Committee Department of Mathematics and Statistics York University 4700 Keele Street Toronto, Ontario, Canada M3J 1P3 fax: 416-736-5757 bioinf.recruit@mathstat.yorku.ca www.math.yorku.ca/Hiring Complete applications must be received by March 31, 2004.

Ronald Pearlman <ronp@yorku.ca>

Other

AFLP GeneMapper

Hi, Has anyone had any success using the ABI software "GeneMapper" to analyze AFLP data collected on an ABI 3730 capillary machine? If so, please let me know. Thanks, Tom tdevitt@socrates.berkeley.edu

AFM microdissection

Dear members:

We are trying to set up the LMM-LPC technique in our group to amplify DNA from single bands in Drosophila polytene chromosomes. We have been using PALM technology with an Olympus microdissection system, but found some problems related to adapt polytene squash technique on LMPC-membrane slides. Precisely, we find that, when dissected salivary glands are squashed on top of membrane slide by applying pressure on the

cover slide, the membrane becomes impregnated by the squashing solution that contains acetic and lactic acids, producing a rugged surface that impairs the chromosome spreading and their microscopic observation. Could you suggest a way to avoid this inconvenience? Also, after cover slide is taken off, slides are dehydrated with ethanol which gets under the membrane and leaves air bubbles after ethanol dries up. We are following our in situ hybridisation protocol to make polytene spreads, but I wonder whether other protocols suit best the laser-based microdissection. Could you give us a reference of somebody that has succeed in polytene band microdissection?

We have tried to do LMM-LPC microdissection on slides without membrane and found that we have to apply multiple laser shots to catapult most of

the polytene band. Doing this we are never sure the we recover the whole

band and, most important, we are afraid that DNA could be fragmented into pieces too small for our purposes (we need to amplify a minimun of 5 kbs). Is there a way to adjust the focus of the laser to improve catapulting or, we really need to make the spread on the membrane? A final question that intrigues us is whether such small ammounts of DNA

(contents of a band ranges from 50 to 150 DNA kilobases) are sufficient to PCR amplification.

I am addressing you in the hope that you will be able to guide us to solve our problems. May be you know of somebody that is using this technique to microdissect polytene chromosomes. Hope to hear from you soon and thank you in advance for your help. Sincerely, Antonio Fontdevila Professor of Genetics Departament de Genètica i Microbiologia Universitat Autònoma de Barcelona 08193 Bellaterra Spain Phone 34-93-5811083 Fax 34-93-5812726

AMOVA question answers

Dear Evoldir members,

Several weeks ago I posted a question about AMOVA on Evoldir. I have received several answers and several requests for a synopsis, which are included here. Thank you very much.

Yours sincerely, Miriam Richards

>My question is, am I correct that more complicated, multilevel AMOVA >models have >not been derived? Or if they have, could somebody steer me in the right >direction? A colleague and I intend to derive the models if this has not >been done previously, but we don't want to reinvent the wheel.

1. These analysis of variance "models" have certainly been implemented before, and I guess some statistical packages could certainly handle such additional levels in the hierarchy. However, they do not use molecular distances, but the principles would be exactly the same regarding degrees of freedom. Implementing it yourself would certainly require some major programming efforts. I think the software GDA incorporates one additional level in the hierarchy compared to that implemented in Arlequin. Also be careful that by including many levels in the hierarchy, the degrees of freedom can become quite small, and you would need quite a lot of samples to get significant results.

2. you can simply use the three level analysis to get what you want, if you reorganise your data between runs. E.g., first you do country, region, and within region, then you do region, subpop, and family, and finally you do subpop, family, and individuals. This should serve the purpose, although you will realize that between runs the partitioning may deviate by few tenth of percents.

PS I did that with plants between regions, populations, subpopulations, and individuals, and had no problems to publish.

3. Amova is just like Anova with respect to models. The sums of squares decompositions can be set up in the same way, whatever the model. To my knowledge, software for nested models for 3 levels are all that is generally available. I have myself, on special occasions,

worked out cross-classified models and 4-level nests, on a óne-off basis, as needed, and virtually anything is possible, but I doubt that generic software exists for more than the 3'level nest. There never seemed to be much point in reinventing SAS.

4. The program GDA, available from Paul Lewis (http://lewis.eeb.uconn.edu/lewishome) at least comes closer to what you want, as it will handle 4 levels of hierarchy for F-statistics if I am not mistaken. The models for adding additional levels of hierarchy are really just extensions of the simpler models in a hierarchical ANOVA-like structure – see Bruce Weir's Genetic Data Analysis II textbook (1996, Sinauer) for an explanation. As I see it, the downside of having so many levels of hierarchy in your analysis might be a lack of precision for the F-statistic estimates at the various levels unless you have a huge data set. Anyway, good luck!!

Miriam H. Richards Dept. Biological Sciences Brock University St. Catharines, ON L2S 3A1 Phone: 905 688 5550 x4406 Fax: 905 688 1855

Miriam Richards <miriam.richards@brocku.ca>

Avise book

Dear Friends and Colleagues,

This note is to announce my latest book: "The Hope, Hype, and Reality of Genetic Engineering: Remarkable Stories from Agriculture, Industry, Medicine, and the Environment".

It provides an extensive tour into the stranger-than-fiction world of genetic engineering (including ecological and evolutionary issues), and how researchers are fashioning a medly of genetically modified organisms to serve human needs. For more information, visit www.oup.com/us and search by title.

Sincerely,

John C. Avise

å John C. Avise, Ph.D. Department of Genetics Life Sciences Building University of Georgia Athens, GA 30602 avise@uga.edu 706-542-1456 fax: 706-542-3910

Beetle diseases

Dear colleagues,

I am looking for sexually transmitted parasites that infest beetles from the genus Tribolium and Tenebrio, and that have a negative impact of their host fitness. Can anyone help me ? Any references, names, ideas or suppositions are welcome !

Thanks in advance,

Kind regards,

Nathalie Charbonnel

Centre de Biologie et de Gestion des Populations (CBGP) Campus International de Baillarguet 34 988 Montferrier s/Lez cedex Tél : 33 (0)4 99 62 33 02 Fax : 33 (0)4 99 62 33 45 E-mail: Nathalie.Charbonnel@ensam.inra.fr

Soutenez le mouvement SAUVONS LA RECHERCHE : http://recherche-en-danger.apinc.org/

CNN evolution poll

Today a CNN poll confirms what educators and researchers - and by far the majority of Americans' perspective that evolution is at the core of any meaningful biological sciences curriculum.

See the poll today at www.cnn.com at of 9:18 this morning:

Should the word "evolution" be removed from Georgia's science curriculum?

Yes 15% 1869 votes

No 85% 10867 votes

Total: 12736 votes

Spread the good word!!!

Cheers,

Jim Lyons-Weiler http://bioinformatics.upmc.edu

"Lyons-Weiler, James" <lyonsweilerj@upmc.edu>

Carp samples

Hello everyone, I am estimating phylogenetic relationship between indigenous common carp in Vietnam and foreign common carp. Could you have me to collect some wild Amur common carp samples? It is appreciate. Cheers

Binh Thai Master Student School of Ecology and Environment Deakin Unversity Warrnambool VIC 3280 AUSTRALIA Tel: 61.3.55633569, 61.3.55615831 Mob: 0408038242 http://www.deakin.edu.au/sch_ecol_env/-research/mol_ecol_bio/home.htm

Binh Thai <tbt@deakin.edu.au>

DNA from pleopods

Does anybody out there have a technique to isolate total genomic DNA from ethanol preserved pleopods of freshwater crayfish? We are trying to get enough DNA from one pleopod (this is all we have to work with - about 1 - 1.5 cm long) to be able to PCR amplify multiple gene regions.

Note that some of the pleopod samples are quite old (up to 100 years), and that there seems to be a PCR inhibitor in the extracts trialled so far, perhaps this is from the pigment in the exoskeleton.

Thank you in advance.

Mark Schultz mbsc@deakin.edu.au

DNA sample

Hi everyone!

I would like to know how much tissue do I need to obtain 100 nanograms of DNA ??

The animal in this case is copepods or other crustacean.

Any idea? even a rough estimation will be Ok for me, thanks in advance,

Rodrigo romadryn@yahoo.com

Douglas Falconer

Dear colleagues

I am sorry to pass on some sad news.

Professor Douglas Falconer died on 23 February, in hospital in Edinburgh, aged 90. His health had been declining for some time, and he was almost blind. He had a fall at home last week, and broke his leg. He died after an apparantly successful operation to pin it.

He is survived by his wife Margaret and two sons. Her address is 21 Mansionhouse Road, Edinburgh, EH9 1TZ.

Funeral arrangements have still to be made.

Bill

Prof W G Hill Institute of Cell, Animal and Population Biology University of Edinburgh West Mains Road, Edinburgh, EH9 3JT Tel: +44(0)-131-650 5705. Fax: +44(0)-131-650 6564 e-mail: w.g.hill@ed.ac.uk

Drosophila stocks

Dear Colleagues,

The Coyne Lab is discarding a number of its Drosophila stocks listed below. If you would like a vial of these flies, please contact me, Susannah Elwyn (elwyn@uchicago.edu) by March 14, 2004. We are willing to send vials if you provide us with a FedEx or UPS number, covering the cost of shipping.

Cheers, Susannah

D. simulans

e ebony (chromosome 3) ro rough eyes (chromosome 3) Sim line #2 wild type stock, collected in Winters, CA 1992

D. mauritiana

w, f white, forked (X chromosome) j; irr jaunty, irregular (chromosome 2,3) sn; irr singed; irregular (chromosome 1,3) Maur B/S line B wild type stock MS 34 wild type from Bill Ballard

D.sechellia w, f white, forked (X chromosome) (1-4, 56 [D. simulans locations] cn, pur cinnabar, purple (chromosome 2) SY 034 isofemale line collected on Avocado fruit 4/98 by B. Ballard

D. melanogaster St. Croix Cave Bay (line A rep B)

–

Susannah Elwyn Senior Research Technician Laboratory of Jerry Coyne Dept. of Ecology and Evolution University of Chicago 1101 E. 57th St. Chicago, IL 60637 phone: (773)702-1106 FAX: (773)702-9740 elwyn@uchicago.edu

Susannah Elwyn <elwyn@uchicago.edu>

ElsevierJournal BoardResigns

In line with recent discussion and with U. Conn. Faculty Senate recommendations, the editorial board of the _Journal of Algorythms_ has resigned and will start a competing journal. There was an article on the http://chronicle.com (you may have to be a member to see it) entitled "Editorial Board of Scientific Journal Quits, Accusing Elsevier of Price-Gouging".

Dr. Patrick D. Lorch

plorch@email.unc.edu http://www.unc.edu/˜plorch/lorch.html Department of Biology W: 919-843-2320 University of North Carolina F: 919-962-1625 at Chapel Hill CB#3280, Coker Hall Chapel Hill, NC 27599-3280 USA

Evol questions peer instruction

A physicist friend loaned me a book called "Peer Instruction: a User's Manual" by Eric Mazur. It describes an interactive, concept-based method of teaching physics, complete with hundreds of concept questions that could be asked during lecture. Does anyone have a similar bank of questions for the teaching of genetics and evolution?

The questions are multiple choice, but complicated and difficult enough that most students benefit from talking to the students around them to understand the answer. The idea is that the instructor projects the question and the students hold up a card indicating what they think is the right answer ("A, B, C, or D"). Students then turn to 3-4 of the students around them to talk about the question for several minutes. Then they "vote" again. What Mazur finds is that the students who know the answer are quite convincing in their explanations and teach their peers how to think about the question. Those who had the wrong answer initially usually had weaker arguments supporting their decision and were likely to change their answer on the second round of voting.

I want to try this technique in my Genetics and Evolution course, a course for first-year biology majors that enrolls about 80 students per semester.

Helen Young hjyoung@middlebury.edu

Helen Young Biology Department Middlebury College Middlebury, VT 05753 (802) 443-2556 hjyoung@middlebury.edu http://community.middlebury.edu/˜hjyoung/

"Young, Helen" <hjyoung@middlebury.edu>

Freqpars format

I am having difficulty converting my nuclear SNP frequencies into the "freqpars" file format. It looks like most people using frequency parsimony are starting with a BIOSYS file and using Swoffords BIO2frq program in the FREQPARS package to convert it to a freqpars file format. This can then be imported into PAUP* to generate the appropriate matrices for frequency parsimony. It appears BIOSYS-2 is no longer available from the ftp site at Colorado State. Is there an alternative program to generate the freqpars format or can someone explain what line 4 in the freqpars file format is for (e.g. 6A,5F4.2)?

Thank you,

Justen

Justen Whittall Noble Hall 2263 Department of Ecology, Evolution and Marine Biology University of California (805) 893-7814 Santa Barbara, CA 93106 whittall@lifesci.ucsb.edu

GCrich sequencing

Dear All, I am having trouble for sequencing highly G+C rich PCR products of nuclear ITS rDNA genes, using the BigDye ABI chemistry.

Basically, the sequences start very nicely, with high and distinct peaks, and suddendly crash after a string of GGGGGGGGCCC. I am not sure if this is only due to the high GC content, or also to the secondary structure that ITS fragment can take. I tried a GC-buffer from Invitrogen, I tried different concentrations of DMSO, I tried to increase temperature for the extension-step(up to 72 deg, rather than the suggested 60). Without success.

I would appreciate a lot any advices, suggestions, on this matter, Many thanks in advance, Best Regards Colomban

vargas@imcs.marine.rutgers.edu

GeneConcepts survey

Changes in our understanding of the structure and function of genes have occurred through the concept's one hundred year history but have accelerated rapidly in recent years. The Representing Genes project, funded by NSF, is an interdisciplinary group of researchers examining the current status of the concept and how researchers in different fields have reconceived it to meet their particular needs. We aim to gather the views of the widest possible range of biological researchers and ask for your assistance in completing a web-based survey based on a series on intriguing cases in contemporary genomics. Please take the opportunity to be part of this project.

The survey is posted at: http://surveyweb.ucsur.pitt.edu/sw/wchost.asp?st=gene and will remain accessible through the end of March.

Although survey responses are anonymous there is an opportunity to request an information package of annotated bibliographies on the cases mentioned in the questionnaire, and to request notification of the published results in due course.

Please report any difficulties to the researchers: kstotz@pitt.edu

Karola Stotz, PhD Department of History and Philosophy of Science 1017 Cathedral of Learning, University of Pittsburgh, Pittsburgh, Pa 15260, USA phone 412-624-9177 mobile 412-726-9766 Home page: http://www.pitt.edu/˜kstotz/ Genes Project: http://www.pitt.edu/˜kstotz/genes/genes.html Private: 218 Elysian St, Pittsburgh, Pa 15206, USA, mobile 412-726-9766

"She was not quite what you would call refined. She was not quite what you would call unrefined. She was the kind of person who keeps a parrot."

Karola Stotz <karola.stotz@verizon.net>

Genome walking answers

Dear colleagues,

Here are all the replies to the Genome walking question that I asked last year. Sorry for the delay in posting this reply, but I wanted to have time to trial the kit!

I ended up using the Sigma Vectorette System, with some success.

A special "Thank you" to all those people that took the time to reply to my email.

Kind regards, Adele

Original Email

Dear colleagues, I am studying metallothionein (MT) genes that are involved in Heavy Metal responses in mussels I have isolated some coding gene sequence(s) and want to use a PCR based DNA walking method to isolate the entire gene sequence(s) for use in populations surveys. Is there anyone out there who has used the Invitrogen TOPO Walker Kit or SIGMA's Universal Vectorette System who could give me some advice as to their relative effectiveness? Any other advice/kits that could be useful?

Many thanks, Adele

Answers Summary

Clonetech

I have had repeated success with Clonetech (now BD-Sciences, I think) Universal Genome Walker kit. I have used this for several species (from mice to lizards) and for many genes. For the most part, I followed the kit's instructions, but used annealing temperatures about 2 degrees lower than recommended and used 2X more library (template) in the PCR reactions than recommended. In my experience, success or failure relied heavily on how good your gene-specific primers were.

I haven't used either of the kits you mention, but have used the Clontech Genome Walker kit for this purpose, with good success.

I've been using the GeneWalker Kit - Clontech - to obtain the complete sequence of the genes involved in the carotenogenic pathway...until know the kit worked very well and results are very good. Hope this is helpfull and if you need more informations just ask me.

I have used the Universal GenomeWalker Kit from Clontech (now BD Biosciences) and have, frankly, been surprised at how well it works. Out of seven "walks", I have only had one failure (and that due to my faulty primer design). I have been using it in plants (wild beets), but it should be fine for any uncharacterized genome.

When I was deciding which was the best approach for my work I considered both the Universal Vectorette kit from SIGMA and the Universal GenomeWalker Kit from Clontech. The kit from Sigma does not give any information about linkers sequence while the Clontech one is nicely explained in the manual and in a paper from NAR (SIEBERT, P. D., CHENCHIK, A., KELLOGG, D. E., LUKYANOV, K. A. and LUKYANOV, S. A., 1995. An improved PCR method for walking in uncloned genomic DNA. Nucleic Acids Res. 23: 1087-1088). So I choose the Clontech kit, which has been working very well, allowing 10kb genomic walkings in several steps (typically 500 bp to 2500 bp each) and I would recommend it.

