EvolDir

July 1, 2007

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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Albuquerque EvolutionaryPhysiology Jun6-10

A symposium on ???Evolutionary Physiology of Mammals??? will be held as part of the 87th Annual Meeting of the American Society of Mammalogists in Albuquerque, New Mexico (6-10 June, 2007).

Date of symposium: Saturday, June 9th, 3:30-5:30 pm

Speakers:

Dr. Ted Garland, UC Riverside "Phylogenetic approaches in mammalian evolutionary physiology"

Dr. Jay F. Storz, University of Nebraska "Gene duplication and the evolution of physiological pathways"

Dr. Roberto Nespolo, Universidad Austral de Chile "Quantitative genetic approaches in mammalian evolutionary physiology"

Dr. Jack Hayes, University of Nevada-Reno "Testing the aerobic capacity model for the evolution of endothermy"

For more details regarding the meeting see: http://asm007.unm.edu/ Jay F. Storz School of Biological Sciences University of Nebraska Lincoln, NE 68588 Phone: 402/472-1114 E-mail: jstorz2@unl.edu

http://www.biosci.unl.edu/faculty/Storz/index.html
Jay F Storz <jstorz2@unlnotes.unl.edu>

Boston Self-Adaptive Self-Organizing Systems Jul9-11

CALL FOR PARTICIPATION First IEEE International Conference on Self-Adaptive andSelf-Organizing Systems (SASO 2007) July 9-11, 2007Boston, Mass., USAhttp://projects.csail.mit.edu/saso2007/ Sponsored by IEEE Computer SocietyTechnical Co-Sponsors: ACM SIGOPS, ACM SIGART, IEEE SMC Society REGISTRATION DETAILS http://www.regonline.com/SASO_reg ADVANCE PROGRAM http://projects.csail.mit.edu/saso2007/program.html Sunday, July 8, 2007 Tutorials——— * "Global-to-Local Programming: Design and Analysis for Amorphous Computers" Radhika Nagpal and Daniel Yamins (Harvard University, USA) * "Introduction to Complex Systems and Applications to Engineering" Yaneer Bar-Yam (New England Complex Systems Institute, USA) * "Engineering Self-Organizing Applications" Sven A. Brueckner and H. Van Dyke Parunak (NewVectors LLC, USA) * "Peer-to-Peer Systems and Gossip Algorithms" Mark Jelasity (Hungarian Academy of Science and University of Szeged, Hungary)

Monday, July 9, 2007 Keynote Address 1————— "99% (Biological) Inspiration"Michael G. Hinchey, NASA, USA Research Track, Session 1: Design

Methodology,
Foundations————————————————
—-

“Novel Mathematics-Inspired Algorithms for Self-Adaptive Peer-to-Peer Computing” Steve Ko, Indranil Gupta (University of Illinois at Urbana Champaign, USA), Yookyung Jo (Cornell University, USA) * “Self-Organizing Replica Placement – A Case Study on Emergence” Klaus Herrmann (University of Stuttgart, Germany) * “A Space- and Time-Continuous Model of Self-Organizing Robot Swarms for Design Support” Heiko Hamann, Heinz Woern (University of Karlsruhe, Germany) * “A Nonlinear Multiagent System Designed for Swarm Intelligence: The Logistic MAS” Rodolphe Charrier, Francois Charpillet, Christine Bourjot (LORIA and Nancy University, France) Research Track, Session 2: Provocative
Ideas————————————————
“Text and Graphics Control on a Paintable Computer” William Butera (Intel, USA) * “Neural Network of a Cognitive Crow: An Interacting Map Based Architecture” Vishwanathan Mohan, Pietro Morasso (University of Genova, Italy) * “Evolution of Cooperative Information Gathering in Self-Replicating Digital Organisms” Benjamin Beckmann, Philip McKinley, David Knoester, Charles Ofria (Michigan State University, USA) Research Track, Session 3:
Synchronization/Desynchronization————————
————————

“Firefly-Inspired Heartbeat Synchronization in Overlay Networks” Ozalp Babaoglu, Toni Binci (University of Bologna, Italy), Mark Jelasity (Hungarian Academy of Science and University of Szeged, Hungary), Alberto Montresor (University of Trento, Italy) * “Desynchronization: The Theory of Self-Organizing Algorithms for Round-Robin Scheduling” Ankit Patel, Julius Degesys, Radhika Nagpal (Harvard University, USA) * “Clustering Distributed Energy Resources for Large-Scale Demand Management” Elth Ogston (Vrije Universiteit Amsterdam, The Netherlands), Astrid Zeman, Mikhail Prokopenko, Geoffrey James (CSIRO ICT Center, Australia) Plenary Panel 1———— “An Industrial Perspective on Self-Adaptive and Self-OrganizingSystems”Panel Chair: J.P. Martin-Flatin, NetExpert, SwitzerlandPanelists: * Bruno Klauser, Cisco, Switzerland * Ashvin Sanghvi, Microsoft, USA * Fabrice Saffre, BT, UK * Mark Berman, BBN Technologies, USA * Gregory T. Sullivan, BAE Systems, USA * Scott Alexander, Telcordia, USA

Tuesday, July 10, 2007 Research Track, Session 4: P2P Systems————————————————
“Merging Intra-Planetary Index Structures: Decentralized Bootstrapping of Overlays” Anwitaman Datta (National Technical University, Singapore) * “An Amortized Tit-for-Tat Protocol for Exchanging Bandwidth instead of Content in P2P Networks” Pawel Garbacki, Dick Epema (Delft University of Technology, The Netherlands), Maarten van Steen (Vrije Universiteit Amsterdam, The Netherlands) * “Aggregation Dynamics in Service Overlay Networks” Pietro Michiardi (Institut Eurecom, France), Paul Marrow, Richard Tateson, Fabrice Saffre (BT, UK) Research Track, Session 5: Data Collection and
Aggregation————————————————
—-

“Shruti: A Self-Tuning Hierarchical Aggregation System” Praveen Yalagandula (HP Labs, USA), Mike Dahlin (University of Texas at Austin, USA) * “An Autonomy Oriented Computing (AOC) Approach to Distributed Network Community Mining” Bo Yang (Jilin University, P.R. China), Jiming Liu (University of Windsor, Canada) * “Self-Organized Data-Gathering Scheme for Multi-Sink Sensor Networks Inspired by Swarm Intelligence” Yuichi Kiri, Masashi Sugano, Masayuki Murata (Osaka University,

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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

Cambridge SystemsBiol Jul13

Population and Evolutionary Approaches to Biological Systems

A One Day Symposium by the Cambridge Systems Biology Centre

Friday 13th July Lecture Theatre, Department of Biochemistry (Sanger (new) Building, Tennis Court Road)

Register before by 10th July at http://www.sysbiol.cam.ac.uk/PopEvoMeet Programme includes

Paul Flicek, European Bioinformatics Institute, Hinxton Individual variation identifies evolutionary patterns between species

Francois Balloux, Department of Genetics, Cambridge Worldwide distribution of human genetic diversity

Andrea Manica, Department of Zoology, Cambridge Worldwide distribution of human phenotypic diversity

Derek Smith, Department of Zoology, Cambridge The systems biology of influenza

Julia Gog, Applied Maths and Theoretical Physics, Cambridge Disease dynamics at different scales

Michael Akam, Department of Zoology, Cambridge Evolving mechanisms of pattern formation: Segmentation in arthropods

Johannes Jaeger, Department of Zoology, Cambridge Developmental and evolutionary dynamics of the gap gene system.

Chris Gilligan, Department of Plant Sciences, Cambridge Disease in a changing landscape

Balázs Papp, University of Manchester & BRC Szeged A systems approach to understand the condition dependency of genetic interactions.

Steve Oliver, University of Manchester & Department of Biochemistry, Cambridge Genomic approaches to speciation and fitness: old wines in new bottles.

Organisers Steve Russell (s.russell at gen.cam.ac.uk) and François Balloux (fb255 at mole.bio.cam.ac.uk)

fb255@mole.bio.cam.ac.uk fb255@mole.bio.cam.ac.uk

Edinburgh SpeciationSymposium Aug30

SPECIATION SYMPOSIUM; 30th August 2007; Edinburgh, UK

Speakers: Jim Mallet (UC London); Alfried Vogler (Imperial London); Nick Barton (Edinburgh); Christian Lexer (Kew); H Peter Comes (Salzburg); Mike Ritchie (St Andrews); Roger Butlin (Sheffield); John Willis (Duke); Salvatore Cozzolino (Naples); Simon Hiscock (Bristol); Chris Jiggins (Cambridge); Peter Linder (Zurich)

Speciation Symposium programme: www.systass.org/biennial2007/symposia.shtml#speciation

Hosted at the Systematics Association Biennial Conference

CLOSING DATE FOR REGISTRATION: 30 JUNE

Late registration fee applies after this date

Registration and further details: www.systass.org/biennial2007

Sponsors: Systematics Association, Linnean Society, Genetics Society, Molecular Ecology, Botanical Society of the British Isles.

Jess Barrett <JBarrett@rbge.ac.uk>

HarvardU IslandBiogeography Oct5-6

Harvard University's Center for the Environment and Museum of Comparative Zoology are pleased to announce a symposium:

The Theory of Island Biogeography at 40: Impacts and Prospects

to be held October 5-6, 2007.

Speakers:

Sonya Clegg Brian Farrell Peter Grant and Rosemary Grant Rosemary Gillespie Ilkka Hanski Robert Holt Stephen Hubbell Mark Lomolino Jonathan Losos Robert Ricklefs Thomas Schoener Daniel Simberloff John Terborgh Mark Vellend Robert Whittaker Edward O. Wilson

For more information: http://www.mcz.harvard.edu/events/island_biogeography/

"Jonathan B. Losos" <jlosos@oeb.harvard.edu>

Marseilles 11thEvolBiol Sep19-21 Online

Dear colleagues,

As you probably know, the 11th Evolutionary Biology Meeting will take place in Marseilles on September 19-21.

The first accepted abstracts are online! http://www.up.univ-mrs.fr/evol-cgr/first_accepted_abstracts.html Do not hesitate to see our website for more information: registration, hotels, former programmes... http://www.up.univ-mrs.fr/evol-cgr/ all the best,

– Julie Perrot Logistical Organisation Committee egee@up.univ-mrs.fr

EA 3781 Evolution Biologique Université d'Aix Marseille I - case 19 Centre St Charles 3 Place Victor Hugo 13331 Marseille Cedex 3 33491106489 http://www.up.univ-mrs.fr/evol We are organizing the 11th Evolutionary Biology Meeting at Marseilles - 19-21 September 2007 http://www.evolutionary-biology.org http://www.up.univ-mrs.fr/evol-cgr/ egee@up.univ-mrs.fr

Nairobi MEEGID IX Oct30-Nov1

MEEGID IX Nairobi, Kenya. 30th October-1st November 2008. Call for conferences/symposia proposals and papers

The 9th International Meeting "Molecular Epidemiology and Evolutionary Genetics of Infectious Diseases" (MEEGID IX) will be held in Nairobi, Kenya, 30th October-1st November 2008. As for the 8 first MEEGID meetings, it will be co-organized by the Centers for Disease Control and Prevention (CDC; http://www.cdc.gov/) in Atlanta and the Institut de Recherche pour le Développement (IRD; http://www.ird.fr/) in France. The meeting will be hosted by ICIPE (http://www.icipe.org/), which will be co-organizer, together with KEMRI (http://www.kemri.org/), ILRI (http://www.ilri.org/), CDC Kenya (http://www.cdc.gov/malaria/cdcactivities/kenya.htm) and the University of Nairobi (http://www.uonbi.ac.ke/).

The MEEGID meetings are organized in synergy with the new journal Infection, Genetics and Evolution (Elsevier; http://www.elsevier.com/locate/meegid), which scientific topic is identical to that of the MEEGID. Launched only 6 years ago, Infection, Genetics and Evolution is now published with 6 issues per year, and is covered by Medline and Index Medicus, starting from the 1st issue. It has been quoted 3.5/5.0 ("very good") by the US National Library of Medicine. It is now covered by ISI and an official impact index will be available soon. Nonofficial 2005 impact factor has been evaluated by Elsevier at 3.554 (http://www.th.ird.fr/downloads/edito.pdf).

Communications on genetics, genomics, proteomics, population biology, mathematical modelling, bioinformatics are welcome. They can deal with the host, the pathogen, or the vector in case of vector-borne diseases. Papers considering host + pathogen or pathogen + vector (co-evolution) are particularly encouraged. All pathogens are within the scope of MEEGID: viruses, parasitic protozoa, helminths, fungal organisms, prion. All infectious models can be considered, including those of veterinary or agronomical relevance.