Invitrogen TOPO

I have used TOPO walking and had success, though this was quite variable. I suspect that it worked when the kit was new, but then deteriorated. I bought three kits in my life, and this always seemed to be the case. I have heard others say similar things about the TOPA TA cloning kit, so it could be a general thing with that enzyme. I haven't used the vectorette system, but some people here swear by it. I suggest trying that.

I have used the TOPO kit - it works fine but it generally only gives you about 1-2 kb long fragments. If you gene is long, you will have to do a lot of walking and end up designing/ordering many primers.

Other suggestions

Have a look at Myrick KV, Gelbart WM Universal Fast Walking for direct and versatile determination of flanking sequence GENE 284 (1-2): 125-131 FEB 6 2002 It works!

Adele Whyte Tuapapa Putaiao Maori Fellow School of Biological Sciences Victoria University of Wellington PO Box 600 Wellington NEW ZEALAND Phone: 64-4-472-1000

Visit the student portal @ http://-www.studentvuw.vuw.ac.nz Adele Whyte <whyteadel@student.vuw.ac.nz>

Genomes to sequence

Dear Colleagues,

John Gerhart and I are chairing an NHGRI working group on Comparative Genome Evolution to make recommendations for genome sequencing targets. There is information on the new program posted at:

http://www.genome.gov/10002189 This working group will address the acquisition of new genomic sequences for one or more of three main purposes: 1) the provision of sequence from critical phylogenetic positions, for example to illuminate the evolution of major morphogenetic or physiological innovations in evolution; 2) at a smaller evolutionary scale, the provision of sequence from species that will allow the optimal identification of conserved functional regions in the existing genome sequence of important non-mammalian model systems; and 3) the provision of information that addresses basic questions about genome evolution such as evolutionary rates; speciation; genome reorganization, origins of variation, etc.

This program is intended to have a scope potentially encompassing all organisms except plants, algae, eubacteria and archaea. This program is for consideration of targets for large-scale genomic sequencing. Proposals for EST sequencing, cDNA sequencing or the development of other genomic resources will not be considered by this procedure, but pilot sequencing may be possible to justify the consideration of an organism.

We seek input from various research communities, and we welcome nominations, supported by as much information as you can provide in the attached spreadsheet (columns and rows can be resized as needed to provide ample space for text), or you can address the list of questions appended at the bottom of this email. We can consider some genomes very soon, since we will be making our first set of recommendations in early April. This sequencing effort will continue, and we are interested in knowing about candidate genomes for future years, from organisms still needing preliminary work. We look forward to hearing from you.

Please cc "Felsenfeld, Adam (NIH/NHGRI)" <felsenfa@mail.nih.gov> on inquiries or recommendations.

Best regards, Laura Landweber

Proposed organism or set of organisms: Contact or lead author: Genome Size: Method of genome size estimate: Sequencing coverage-high, low, or just preliminary: What is the need for the complete genome as opposed to BACs or ESTs: Sequencing strategy (e.g., whole genome shotgun) Phylogenetic or Evolutionary argument(s): Polymorphism level: Availability of DNA: Availability of BACs: Food source/symbionts/contaminants: Argument(s) for the usefulness of the genome sequence for annotating/ informing other genomes: Preliminary data, if any: G/C content: Unusual genome characteristics: Is it an experimental organism? Which experimental tools are available: Medical or Agricultural relevance, if any: Model for any particular biological system(s) or other novelty: Readiness for the genome: Size of research community: Other funding or cDNA projects, etc.: Any anticipated technical challenges: Is preliminary work needed to assess genome readiness?

–

Laura F. Landweber, Associate Professor Ecology & Evolutionary Biology, 223 Guyot Hall Princeton University, Princeton, NJ 08544-1003 http://www.princeton.edu/˜lfl tel 609-258-1947 * fax 609-258-7892 * lfl@princeton.edu

Laura Landweber <lfl@Princeton.EDU>

Gyny levels in ants

Subject: gyny-levels and colony sizes in several ant species

Dear colleagues, I am working on a comparative study on life history aspects in ants and would like to have information on the primary mono-/polygyny and/or mean colony size of the different species hereafter. This information can in many cases not be found in the (accessible) literature, either because the references are so old as to not be included in the on-line databases or because the data have not yet been published. I would therefore very much appreciate it if you should have any information on gyny-levels and colony size in the species listed below and would most kindly be prepared to let me include unpublished data in my study. All due reference and acknowledgement would naturally be given. Cryptopone gilva Gnamptogenys simplicoides Vollenhovia emeryi Strumigenys manga Melissotarsus insularis Camponotus lateralis Camponotus pilicornis Formica gagates Formica selysi Lasius carniolicus Lasius flavus Crematogaster scutellaris Leptothorax unifasciatus Manica rubida Myrmica rubra Myrmica sabuleti Solenopsis fugax Tetramorium caespitum Pachycondyla villosa Plectroctena subterranea

–

mathieu.molet@ens.fr

Laboratoire d'Ecologie Université Paris 6 - Pierre et Marie Curie 7 quai Saint-Bernard 75005 Paris FRANCE

batiment A, 7ème étage, pièce 713 tel: 01.44.27.26.94 mobile: 06.70.20.29.38

Halimolobus samples

Dear evoldir members

I am looking for samples of Halimolobus berlandieri (Brassicaceae) for a phylogenetic study. I prefer seeds but any kind of tissue that contains DNA would be fine. If there is anyone that can help me, please contact me directly via alf.ceplitis@cob.lu.se

Many thanks,

Alf Ceplitis

Alf Ceplitis, PhD Department of Cell and Organism Biology (Genetics) Lund University Sweden

Postal address: Solvegatan 29, SE-22362 Lund Phone: +46 46 2227857 Fax: +46 46 147874

HighGC sequencing answers

Hello, some of you asked me to post the answers to my question of last week:

“Dear All, I am having trouble for sequencing highly G+C rich PCR products of nuclear ITS rDNA genes, using the BigDye ABI chemistry. Basically, the sequences start very nicely, with high and distinct peaks, and suddendly crash after a string of GGGGGGGGCCC. I am not sure if this is only due to the high GC content, or also to the secondary structure that ITS fragment can take. I tried a GC-buffer from Invitrogen, I tried different concentrations of DMSO, I tried to increase temperature for the extension-step(up to 72 deg, rather than the suggested 60). Without success. I would appreciate a lot any advices, suggestions, on this matter, Many thanks in advance, Best Regards Colomban”

HERE ARE THE ANSWERS I GOT:

Dear Colomban, This can always be tricky. Have you tried heating up your reaction at 98oC for 10’ before you start cycling? This should help by breaking up any secondary structure that your DNA might have. Hope this helps. Cheers, Anders. CERC Graduate Fellow Center for Environmental Research and Conservation Department of Ecology, Evolution and Environmental Biology 1200 Amsterdam Ave. 10th Floor MC 5557 Columbia University New York, NY 10027 Email: ag2057@columbia.edu Phone: +1 212 854 0377 Fax: +1 212 854 8188

Dear Sir/Madam, Hello....the problem is really simple and solution is very easy.I am getting a very good sequence with such region in ITS ,but initially it was a hectic in the sense that I did Gradient pcr to get the good pcr product,muct be intact product.Then probably you go for cloning the product in a suitable vector and sequence it with the flanking primers.You will get full sequence with both the primers. Let me know if there are any querries... best wishes, mahesh

Mahesh S. Dharne National Center For Cell Science Molecular Biology and Evolution Unit, University campus,Pune, (M.S.),India Tel # 91(20)5690922, Fax #91(20)5692259 web:http://www.nccs.res.in Cellular no: 919822417027

Dear Colomban, are you sequencing cloned products? Otherwise it sounds like you are running into the problem of variability between the two alleles, one of them possibly being a few Gs shorter and therefore messing up the rest of your sequence! Cheers, Christoph

Christoph Schubart Biologie I Universität Regensburg 93040 Regensburg; GERMANY Tel: +49 941 9433093 Fax: +49 941 9433304 for official correspondence please use: christoph.schubart@biologie.uni-regensburg.de

Dear Colomban, Sequence your PCR product from the other side. If you do not reach your desired region, you would have to design new primers within the parts of your PCR products that you can sequence. Good luck, Natalia Martinkova

Dear Colomban, Not that I have a LOT of experience with ABI sequences, but I heard recently that one can add betaine to the BigDye sequencing reactions. I don’t know if you were still in Steve’s lab when I promoted the use of betaine as a magic _PCR_ ingredient, and it makes sense to me that it would improve cycle sequencing (especially of GC-rich regions) just as much. In PCR I use 0.5 to 1 molar (!) betaine – may be worth trying – good luck!

If the ITS regions are nuclear junky?, you may be trying to directly sequence heterozygotic pcr products which cannot be done! That is heterozyogotic in length, not mutation!! One allele may be: GGGGGGGGCCC, and the other may be GGGGGGGGCCC plus or minus any other combination of miscellaneous bases. Just one additional bp will do exactly what you describe in a sequencing run.

Fortunately, you can get around this problem by cloning the pcr products and sequencing the separate alleles. Many people I believe however, are just sequencing from the other direction, but this is not a luxury you can afford if this phenomenon occurs throughout a specific sequence.

Good luck and keep me posted? Si Creer

Colomban,

Applied Biosystems has a GC rich sequencing solution for these issues. We used it when we were doing our microsatellite libraries on organisms that had GC rich genomes. If you need more information on product/part number let me know and I can find out, but maybe try that out.

Melissa

vargas@imcs.rutgers.edu vargas@imcs.rutgers.edu

Journal cost 6

Several months ago there was a brief discussion of journal prices and the challenges faced by libraries. As a result, I thought readers of Evoldir might be interested in the resolution that appears below, which was adopted on Monday by the University Senate at the University of Connecticut.

Kent

***

Resolution

Access to the scholarly literature is vital to all members of the academic community. Scholars and their professional associations share a common interest in the broadest possible dissemination of peer-reviewed contributions. Unfortunately, the business practices of some journals and journal publishers is inimical to these interests and threatens to limit the promise of increased access inherent in digital technologies. Development of library collections is more and more constrained by the rising costs of journals and databases. Faculty, staff, students, and university administrators must all take greater responsibility for the scholarly communication system.

Therefore, the University Senate calls on all faculty, staff, and students of the University of Connecticut to become familiar with the business practices of journals and journal publishers in their specialty. It especially encourages senior tenured faculty to reduce their support of journals or publishers whose practices are inconsistent with the health of scholarly communication by submitting fewer papers to such journals, by refereeing fewer papers submitted to such journals, or by resigning from editorial posts associated with such journals. It encourages them to increase their support of existing journals and publishers whose practices are consistent with the health of scholarly communication.

The Senate also calls on University administrators and departmental, school, college and University committees to reward efforts by faculty, staff, and students to start or support more sustainable models for scholarly communication. It calls on them to provide financial and material support to faculty, staff, and students whose work helps to ensure broad access to the scholarly literature. It also calls on professional associations and the University to invest in the infrastructure necessary to support new venues for peer-reviewed publication.

Finally, the Senate calls on the University Libraries to provide resources that help faculty, staff, and students understand the business practices of different journals and journal publishers and their impact on the health of scholarly communication.

– Kent E. Holsinger kent@darwin.eeb.uconn.edu http://darwin.eeb.uconn.edu – Department of Ecology & Evolutionary Biology – University of Connecticut, U-3043 – Storrs, CT 06269-3043

ML distances

Hi,everyone

Does anybody know if ML distances between groups (not pairwise comparison) are calculated using PAUP, and how to perform them? If not, is there any other program to do them? I only know that evolutionary distances between groups can be calculated in Mega2, but there are only several simple models in Mega2. I want to use more complicated models, for example,GTR+I+G model.

Thanks in advance. Xiaoming Liu Institute of Zoology, the Chinese Academy of Sciences 25 Bei Si Huan Xi Lu, Haidian District, Beijing, 100080 CHINA Email: liuxm@panda.ioz.ac.cn

Xiaoming Liu Institute of Zoology, the Chinese Academy of Sciences, http://www.ioz.ac.cn/ 25 Bei Si Huan Xi Lu, Haidian District, Beijing, 100080 CHINA Tel:86-10-62552630(O) Email: liuxm@panda.ioz.ac.cn

MississippiStateU REU Conservation

Applications are now being accepted for an NSF-funded Research Experience for Undergraduates program in “Conservation Biology in the Southeastern United States” at Mississippi State University. The program will take place during the summer of 2004. Undergraduate students will conduct independent research projects with faculty mentors and participate in group activities that complement individual efforts. This program focuses on building confidence and skills in conservation biology research and targets students who would not otherwise have the opportunity to participate in research activities at their home institution or are from typically underrepresented groups in the sciences. The application deadline is March 15. For more information, please visit the program website: http://csmt.msstate.edu/html/REU/ Mark Fishbein Assistant Professor Director, Miss. St. Univ. Herbarium (MISSA) Department of Biological Sciences Mississippi State University P.O. Box GY Mississippi State, MS

39762 USA ph: (662) 325-7577, -7570 fax: (662)325-7939 email: fish@biology.msstate.edu

Molluscan keys

Dear Evodir members,

I am looking for a good molluscan key (specially for freshwater molluscans). If anybody can send me details I really appreciate it.

many thanks.

H. Munasinghe dhnm@zoo.ruh.ac.lk

NJ phylogenies

Hello Everyone,

If anyone could suggest a way to statistically compare a neighbor joining tree built with genetic distances from microsatellite frequency data to a constrained tree, I'd be very grateful.

I know that NJ is not a likelihood method and I at least cannot use PHYLIP to do such a comparison. Please let me know if you know of a better method of creating a tree from microsatellite data where such a comparison may be possible, or whether there is software available that may allow me to make the comparison regardless. My populations are distant enough that significant mutation has occurred, so methods that ignore mutation will probably not be useful.

Thanks! Ben Blackman bkblackm@indiana.edu

NJ phylogenies answers

Here's the replies I received to my question about comparing constrained alternative topologies of microsatellite based NJ phylogenies from last week. Thanks again for the responses!

Cheers, Ben

Original e-mail > Hello Everyone, > > If anyone could suggest a way to statistically compare a neighbor > joining tree built with genetic distances from microsatellite frequency > data to a constrained tree, I'd be very grateful. > > I know that NJ is not a likelihood method and I at least cannot use > PHYLIP to do such a comparison. Please let me know if you know of a > better method of creating a tree from microsatellite data where such a > comparison may be possible, or whether there is software available that > may allow me to make the comparison regardless. My populations are > distant enough that significant mutation has occurred, so methods that > ignore mutation will probably not be useful. > > Thanks! > Ben Blackman > bkblackm@indiana.edu

Replies: I guess you've tried CONTML? Also, with respect to mutations, Joe Felsenstein mentions the following paper, although cautiously: Wiens JJ. 2000. Reconstructing phylogenies from allozyme data: comparing method performance with congruence. Biol. J. Linnean Soc. 70(4):613-632. Ross Crozier

Hello

In response to your post on the Evoldir: David Hillis wrote a chapter in the book "Advances in molecular ecology" (1998, IOS Press, Amsterdam) about the phyogenetic analysis of frequency data, such as allozyme data, but of course that may also be appicable to microsats. I do not know by heart if the method is suitable for Likelihood analysis, so it may not be of much use to you.

Good luck, Patrick Meirmans

Dear Ben I do not know what you want to do by comparing a NJ tree with a constrained tree. In most cases, construction of an NJ tree with bootstrap values gives sufficient information. This type of NJ trees can easily be constructed from microsatellite data by using Takezaki's program POPTREE or Ota's DISPAN for various distance measures. These two programs are available from my website listed at the bottom of this message. Have you read Takezaki and Nei's Genetics (1996) paper or Nei and Kumar's book "Molecular evolution and phylogenetics", Oxford University Press, 2000, about microsatellite data? Theoretically, of course, it is possible to compare any pair of minimum evolution topologies by using Rzhetsky and Nei's (1993) algorithm, and this can be done by using Rzhetsky and Nei's program (CABIOS 10:409-412, 1994). However, this requires a least-squares distance, and this distance is not necessarily good for microsatellite data (see Nei and Kumar's book, chapter 13). All the papers and softwares mentioned here are available from my website.

You imply that ML trees are usually better than NJ trees. This is a common misconception in systematics. Actually both methods have advantages and disadvantages, as was discussed in Nei-Kumar book. Masatoshi Nei

Hi Ben,

If I understand your query to evoldir correctly, what you want to do is determine whether a distance matrix based on microsatellite frequency matches and is consistent with a hypothetical matrix (a constrained tree/relationship among taxa). Is that correct? If so, people frequently use a Mantel's test to test for independence and lack of association between matrices. But by 'constrained tree' you may mean something more specific. If there is a way to specify your constrained tree as a nested hierarchy within a matrix, this may be one way to go. Alex Buerkle

Dear Ben

I suggest the program Populations (http://www.pge.cnrs-gif.fr/bioinfo/populations/index.php?lang=en) I think that you can compare the tree by bootstrap values...