The papers communicated for MEEGID IX will be published in a special issue of Infection, Genetics and Evolution, as already done for MEEGID VI (Paris, July 2002) and MEEGID VIII (Bangkok, Thailand, November 2006). MEEGID IX will include 10-15 plenary lectures, about 20 specialized symposia, 12-15 "express-debates" (20 mn presentation by only one speaker followed by 40 mn free discussion) and several poster sessions.

Special emphasis through plenary lectures and symposia will be given to health problems of particular interest to Africa: AIDS, malaria, tuberculosis, sleeping sickness, ebola, cattle and crop pathogens. Plenary lectures and symposia will also deal with transversal topics such as population genetics or species concepts. The congress is open to proposals of conferences and symposia.

Awards will be attributed to the best communication, the best communication by a student and the best communication by a scientist from the Southern World on a problem specifically relevant to these areas. Each prizewinner will be offered a free 2-year membership to Infection, Genetics and Evolution.

Abstract submission deadline: 30th July 2008.

Registration Fee: 200.00 euros or equivalent in other currencies; Reduced fees upon request for scientists from developing countries who don't have international funds. Students are exempted from registration fees.

Preliminary registration and abstract submission are possible by email (below). Please provide last name, first name, title, gender, nationality, scientific speciality, professional address, phone, fax, email and website if available. Abstract should follow the format recommended for Infection, Genetics and Evolution for list of references, reference citations, etc. and should not exceed 300 words. Please express your request, either orgal communication or poster.

More information available soon at http://www.th.ird.fr/meegid/meegid.htm Contact:

Michel Tibayrenc, MD, PhD Editor -in-chief Infection, Genetics and Evolution (Elsevier) http://www.elsevier.com/locate/meegid IRD representative in Thailand IRD Representative Office French Embassy 29, Thanon Sathorn Tai, Bangkok 10120, Thailand Tel : + (66 2) 627 2190 Fax : + (66 2) 627 2194 Cel: + (66 8 1) 82 64 056 E-mail : Michel.Tibayrenc@ird.fr Website

: http://www.th.ird.fr Michel.Tibayrenc@ird.fr

PoitiersFrance PopGenetics Aug27-30

dear colleagues,

below the announcement for French scientists wondering to join the annual national meeting PPD

La date de cloture des inscriptions au PPD 2007 est fixée au vendredi 25 juin, les inscriptions se font en ligne sur le http://ppd2007.conference.univ-poitiers.fr Le comité d'organisation

catherine.souty@univ-poitiers.fr

RoyalBotGarden Edinburgh Systematcis Aug28-31

Biennial Conference of the Systematics Association

Royal Botanic Garden Edinburgh, UK

28 - 31 August 2007

Closing date for registration and submission of abstracts: 30th June 2007

Follow the link for further details and registration:

www.systass.org/biennial2007 **Please note that accommodation books up quickly in Edinburgh during the summer**

Meeting information The Biennial conferences of the Systematics Association provide a forum for systematists to present and discuss their research. The format will be a mixture of both open sessions and focused thematic symposia.

Open sessions Contributed papers can be on any topic in systematics. We especially encourage talks and posters from research students and younger postdoctoral fellows.

Thematic sessions Speciation (organisers Richard Abbott and Pete Hollingsworth) Speakers: Jim Mallet (UC London); Alfried Vogler (Imperial London); Nick Barton (Edinburgh); Christian Lexer (Kew); H Peter Comes (Salzburg); Mike Ritchie (St Andrews); Roger Butlin (Sheffield); John Willis (Duke); Salvatore Cozzolino (Naples); Simon Hiscock (Bristol); Chris Jiggins (Cambridge); Peter Linder (Zurich)

Floras and Faunas: Descriptive Taxonomy Serving Biodiversity (organisers: Mark Watson and Christopher Lyal) Speakers include: Bill Baker (Kew); Steve Brooks (NHM London); Ben Collen (Institute of Zoology London); Jane Conner (Timber Press); Jan Dick (CEH Edinburgh); Tony Gutierrez (US Government); Christoph Häuser (SMN Stuttgart); Donald Holbern (GBIF); Stephen Jury (Reading); Sandy Knapp (NHM London); Della Lindsay (Kew); Chris Lyal (NHM London); Tony Miller (RBG Edinburgh); Dave Minter (CABI); Rod Page (Glasgow); Alan Paton (Kew); Mark Watson (RBG Edinburgh); Anna Weitzman (Smithsonian Institute).

Also included, an evening session with demonstrations of projects and systems.

UK Research Councils Systematics Symposium (organisers Amanda Read, Sarah Collinge and Pete Hollingsworth) Speakers: Sandie Baldauf (York); Mark Wilkinson (NHM London); Roger Thorpe (Bangor); Tim Littlewood (NHM London); Lee Hastie (Aberdeen); Malcolm Scoble (NHM London)

'How-to' lectures on emerging technologies and techniques: Putting time back into molecular phylogenetics (Andrew Rambaut, Edinburgh) Geophylogenies: threading evolutionary graphs through earth history (David Kidd, NESCent, Durham NC) Evo-devo of non-model organisms (Catherine Kidner RBG Edinburgh)

Meeting Sponsors: Systematics Association, Linnean Society, Genetics Society, Biotechnology and Biological Sciences Research Council, Natural Environment Research Council

Jess Barrett <JBarrett@rbge.ac.uk>

Taipei BarcodeOfLife Sep16-21 Deadline

If you're thinking about attending the Second International Barcode of Life Conference in Taipei during the week of 17 September, 1 July is an important date.

July 1st is the:

* Deadline for submission of abstracts

* Deadline for applications for travel bursaries for developing country participants

* Last day to register with reduced conference fees

All information and on-line forms are available at the Conference website: www.dnabarcodes2007.org <http://www.dnabarcodes2007.org/> .

We hope to see you in Taipei in September!

Regards to all -

David

David E. Schindel, Executive Secretary

Consortium for the Barcode of Life 202/633-0812; fax 202/633-2938; portable 202/557-1149 Email: SchindelD@si.edu CBOL WEBSITE: http://www.barcoding.si.edu <http://www.barcoding.si.edu Office and overnight delivery address:

National Museum of Natural History Room CE-119 10th & Constitution Avenue, NW Washington, DC 20560

Postal mailing address:

National Museum of Natural History Smithsonian Institution P.O. Box 37012, MRC-105 Washington, DC 20013-7012

schindeld@si.edu schindeld@si.edu

Taipei BarcodeOfLife Sep16-21 DeadlineExtension

The Consortium for the Barcode of Life is extending the deadline for submission of abstracts and applications for travel bursaries until 1 July 2007. Applicants will be informed of decisions by 15 July and the final conference program will be distributed at that time.

Information on the conference and the online systems for submitting abstracts and bursary applications can be found on the conference website at www.dnabarcodes2007.org.

Some people have encountered difficulties when trying to submit abstracts or bursary applications. We apologize for these problems and hope that these software issues have been corrected. Please contact Agnes Balla (ballaa@si.edu) if these problems persist.

Please don't hesitate to contact me if you have questions concerning the conference.

Best regards,

David

David E. Schindel, Executive Secretary Consortium for the Barcode of Life 202/633-0812; fax 202/633-2938; portable 202/557-1149 Email: SchindelD@si.edu CBOL WEBSITE: http://www.barcoding.si.edu

Office and overnight delivery address: National Museum of Natural History Room CE-119 10th & Constitution Avenue, NW Washington, DC 20560 Postal mailing address National Museum of Natural History Smithsonian Institution P.O. Box 37012, MRC-105 Washington, DC 20013-7012

schindeld@si.edu

UGuelph AppliedEvolution May15-16 4

REMINDER: Approximately 2 weeks left to register for the 2007 Peter Yodzis Colloquium in Fundamental Ecology

"Applied Evolution: Understanding the Past, Predicting the Future"

May 15th and 16th 2007 University of Guelph, Guelph, Ontario, Canada

The colloquium will focus on the mechanistic basis of adaptation and the potential to predict adaptive evolution in pure and practical applications. There will be a series of keynote lectures and an open poster session, all at a pace conducive to conversation and interaction.

Confirmed keynote lecturers include:

Graham Bell (McGill University)–"Adaptation of algae to elevated CO2" Michael Lynch (Indiana University)–"Evolutionary genetics/genomics of Daphnia" David Mindell (University of Michigan)–"Applied evolution in understanding disease, criminal justice and cultural change: what the public should know" Patricia Schulte (University of British Columbia)–"Mechanistic basis of adaptation to environmental change: lessons from a small fish" Ruth Shaw (University of Minnesota)–"Inferences about selection: a general solution to an empirical challenge" John Willis (Duke University)–"Genetic analysis of adaptation and reproductive isolation in Mimulus"

For information, go to

http://www.ecologycolloquia.uoguelph.ca/main.shtml

For credit card registration ($55 for students, $130 for non-students, both including GST), go to

http://www.peopleware.net/index.cfm?siteID=-323&eventDisp=07YODZIS

Christina (Chris) Caruso Assistant Professor Department of Integrative Biology University of Guelph Axelrod Building 50 Stone Road East Guelph, Ontario N1G 2W1 CANADA 519-824-4120 ext. 52030 carusoc@uoguelph.ca

carusoc@uoguelph.ca carusoc@uoguelph.ca

UGuelph AppliedEvolution May15-16 5

REMINDER: Approximately ONE WEEK left to register for the 2007 Peter Yodzis Colloquium in Fundamental Ecology

“Applied Evolution: Understanding the Past, Predicting the Future”

May 15th and 16th 2007 University of Guelph, Guelph, Ontario, Canada ponsored by the University of Guelph and Blackwell Publishing

The colloquium will focus on the mechanistic basis of adaptation and the potential to predict adaptive evolution in pure and practical applications. There will be a series of keynote lectures and an open poster session, all at a pace conducive to conversation and interaction. In addition, Blackwell (publishers of the new journal Evolutionary Applications) is sponsoring prizes for the best posters ($150 for first place, $50 for second place). Consequently, we have extended the deadine for submitting a poster title until the end of the week (May 11th).

Confirmed keynote lecturers include:

Graham Bell (McGill University)–“Adaptation of algae to elevated CO2” Michael Lynch (Indiana University)–“Origins of Genome Architecture” David Mindell (University of Michigan)–“Applied evolution in understanding disease, criminal justice and cultural change: what the public should know” Patricia Schulte (University of British Columbia)–“Mechanistic basis of adaptation to environmental change: lessons from a small fish” Ruth Shaw (University of Minnesota)–“Inferences about selection: a general solution to an empirical challenge” John Willis (Duke University)–“Genetic analysis of adaptation and reproductive isolation in Mimulus”

For information, go to

http://www.ecologycolloquia.uoguelph.ca/main.shtml For credit card registration ($55 for students, $130 for non-students, both including GST), go to

http://www.peopleware.net/index.cfm?siteID=-323&eventDisp=07YODZIS

To submit a poster title, go to

http://www.ecologycolloquia.uoguelph.ca/-postercall.shtml Christina (Chris) Caruso Assistant Professor Department of Integrative Biology University of Guelph Axelrod Building 50 Stone Road East Guelph, Ontario N1G 2W1 CANADA 519-824-4120 ext. 52030 carusoc@uoguelph.ca

UWarwick PopGenetics Dec17

Dear Colleagues,

The Population Genetics Group meeting (“the popgroup”) this year will be held on Monday 17th of December to Thursday 20th of December at the University of Warwick conference centre, Coventry, West Midlands, United Kingdom. Further details can be found on the website: http://www.popgroup.org/ <http://-www.popgroup.org/>

Best regards, Dmitry

Dr D.A.Filatov Senior Lecturer in Evolutionary Genetics School of Biosciences University of Birmingham Edgbaston, Birmingham B15 2TT United Kingdom

Dmitry Filatov <d.filatov@bham.ac.uk>

UdoPorto Biodiversity Jul2-3

Conference/ Meeting

TiBE - Trends in Biodiversity & Evolution 2007 Topic: Hybridization & Evolution 2-3 July, 2007 Campus Agrário de Vairão CIBIO, Universidade do Porto

TiBE is an annual meeting organized by InBio, the Portuguese Research Network in Biodiversity and Evolutionary Biology (CBA-University of Lisbon; CIBIO-University of Porto; CEABN-Agronomic Institute of

Lisbon), that aims to join senior researchers, postgraduate and graduate students in Biological Sciences, and promote a relaxing but insightful discussion about themes on Biodiversity and Evolution. Each year a specific subject will be chosen, and recognized senior scientists are invited to report their views, opinions and novel results. Young researchers will also be invited to participate and show their recent and innovative work.

TiBE 2007 will be organized by CIBIO, the Center in Biodiversity and Genetic Resources at the University of Porto, and will be devoted to ?Hybridization & Evolution? which has received considerable attention in recent years by evolutionary biologists, and has been regarded as a unique opportunity to understand evolutionary processes in many groups of organisms.