Best regards

Paulo Russo

Onagraceae micros

Dear members,

Our lab is currently trying to develop a microsatellite library for Camissonia cheiranthifolia (Onagraceae), but we are having some problems. Before the enrichment phase, but after the digestion (with RsaI and BstUI each) and linker ligation several highly concentrated bands appear within the smear on a gel (6-10 bands in the 500-1000bp region). The problem seems to be that the genome has several highly repetitive elements present, which obviously also contain enzyme cut sites. Since these elements are appearing even prior to enrichment we are concerned that this species might not be a good candidate for microsatellite library development as it would likely become heavily biased for these repetitive elements.

Has anyone ever experienced this problem before? If so, how did you handle it? More specifically, has anyone had success (or not) with an Onagraceae species or had a similar result?

Any suggestions or advice on how to proceed would be greatly appreciated.

Karen Samis samisk@biology.queensu.ca

– Karen Samis, MSc. PhD Candidate Biology Department Queen's University Kingston, Ontario, Canada K7L 3N6 613-533-6000 ext. 75125

Karen Samis <samisk@biology.queensu.ca>

Plato program help

Dear EvolDir members,

I am looking for help with a problem I encountered when using the PLATO program.

The problem is like this: When I tried to run PLATO in Mac Classic environment with my file containing both the data and the ML tree in PHYLIP format, the program prematurely aborted and the Classic environment was shut off also. When I tried to run on Mac OS9, the output window stayed open but the program stopped at the beginning of the analysis and could not progress. I checked my file a few times and it seemed to be all right.

My questions are: 1. Has anyone experienced same or similar problem? 2. What might be the cause of this problem and how to solve it?

My data file can be sent if needed. Thanks a lot for any help!

Frank Xie Xie.6@nd.edu

Polyploid software

Hi everyone,

I need a software to perform analyses using molecular marker data (microsatellites) from polyploid species. All the software that I have proved until now seems to be made specially for diploid data. If someone knows about some software that could be useful to me (especially if it can calculate Golstein genetic distance) please let me know.

Thanks for any advice,

Iris irisxkx@yahoo.com

SSB awards

Mini-PEET Awards for Students, Postdocs or Faculty to Enhance Transfer of Taxonomic Knowledge - SSB is pleased to again announce the availability of four awards to enhance the transfer of taxonomic expertise, modeled after the highly successful PEET program at NSF. Unlike the NSF PEET program, awards will not be limited to taxonomically understudied taxa, since the primary purpose is to pass on taxonomic expertise in general. The awards are designed to allow SSB members (students, post-docs, and faculty) to spend a summer or semester apprenticed to an expert in a particular taxonomic group. This would support the PEET goal of passing on taxonomic expertise before it is lost. This could support either a trip for the applicant to the taxonomists' laboratory, or supply funds to allow the expert taxonomist to visit the applicants' laboratory for a period of time. Requests for support may be in any amount up to $4,000. The request should include a brief description of the project, justification of the importance of the taxon, and an itemized budget; the request should be no more than two pages long, not including the curriculum vitae. Requests should be sent to Dr. Keith Crandall, Executive Vice President, SSB. E-mail submissions can be sent to keith_crandall@byu.edu or Dr. Keith A. Crandall, 675 Widtsoe Building, Department of Integrative Biology, Brigham Young University, Provo, UT 84602-5181USA. Review of applications will begin on April 1st 2004. Applicants should NOT be from a laboratory group currently supported by an NSF PEET award.

Scholarships and Travel Awards for Scientists from Developing Countries to Obtain Modern Systematic Training in the US - SSB is pleased to announce the availability of four scholarships for scholars from developing countries to attend workshops and courses in systematics, or to visit a molecular lab for training. The emphasis of this program is the transfer of knowledge to the scholar's home country. This means that the student should currently be in their home country, or have definite plans to return in the near future. Courses such as the Molecular Evolution Workshop at Woods Hole, the applied Systematics Course at Bodega Bay, the Systematic Workshop at the Alan Wilson Center, Massey University, New Zealand, are examples of courses that are appropriate for this funding, in addition to other equivalent opportunities. Support for attending a course will be contingent on admission to the course through the normal admissions process. A letter expressing interest in support and a curriculum vitae should be sent to Dr.Keith Crandall 675 Widtsoe Building, Department of Integrative Biology, Brigham Young University, Provo, UT 84602-5181USA; email-keith_crandall@byu.edu. The letter should include a discussion of how the knowledge acquired will be transferred to the country of the scholar's origin, and a justification of the course itself as providing appropriate training. Applications will be evaluated as they are received.

"Keith A. Crandall" <keith_crandall@byu.edu>

Salmo primers

Dear Evoldir Members,

I am inquiring if anyone has knowledge of, or is in the process of developing, primers for a locus which can determine sex in the Atlantic Salmon (Salmo salar). I have searched the literature but thus far have come up empty handed. Any help would be very much appreciated.

Many thanks,

Anne-Marie Gale University Laval

Anne-Marie.Gale@giroq.ulaval.ca Anne-Marie.Gale@giroq.ulaval.ca

SeqAlignment Editor

I'm looking for a good, simple and robust multiple sequence alignment editor that will run well on Windows XP. I need software that will cope with large MSAs (up to 1000 sequences) although it does not have to do much more than allow rudimentary alignment editing.

Thanks for your suggestions

David

Dr David S Horner

"I know the human being and fish can coexist peacefully" - George W. Bush Sept 20 2000

Dipartimento di Scienze Biomolecolari e Biotecnologie Università degli Studi di Milano via Celoria, 26 - 20133 Milano, Italy Tel. (+39) 02 50314916 Fax (+39) 02 50314912 e-mail: david.horner@unimi.it

David Horner <david.horner@unimi.it>

SeqAlignment software

Hello all, I need a good and easy-to-use software to deal with multialigment sequence for teaching. I don't need powerful or complexe analysis tool, just good compatibilities with PAUP, clustal W, and option to print sequences.

Thanks for any advice.

Alex Baumel Institut Méditerranéen d'Ecologie et de Paléoécologie UMR-CNRS 6116 - Université Aix-Marseille III

IMEP - Bat. Villemin Europole de l'Arbois BP80 - 13545 Aix en Provence Cedex 04

Tel. : (33) 04 42 90 84 53 Please, visit our web site : http://www.imep-cnrs.com Alex Baumel <alex.baumel@univ.u-3mrs.fr>

Shipping Ecoli

Dear colleagues,

As part of an ongoing joint project between a Spanish and an US institution, we plan to ship petri dishes containing solid media with growing colonies of commercial strains of E. coli transformed with inserts from cDNA libraries constructed in Spain, to the American institution, for their screening and high-throughput sequencing. We would like to hear from other people with experience in shipping this kind of material to the US from Europe. We anticipate some issue with the US customs service.

thank you for your help

miquel

——— Miquel A. Arnedo

Departament Biologia Animal Universitat de Barcelona Av. Diagonal 645, E-08028 Barcelona, Spain Tel. +34 93 403 4808 Fax. +34 93 403 5740

http://www.ub.es/geisan/arnedo_english.HTML

SlopePermutation

Hi Everyone

I would be very grateful if anyone can suggest software that will test by permutation the statistical difference in slopes such as a pair of isolation-by-distance slopes from comparable sample sets).

* The data are pairwise, so a permutation approach of some kind is needed to overcome statistical non-independence (and likely different N contributing to each slope).

* Permuting the difference in slope is not the same thing as bootstrapping each slope to get SEs and seeing if they overlap (e.g. this does not account for holes in the data and different N)

Bohonak's IBD seems to do the latter.

It has been suggested that a new function in GENEPOP 3.4 does what we want, but it does not seem to.

Thanks a lot Paul

Dr. Paul Sunnucks Senior Lecturer Department of Genetics La Trobe University Bundoora 3086 Victoria Australia phone (office) + 61 3 9479 2264 phone (lab) + 61 3 9479 3636 fax + 61 3 9479 2480 email p.sunnucks@latrobe.edu.au http://www.latrobe.edu.au/genetics/staff/sunnucks/-homepage/

SlopePermutation answers

Hi Everyone

Thanks to everyone who responded concerning permuting slopes.

There were twice as many who wanted to know the answer as those who had something to contribute to the answer, so this is obviously an area of interest!

I have not checked out all the responses in detail yet, so it remains to be seen if there is something here that does what we want, but several look promising.

Thanks again Paul

My original question...

'I would be very grateful if anyone can suggest software that will test by permutation the statistical difference in slopes such as a pair of isolation-by-distance slopes from comparable sample sets).

* The data are pairwise, so a permutation approach of some kind is needed to overcome statistical non-independence (and likely different N contributing to each slope).

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Bohonak's IBD seems to do the latter.

It has been suggested that a new function in GENEPOP 3.4 does what we want, but it does not seem to.

Thanks a lot Paul'

Answers (in order that they were received):

(1) But a paired t-test does the same thing! You could simply calculate the difference in slopes, and the associated standard error (which is just the denominator in a paired t.test). If you have several of these slopes, then you can put the differences into a weighted ANOVA to get a single analysis.

> * Permuting the difference in slope is not the same thing as > bootstrapping each slope to get SEs and seeing if they overlap (e.g. > this does not account for holes in the data and different N) > But you could both slopes boostrap simultaneously and use the difference in slopes as the statistic you calculate.

Does your stats department have a consultancy service? This looks like a problem that can be solved easily, if you sit down with them and spend a few minutes explaining the problem. Alas Finland is a bit far away.

Bob

– Bob O'Hara

Dept. of Mathematics and Statistics P.O. Box 4 (Yliopistonkatu 5) FIN-00014 University of Helsinki Finland Telephone: +358-9-191 23743 Mobile: +358 50 599 0540 Fax: +358-9-191 22 779 WWW: http://www.RNI.Helsinki.FI/~boh/ (2)

I have written such a program that would run under the mathematics computer language Maple (Waterloo inc, Canada). Attached is a MS in press for Molecular Ecology (INDIVIDUAL ASSIGNMENT METHODS REVEAL RESTRICTED DISPERSAL DESPITE NO DETECTABLE INCREASE OF GENETIC DIFFERENCES WITH DISTANCE IN ATLANTIC SALMON SALMO SALAR AND BROOK CHARR SALVELINUS FONTINALIS . Vincent Castric, Louis Bernatchez), where I compared IBD patterns is two salmonid species (salmon and charr). I short, I used a bootstrap method to test for a difference in the IBD slopes between the two species: I first estimated the difference in slope on the real data (slope salmon - slope charr). I then bootstraped the data sets over loci, and estimated the difference in slope for each replicated bootstraped data sets. This provided a distribution of the difference in slope that I tested for an overlap with zero.

Please let me know if you would like to get the worksheet. Alternatively, I could also run the data on my computer.

I hope this helps, Vincent. Vincent CASTRIC

Equipe "Evolution des systèmes d'auto-incompatibilité" Laboratoire de Génétique et Evolution des Populations Végétales (UMR 8016 du CNRS) Université de Lille 1- Bâtiment SN2- Bureau 108 59655 Villeneuve D'Ascq cedex FRANCE

Tel: 03 20 33 59 23 Fax: 03 20 43 69 79 Courriel: Vincent.Castric@univ-lille1.fr http://www.univ-lille1.fr/gepv/perso_pages/PagepersoVincent_c.htm

(3) You can set things up in a standard general linear model framework (e.g. geographic distance, two categories, interaction term) with genetic distance/Fst/Nm as the response variable. Then permute the response values to get significance for the coefficients in your model. See my attached paper for an example, and also the references to Manly's work are quite useful. Manly used to distribute a little PC program that would do many useful permutation tests called "RT", which cost about US$ 60 and was terrific for such analyses.

Good luck!

Cynthia Riginos riginos@duke.edu

Department of Biology 139 Life Sciences Dr, Biosciences Bldg. Box 90338 Duke University Durham, NC 27708 phone: 919-660-7431 fax: 919-660-7293

(4)

In case you don't find an available software package for your slope permutations, I've written some code in Matlab that is a bit clunky (i.e. runs pretty slowly and doesn't look pretty) but will do what you want. The test combines data from the two observed groups (of matrix size n1

— / —

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

Software Clann

We wish to introduce Clann, Software for investigating phylogenomic information using supertrees. The word "Clann" is the Irish word for "family".

This version of Clann (2.0.1) implements four supertree methods (which are used as optimality criteria):

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

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

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

Software Clann 2

Hi all,

Further to the release of Clann recently, some serious errors in the manual were identified. These have been corrected and a new version of the manual is now available at:

http://bioinf.may.ie/software/clann/data/ClannManual.pdf If you have downloaded a copy of Clann, you need this update.

Thanks, Chris.

Clann homepage:

http://bioinf.may.ie/software/clann/
chris.creevey@MAY.IE

Software IM divergence

IM is a program, written with Rasmus Nielsen, for the fitting of an isolation model with migration to haplotype data drawn from two closely related species or populations. IM is based on a method originally developed by Rasmus Nielsen and John Wakeley. Large numbers of loci can be studied simultaneously, and different mutation models can be used.

http://lifesci.rutgers.edu/~heylab/HeylabSoftware.htm

Jody Hey Department of Genetics Rutgers University Nelson Biological Labs (rm B326) 604 Allison Rd. Piscataway, NJ 08854-8082 732-445-5272 fax 732-445-5870 hey@biology.rutgers.edu http://lifesci.rutgers.edu/~heylab/

Software LVB phylogeny

LVB (D. Barker 2004, Bioinformatics, 20, 274-275) is a free computer program to seeks parsimonious trees from a nucleotide multiple alignment. It uses a heuristic search suited to moderately large data sets.

The program and Web page have recently been improved. LVB 2.1 may be downloaded for Windows, MacOS X, Linux or as source code at

http://www.rubic.reading.ac.uk/lvb/ The Institut Pasteur has kindly installed LVB 2.1 on its Biological Software Web server <http://bioweb.pasteur.fr/intro-uk.html>. To run LVB over the Web at Institut Pasteur, click

http://bioweb.pasteur.fr/seqanal/interfaces/lvb.html Finally, for large-scale use, LVB may be launched through a Perl "wrapper" in the free BioPerl library:

http://bioperl.org/ The module is Bio::Tools::Run::Phylo::LVB.pm in bioperl-run. It was tested with BioPerl 1.4, but at the time of writing is found with the HEAD code.

Best regards,

Daniel

Software SCANMS

Dear Colleagues,

SCANMS is a utility that, when used together with Richard Hudson's coalescent simulator MS, allows you to make parametric bootstraps of a sliding window analysis of various neutrality test statistics.

Currently supported statistics are Tajima's D, and Fu and Li's D* and F*. The joint distributions of window minima and maxima that SCANMS outputs may be used to correct for multiple comparisons in sliding window analyses of these statistics.

SCANMS is available for download from http://www.lcb.uu.se/~dave/SCANMS SCANMS, being quite simple, should work on any platform to which Perl has been ported. This list includes Windows, Mac Classic and Mac OS X (where it should Just Work). But it has only been tested on Linux and Mac OS X. If you have feedback about the use or installation of SCANMS please contact me.

From the website you can also get a preprint of a short application note to appear in Bioinformatics. This manuscript briefly discusses the effect of recombination on the joint distribution of window extrema of Tajima's D.

SCANMS is open source software and may be freely modified and re-distributed under the terms of the Academic Free License, v. 2.

Best Regards. +– David Ardell tel : 46 (0) 18 471 6694 Linnaeus Centre for Bioinformatics fax : 46 (0) 18 471 6698 Uppsala University Biomedical Center http://www.lcb.uu.se/~dave Husargatan 3, Box 598, SE 751 24 Uppsala SWEDEN.

Software WinPop 2 0 2

Hello EvolDir

I have just posted an update to Winpop version 2.0. This update includes:

- new assortative matings interface, with a mating matrix to choose from (no models change at the moment)

- addition of gene drift with hard (with elimination of individuals) and soft (without elimination of individuals) selection

- addition of frequency dependent selection (same from version 1.0)

- minor bugs correction

To install it, download the compressed pack from

http://evol.biology.mcmaster.ca/paulo/soft.php run the setup.exe. The new version will be copied over the old one.

Please, if you have any bug to report send me an email (nuinp@mcmaster.ca). And if you are using it in any population genetics course send your opinions.

Thanks

Paulo Nuin Post-Doctoral Fellow Dept of Biology McMaster University Hamilton ON Canada

Paulo Nuin <nuin@terra.com.br>

Spider crabs

Dear colleagues,

We are trying to find some genetic variability within the spiny spider crabs Maia squinado (Brachyura: Heterotremata: Majoidea). So far we have not been very sucessful. Any info you can provide will be very appreciated.

Best wishes,

David.

– David Posada Departamento de Bioquímica, Genética e Inmunología Facultad de Ciencias Universidad de Vigo Vigo 36200, Spain Phone: +34 986 812038 Fax: +34 986 812556 Email: dposada@uvigo.es Web: darwin.uvigo.es

Squat lobster samples

Dear colleagues, My name is Patricia Pérez Barros and I am a PhD student at CADIC, Ushuaia (Argentina) under the supervision of Dr. Gustavo Lovrich. Part of the aim of my project is to study the phylogeography of the squat lobsters Munida gregaria and M. subrugosa. I am writing to you in the hope that you may be able to help me obtaining samples. I would only require a small amount of specimens of each species stored in ethanol (96%). If this would not be possible, could you provide me with any contacts that may be able to help me? Thanking you in advance for your cooperation in this matter. Any help you could provide me with would be greatly appreciated.

Kindest Regards,

Patricia.

Lic. Patricia Pérez Barros Centro Austral de Investigaciones Científicas (CADIC-CONICET) CC 92 - V9410BFD Ushuaia Tierra del Fuego Argentina

Tel: +54-2901-422310 // 422314 // 422278 FAX: +54-2901-430644 http://www.cadicush.org.ar patopb@yahoo.com

Topology Newick to Nexus

Dear Colleagues,

I am wondering if anyone is aware of any program that could detect the frequency of different topologies +given a group of trees for same taxa. PAUP has a very similar option in calculating consensus trees, but +it gives a table of partition or group frequencies, not the overall tree topology frequencies.

Also, I am trying to convert tree files from Newick to Nexus format. Does anybody know the programs to do this?

Your information is highly appreciated!

Tuo Shi

Institute of Marine and Coastal Sciences Rutgers University 71 Dudley Road, New Brunswick, NJ 08901 Phone: (732)-932-6555 ext. 332 Fax: (732)-932-4083 Emai: tuoshi@imcs.rutgers.edu http://www.marine.rutgers.edu/ebme/index.html

TreeFile publication

Hello,

Does anyone know how to take tree files from PAUP, MrBayes, or TreeView and import them into Adobe Illustrator or Photoshop so that they can be manipulated and eventually inserted into a Word file for publication? TreeView only allows you to save files as .emf or .wmf and Adobe doesn't recognize those files.

Thanks, Connie – Connie J. Mulligan, PhD Assistant professor Department of Anthropology PO Box 117305 University of Florida Gainesville, FL 32611 Tele: (352) 392-2253, ext 248 Fax: (352) 392-6929 email: mulligan@anthro.ufl.edu website: http://www.clas.ufl.edu/users/mulligan/Webpage/index.html

TreeFile publication answers

Hello,

So many responses to my query about saving tree images to drawing programs (see below)! Lots of people asked for the responses, so I've collected a sample of the sugestions below. Basically, it seems like everything is easier on a Mac. My problem (on a PC) seems to have been that the .emf figures are so large when they are opened in Illustrator that I didn't see any of the tree until I had Zoomed out and Scaled the tree down. None of the cut-and-paste suggestions have worked for me. Thanks to everyone.

Initial query: Does anyone know how to take tree files from PAUP, MrBayes, or TreeView and import them into Adobe Illustrator or Photoshop so that they can be manipulated and eventually inserted into a Word file for publication? TreeView only allows you to save files as .emf or .wmf and Adobe doesn't recognize those files.

Responses: >Actually, Adobe Illustrator 10 (Windows) WILL directly open either .emf or .wmf files saved by

TreeView. I don't know why you have been having trouble with that. I just re-verified that I can double-click, at the directory display level in Windows, on a .wmf from TreeView and Adobe Ill. 10 comes right up with that file in hand and is ready to edit it. What seems to be trickier is finding the right format in which to EXPORT them, after alterations, so that the Microsoft office suite can deal with them. I have had the best luck by far saving them as bitmap files, .bmp. Then either PowerPoint or Word will take them up in at least somewhat manipulable form, with everything intact.

Good luck with it...

Ward

Ward Watt Prof. of Biology, Stanford

>What version of Illustrator are you using? Illustrator 9 reads WMF and EMF files. TreeView scales the trees a little awkwardly (too small for WMF, too big for EMF), but Illustrator will read the files.

Regards

Rod

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

>The easiest way (at least for me) to manipulate trees made in PAUP and MrBayes (which uses PAUP to crunch the data it generates into a tree) is to do the following. Construct the tree by whatever method you like. Under "Trees" along the top of the screen, choose the "Print Trees" option. A dialog box will pop up with options for printing the tree. Choose "Preview". This will give you an idea of what the final tree will look like. Go back one step if you want to change the look of the tree (for example, from a slanted cladogram to a phylogram). Once you are happy with the tree, choose "Preview" again. On the left side of the screen, there will be an option to save the resulting tree as a PICT file. Save it to where you like under whatever name you like. Open this file in the graphics program you like and you should be able to manipulate the file, such as thicken the branches and change the font of the names. Sometimes you will have to ungroup the elements of the tree, so select the whole figure and check the status of the grouping. If it is one unit, deselect to the individual elements. I've had great success with this method using the programs CorelDraw, FreeHand and Canvas to produce publication-grade trees for a variety of journals (make sure to save the manipulated file in TIFF format at 300 dpi or higher since this is what most journals like/want).

Hope this helps.

Cheers,

Scott

>From PAUP*'s Print Tree window, select Print Preview. In this window, click the Save As File button. This saves as a *.pict format file which can then be opened by Illustrator.

Note that Barry Hall's new book, Phylogenetic Analysis Made Easy, has some great suggestions for data pipelines and file manipulation like this.

Dave Fitch

>I am myself unhappy about these same things. I used to copy the trees from treefile either by control C or as .emf (depending on the treeview version) into power point and work with them there. If you click on the tree in power point and try to ungroup it in the drawing option, the program will ask you whether you want to convert the inserted object into a windows drawing object. Agree, and it will recognize text and lines as such, but it will lose some of the exact line positions, so the tree does not look absolutely perfect any longer (can be edited by hand, but this is a horrible lot of work and depends on your printer in the end, i.e., it might not look in print exactly as on the screen). I would therefore be happy to learn how others are doing it. There must be an easier trick. Please let me know the other answers as well.

regards,

Judith

>I save the tree as a pict file in PAUP, then simply use the 'Insert> File' option using Powerpoint. If you double click on the image, Powerpoint will then ask you to convert, which will then ungroup the figure. You can then scale down all the tree branches (n.b. it is important to scale ALL the

— / —

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

Triploid micros

Hello- I would like to use microsatellite data to calculate allelic and genotypic diversity (including richness and evenness) for populations with both diploid and triploid individuals. I was wondering if there was a program designed to calculate these values that can accomodate polyploid data (the ones that I am familiar with seem to be limited to diploid data).

Thanks, Maurine maurine_neiman@hotmail.com

Triploid micros answers

Hi everyone-

A lot of people requested that I post responses to my question regarding microsatellite diversity in triploids. The responses are listed below in the order in which they were received. Thanks so much for all your suggestions! They were very helpful.

cheers, Maurine

Original question: Hello- I would like to use microsatellite data to calculate allelic and genotypic diversity (including richness and evenness) for populations with both diploid and triploid individuals. I was wondering if there was a program designed to calculate these values that can accomodate polyploid data (the ones that I am familiar with seem to be limited to diploid data).

Thanks, Maurine Neiman mneiman@bio.indiana.edu

Responses:

Hi,

It depends how you want to define diversity, and what your data looks like.

If you can score genotypes: i.e. you can tell that the difference between individuals carrying alleles (a,a,b) and individuals carrying (a,b,b) then you should try looking at

Hardy OJ, Vekemans X (2002) SPAGEDi: a versatile computer program to analyse spatial genetic structure at the individual or population levels. Molecular Ecology Notes 2, 618-620.

Which correctly handles polyploids (at least, 2n-ploids - I'm not so up on triploids. Are they sexual?)

Also have a look at

Thrall PH, Young A (2000) AUTOTET: A program for analysis of autotetraploid genotypic data. Journal of Heredity 91, 348-349. Which may give you some ideas.

If you cannot score genotypes, i.e. you can see which alleles each individual is carrying, but not the dosage: a,a,b = a,b,b -> “a,b”

Then things are less straight-forward. You can use the gel/banding phenotypes to measure diversity.

I have written a program (I'm writing the paper at the moment) that calculates the commonly used phenotype-diversity stats. If you are interested, email me and I can send you a copy plus my reference list. Its designed for sexual 2n allopolyploids, but I see no reason why the stats couldn't be used for a triploid (asexual or otherwise).

Please let me know if you find any other software that people use for triploids - I would be interested to know about it.

Darren – Darren Obbard Plant Sciences,Oxford darren.obbard@plants.ox.ac.uk Mobile: +44 07968 838 635 Home: +44 01603 259 670

Hello,

I wrote a software (Spagedi) that can accomodate different levels of ploidy to compute different statistics related to population differentiation. You can get it from http://www.ulb.ac.be/sciences/lagev/ Good luck,

Olivier Olivier Hardy Chargé de recherches FNRS / Postdoctoral Researcher Université Libre de Bruxelles Laboratoire de Génétique et Ecologie Végétales Chaussée de Wavre, 1850 B-1160 Bruxelles Belgium Tel: +32 (0)2 650 91 69 Fax: +32 (0)2 650 91 70

http://www.ulb.ac.be/sciences/lagev/ Hi Maurine, I saw your question on EvolDir, I have been struggling with this myself as well. Almost all programs that are available are only able to deal with diploids. To overcome this, I wrote some programs myself, to do stuff like this. They might to some extent be what you are looking for. One is a program that reads genetic data (of any ploidy) and helps you in determining which individuals have the same genotype, with respect to errors/missing data/mutations. The other program reads the genotype data and can output diversity indices (including eveness, I wonder what you mean by richness, btw), and test through permutation for differences in the genotypic composition of populations and also tests through bootstrapping whether populations differ in genotypic diversity (which I guess is of primary importance for you). You can find the programs on http://www.science.uva.nl/˜meirmans . For other tests on polyploids I recommend the program Spagedi by Olivier Hardy and Xavier Vekemans.

Good luck with the analysis.

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

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

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

Hi Maurine,

I am working in a tetraploid species, and I have the same problem with the software. Nowadays, I am using POPULATION, and AUTOTET. With >POPULATION you can analyse haploid, diploid or polyploid individuals. You can calculate distances between individuals, populations, phylogenetic trees, >and allelic diversity. AUTOTET is only for autotetraploid data.

I hope that it can help you. On the other hand, could you send me any reply that you received, please?

Saludos

Miguel Angel

Dr. Miguel Angel González Pérez Departamento de Biología

— / —

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

Walter Fitch prize

CALL FOR APPLICATIONS FOR THE WALTER FITCH PRIZE COMPETITION

Competition:

The Walter M. Fitch Prize is awarded to the young investigator who makes the best presentation at the Walter M. Fitch Symposium of the annual meeting of the Society for Molecular Biology and Evolution (SMBE), which this year will take place June 17-20, 2004, at Penn State University.

Eligibility:

Applicants must be current graduate students or postdoctoral researchers who obtained the primary doctoral degree no earlier than June, 2003. Contestants must also be members of SMBE.

Application:

Submit an abstract of an oral presentation by March 31, 2004, using the online submission form (http://www.outreach.psu.edu/C&I/genomes/). Make certain to designate your abstract as “Fitch Prize Competition” (tick the approprite box on the web form).

Also, be sure to register for the SMBE annual meeting (http://www.outreach.psu.edu/C&I/genomes/).

For more information about SMBE (including the Walter Fitch Prize), see also the society website (http://www.smbe.org).

John Avise President, Society for Molecular Biology and Evolutionn John C. Avise, Ph.D. Department of Genetics Life Sciences Building University of Georgia Athens, GA 30602 avise@uga.edu 706-542-1456 fax: 706-542-3910

John Avise <avise@uga.edu>

PostDocs

ArizonaStateU CompEvolBiol

Postdoctoral Position Computational Evolutionary Biology and Comparative Genomics Arizona State University

A postdoctoral position is available in the areas of computational evolutionary biology and comparative genomics. The successful candidate will join ongoing research projects examining the evolution of genome structure and spatial organization and/or studies of the fidelity of sequence alignment and the downstream consequences of error on high-through-put analysis. Additional research topics are possible depending on the qualifications and interests of the candidate.

Doctoral degree in biology, genetics, or a related area prior to appointment and not currently serving a permanent faculty position required. Background in evolutionary biology or theory; experience with computer programming, statistics or data analysis desired. The initial appointment is for one year and is renewable upon satisfactory performance. Applications (including a CV, research statement, and names/contact info for two references) and questions must be submitted to msr@asu.edu (email preferred) or

Michael Rosenberg School of Life Sciences PO Box 874501 Arizona State University Tempe, AZ 85287-4501

Phone 480-965-1578 http://lsweb.la.asu.edu/rosenberg Applications will be reviewed beginning March 31, 2003; if not filled, weekly thereafter until the search is closed. Arizona State University is an Equal Opportunity/Affirmative Action Employer.

Michael S. Rosenberg, Ph.D. Assistant Professor School of Life Sciences / Arizona State University msr@asu.edu http://lsweb.la.asu.edu/rosenberg

ArizonaStateU Drosophila

An NIH funded postdoctoral position is immediately available for a Drosophila geneticist to participate in a project dealing with the analysis of existing images capturing gene expression patterns in embryos. The selected individual will be responsible for annotation of gene expression patterns as they are compiled into an image searchable database. There will also be opportunities, in a non-experimental setting, to participate in research leading to the characterization of genome-wide networks of gene interactions underlying embryonic development (see Kumar et al. in Genetics 162:2037-2047, 2002). Candidates must have experience in a wide range of standard Drosophila techniques; candidates with additional experience in the genetic manipulation of gene expression in embryos will be preferred. A Ph.D. in biology, genetics, or a related discipline is required. Initial appointment will be for one year and is renewable upon satisfactory performance. Applicants must submit a complete curriculum vitae and names and contact information for two references to Sudhir Kumar, Box 874501, School of Life Sciences, Arizona State University, Tempe, AZ 85287-4501. (email: s.kumar@asu.edu; fax: (480) 965-6899; Tel: (480) 727-6949: Internet: http:///www.kumarlab.net/). Review of applications will begin starting March 31, 2004 and thereafter on the 1st and 15th of each month thereafter unt il the search is closed. Arizona State University is an Affirmative Action/Equal Opportunity Employer.

Dr. Sudhir Kumar, Director Center for Evolutionary Functional Genomics, Arizona Biodesign Institute Associate Professor, School of Life Sciences Affiliate Professor, Department of Computer Science & Engg. Address: Life Sciences A-351 Arizona State University Tempe, AZ 85287-4501 Tel: (480)-727-6949 (office) (480)-727-6947 (lab) Fax: (480)-965-6689 Email: s.kumar@asu.edu Center: http://www.azbio.org/efg Lab: http://www.kumarlab.net/ Software: http://www.megasoftware.net/

Atlanta SocialInsects

POSTDOCTORAL POSITION IN SOCIAL INSECT BIOLOGY

A full-time Postdoctoral Research position is available to pursue a variety of potential studies in social insect biology. Candidates with interests in social insect genomics, population structure, hybridization, development, behavior, or evolution are encouraged to apply.

Position is available immediately and the starting date is flexible. Funding is for at least two years and starting salary will be commensurate with experience. Applicants should have a Ph.D. in genetics, genomics, behavior, entomology, evolution or a related field and have demonstrated research excellence.

Interested applicants should send CV, names and e-mail addresses for three references, and a one-page letter of interest including a proposed start date to michael.goodisman@biology.gatech.edu. Alternatively, applications can be sent to Michael A D Goodisman, Assistant Professor, School of Biology, The Georgia Institute of Technology, 310 Ferst Drive, Atlanta, GA 30332-0230, United States. For additional information visit http://www.biology.gatech.edu/professors/goodisman.html or send an e-mail to the application address.

Michael A D Goodisman Assistant Professor School of Biology The Georgia Institute of Technology Cherry Emerson Bldg A110 310 Ferst Drive Atlanta, GA 30332-0230 United States

webpage: http://www.biology.gatech.edu/professors/goodisman.html email: michael.goodisman@biology.gatech.edu office: 404-385-6311 lab: 404-385-6312 fax: 404-894-0519

Barcelona Bioinformatics

Postdoctoral position in Bionformatics in Barcelona.

The Spanish National Genotyping Center (NGC) seeks one postdoc. The successful candidate will carry data analysis related to population genetics of the NGC's high-throughput SNP genotyping operation. He or she will be required to initiate and lead the development and implementation of the database and data analysis tools necessary for the project. Candidates should have a PhD and expertise in Bioinformatics and Genomics. Other requirements are experience in extant genomics-oriented software, particularly health- and population-oriented tools. Programming skills (C++, Java, Perl or other languages will be considered) and experience in database construction (working knowledge of SQL) will also be considered.

Salaries will be conmensurate to experience. Contracts will have one year duration, with the possibility of extensions of up to three years.