We hope that the University Campus of Vairão, located in a beautiful rural area north of Porto, will provide an excellent atmosphere for such scientific forum in one of the most interesting and stimulating areas of Biology.

Invited speakers Michael Arnold, Department of Genetics, University of Georgia, USA Fred Allendorf, University of Montana, USA Manuela Coelho, Universidade de Lisboa, Portugal

More Information by e-mail: tibe@mail.icav.up.pt or at http://cibio.up.pt/ <http://cibio.up.pt/> – Paulo Celio Alves

1. CIBIO, Centro de Investigação em Biodiversidade e Recursos Genéticos Universidade do Porto Campus Agrario de Vairao 4485-661, VAIRAO Vila do Conde, PORTUGAL Tel: ++351252660411 Fax: ++351252661780

2. Dep. Zoologia-Antropologia, Faculdade de Ciencias do Porto Universidade do Porto 4099-002 Porto, PORTUGAL Tel: ++351223401400

e-mail: pcalves@fc.up.pt

Paulo Celio Alves <pcalves@fc.up.pt>

Zurich SexualReproduction Sep14-15

EU Marie Curie Research and Training Network SexAseX organizes a two-day conference on

PARADOX OF SEXUAL REPRODUCTION: THEORY AND DATA

The conference focuses on the empirical approaches to the test hypotheses for maintenance of sex and how the recent data interact with the theory. Members of the SexAseX network will present the results of the network project.

Invited speakers include: Sebastian Bonhoffer (ETH-Zürich), Arjan de Visser (Wageningen University), Bas Ibelings (EAWAG), Hinrich Schulenburg (University of Tübingen), Thomas D'Souza (University of Tübingen), Nico Michiels (University of Tübingen), Christoph Vorburger (University of Zürich), Ellen Decaestecker (K. U. Leuven), Jochen Vandekerkhove (SexAseX), Dunja Lamatsch (SexAseX), Maria Joao Martins (SexAseX), Saskia Bode (SexAseX), Oliver Schmit (SexAseX), Sofia Adolfsson (SexAseX), Andrew Park (SexAseX), Radka Symonova (SexAseX) and Ruza Bruvo (SexAseX).

The seminar takes place in EAWAG Dübendorf (close to Zürich, Switzerland) on 14th and 15th of September. For exact location, visit Eawag homepage http://www.eawag.ch/kuerze/standorte/anreise_dd/index_EN If you are interested in participating, please send an email to Christiane Rapin (christiane.rapin@eawag.ch). Registered participants are welcome to present a poster, in that case please send the title of your poster with your registration. Participation is free.

Jukka.Jokela@eawag.ch Jukka.Jokela@eawag.ch

GradStudentPositions

Amsterdam YellowcressEvol 10
DiseaseDynamics 11
EAWAG Switzerland FrogAdaptation 12
ETH Zurich 3 PopGenet 12
ETH Zurich PlantEvol 13
INRA Rennes AphidEvolGenomics 14
Iceland subterranean amphipods 14
ImperialCollegeLondon PlantSpeciation 15
Innsbruck HumanHistory 16
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TrinityCollege IrishBiodiversity 20
UArkansas EnvGenomics 21
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UPotsdam EvolEcolModelling 27
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Amsterdam YellowcressEvol

The following position for a PhD student is available in Amsterdam, please bring it to the attention to prospective candidates. See also http://www.science.uva.nl/ibed/vacancies.cfm/3E2203AA-1321-B0BE-68890EC278020B44 Universiteit van Amsterdam The Universiteit van Amsterdam (UvA) is a university with an internationally acclaimed profile, located at the heart of the Dutch capital. As well as a world centre for business and research, Amsterdam is a hub of cultural and media activities. The Universiteit van Amsterdam is a member of the League of European Research Universities. The Faculty of Science at the Universiteit van Amsterdam is one of Europes foremost institutions of higher education and research in its chosen fields of specialization. It plays an active role in international science networks and collaborates with universities and industry. The Faculty has approximately 2,000 students and 1,500 staff members spread over four departments and ten research institutes. Each institute has its own research programme, a substantial part of which is externally funded by the Netherlands Organization for Scientific Research (NWO), the Dutch government, the EU and various private enterprises. The Institute of Biodiversity and Ecosystem Dynamics (IBED) is one of the ten research institutes of the Faculty of Sciences.

In the context of IBEDs participation in the Centre for Wetland Ecology there is a vacancy for a PhD student 1,0 fte vacancy number 07-1038 For both internal and external candidates project: Diversity and adaptation in the genus Yellow Cress (Rorippa) in response to flooding

When faced with environmental stress, plants may either try to avoid the environmental adversity or try to tolerate it while it lasts. An avoidancetolerance continuum may therefore provide an important axis of specialisation underlying the diversity of populations and communities. Our main objective is to investigate whether an avoidance-tolerance trade-off in response to flooding underlies genetic diversity in the genus Rorippa. More specifically, the following questions will be addressed: 1) How do Rorippa plants respond to deep and shallow flooding and how do tolerance- and avoidance related traits affect growth under both types of flooding? We will expose different genotypes of Rorippa sylvestris and Rorippa amphibia and their hybrids to clear and deep/turbid flood water. In each treatment we will measure traits related to tolerance and avoidance strategy, assess how they are related to each other, and how they affect plant performance. 2) Is the variation in these adaptive responses related to variation in (expression of) key genes that are known to be involved in flooding responses? We will link the adaptive responses to variation in expression of candidate genes, building forth on the existing knowledge on Arabidopsis thaliana. We will also assess the expression of the candidate genes during submergence in the field. 3) To which extent can variation in the selected candidate genes explain current distribution of Rorippa along flooding gradients? To test if selection on tolerance traits predominates over other, unknown, selection forces and demographic processes, we will compare genetic variation in putative tolerance genes with selectively neutral markers in natural Rorippa populations encompassing a broad geographical range.