Please contact Francesc Calafell (francesc.calafell@upf.edu) or Arcadi Navarro (arcadi.navarro@upf.edu) Unitat de Biologia Evolutiva Facultat de Ciències de la Salut i de la Vida Universitat Pompeu Fabra 08003 BARCELONA Phone: 00 34 93 5422841

Francesc Calafell <francesc.calafell@upf.edu>

BrighamYoung PlantSyst

Postdoctoral Position in Evolutionary Plant Systematics

An NSF-funded position is available in the Johnson lab to work on phylogenetic reconstruction and evolutionary inference within the Phlox family in a research environment emphasizing low-copy nuclear genes, qualitative and quantitative analysis of morphological features, and construction and screening of cDNA libraries. Support is available for up to 2.5 years (Salary $30K plus benefits; starting date negotiable, on or after 1 July 2004; applications will be considered until a suitable candidate is found). An important responsibility of the successful candidate will be development and optimization of nuclear loci for multigene phylogenetic analysis, including novel marker selection from genomic libraries. The ideal applicant would fit one of two profiles: (1) experience in rigorous coding and analysis of morphological data combined with basic molecular skills in modern DNA-based PCR and sequencing methods. Aptitude in cloning and cDNA/genomic library construction, or willingness to learn as a first priority, is desirable; (2) moderate to advanced molecular biology skills, including primer design/optimization, cloning, and cDNA/genomic library construction/screening with thorough familiarity of conceptual issues and methods of phylogenetic inference. This individual will join a lab with graduate and undergraduate students actively involved in evolutionary plant systematics. The Johnson lab is part of an interactive core research group in evolutionary biology at Brigham Young University, with substantial depth in molecular systematics, population genetics, phylogenetics, coevolution, computational biology, and molecular evolution; this postdoctoral position provides opportunities for interaction and potential collaboration on related projects within our growing evolutionary biology group (Byron Adams, Keith Crandall, Leigh Johnson, David McClellan, Duke Rogers, Jack Sites, Michael Whiting). Interested researchers should contact: leigh_Johnson@byu.edu for more information.

leigh_johnson@byu.edu leigh_johnson@byu.edu

EmoryU MolPopGenet

EMORY - CENTER FOR DISEASE ECOLOGY

POSTDOCTORAL POSITION IN MOLECULAR POPULATION GENETICS

Applications are invited for a postdoctoral position in the laboratory of Les Real, Center for Disease Ecology, Emory University and in association with the Viral and Rickettsial Zoonoses Branch of the Centers for Disease Control and Prevention (CDC). The position is funded through a NIH sponsored research project on the phylogeography and spatial dynamics of infectious diseases. The project is a collaboration between Emory and the CDC to understand the molecular evolution and population genetic structure of viral pathogens in epidemic and endemic regions using RNA viral diseases as model systems. The applicant should have familiarity with theoretical model building in molecular evolution and the use of molecular data in population genetic analysis. A familiarity with modeling and computer simulation is essential.

The position is initially for two years (extendible to five) at a starting salary of $35,000 - $40,000 depending on experience. To apply, please send, FAX, or e-mail a curriculum vitae, statement of research interests and experience with computational techniques, and the names and addresses of three potential references to: Leslie Real Department of Biology Center for Disease Ecology 1510 Clifton Road Emory University Atlanta, GA 30345

E-mail: lreal@biology.emory.edu Phone: (404) 727-4099 FAX: (404) 727-2880

Consideration of applications will begin March 1, 2004 and continue until a suitable candidate is found.

Leslie A. Real Asa G. Candler Professor Director, Center for Disease Ecology Department of Biology 1510 Clifton Road Emory University Atlanta, GA 30322 Voice: (404) 727-4099 Fax: (404) 727-2880 e-mail: lreal@biology.emory.edu

lreal@Biology.Emory.Edu

ImperialCollege BactEvol PopGenet

Several postdoc positions are available at the Department of Infectious Disease Epidemiology, based at St. Mary's Campus of Imperial College London (http://www1.imperial.ac.uk/medicine/about/divisions/pcphs/ide/default.html)

Position 1. Post: Postdoc, Emerging infectious mycoses Ref: 2004/174 Salary: £21,368-£31,142 including London Weighting Length of Appointment: 18 months, with extension dependant on further funding

This established project is focused on investigating the population genetics and evolution of Penicillium marneffei in South East Asia. The goal of the project is to gain a better understanding of the spatial and genetic ecology of the new and emerging mycoses that are associated with the global increase in HIV. The position will involve (i) extending a multi-locus typing system to study spatial population genetic structure in clinical isolates and (ii) investigating sources of infection by developing assays to detect the organism in the environment with the aim of determining genetic variation in virulence/fitness. The successful candidate will have a PhD in genetics or molecular microbiology, as well as experience in bioinformatics and the ability to work unsupervised in the field (Thailand). Additional information concerning the nature of the research to be undertaken can be obtained by contacting Dr Matthew Fisher. e-mail: mcfisher@ic.ac.uk.

Positions 2, 3, 4. Molecular epidemiology and modelling of gonorrhoea transmission in London. Three

Wellcome Trust-funded positions are available to apply new molecular epidemiological approaches and infectious disease modelling to identify clusters of linked cases of gonorrhoea in London. Applicants for one postdoctoral position (18 months), Ref: 2004/171 and a Technician grade E position (12 months), Ref: 2004/172 should have experience in molecular microbiology and preferably in working with bacterial pathogens; a PhD is essential for the former post.

The second Postdoctoral Research Associate Ref: 2004/173 will be responsible for statistical analyses, including developing spatial models to link molecular and epidemiological data. Applicants should have a PhD, or an MSc with work experience, preferably in statistics or a subject involving a strong mathematical component. Experience in infectious diseases would be an advantage. The position is for 12 months from 1 July 2004.

Research Associate posts: £21,368 - £31,142 inclusive of London Allowance, Technician: £19,042 - £21,469 plus £2,262 London Allowance

Further details of the experimental posts can be obtained from Prof Brian Spratt FRS (b.spratt@imperial.ac.uk) and on the modelling post from Dr Azra Ghani (a.ghani@imperial.ac.uk).

To obtain an information pack, please contact the Recruitment Assistant, Human Resources Division, Imperial College, St Mary's Campus, Norfolk Place, London W2 1PG, tel: 020 7594 3627, email: g.brennan@imperial.ac.uk quoting the relevant reference number.http://www.ic.ac.uk/employment/ Closing date: 11 March 2004. See advertisment in Nature, Feb 26th 2004.

matthew.fisher@imperial.ac.uk

IndianaU PollinationBiol

Postdoctoral Research Position in Pollination Biology and Population Genetics

A postdoctoral research position is available in a collaborative study of the pollination ecology and population genetics of acacias in Kenya. Research projects will involve field ecological experiments in Kenya as well as genetic studies using microsatellite markers to estimate patterns of paternity and gene flow. The position will be based at Indiana University South Bend, and field work will be conducted at Mpala Research Centre, Kenya. Ideally, applicants should have both field ecological experience working with plants and/or insects and laboratory experience working with molecular markers, but exceptional candidates with experience in other areas will be considered. Stipend is $30-35,000/year, and I expect the position to be available in May 2004. Deadline for applications is 7 March 2004. The duration of the postdoc is 2 years, with a likely third year. Please e-mail a brief letter of application detailing your research experience, and attach curriculum vitae and names, addresses, and phone numbers of at least three references. Send e-mail to Dr. Andrew Schnabel (aschnabe@iusb.edu).

Andrew Schnabel Department of Biological Sciences Indiana University South Bend South Bend IN 46634 Phone: 574-237-4413 Fax: 574-237-6589

Smithsonian ConsGenet

Postdoctoral Research Positions in Conservation Genetics

Up to two postdoctoral research positions are available in a collaborative study of population genetics of Hawaiian forest birds, invasive mosquitoes and avian malaria in the Genetics Program at the Smithsonian Institution (one position will be sited in Washington, DC and the other at the Academy of Natural Sciences, Philadelphia). Research projects will involve the application of microsatellite and other molecular markers, analysis of population genetic data, and preparation of publications. Ideally, applicants should have experience in all of the above, but exceptional candidates with experience in other areas or methods will be considered. The stipend is $30,000 plus funding of medical insurance. Deadline for applications is 15 March 2004, and we expect the positions to begin to be available in May 2004. The duration of the postdocs is one year, with a likely second year. Please e-mail a brief letter of application detailing your experience in evolutionary and molecular genetics and containing the names, addresses and phone numbers of at least three references; attach curriculum vitae and relevant publication reprints. Send an email to both:

Dr. Robert Fleischer and Dr. Dina Fonseca Fleischer.Robert@nmnh.si.edu fonseca@acnatsci.org

Robert C. Fleischer Genetics Program Department of Systematic Biology National Museum of Natural History Smithsonian Institution 3001 Connecticut

Ave., NW Washington, DC 20008-0551, USA 202-673-4842; 202-673-0040 fleischer.robert@nmnh.si.edu USE STREET ADDRESS

Smithsonian ConservationGenet

Postdoctoral Research Positions in Conservation Genetics

Two postdoctoral research positions are available in a collaborative study of population genetics of Hawaiian forest birds, invasive mosquitoes and avian malaria in the Genetics Program at the Smithsonian Institution (one position is sited in Washington, DC and the other at the Academy of Natural Sciences, Philadelphia). Research projects will involve the application of microsatellite and other molecular markers, analysis of population genetic data, and preparation of publications. Ideally, applicants should have experience in all of the above, but exceptional candidates with experience in other areas or methods will be considered. The stipend is $30,000 plus funding of medical insurance. Deadline for applications is 1 March 2004, and we expect the positions to begin to be available in May 2001. The duration of the postdocs is one year, with a likely second year. Please e-mail a brief letter of application detailing your experience in evolutionary and molecular genetics and containing the names, addresses and phone numbers of at least three references; attach curriculum vitae and relevant publication reprints. Send email to both:

Dr. Robert Fleischer and Dr. Dina Fonseca Fleischer.Robert@nmnh.si.edu fonseca@acnatsci.org

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

Robert Fleischer <Fleischer.Robert@NMNH.SI.EDU>

Spain Evol

Plant ecologist

By the present we are seeking two postdoctoral scientists to participate in the next call for the Juan de la Cierva program (Ministry of Science and Technology of Spain). The applicants will be associated to the project:

The evolution of Heterostyly: new tests of the Darwinian hypothesis of Lloyd and Webb. BOS2003-07924-CO2-00. This project ends in December 2006. The interested candidates can see an abstract in: http://webs.uvigo.es/plantecology/ by clicking in proyectos vigentes.

The project consists on two subprojects leaded by Dr. Juan Arroyo (University of Seville) and Dr. Luis Navarro (University of Vigo).

The main task of the applicant associated to the University of Vigo group (Dr. Luis Navarro) will be related to the study of evolution of heterostyly in the South African genus Nivenia.

The main task of the applicant associated to the University of Seville group (Dr. Juan Arroyo) will be related to the study of evolution of heterostyly in the genus Narcissus.

It is interesting that candidates will be able to speak Spanish. More additional information will be posted to the interested candidates.

Applicants could send a CV and recommendations letters to:

>Luis Navarro >Departamento de Biología Vegetal >Facultad de Ciencias >Universidad de Vigo >Phone: (+34) 986 812619 >Email: lnavarro@uvigo.es >http://webs.uvigo.es/lnavarro/ or

>Dr. Juan Arroyo >Dept. Biología Vegetal y Ecología >Universidad de Sevilla >Apartado 1095, E-41080 Sevilla, Spain >Email: arroyo@us.es >Phone: #34 95 455 7058 >Fax: #34 95 455 7059 >http://www.farmacia.us.es/rnm210 Rocio Perez Barrales Depto. de Biologia Vegetal y Ecologia Apdo. 1095 E-41080 Sevilla ropeba@us.es Tlf: ++34-954-557056 Fax: ++34-954-557059

ropeba@us.es

TuftsU MolEvolInfDisease

Category: Postdocs

Position announcement: TuftsU_MolEvolInfDisease Applications are invited for postdoctoral fellow(s) to study molecular evolution of certain agents of infectious disease and their hosts. Work in the lab centers upon two NIH-funded projects involving two distinct pathogen-host systems. The first is aimed at elucidating the population structure of Plasmodium falciparum in malaria endemic regions in the world?s tropics. The second involves study of the ecological interaction of hosts, vectors, and pathogens of Lyme borreliosis, with particular focus on those aspects of the interactions which are mediated by genomic factors. Candidates seeking to work on either of these projects should have strong skills in molecular biology and fluency with the theoretical aspects of evolutionary analyses. A background in parasitology, entomology and/or microbiology is highly favorable. The incumbent(s) would join a unique research group within the Division of Infectious Diseases (DID) at the Tufts University Vet School. The campus is located in a rural setting approximately 30 miles west of Boston. Salary for these position(s) are highly competitive and based on experience. Interested parties should send C.V., two reprints, and list of three references to:

Keith Reddig c/o Rich Lab 200 Westborough Rd. Tufts University SVM. North Grafton, MA 01536 Richlab_2003@yahoo.com 508.887.4921

UAngers SexualSelection

Mating strategies and sexual selection in European newts

There is an opportunity of a 12-month post-doctoral position (EU 6th Framework) in the laboratory of animal ecology in Angers (France). The main research topic of the laboratory is evolutionary ecology and behavioural ecology of vertebrates in hydrosystems. Urodeles can display an unusual mating system where females may accept several males and males may sire offsprings of several females during the breeding period. Additionally, in the genus Triturus males seem unable to force female choice. In such a system, females could display a large flexibility in their mating strategies, ranging from monandry to promiscuity, depending on environmental conditions and the quality of mating partners. However, little is known about mating strategies in urodeles. The project aims at investigating the behavioural bases of sexual selection in newts and how this may condition the development of alternate mating strategies. The applicant is to address these issues using laboratory experiments and empirical field data. Experience in designing mate choice experiments and molecular techniques of paternity assignement are most required. Modelling skills in the evolution of mating systems would also be appreciated. The funding of the project is partly conditional to the quality of the applicant. The deadline for candidate application is February 14th 2004. The position starts in September 2004 and is applicable to all EU members but French. The applicant should not have been living in France for the last 3 years. Please send a CV and a list of publications by e-mail only.

Contact: Pr. Thierry LODE Laboratoire d'Ecologie Animale Faculté des Sciences Université d'Angers Campus de Belle-Beille 2 bd Lavoisier F-49045 Angers France e-mail: thierry.lode@univ-angers.fr

Laboratory of Animal Ecology Angers university Faculté des Sciences Campus de Belle-Beille 2 bvd Lavoisier F-49045 Angers France http://sciences.univ-angers.fr/-ecologie/

UCRiverside MolEvol

NSF-funded Postdoctoral Position Molecular Evolution of Wolbachia University of California, Riverside

We are soliciting applications for a postdoctoral research position on the molecular evolution and phylogenomics of Wolbachia. This research is part of a five-year Frontiers in Integrative Biological Research (FIBR) grant from NSF (lead PI, Jack Werren, University of Rochester). Candidates should have a strong background in molecular evolutionary, phylogenetic, and bioinformatic methods. Familiarity with endosymbiotic bacteria, host-parasite evolution, molecular biology, terrestrial arthropods, and/or programming skills are also desirable.

The postdoctoral position is available in the laboratory of Cheryl Hayashi at the University of California, Riverside. The successful candidate will be expected to work collaboratively with other Wolbachia-FIBR researchers and will also have the opportunity to develop her/his own research project. The position is scheduled to begin on August 1, 2004, but the exact start date is negotiable. Applications, including a CV, statement of research interests, copies of relevant publications, and three letters of reference, should be sent to: Cheryl Hayashi, Department of Biology, University of California, Riverside, CA 92521. Review of completed applications will begin on March 15, 2004. The University of California is an Equal Opportunity/Affirmative Action employer.

"Cheryl Y. Hayashi" <chayashi@citrus.ucr.edu>

UCambridge BirdMelanism

The following position will be advertised in this week's Nature.

Postdoctoral Research Associate, Department of Zoology, University of Cambridge

A Post-doctoral Research Associate is required to work on a NERC-funded project on the evolutionary genetics of melanism in birds. The project will investigate the role of candidate loci in the evolution of melanic patterning in various avian lineages. The research group occupies a newly refurbished lab and office space, and has diverse ongoing projects in adaptive evolutionary genetics. The Zoology Department achieved the highest research rating (5*) and provides a stimulating and interactive environment.

Candidates should have a Ph.D. in evolutionary biology, molecular ecology, population genetics or a related field. Salary will be on the RA1A scale (GBP18,265 - 27,339 pa). The appointment will be for up to three years subject to satisfactory completion of a six month probationary period.