Tasks The department where PhD is going to work is the Institute for Biodiversity and Ecosystem Dynamics. IBED research covers a wide range of subjects, both in pure fundamental and in applied research. Research is directed to the development of fundamental knowledge of the dynamics of ecosystems at all relevant levels, from genes to communities. Common to all IBED research is a multidisciplinary approach to the study of the interactions among organisms and between organisms and their environment, and the emergent dynamics at different spatial and temporal scales. Strategic research concerns topics such as sustainable harvesting, climate change, desertification, prevention of toxic algal blooms, conservation of endangered species, and the potential impact of the introduction of transgenic crops. The Centre for Wetland Ecology is a partnership of the Netherlands Institute of Ecology (NIOO-KNAW), Radboud University Nijmegen (RU), Utrecht University (UU) and the University of Amsterdam (UvA). It is the main research centre for wetland ecology in the Netherlands. Its mission is twofold: (i) increase the fundamental knowledge of the functioning of wetlands and shallow lakes and the of the organisms they contain, and (ii) exploit and utilize this knowledge in order to bring solutions to the many problems that such ecosystems are faced with today. The concentration of knowledge on wetland functioning embodied in the CWE

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DiseaseDynamics

Phd project: Dynamics of infectious diseases: mathematical modelling and experiments

Lelystad, The Netherlands

Wageningen University, Department of Animal Sciences

Job description

This research project aims to obtain a better understanding of the disease transmission during outbreaks of highly transmissible diseases in livestock. The research team where this project will be carried out has developed experimental methods and mathematical modelling approaches for studying disease transmission. Both these experiments and the mathematical modelling play an important role in present-day thinking about control measures against disease spread. This PhD project aims to expand the existing experimental methods and modelling approaches to situations where transmission occurs over some distance, for example between cages, between stables, or between farms. The PhD student will be conducting experiments and develop the models to analyze the experimental results.

This research project is funded by the Ministry of Agriculture, Nature and Food Quality. The relevance to the Ministry lies in its need to design well-founded intervention strategies for combating epidemic spread of highly transmissible diseases in livestock, such as avian influenza, classical swine fever and foot-and-mouth disease.

This research will be carried out in Lelystad, the Netherlands, at the Quantitative Veterinary Epidemiology cluster of the Division of Infectious Diseases of the Animal Sciences Group (ASG), where experts both in mathematical modelling and in conducting transmission experiments will provide guidance. The project will be carried out under supervision of Prof. dr ir. M.C.M. de Jong, head of the Quantitative Veterinary Epidemiology group at Wageningen University, also part of ASG.

Requirements

University Graduate

with an interest in quantitative approaches in infectious disease epidemiology, holding an MSc degree in Biology, Animal Science or Veterinary Medicine. Candidates with experience in theoretical biology, evolutionary biology and/or population biology are especially encouraged to apply.

Organization

Wageningen University, Department of Animal Sciences Quantitative Veterinary Epidemiology

The PhD student will be employed by Wageningen University and based with the Animal Sciences Group (ASG) in Lelystad, The Netherlands

Conditions of employment:

We offer you a full-time position for a period of one year with a possibility of extension for 3 years. Gross salary per month â¬1956, $-inthefirstyearrisingto$â¬2502, $-permonthinthefourthyear$

Employment basis: Temporary for specified period

Duration of the contract: 1 year + 3 years

Maximum hours per week: 38

Additional Information

Additional information about the vacancy can be obtained from:

prof.dr.ir. M.C.M. de jong

Telephone number: +31 317 482012

E-mail address: mart.dejong@wur.nl

Application

You can apply for this job before 07-07-2007 by sending your application to:

Wageningen University, Department of Animal Sciences

Marijkeweg 40, 6709 PG Wageningen

S.P. van Ee

Postbus 338

6700 AH Wageningen

E-mail address: sandra.vanee@wur.nl

When applying for this job always mention the vacancy number AT DIE 2007-013.

EAWAG Switzerland FrogAdaptation

Eawag is the Swiss Federal Institute for Aquatic Science and Technology, a Swiss-based and internationally operating aquatic research institute within the ETH domain

The department of Aquatic Ecology (Dr Katja Räsänen, ETH-Zurich and Eawag) has an opening for a

PhD student for studies on adaptive divergence of Rana arvalis in response to acidification

The project investigates the relationship between selection, gene flow and adaptive maternal effects in natural populations of the moor frog (Rana arvalis) in Sweden, and is conducted in collaboration with Dr Anssi Laurila, EBC, Uppsala University, Sweden. The work involves field surveys, laboratory experiments and molecular genetics. The student will be based at Eawag, with annual visits to Sweden.

A diploma or M.Sc. (or equivalent) degree in biology or related area is mandatory. The ideal candidate has a strong interest in evolutionary ecology, is independent and works well in a team. Experience in molecular genetics and fieldwork is desirable. This Swiss National Science foundation position is funded for three years and will be filled as soon as a good candidate is found (target date 1 September 2007).

The Department of Aquatic Ecology situates in Duebendorf (near Zurich) and offers a dynamic environment with broad expertise in ecology and evolution. The student will also interact with graduate students in the group of Prof. Jukka Jokela as well as at the Institute of Integrative Biology, ETH (http://www.ibz.ethz.ch/index_EN). The working language is English.

The applicant should send an application letter with a statement of research interests and relevant experience, curriculum vitae with a list of publications (if any), copies of academic qualifications and the names and e-mail addresses of three referees.

For further information, consult www.eawag.ch <http://www.eawag.ch/> or contact Katja Räsänen (katja.rasanen@eawag.ch).

Please submit your application by 13 July 2007 to Sandra Isenring, Eawag, Human Resources, P.O. Box 611, 8600 Dübendorf or Email recruiting@eawag.ch.

Katja Rasanen <katja.raesaenen@eawag.ch>

ETH Zurich 3 PopGenet

Three funded PhD studentships in Population Ecology and Population Genetics at the Professorship of Ecosystem Management, ETH Zurich, Switzerland.

Title: Integrating genetic diversity and phenotypic plasticity into plant population responses to climate change in the Alps

Start Date: January 2008

The Professorship of Ecosystem Management is offering three PhD positions in Plant Ecology and Ecological Genetics to address the relative importance of intrinsic adaptive variation, local (pre-) adaptation and phenotypic plasticity to Alpine plant populations abilities to adapt to climate change.

All three projects will be supervised by Prof. Dr. Jaboury Ghazoul, Dr. Andrea R. Pluess and Dr. Chris Kettle, and will form part of the BIOCHANGE platform at ETH Zurich.

*Project: * Alpine plant populations are predicted to shift to higher elevations in response to climate change. Under such conditions core populations will move to higher elevations currently occupied by peripheral populations occupying the present species range limits. Should conservation efforts prioritize the current core populations which are predicted to contain greater genetic diversity or small isolated peripheral populations?