The closing date for applications is 26th February 2004. Applicants will have to fill in an application form, including details of two professional referees. Application forms are available from Anne Garlick, email: ag318@hermes.cam.ac.uk , tel: +44-(0)1223-336621

For further information please contact Nick Mundy at: nim21@cam.ac.uk Website:http://www.zoo.cam.ac.uk/zoostaff/egg. Closing date for applications: 26th February 2004.

nim21@cam.ac.uk

UCollegeLondon Biogeography

A three-year Post-doctoral Research Fellow is required to investigate gene genealogies and phylogeography of Amazonian butterflies (Heliconiinae and Ithomiinae). The work will employ a novel, reductionist approach to the biogeography of a "suture zone" in Peru to test models of the evolution of Amazonian biodiversity. The successful applicant will have experience and interest in mtDNA and nuclear gene technology and data analysis to test evolutionary hypotheses. It is also hoped to employ a PhD student starting at the same time to work on this project, and there will be assistance available from a technician. Salary will start at points 6-8, (£22,445 - £24,325, including London Weighting, pay award pending), depending on experience, funded by a 3-year NERC research grant. For further details of this post, see http://abacus.gene.ucl.ac.uk/jim/dmp/postdocad.html To apply, send CV, names, addresses, phone numbers and email addresses of two referees, and a covering letter explaining how you could contribute to the project, to James Mallet, Galton Laboratory, UCL. For full contact and research group details, see http://abacus.gene.ucl.ac.uk/jim/ . Closing date: Thursday 15 April 2004, or until a suitable candidate is found.

** UCL Taking Action For Equality **

Jim Mallet http://abacus.gene.ucl.ac.uk/jim/

UEdinburgh Mimicry

MOLECULAR BASIS OF MIMICRY POSTDOC POSITION IN EDINBURGH

A three year BBSRC-funded postdoctoral position is available at the University of Edinburgh to study the genetic basis of mimicry in Heliconius melpomene.

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

The applicant should have a PhD in a relevant field and molecular biology experience, either in developmental or population genetics. This project is a collaboration between the laboratories of Chris Jiggins (http://homepages.ed.ac.uk/cjiggins) and Mark Blaxter (http://www.nematodes.org/) in the School of Biology at the University of Edinburgh, forming part of a very strong population genetics and evolutionary biology group. The project also forms part of an international collaboration with the laboratories of Owen McMillan in Puerto Rico and Eldredge Bermingham in Panama.

Please contact Chris Jiggins (Chris.Jiggins@ed.ac.uk) in the first instance to discuss the project, attaching a current CV and a statement of research interests.

Chris Jiggins I.C.A.P.B. (Institute of Cell, Animal & Population Biology) University of Edinburgh King's Buildings West Mains Road Edinburgh EH9 3JT Scotland UK

Web site: http://homepages.ed.ac.uk/cjiggins Tel. 0131 650 8624

Chris Jiggins <chris.jiggins@ed.ac.uk>

UEdinburgh MosquitoImmuneGenes

Two Jobs. One Post-Doctoral Researcher. One Research Assistant.

Molecular Evolution of Mosquito Immune System Genes

At The University of Edinburgh, School of Biological Sciences / ICAPB

1) Postdoctoral Research Fellow (quote ref: 3001274)

Required for a Wellcome Trust funded project to investigate patterns of DNA polymorphism at immune system genes of Anopheles mosquitoes. The candidate requires a PhD with molecular biology experience and an emphasis on population genetics and/or phylogenetics. The candidate will be experienced with DNA extraction, sequencing, alignment and analysis. Helpful, but not necessary, is an interest in statistical tests for positive selection, phylogenetics, and appreciation of the invertebrate immune system. The successful candidate will join an interdisciplinary institute with exceptional strengths in evolution, population genetics and immunology (http://www.icapb.ed.ac.uk/)

Fixed term: 36 months Salary scale: £18,265 - £27,339 pa (under review) Hours: Full-time Start date: 1st April 2004 (negotiable) Fixed term: 36 months Supervisor: Tom Little Enquiries: tom.little@ed.ac.uk

Please quote ref: 3001274 Closing date: 02 Mar 04

2) Graduate Research Associate (quote ref: 3001275)

Required for a Wellcome Trust funded project to assist with the investigation of patterns of DNA polymorphism at immune system genes of Anopheles mosquitoes. Experience in molecular biology (DNA extraction, PCR and sequencing) is essential. Some understanding of population genetics and/or phylogenetics could be helpful. The successful candidate will join an interdisciplinary institute with exceptional strengths in evolution, population genetics and immunology (http://www.icapb.ed.ac.uk/)

Fixed term: 36 months Salary scale: £18,265 - £20,311 pa (under review) Hours: Full-time Start date: 1st April 2004 (negotiable) Fixed term: 36 months Supervisor: Tom Little Enquiries: tom.little@ed.ac.uk

Please quote ref: 3001275 Closing date: 02 Mar 04

To apply online or view more job opportunities, visit our website (www.jobs.ed.ac.uk). Alternatively, telephone the recruitment line on 0131 650 2511.

Informal Inquiries to Tom.Little@ed.ac.uk See also http://www.icapb.ed.ac.uk/ and http://www.icapb.ed.ac.uk/people/little.html Formal Application must be made through the website: www.jobs.ed.ac.uk Or by phoning 0131 650 2511

Tom Little, SBS Research Fellow Institute for Cell, Animal and Population Biology University of Edinburgh, Kings Buildings West Mains Rd, Edinburgh, U.K.EH9 3JT, UK

phone: 0131 650 7781, Fax: 0131 650 6465 email: tom.little@ed.ac.uk

UEdinburgh PlantDiversity

A postdoctoral position for a NERC funded project to study DNA sequence diversity in natural populations of the plant Arabidopsis lyrata. The position is with D. Charlesworth in the population genetics group in the Institute of Cell, Animal and Population Biology (ICAPB), University of Edinburgh, and is for a fixed term of 30 months.

The work will involve studying several genes in multiple populations of the subspecies petraea over its distribution range in Europe, and also divergence from suitable outgroup species. Candidates should be interested in population genetics and evolution, ideally with an interest in plants. Experience with PCR amplification and DNA sequencing, including some familiarity with methods of analyses of sequences is required.

To find out more deails, contact Deborah.Charlesworth@ed.ac.uk. Applications for the post should be made via the web site at https://www.jobs.ed.ac.uk/jobs/-index.cfm?action=3Djobdet&jobid=3D3001314

The Job Reference is 3001314 The salary scale is £ 18265 - £ 27339

The starting date should be as soon as possible after April 1st 2004. –

Professor Deborah Charlesworth Institute of Cell, Animal and Population Biology University of Edinburgh Ashworth Lab. King's Buildings, W. Mains Rd., Edinburgh EH9 3JT, UK Tel: (+44)(0)131 650 5751 Fax: (+44)(0)131 650 6564 Deborah.Charlesworth@ed.ac.uk Deborah.Charlesworth@ed.ac.uk

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UGranada FlowerEvol

Dear colleagues,

My research group is looking for a post-doctoral candidate who has recently (within the last 3 years) finished his/her (PhD) thesis, and who is interested in applying for a Juan de la Cierva postdoctoral grant to join our project BOS2003-0949 entitled "Flowering evolution in Erysimum mediohispanicum: microevolution, genetic architecture and interspecific comparisons. If funded, the grant provides support for 3 years, with a salary of approximately 24000 per annum. The main task of this project will be the development of molecular markers in the plant Erysimum mediohispanicum, followed by their use in the detection of loci in the standard chromosomes which might be associated with changes in the shape of the flowers. Interested people should contact Jose M Gomez (e-mail: jmgreyes@ugr.es), and should provide both CV and a description of their research experience. Best wishes,

Jose M. Gomez Departamento de Biologia Animal y Ecologia Universidad de Granada Spain

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ULaval SalmonidEvol

POSTDOCTORATE or Ph.D. POSITION IN SALMONID EVOLUTIONARY FUNCTIONAL GENOMICS

We are currently looking for either a postdoctorate or Ph.D. candidate to be involved in our ongoing research project regarding the elucidation of functional genomic bases of growth and anadromy in salmonid fishes. This multidisciplinary project is funded by FQRNT (Quebes) and NSERC (Canada) and is also part of the research program of the Canadian Research Chair in conservation genetics of aquatic organisms.

The originality and interest of this project is based upon a multidisciplinary approach integrating genomics, physiology and immunology. The use of charr species (Salvelinus) as a model system offers particular interest for investigating the functional genomic bases of growth and anadromy. Namely, some of these species are well differentiated in terms of growth potential and physiological adaptations to seawater. Yet, such species can interbreed in laboratory and natural conditions, which offers a unique oportunity to investigate the basis of heterosis and outbreeding depression at the functional genomics level.

The specific objective of the proposed research will be to apply microarray technology for quantifying gene expression profiles in pure brook and arctic charr, as well as in their hybrid crosses in order to determine and compare the nature and number of genes potentially involved in differential growth in both freshwater and saltwater. A 16000 gene microarray recently developped in salmonids is already available to achieve this work.

We are primarily looking for a candidate with strong laboratory expertise in functional genomics, a solid theoretical background in evolutionary biology, quantitative genetics or comparative physiology, as well as expertise in management and analysis of large data bases.

The position is available now.

To apply, please send a cover letter describing your research interests, a complete CV and names of three references by e-mail to Louis.Bernatchez@bio.ulaval.ca

To learn more about

Quebec city : http://www.quebecweb.com/tourisme/-

quebec/villequebec/introang.html Laval University : http://www.ulaval.ca/ The Biology department and our research programs: http://www.bio.ulaval.ca/-index-alt.html

Louis Bernatchez, Titulaire de la Chaire de recherche du Canada en conservation genetique des ressources aquatiques Departement de biologie, Pavillon Charles-Eugene Marchand, Universite Laval, Sainte-Foy, QC G1K 7P4 Canada

Tel: 1 418 656-3402 Fax: 1 418 656-2043 Couriel: Louis.Bernatchez@bio.ulaval.ca Toile: http://-www.bio.ulaval.ca/contenu-fra/professeurs/prof-l-bernatchez.html

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UPittsburgh Bioinformatics

Bioinformatics/Computational Biology Position -

The University of Pittsburgh Cancer Institute and the Benedum Oncology Informatics Center announce a one or two-year Postdoctoral Fellowship in Oncology Informatics. The successful applicant will work well on a multidisciplinary research team on the optimization of computational approaches to the pre-interpretive and interpretive analysis of high throughput genomic and proteomic data, and will enjoy opportunities to interface directly with >20 UPCI-affiliated cancer researchers and colleagues in biostatistics, human genetics, computer science and pathology, in a dynamic, fast-paced, cutting edge research institute. Qualifications include a background in the biological sciences, with demonstrable programming experience in C++ or JAVA. Demonstrated experience with coding alignment algorithms, concepts of statistical learning, computational structural biology and computational genomics a plus. The fellow will be encouraged to complement their previous training with the many excellent courses offered at the University of Pittsburgh in machine learning, biostatistics, computational biology and bioinformatics. A second year of funding is dependent on the availability of funding. Applicants should send a cover letter describing their background and experience, a curriculum vitae, and three letters of recommendation to

Contact:

Dr. James Lyons-Weiler Benedum Oncology Informatics Center The University of Pittsburgh Cancer Institute Room 304 Cancer Pavilion 5150 Centre Avenue Pittsburgh, PA 15232 (412) 623-7866 lyonsweilerj@msx.upmc.edu

GEDA http://bioinformatics.upmc.edu/GE2/-GEDA.html University of Pittsburgh Cancer Institute http://www.upci.upmc.edu/ Center for Biomedical Informatics http://www.cbmi.pitt.edu/ Interdisciplinary Biomedical Graduate Studies Program http://www.gradbiomed.pitt.edu/ Applied Bioinformatics http://www.openmindjournals.com/-bioinformatics.html

UPittsburgh FloralEvol

Postdoctoral Associate in Floral Development and Evolution

Applications are invited for a postdoctoral position to study plant mating system evolution in Susan Kalisz's lab. The goal of the project is to understand mechanisms that generate floral developmental flexibility and their role in influencing mating system evolution. Molecular genetic and candidate gene approaches in comparative studies of the genus Collinsia and the model Antirrhinum majus, both in the Scrophulariaceae will be used. Applicants well versed in molecular techniques will be given preference. Our lab is a member of the NSF-supported MORPH Research Coordination Network http://www.colorado.edu/eeb/MORPH Funding is available for two years, with a competitive salary and full benefits. The position is available beginning May 1, 2004. The University of Pittsburgh is an equal opportunity employer.

Interested applicants should send a CV, brief statement of research interests and experience, and contact information for three references via email to:

Susan Kalisz Department of Biological Sciences University of Pittsburgh 4249 Fifth Avenue Pittsburgh, PA 15260 USA E-mail: kalisz@pitt.edu Phone: 412 624-4281

UPuertoRico EvoDevo

Postdoc Postion- Genetic and Developmental Architecture of Wing Pattern Variation in Heliconius Butterflies

Project Description: A postdoctoral fellowship is available to study the genetic and developmental basis of wing pattern variation in the neotropical butterfly Heliconius erato. The researcher will join an NSF-funded project that will utilize microarray technology to study temporal and spatial variation in gene expression during wing pattern development. The project is a collaboration between Owen McMillan at the University of Puerto Rico and Fred Nijhout and Bob Reed at Duke University. It builds on over a century of ecological, behavioral, and genetic analysis to understand the developmental basis of H. erato's extraordinary adaptive radiation in aposomatic wing patterns.

Although the researcher will be based in Puerto Rico, we expect strong interactions with collaborators at Duke University. Furthermore, there will be ample opportunity for research collaborations with other colleagues working on Heliconius. The postdoc will primarily be responsible for i) overseeing the characterization of a H. erato cDNA library, ii) leading the production of an integrated genetic map of the H. erato color pattern radiation using candidate genes, AFLP, and microsatellites (an ongoing collaboration with Durrell Kapan (UPR) and David Heckel (Max-Planck-Institut für Chemische Ökologie), and iii) coordinating, with Chris Jiggins (University of Edinburgh), the generation of a comparative genomic framework to study wing pattern convergence between of H. erato and it's co-mimic, H. melpomene.

Job Period: 1 June 2004 - 31 May 2006.

Salary: $34,000/year plus medical (and dental!).

Qualifications: Ph.D. with experience in molecular genetic techniques including DNA sequencing, library subtraction, and mutation detection. Experience with genetic linkage and QTL analysis and/or analysis of gene expression data is helpful, but not a requirement. A hearty sense of humor, offensive driving skills, and appreciation of life in the tropics is also recommended.

Additional Information: The postdoc will join an active molecular evolution group studying a diverse array of questions ranging from the evolutionary biology of infectious diseases to the reproductive biology of land iguanas. See http://zephyr.hpcf.upr.edu/~mcmi-lab/ for added details. Genomic facilities at the University of Puerto Rico are first-rate and include equipment for high-throughput sequencing and genotyping and for printing and analyzing microarrays. Core genomic facilities are augmented by a fledging Bioinformatics Center supported by Puerto Rico's High Performance Computing Center.

Please send CV (including the names and addresses of three referees) and cover letter in PDF format to Dr. W. Owen McMillan (wmcmilla@rrpac.upr.clu.edu). Inquiries welcome. The University of Puerto Rico is an Affirmative Action/Equal Opportunity Employer. –

W. Owen McMillan Associate Professor Department of Biology University of Puerto Rico- Rio Piedras P.O. Box 23360 San Juan, PR 00931-3360

wmcmilla@rrpac.upr.clu.edu http://-zephyr.hpcf.upr.edu/~mcmi-lab/ phone (office): 787-764-0000 [(1)2909] phone (lab): 787-764-0000 [(1)2902, (1)2853] phone (home): 787-764-3564 fax: 787-764-3875

Owen McMillan <wmcmilla@rrpac.upr.clu.edu>

UQueensland Eukaryotic Genomics 2

POSTDOCTORAL POSITION AVAILABLE EVOLUTION OF EUKARYOTIC GENOMES

Institute for Molecular Bioscience The University of Queensland Brisbane, Australia

A postdoctoral position in comparative eukaryotic genomics will be available from May 2004 within the Australian Research Council (ARC) Centre in Bioinformatics based at the Institute for Molecular Bioscience, University of Queensland.

The successful applicant will work closely with Professor Mark Ragan and will take primary responsibility for extending to eukaryotic (including mammalian) genomes the automated identification, alignment and phylogenetic analysis of orthologous genomic regions, including but not limited to genes.

Applicants must have strong programming skills, and be fully conversant with likelihood-based phylogenetic inference. Experience with eukaryotic genomes and gene structure, relational databases and high-performance computing would be highly beneficial.

Highly motivated applicants who have, or will soon receive, a PhD or equivalent degree in a relevant field (e.g. bioinformatics, genomics, mathematics, molecular biology) are encouraged to send a covering letter, CV, and contact information for three academic referees to m.ragan@imb.uq.edu.au. Appointment will normally be made for two years contingent on successful annual performance review, with possibility for extension to a third year.

The Institute for Molecular Bioscience brings together more than 350 researchers in fundamental mammalian cell and molecular biology, developmental biology, structural biology, biological chemistry, genomics, proteomics, computational biology and bioinformatics. Together with more than 200 researchers from CSIRO Livestock Industries and Plant Industry, IMB is based in the new A$105M Queensland Biosciences Precinct, the largest bioscience research initiative in the Southern Hemisphere. IMB researchers enjoy superb infrastructure including high-performance computing and database infrastructure under a research alliance with IBM.