We will investigate the relative importance of intrinsic adaptive variation, local (pre-) adaptation and phenotypic plasticity to Alpine plant populations abilities to adapt to climate change. Key questions include: 1) Does local adaptation and phenotypic plasticity in high-altitude peripheral populations infer an advantage over core populations under predicted climate change scenarios? 2) Do small peripheral populations which are predicted to have lower genetic diversity than large central populations, have reduced adaptive potential? 3) Does gene flow via pollen between core and peripheral populations undermine local adaptation of peripheral populations and can this lead to outbreeding depression. These questions will be addressed using field-based reciprocal transplant experiments, experimental populations in climate-controlled chambers, artificial inter-population breeding experiments and direct and indirect measures of gene flow using molecular markers.

Requirements: We are seeking three highly motivated applicants, with a desire to work on the ecology and genetics of alpine plants in the context of climate change. Applicants should have a B.Sc and M.Sc degree, preferably with experience in experimental population biology, statistics, and ideally molecular work. Excellent spoken and written English is required, and German would be highly advantageous though not strictly necessary. Applicants should enjoy working both in the field (Swiss pre-alpine and alpine area) and in the laboratory. The three PhD positions will be part of a team of researchers working on the general theme of plant responses to climate change in alpine systems, and will also be members of the Ecosystem Management group, led by Prof. Jaboury Ghazoul. Therefore, we place a strong emphasis on cooperation and team work. Requests for additional information on the three positions offered, or other informal enquiries, should be made to Dr. Pluess andrea.pluess(at)env.ethz.ch, tel: +41 (0)44 632 89 75. Information about the research group can be found at http://www.ecology.ethz.ch/ *Conditions of Employment:* Three years appointment at ETH, Zurich. Starting Salary: minimum 37,600 Swiss Francs per year.

*Application: * Please send a letter of motivation, CV and names and addresses of two academic referees to Dr. Andrea Pluess, by e-Mail (andrea.pluess(at)env.ethz.ch).

Deadline: 10th July 2007

chris.kettle@env.ethz.ch chris.kettle@env.ethz.ch

ETH Zurich PlantEvol

ETH Zurich, Switzerland PhD position in Evolutionary Ecology / Plant Mating System Evolution

A 3-year graduate position is available at the Institute of Integrative Biology, ETH Zurich, to work on plant mating system evolution. The project seeks to understand the effect of the mating system on the genetic architecture of morphological and life history traits and on the ability to adapt to a changing environment.

Project description: Studies of plant mating systems have long focused on the evolutionary advantages and disadvantages of inbreeding and outbreeding. The project reverses the chain of causation to ask how the mating system affects the genetic composition of a population. The research involves a combination of field surveys of realized mating systems in natural populations and assessments of genetic variance components for a set of ecologically relevant traits. The work includes crossing experiments, molecular marker techniques and quantitative genetics analysis.

The Institute of Integrative Biology consists of a dozen groups working in diverse fields of Ecology and Evolution. For more information, contact Yvonne Willi (yvonne.willi@agrl.ethz.ch <mailto:yvonne.willi@agrl.ethz.ch>) or see http://www.ibz.ethz.ch/ and http://www.path.ethz.ch/ The applicant is expected to have a University degree in Natural Sciences which allows entering a PhD program, and very good organizational, analytical and writing skills. Motivated applicants should submit a 1 page letter that summarizes interests and relevant experience, CV including score transcripts, and contact information for 3 references (all as PDFs) to yvonne.willi@agrl.ethz.ch <mailto:yvonne.willi@agrl.ethz.ch>

Yearly salary: CHF 34? -40?000.-

Closing date: August 1, 2007

Yvonne Willi <yvonne.willi@agrl.ethz.ch>

INRA Rennes AphidEvolGenomics

PhD position available at INRA Rennes (France) on Aphid Evolutionary Genomics (URGENT, deadline is 29 June 2007). The position is open to non-French and French students. However, it is preferable that the candidate has just obtained his "Master 2" in France. Otherwise, there might be difficulties to obtain a proof of equivalence (please contact the University of Rennes, Ecole doctorale VAS in case of doubts).

The financing for that position has been obtained; however, it is necessary that the candidates i) contact me immediately ii) apply to the open competition organised by the University of Rennes ("Ecole doctorale VAS"); the deadline for sending a written application (including a CV, a program of the courses followed in the last two years, the manuscript corresponding to the "Master 2", a letter of motivation) is extremely soon: 29 June 2007. The website of the "Ecole doctorale VAS" is http://www.vas2.univ-rennes1.fr/ Attention, navigating through this website is a difficult adventure: first click on "Présentation", then click on "Inscription au concours 2007" in the left column.

The aim of the work is to use the growing sequence data for aphids to study their genome in an evolutionary perspective, comparing it to that of other insects. A special focus will be put on multigenic families, in order to detect patterns specific to aphids, that would be related to their adaptive potential. Most of the work will consist in bioinformatic analyses, and phylogenetic studies. The student will use data from the complete genome sequencing of Acyrthosiphon pisum and EST collection from different aphid species. This will be a starting point to describe the specificities of the aphid genome, and for describing which genes have been duplicated and which genes have atypical evolutionary rates (relaxed selection, positive selection, etc).

Website of my research group: http://www.rennes.inra.fr/umrbio3p/equipes/insectes/insectes.htm Recent related publications: SABATER-MUÑOZ, B., F. LEGEAI, C. RISPE, J. BONHOMME, P. DEARDEN et al., 2006. Large-scale gene discovery in the pea aphid Acyrthosiphon pisum (Hemiptera). Genome Biol. 7: R21 RISPE, C., F. DELMOTTE, R. C. H. J. VAN HAM and A. MOYA, 2004. Mutational and selective pressures on codon and amino acid usage in Buchnera, endosymbiotic bacteria of aphids. Genome Res. 14: 44-53. Please contact me before sending your application the the "Ecole doctorale VAS" and send me along a letter of support from the person advising your research in "Master 2".

Claude Rispe (claude.rispe@rennes.inra.fr)

Dr Claude Rispe UMR Bio3P, Institut National de la Recherche Agronomique, domaine de la Motte BP35327 35653 Le Rheu cedex - France

E-MAIL ADDRESS : claude.rispe@rennes.inra.fr

Tel (from France): 02 23 48 51 53 Tel (international): (+) 33 2 23 48 53 Fax (from France): 02 23 48 51 50 Fax (international): (+) 33 2 23 48 51 50

website (click on the insect) http://www.rennes.inra.fr/umrbio3pE/

claude.rispe@rennes.inra.fr claude.rispe@rennes.inra.fr

Iceland subterranean amphipods

PhD position at the University of Iceland, Reykjavik.