The ARC Centre in Bioinformatics is a new initiative of the Australian Research Council. The Centre aims to understand the mammalian cell as a complex system of molecular networks. It links researchers at four Australian universities and overseas in algorithmics, statistics, machine learning, pattern discovery, mathematical modelling and simulation, 3-D visualisation, advanced databases, and high-throughput experimental validation.

For more information please contact Mark Ragan.

UWashington StatGenetics

Two-year Postdoctoral positions available. Department of Statistics, University of Washington, Seattle, WA.

A 100% postdoctoral research position is available. Starting date, as soon as possible after June 2004 (flexible). Length: two years, subject to satisfactory performance and availability of funding.

Opportunity for a statistical geneticist to work as a postdoctoral Research Associate under the supervision of Dr. Elizabeth Thompson, in the Department of Statistics on the development of statistical and computational methodology in the area of the genetic analysis of complex traits. Our current focus is in the area of Monte Carlo likelihood methods for the analysis of genetic data on pedigrees. This research is funded by NIH grant GM 46255, recently continued through November 2007: salary and benefits will be in accordance with NIH postdoctoral scales, and University of Washington policies.

Further information about this research can be found on the web at http://www.stat.washington.edu/-thompson/Genepi. Additional information on education and research in Statistical Genetics at the University of Washington can be found at http://-depts.washington.edu/statgen/ Requirements: Ph. D. in Statistics, Biostatistics, or a related field practical knowledge of computing in a workstation environment, including programming experience. Some knowledge/experience in genetics or molecular biology.

Enquiries BY PLAIN TEXT E-MAIL ONLY PLEASE, should be sent to Professor Elizabeth Thompson, (thompson@stat.washington.edu). Please do NOT send email attachments as WORD documents, HTML etc. If you wish to provide supporting information, please send a reference to a web page (preferred) or PDF attachments ONLY. If applying, please provide email addresses of 3 referees.

The University of Washington is building a culturally diverse faculty and strongly encourages applications from women and minority candidates. AA/EOE.

UppsalaU 2 Evol

2 Post-docs in Molecular Evolution / Evolutionary Genomics in Uppsala

We seek enthusiastic post-docs who will join a group working with various aspects of molecular evolution and evolutionary genomics. These include studies of male-biased mutation, mutation rate variation, the evolution of isochores, selection, sex chromosome evolution and microsatellite evolution. We combine in-house DNA sequencing and genotyping with large-scale in silico analysis of sequence and SNP data from public databases. In both cases data are analysed within a molecular evolutionary context, either using common programs or through own programming.

Project will be decided together with the successful candidates, and will depend on the expertise and interests of the candidates. A selected list of recent publications to indicate ongoing activities is given below. For further information please visit http://www.ebc.uu.se/evbiol/-Research/evolmolec.html . The laboratory is situated in the recently-built Evolutionary Biology Centre of Uppsala University and is equipped with large-scale sequence and genotype facilities including 96-capillary DNA sequencing, pyrosequencing, DHPLC and real-time PCR. The working atmosphere is international with a regular recruitment of post-docs. The Centre is an exciting arena for multi-disciplinary research in evolutionary biology, housing some 400 scientists and graduate students, with research programs in ecology, systematics, genetics, genomics, functional genomics and developmental biology. Uppsala University is the oldest in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated close to Stockholm.

Informal inquiries and applications should be sent to the address indicated below. Previous experience of research in molecular evolution is of merit, and may have been in the form of experimental or theoretical work. Please include with the application a full CV, a statement of research interests and the name and address of at least two referees. The positions are initially for two years, with possibilities for prolongation after this period.

Professor Hans Ellegren Dept of Evolution, Genomics and Systematics Evolutionary Biology Centre Uppsala University Norbyvägen 18D SE-752 36 Uppsala Sweden

Email: Hans.Ellegren@ebc.uu.se Phone: +46-18-4716460 Fax: +46-18-4716310 Web address: http://www.ebc.uu.se/evbiol/index.html Brohede, J, Arnheim, N & Ellegren, H (2004) Single molecule analysis of the hypermutable tetranucleotide repeat locus D21S1245 through sperm genotyping: a heterogeneous pattern of mutation but no clear male age effect. Molecular Biology and Evolution, in press.

Ceplitis, H & Ellegren, H (2004) Adaptive molecular evolution in HINTW, a female-specific gene in birds. Molecular Biology and Evolution, in press.

Lawson-Handley, L., Ceplitis, H. & Ellegren, H. (2004) Evolutionary strata on the chicken Z chromosome: Implications to sex chromosome evolution. Genetics, in press.

Bartosch-Härlid, A, Berlin, S, Smith, NGC, M, AP & Ellegren, H (2003) Life history and the male mutation bias. Evolution 57: 2398-2406.

Ellegren, H, Smith, NGC & Webster, MT (2003) Mutation rate variation in the mammalian genome. Current Opinion in Genetics and Development 13:562-568.

Sundström, H, Webster, MT & Ellegren, H (2003) Is the rate of insertion and deletion mutation male-biased? -Molecular evolutionary analysis of avian and primate sex chromosome sequences. Genetics 164: 259-268.

Smith NGC, Webster, MT & Ellegren, H (2002) Deterministic mutation rate variation in the human genome. Genome Research 12:1350-6.

UppsalaU ConsGenet

Post-doc in Conservation Genetics in Uppsala

We seek a competitive post-doc who will join a group working with carnivore conservation genetics (mainly wolves and wolverines). Although partly conducted on a global scale, a main line of research centers on the situation on the Scandinavian peninsula, for which extensive information about demographic trends is available for these species. To obtain a better understanding on the history of the populations we are combining the use of diverse molecular markers, including maternally inherited mitochondrial DNA sequences and paternal Y chromosome haplotypes. We are also studying biparental autosomal markers: microsatellites, single nucleotide polymorphisms (SNPs) and MHC sequences. Key questions include inbreeding, immigration and hybridization. The successful candidate will work mainly with the development of new molecular approaches for the study of conservation genetics.

A selected list of recent publications to indicate ongoing activities is given below. For further information please visit http://www.ebc.uu.se/evbiol/Research/Conservation.html The laboratory is situated in the recently-built Evolutionary Biology Centre of Uppsala University and is equipped with large-scale sequence and genotype facilities including 96-capillary DNA sequencing, pyrosequencing, DHPLC and real-time PCR. The working atmosphere is international with a regular recruitment of post-docs. The Centre is an exciting arena for multi-disciplinary research in evolutionary biology, housing some 400 scientists and graduate students, with research programs in ecology, systematics, genetics, genomics, functional genomics and developmental biology. Uppsala University is the oldest in Scandinavia and the city of Uppsala is a vibrant student town with beautiful surroundings conveniently situated close to Stockholm.

Informal inquiries and applications should be sent to the address indicated below. Previous experience of research in conservation genetics of merit. A strong background in molecular genetics is required. Please include with the application a full CV, a statement of research interests and the name and address of at least two referees. The position is initially for two years, with possibilities for prolongation after this period.

Professor Hans Ellegren Dept of Evolution, Genomics and Systematics Evolutionary Biology Centre Uppsala University Norbyvägen 18D SE-752 36 Uppsala Sweden

Email: Hans.Ellegren@ebc.uu.se Phone: +46-18-4716460 Fax: +46-18-4716310 Web address: http://-www.ebc.uu.se/evbiol/index.html Flagstad, Ø., Hedmark, E., Landa, A., Br, H., Persson, J., Andersen, R., Segerström, P. & Ellegren, H. (2004) Colonization history and noninvasive monitoring of a re-established wolverine population. Conservation Biology, in press.

Flagstad, Ø, Walker, CW, Vilà, C, Sundqvist, A-K, Fernholm, B, Hufthammer, AK, Wiig, Ø, Koyola, I & Ellegren, H (2003) Two centuries of the Scandinavian wolf population: patterns of genetic variability and migration during an era of dramatic decline. Molecular Ecology 12: 869-880.

Hellborg, L & Ellegren, H (2003) Y chromosome conserved anchored tagged sequences (YCATS) for the analysis of mammalian male-specific DNA. Molecular Ecology 12: 283-291.

Rueness, EK, Stenseth, NC, O'Donoghue, M, Boutin, S, Ellegren, H & Jakobsen, KS (2003) The phylogeography of the Canadian lynx: coinciding genetic and ecological spatial structuring. Nature 425: 69-72.

Vilà, C, Sundqvist, A-K, Flagstad, Ø, Seddon, J, Björnerfeldt, S, Kojola, I, Casulli, A, Sand, H, Wabakken, P & Ellegren, H (2003) Rescue of a severely bottlenecked wolf (Canis lupus) population by a single immigrant. Proceedings of the Royal Society London, Series B 270: 91-97.

Vilà, C, Walker, CW, Sundqvist, A-K, Flagstad, Ø, Andersone, Z, Casulli, A, Kojola, I, Valdmann, H, Halverson, J & Ellegren, H (2003) Combined use of maternal, paternal and bi-parental genetic markers for the identification of wolf-dog hybrids. Heredity 90:17-24.

Seddon, JM & Ellegren, H (2002) MHC class II genes in European wolves: a comparison with dogs. Immunogenetics 54: 490-500.

Hedrick, P, Fredrickson, R & Ellegren, H (2001) Evaluation of d2, a microsatellite measure of inbreeding and outbreeding, in wolves with a known pedigree. Evolution 6:1256-1260.

Sundqvist, AK, Ellegren, H, Olivier, M & Vilà, C (2001) Y chromosome haplotyping in Scandinavian wolves (Canis lupus) based on microsatellite markers. Molecular Ecology 10: 1959-1966.

Walker, CW, Vilà, C, Landa, A, Lindén, M & Ellegren, H (2001) Genetic variation and population structure in Scandinavian wolverine (Gulo gulo) populations. Molecular Ecology 10: 53-63.

Hans.Ellegren@ebc.uu.se

Vienna LocalAdaptation

Postdoctoral position available

A postdoctoral position is available for two years in the laboratory of Christian Schlotterer. The laboratory focuses on molecular approaches to understand adaptation of local populations. The candidate is expected to work on aspects linked to adaptation and behavior in Drosophila montana and close relatives. Depending on the interests of the candidate the focus of the project could be developed during the project.

Current members of the laboratory come from Austria, China, France, Germany, Italy and Scotland. The laboratory operates bilingually, allowing non-German speaking researchers to integrate easily.

Vienna provides a stimulating scientific environment with a number of research groups focusing on population genetics and evolutionary biology: Reinhard Burger, Ulf Dieckmann, Dustin Penn, Karl Sigmund, Peter Schuster and Claus Vogl. Apart from good science, Vienna also offers an active cultural life (2 operas, 2 world class concert houses, numerous museums and the famous coffee houses) and attractive recreation opportunities (alps are close by and you can sail within the city area!).

European citizens less than 36 years old with a background in evolutionary biology or related areas are encouraged to apply. Salary is highly competitive.

Further questions concerning the project and applications should be directed to Christian Schlotterer (Christian.schloetterer@vu-wien.ac.at). Preferred starting date is April/May 2004.

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

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

WalnutCreek MicrobeGenomics

Postdoc position Comparative community genomics of the gut microbiota. DOE Joint Genome Institute

An NIH-funded postdoctoral position is available to study the diverse microbial community that inhabits the gastrointestinal tract, specifically that of humans and mice. This community has important roles in host physiology, is rich in ecological interactions, and has potential for providing clues to the evolution of commensalism and pathogenicity. Some specific objectives of the project include understanding the diversity within the gut, the main differences between commensals and their pathogenic relatives, and the paths of horizontal gene exchange within the gastrointestinal environment. We are looking for a postdoctoral researcher to participate in all aspects of the project, such as production and screening of BAC libraries, and comparative sequence analyses of the obtained sequences. Applicants should have skills in evolutionary genetics, genomics, computational biology or microbiology. Programming abilities a plus.

The person will be based in the Evolutionary Genomics Department of the DOE Joint Genome Institute (http://www.jgi.doe.gov/programs/comparative/-), but will also have the opportunity to interact with the laboratory of Howard Ochman at the University of Arizona at Tucson. The DOE Joint Genome Institute, established on January 1, 1997, is a consortium of scientists, engineers and support staff from the U.S. Department of Energy's Lawrence Berkeley, Lawrence Livermore and Los Alamos National Laboratories, and is located in Walnut Creek, a nice community approximately 25 miles from San Francisco and 20 miles from Berkeley, with easy access to many locations in the Bay Area.

Please send inquiries and applications to Pilar Francino at mpfrancino@lbl.gov. Applications should include a cover letter describing your research interests, a CV and names of three references. – M. Pilar Francino, Ph. D. Research Scientist Genomics Division, Lawrence Berkeley National Lab and Evolutionary Genomics Department, DOE Joint Genome Institute 2800 Mitchell Drive Walnut Creek, CA 94598

phone: (925) 296-5872 fax: (925) 296-5666 e-mail: mpfrancino@lbl.gov e-mail: mpfrancino@lbl.gov

WorkshopsCourses

NatlUnivIreland Phylogenetics Apr12-16

PHYLOGENOMICS AND HIGH-THROUGHPUT PHYLOGENETICS COURSE

Location: National University of Ireland Maynooth. Dates: April 12-16th 2004 inclusive. Registration deadline: March 15th, 2004. Website: http://-bioinf.may.ie/Phylogenomics/ Background

Phylogenomics and phyloinformatics are two terms that relate to the processing of large amounts of genomic data with a view towards producing organismal phylogenies based upon those data. The two main methods of analysis include supermatrix and supertree analysis. We have no particular preference for either approach and will present both kinds of solution along with cautionary tales about each.

Who is this course for?

This course is designed to be of the most benefit to those researchers that have a small amount of familiarity with phylogenetic analysis and intend on setting up and using a system for performing phylogenetic analysis on the genome level. The level at which the course is being taught is introductory to intermediate. This is NOT an advanced level course. If there is demand for such a course, it could be organised in the future.

Students are encouraged to bring their own data.

Website: http://bioinf.may.ie/Phylogenomics/ Regards,

James

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

PloenGermany InnateImmunity May6-9

WORKSHOP

Innate immunity: bridging the gap between ecology and molecules. 6.-9. May 2004 Ploen (near Hamburg), Germany.

GRANTS: Thanks to funding by the VolkswagenStiftung, up to 30 grants are now available for travel and accomodation for young researchers, preferentially at the level of PhD or young postdocs, to attend this workshop. You are invited to present your work in a poster and 1-2 slides advertising the main message in a special seminar.

TOPIC: The field of immunology is currently progressing rapidly with the study of innate immunity, often using the immune system of invertebrates as a model. In parallel, there is an intensifying focus of ecologists and evolutionary biologists on aspects of immunity. The goal of this workshop is to bring together people from these fields and to generate a discussion bridging the boundaries of the fields, in order to achieve a unified understanding of the evolution of innate immunity.

APPLICATION: Please send an e-mail with the subject header “VW” to “kurtz@mpil-ploen.mpg.de”, containing the following information: your name and institutional address, a short CV (including a publication list, if available) and an abstract of the planned poster. Application deadline is March 15, 2004.

PARTICIPANTS: For your information, here is a provisional list of attendees:

Shelly Adamo, Department of Psychology, Dalhousie University, Canada Aneil Agrawal, Indiana University, Bloomington, USA Michael Boots, University of Stirling, UK Thomas C.G Bosch, University of Kiel, Germany Martin Brinkhoff, University of Bern, Switzerland George Dimopoulos, Johns Hopkins School of Public Health, Baltimore, USA Dieter Ebert, University of Fribourg, Switzerland Peter Hammerstein, Humboldt-Universität zu Berlin, Germany Dan Hultmark, Umea University, Sweden Hilary Hurd, Keele University, UK Gregory Hurst, University College London, UK Francis Jiggins, Universtiy of Edinburgh, UK Jacob C. Koella, Universite Pierre et Marie Curie, France Lex Kraaijeveld, Imperial College at Silwood Park, UK Tom Little, University of Edinburgh, UK Yannick Moret, University of Sheffield, UK Matthias Noellenburg, VolkswagenStiftung, Hamburg, Germany Thomas Roeder, Zentrum für Infektionsforschung Wuerzburg, Germany Rebeca Rosengaus, Northeastern University, Boston, USA Paul Schmid-Hempel, ETH Zürich, Switzerland Hinrich Schulenburg, University of Muenster, Germany Mike T. Siva-Jothy, University of Sheffield, UK Valerie Smith, University of St Andrews, UK Kenneth Soederhall, Uppsala University, Sweden Tina Trenczek, University of Giessen, Germany Ken Wilson, University of Stirling, UK

We are looking forward to receive your applications.

Joachim Kurtz Department of Evolutionary Ecology, Max-Planck Institute of Limnology, Ploen, Germany

Jens Rolff University of Sheffield, Department of Animal and Plant Sciences, UK

Dr. Joachim Kurtz

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Prague SNPcourse May1

Teaching Course on SNP genotyping during 14th EC-

CMID in Prague, May 1-4, 2004

On Saturday, May 1st, 2004, 14.00-17.30 for the first time at ECCMID (European Congress of Clinical Microbiology and Infectious Diseases) four teaching courses will be organised by ESCMID Study Groups within the Congress premises.

One of these courses is about SNP genotyping. It is organized by the ESCMID Study Group on Epidemiological Markers (ESGEM).

Teaching courses can be booked on-line (see "On-line Registration" at http://www.akm.ch/eccmid2004/) or by means of an enclosed registration form (pdf) for a separate registration fee of EUR 50. A limited number of places is available, which will be filled on a first-come basis.

TITLE OF THE COURSE:

Single Nucleotide Polymorphism (SNP) Detection and other New Technologies for Genetic Characterisation of Bacteria and Infectious Disease Susceptibility Testing organised by the ESCMID Study Group on Epidemiological Markers (ESGEM).

Topics * The potential of Single Nucleotide Polymorphisms (SNPs) for bacterial strain typing and identification * The potential of SNP genotyping for infectious disease susceptibility studies * Methods for SNP discovery in bacterial genomes * SNP genotyping based on mass spectrometry * SNP genotyping based on microarray approaches * SNP genotyping using pyrosequencing * Flow cytometry methods and bead arrays for bacterial strain genotyping * Question and answer session to the faculty

Faculty * Sylvain Brisse, Institut Pasteur, Paris, F * Richard Goering, Creighton University School of Medicine, Nebraska, USA * Lauren Cowan, CDC, Atlanta, Georgia, USA (to be confirmed) * Neil Woodford, ARMRL, SRMD, Health Protection Agency, London, UK * Marieke Emonts, Laboratory of Paediatrics, Erasmus Medical Center, Rotterdam, NL * Sascha Sauer, Max-Planck Institute for Molecular Genetics, Berlin-Dahlem, DE * Mark Achtman, Max-Planck Institute, Berlin, DE

For more information about ESGEM activities please see the ECCMID web site (http://www.escmid.org/sites/index.asp) and go to 'study groups').

– Dr. Sylvain BRISSE Unité Biodiversité des Bactéries Pathogènes Emergentes Biodiversity of Emerging Bacterial Pathogens Unit INSTITUT PASTEUR 25-28 rue du Docteur Roux 75724 Paris cedex 15 FRANCE Tel : 00 33 (0) 1 40 61 33 57 Fax: 00 33 (0) 1 45 68 88 37 E-mail : sbrisse@pasteur.fr

Sylvain Brisse <sbrisse@pasteur.fr>

RiodeJaneiro Complexity Nov 2

Workshop on Complexity and Philosophy Co-hosted by:Federal university of Rio de JaneiroInstitute for the Study of Coherence and EmergenceCathedra for the Study of Complexity (Instituto de Filosofia de La Habana) Calling Notice November 2004, Rio de Janeiro(exact dates to be determined shortly) Call for Participants I am writing to you today to inform you about the upcoming two-day Complexity and Philosophy workshop to be held this November (2004) in Rio de Janeiro and hosted by the Institute for the Study of Coherence and Emergence(http://www.isce.edu), U.F.R.J. (Federal university of Rio de Janeiro), and the Cathedra for the Study of Complexity (Instituto de Filosofia de La Habana) . The aim of this meeting is to explore the philosophical implications of the fledgling science of complex systems. This workshop complements the 2nd Biennial International Seminar on the Philosophical, Epistemological and Methodological Iimplications of Complexity Theory that was held in Havana, Cuba, January 2004. The larger international seminar provides a forum to discuss complexity and philosophy-related issues in general, whereas the aim of the smaller workshop event is to consider specific issues at a greater length with more time made available for discussion rather than presentation. The location for the workshop event is expected to change location each time it is held. In 2002 the event was held in Norwood (just outside Boston) in the US. This time we are pleased to announce that the next event will be held in Rio de Janeiro, with the very generous assistance of the Federal university of Rio de Janeiro. Call for Papers Potential attendees are encouraged to submit papers on the following topics: Status, limits and legitimacy of knowledge regarding complex systems Relationship between linear and nonlinear philosophies Complexity-based ethics Frameworks for the analysis of complex systems Complex limits to 'theories of everything' Complexity and the social sciences Complexity and globalization Complexity and human subjectivity All paper submissions will be considered for publication in the international journal Emergence: Complexity and Organization (depending upon suitability), and/or publication in an edited book of papers to be published by IAP Press as part of ISCE's Managing the Complex Book Series. Selected papers from the previous event have appeared in Nonlinear Dynamics, Psychology and the Life Sciences, and this journal may again prove to be a publishing avenue for selected papers. All papers will be considered for publication even if time cannot be found for the papers to be presented at the conference itself (the emergent properties of such an event and the organiser's hope to focus on discussion/dialogue rather than a standard presentation format may at times dictate the proceedings). Provisional Timetable Please let Caroline Richardson (complexityworkshop@isce.edu) know of your interest in attending this event as soon as possible. Attendance at the event will be strictly limited to 30 so as to encourage genuine dialogue amongst participants - selection of attendees will be determined simply on a first come first serve basis. A block of 30 rooms will be reserved for the event and a reduced room rate (that includes breakfast) will be negotiated. Final details concerning hotel rates will be made available in the next month or so. Extended abstracts of at least 1000 words to be submitted to Dr. Kurt Richardson (kurt@kurtrichardson.com) by end of July, 2004. The decision by the academic board (which will comprise members of I.S.C.E.'s fellowship) to encourage submission of a full paper - to be no longer than 5000 words - will occur by end of August, 2004. Full papers to be submitted by end of October, 2004. The decision as to what papers will be published and in what form will occur shortly after the closing of the conference. It is hoped that participants will play an integral role in the development of the event timetable before and during the event. The exact cost of registration will be determined shortly, but fees are expected to be around US$300. As well as administrative and location costs, fees will also cover lunch during the event as well as a Brazilian-style dinner event at the close of the second day. Participants will be responsible for their own hotel costs. If you would like to attend the workshop please send an email to Caroline Richardson (complexityworkshop@isce.edu) with the following information: Name, academic affiliation and status if any, address, phone, fax, and email. Caroline will contact you for further information re hotel confirmation and payment of workshop fees. If you have any questions at all please do not hesitate to contact Kurt or Caroline (complexityworkshop@isce.edu).

Seattle RockfishConservation Mar2-3

Conservation of North Pacific Rockfishes: Ecological Genetics and Stock Structure

Sponsored by NOAA Fisheries and the Northwest Fisheries Science Center

Conservation Biology Division

Fishery Resource Analysis and Monitoring Division

2 -3 March 2004, Seattle Washington U.S.A.

Objectives:

* To bring together researchers and managers to help define current stock structure issues related to conservation and recovery of rockfishes * To provide an understanding of current opportunities (and limitations) of new technologies such as molecular genetics, otolith microchemistry, and ultrasonic telemetry. * To foster interactions between ecologists and geneticists and to create synergistic new collaborations that address long-standing conservation and recovery problems. * To provide priorities for conservation research and suggestions for future directions, with respect to important species/guilds and to critical biological problems involving rockfishes.

Structure:

* Speakers will include established ecologists, geneticists and fishery managers * Posters on a broader range of groundfish topics are welcome. * Formal and informal opportunities for discussion and debate

Plenary Speakers:

* Dr. Jenn Caselle, University of California, Santa Barbara * Mr. Daniel Gomez-Uchida, Oregon State University * Dr. Christopher G. Lowe, California State University, Long Beach * Dr. Lisa Seeb, Alaska Department of Fish and Game * Dr. Russell D. Vetter, NOAA Fisheries, SW Fisheries Science Center * Dr. Peter Wimberger, University of Puget Sound

Product:

* Compilation of extended abstracts to be published as a NOAA Technical Memorandum and made available for download via the World-wide Web

Venue:

* Northwest Fisheries Science Center, Montlake Campus, 2725 Montlake Boulevard East, Seattle, Washington (Picture identification currently required for entry to this Federal facility) * Directions: http://www.nwfsc.noaa.gov/contact/map.cfm

For further information and advance registration, please contact:

Paul Moran, 206-860-3245, paul.moran@noaa.gov

<mailto:paul.moran@noaa.gov>

Abstract submission:

* Titles for posters and oral presentations due 23 February (please indicate preference) * Abstracts for poster and oral presentation are due at check-in, 2 March * Maximum 1000 words, not including references, and 1 - 2 tables or figures * Formatting examples for NOAA Technical Memorandum series at: http://www.nwfsc.noaa.gov/publications/-techmemos/index.cfm

Registration:

* There is no registration fee associated with this workshop * To register simply send email to paul.moran@noaa.gov <mailto:paul.moran@noaa.gov>

Early registration is appreciated to facilitate planning

Ewann A. Berntson, Ph.D. Conservation Biology Division Northwest Fisheries Science Center 2725 Montlake Blvd. E Seattle, WA 98112 Phone: (206) 860-3278 Fax: (206) 860-3335 ewann.berntson@noaa.gov

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Smithsonian ConservatonGenetics Aug16-27

American Genetic Association Laboratory of Genomic Diversity - National Cancer Institute The Smithsonian Institution^{1}s Conservation & Research Center announce a course

^{3}RECENT ADVANCES IN CONSERVATION GENETICS^2

August 16-27, 2004

At the Smithsonian Institution's Conservation & Research Center in Front Royal, Virginia, outside Washington, DC, the AGA and the LGD are presenting a 10-day intensive course in methods, interpretation, and applications of molecular genetic analyses for conservation of endangered species. This course will be taught by scientists with expertise and a variety of personal experiences in this important field. Participants will learn how to develop and interpret a wide range of genetic data.

COURSE DIRECTOR: Stephen J. O'Brien, Chief, Laboratory of Genomic Diversity, National Cancer Institute-Frederick, MD, USA

TOPICS include: Sample collection and processing PCR-based technologies for polymorphism detection Genetic analysis: bioinformatics and the use of molecular genetic databases estimating relative genetic diversity with gene markers phylogenetic algorithms: their use and interpretation phylogeography subspecies and population substructure demographic and genetic simulation modeling of small populations kinship and paternity assessment Host-pathogen interactions Conservation management applications

TUITION: US $2,000 (includes housing, all meals, and airport transfers) Deadline for receipt of applications: March 15, 2004. Admission is competitive; participants will be limited to 24. Limited financial aid is available.

The web page is:

http://home.ncifcrf.gov/ccr/lgd/geneticscourse/-congen_2004/index_2004.asp

or contact:

Ms. Jan Martenson, Course Coordinator, e-mail: noah-scrc@ncifcrf.gov NCI-Frederick, P.O. Box B Frederick, MD 21702-1201 Phone: 301/846-7513 FAX: 301/846-6327

Al Roca <roca@ncifcrf.gov>

Valencia AsexualOrigins Apr16-18

Second Announcement

Workshop "Origin and Spread of Asexuals" (16-18 April 2004; Valencia, Spain)

PARTNER-European Science Foundation

Presentation

The workshop "Origin and Spread of Asexuals" will be held 16-18 April 2004 in Valencia (Spain). The workshop is organized in the frame of PARThenogenesis NetwoRk (PARTNER; http://www.nioo.knaw.nl/-NETWORKS/PARTNER), a network funded by the European Science Foundation. The workshop is organized by Manuel Serra (University of Valencia) and Claudia Ricci (University of Milan). We address to young scientists starting an independent research career, post-docs and advanced graduate students for inviting them to attend the workshop. The workshop is aimed to study the origin of asexual reproduction from sexual ancestors and their maintenance and spread. The focus is on how molecular mechanisms, reproductive cytological mechanisms, life-history traits and population features may affect the origin and maintenance of asexuality. The workshop will stress the link between proximate and evolutionary causes of asexuality, using a comparative approach. As a related topic, the origin, advantages and maintenance of partial asexuality (e.g., cyclical parthenogenesis) will be addressed. The following topics will be considered: (1) Becoming asexual; (2) Cytological mechanisms to produce asexual eggs and seeds; (3) Avoiding genomic problems and evolving in the absence of sex (mutational load, capacity of asexuals to adapt to environmental novelties); (4) Partial asexuality: advantage and instability; (5) The fate of asexual taxa: dynamics aspects. The workshop will consist of 14 talks given by senior scientists (see below), followed by discussion sessions.

Site and schedule

The workshop site will be the residence of the University of Valencia "Colegio Mayor Rector Peset" (http://www.uv.es/cmrpeset/), located at Valencia downtown. Meals will be served in the workshop site. Accommodation will be provided also in the workshop site and in hostels at walking distance. The meeting will start on Friday, April 16, with a welcome lunch. Workshop sessions will run from the 15:00 h of Friday, April 16, to the 13:00 of Sunday, April 18. After the last session, the meeting will end with a farewell lunch.

Applications

Applications should include a short CV and a brief description of his/her current research topic (less than 400 words). The selection will be performed on the base of research record and topic, and the scope of the European network. The workshop organization will cover the accommodation costs in the facilities provided by the organization for the invited attendants, but cannot cover their travel expenses. Applications, preferably through e-mail, should be submitted before February 15, 2004, to

Manuel Serra (Manuel.Serra@uv.es) Institute Cavanilles of Biodiversity and Evolutionary Biology University of Valencia A.O. 2085 E46071-Valencia (Spain)

Expected speakers

* Bengt O. Bengtsson, Lund University, Sweden * Brian Charlesworth, University of Edinburgh, Scotland, UK * Charles E. King, Oregon State University, USA * Fabrice Vavre, Université Claude Bernard - LYON1, France * Graham Bell, McGill University, Canada * Hugh Loxdale, Rothamsted Research, United Kingdom * Isa Schoen, Royal Belgian Institute of Natural Sciences, Belgium * Jean-Christophe Simon, INRA, France * Koen Martens, University of Amsterdam, The Netherlands * Matthew Meselson, Harvard University, USA * Nico Michiels. University of Muenster, Germany * Peter van Dijk, Netherlands Institute of Ecology, Holland * Santiago Elena, Institute of Molecular and Cell Plant Biology, Spain * Valerio Scali, University of Bologna, Italy

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WoodsHole MolEvol Jul25-Aug6

Workshop on Molecular Evolution

http://workshop.molecularevolution.org/ Michael P. Cummings, Director

25 July - 6 August 2004 plus extended special topics session 6 August - 13 August 2003

Application Deadline 1 March 2004

The Workshop on Molecular Evolution has been the finest course of its type in the world since it was started in 1988. The Workshop consists of a series of lectures, demonstrations and computer laboratories that cover various aspects of molecular evolution. A distinguishing feature of the Workshop is a well-equipped computer laboratory with Linux workstations and servers for comparative analysis of molecular data. Authors and experts in the use of computer programs and packages such as Clustal W and Clustal X, FASTA, GCG, LAMARC, MrBayes, PAML, PAUP*, and PHYLIP provide demonstrations and consultations. This two-week program is designed for established investigators, postdoctoral fellows, and advanced graduate students with prior experience in molecular evolution and comparative genomics. Scientists with a strong interest in molecular evolution, systematics, and population genetics are encouraged to apply. Enrollment is limited to 60 students, and 15 students will be admitted to an extended topics session for the purpose of analyzing their research data sets. Many participants find the extended topics session to be especially useful.

Topics to be covered include:

* Databases and sequence matching: database searching: protein sequence versus protein structure; homology; mathematical, statistical, and theoretical aspects of sequence database searches * Phylogenetic analysis: theoretical, mathematical and statistical bases; sampling properties of sequence data; Bayesian analysis, hypothesis testing * Character analysis in a phylogenetic context: analysis of quantitative and discrete characters; hypothesis testing * Maximum likelihood

theory and practice in phylogenetics and population genetics: coalescent theory; maximum likelihood estimation of population genetic parameters * Bayesian methods in phylogenetic analysis * Molecular evolution integrated at different levels: population biology; biogeography; ecology; systematics and conservation * Molecular evolution and development: gene duplication and divergence; gene family organization; coordinated expression in evolution * Comparative genomics: genome content; genome structure; genome evolution * Transposable elements: types; history; evolutionary dynamics; as a major component of genomes

Preliminary List of Faculty -

Peter Beerli Michael Cummings Scott Edwards Jonathan Eisen Joseph Felsenstein Claire Fraser Mary Kuhner Paul Lewis Axel Meyer Michael Miyamoto William Pearson David Rand Margaret Riley Fredrik Ronquist David Swofford Steven Thompson Paul Turner Daniel Voytas Ziheng Yang Anne Yoder Shozo Yokoyama

Partial funding support for the Workshop comes from the National Science Foundation (NSF), National Aeronautics and Space Administration (NASA).

Fee: $1500 (room and board at no additional charge), plus an additional $750 for the extended topics session.

Application Form at http://www.mbl.edu/education/-admissions/applications/ – Michael P. Cummings Center for Bioinformatics and Computational Biology University of Maryland Agri/LFSc Surge Building #296 College Park, MD 20742-3360 USA mike@umiacs.umd.edu 301.405.9903 voice 301.314.1341 facsimile http://serine.umiacs.umd.edu/

Instructions

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

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

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

The message will be stored until the middle of the night (local time). At a predetermined time, the collected messages will be captured and then processed by programs and filters. So please do not expect an instant response.

Afterward

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