A PhD project on subterranean amphipods in Iceland – phylogeny and population structure

Two species of subterranean amphipods, Crangonyx islandicus and Crymostygius thingvallensis, were recently found in Iceland. This finding is unique for the biota of Iceland, and northern Europe. These species are the only endemic animals found in Iceland. Furthermore, one of the species defines a new family within the Amphipoda. The two main aims of the project are:

1. The phylogeny of the two species. Did the two species colonize Iceland after the last glacial period or have they existed in Iceland throughout its geological history, possibly for 40 million years? Aside from the geographical isolation from other countries and a northerly position, Iceland is a geologically young island. Being centered on a volcanic hot spot on the Atlantic ridge, its geology is affected by volcanism and tectonics. 2. Analyses of the population structure of Crangonyx islandicus within Iceland. Does the divergence of populations reflect geological separation of the areas within Iceland? The study will relate genetical information and the extensive knowledge of the geology of Iceland.

Genetic relationship among and within species will be studied by sequencing of three genes, mtDNA COI and 16S rRNA, and the nuclear gene 18S rRNA. These genes have been extensively used in studies of phylogeny and biogeography. Sequence information is already known from several related species. In addition, related species from Europe and N-America will be sampled and sequenced. Variation in morphology and life-history will be analysed. Applicants should have a masters degree, with some experience of molecular biology, phylogenetics or population biology. Salary for the PhD student are paid by the University of Iceland research fund for doctoral studies. Further information is provided by Snæbjörn Pálsson, snaebj@hi.is, www.hi.is/ ˜ snaebj . Further reading: Kristjánsson BK and Svavarsson J 2004. Journal of Natural History 38: 1881-1894. Svavarsson J and Kristjánsson BK 2006. Zootaxa 1365: 1-17. Kristjánsson BK and Svavarsson J 2007 The American Naturalist, volume 170 (http://www.journals.uchicago.edu/cgi-bin/-resolve?id=doi:10.1086/518951)

snaebj@hi.is

ImperialCollegeLondon PlantSpeciation

SPECIATION IN PLANTS ON AN OCEANIC ISLAND

PhD Studentship (restricted to UK residents) Imperial College London

Location: Silwood Park Campus, Ascot

Supervision: Dr Vincent Savolainen (Imperial College London & Royal Botanic Gardens, Kew), in collaboration with Dr Bill Baker (Royal Botanic Gardens, Kew), Dr Darren Crayn (Royal Botanic Garden, Sydney), and Mr Ian Hutton (Lord Howe Island)

The origin of species diversity has challenged biologists for over two centuries. Charles Darwin recognized that allopatry, species divergence resulting from geographical isolation, is a driving force of speciation, but he also thought populations could diverge into separate species in the absence of geographical isolation, a mechanism now called sympatric speciation. During the last decade, mathematical models have shown that sympatric speciation is theoretically possible, but extremely few examples have been documented in nature. Last year, Savolainen and colleagues provided complete evidence for sympatric speciation in a case study of two species of palm (Howea) on a remote oceanic island, Lord Howe Island (LHI), Australia (Savolainen & al. 2006. Sympatric speciation in palms on an oceanic island. Nature 441: 210-2133). Natures own coverage of this paper claimed that [Lord Howe] Island hosts double boost for evolutionary theory and that experts say the big question now is whether sympatric speciation is widespread or rare. Here the investigation will be broadened to other vascular plants of LHI with the aim to evaluate whether this evolutionary phenomenon is more common than previously thought.

LHI is a minute subtropical island of less than 12 km2, situated 580 km off the eastern coast of Australia. The island was formed by volcanic activity 6.4-6.9 my ago. Its flora comprises 241 vascular plant species of which 105 are endemic. Geographic isolation in most outcrossing angiosperms is not realistically possible on LHI and thus it is an ideal site on which to test the four criteria for sympatric speciation: 1) species sympatry, 2) sister relationships, 3) reproductive isolation, and 4) that an earlier allopatric phase is highly unlikely. Numerous plant genera, like Howea, are represented by more than one endemic species on the island, which may well be products of sympatric speciation. The student will look at new pairs/groups of endemics:

(i) The student will combine existing DNA sequence data from GenBank with new data collected and produced during the project to reconstruct evolutionary relationships for five pairs/groups of endemic taxa. Using phylogenetic methodology, in each case the student will evaluate whether theses island endemics are sister taxa. Molecular clock methods will then be used to date the divergence events, which will be compared with the known geological history of LHI. (ii) During fieldwork, the student will also document species sympatry and habitat variables at a fine scale. Chromosome counts will also be made for all of these species to evaluate for possible polyploid or hybrid speciation events. (iii) The expected distribution of interspecific divergence (Fst) for species that evolved in allopatry is different from that expected for species that diverged with gene flow. For three pair/group of sympatric species on the island, the student will sample at least 10 individuals from five populations, estimate basic population genetic parameters, and produce genome scans. Genome scans will consist of at least 200 variable AFLP loci, for which Fst will be estimated and compared to neutral expectations from simulations based on the observed average Fst between the pairs of species. Computer simulations and calculation of significance levels will be carried out with the software Dfdist and DetSel. Outlier loci will be identified and the shape of the Fst distribution will be described. The genome scans will reveal a signature of the process of speciation, e.g. providing support for sympatric or parapatric speciation versus independent colonisation events on LHI.

To apply: Please send a letter of motivation, full CV and contact details of two referees as a single pdf file to v.savolainen@kew.org by Friday 29 June 2007. Interviews should be held between 4 and 6 July.

V.Savolainen@kew.org

Innsbruck HumanHistory

PhD-thesis: Phylogenetic reconstruction of human settlement in south-east Asia

Theme: The human settlement in south-east Asia is only known along general lines. The aim of this research project is to reconstruct migration routes and phylogenetic structures of selected south-east Asian populations by using modern yet established molecular DNA-typing technologies (DNA-high-throughput-sequencing; SNP-multiplex-typing) and appropriate phylogenetic algorithms.

Work conditions: We offer a full-time PhD-position in the frame work of the Austrian FWF Translational-Research project "EMPOP - an innovative mitochondrial DNA database" for a period of 3 years. The Institute of Legal Medicine at the Innsbruck Medical University, Austria, disposes a high-tech infrastructure for molecular DNA analytics. Through the establishment of the mitochondrial DNA database EMPOP (www.empop.org), the Institute of Legal Medicine in Innsbruck holds a worldwide key position in the field of forensic mtDNA analyses.

Job description: Generation of mtDNA control region sequences of selected south-east Asian populations; Determination of the mitochondrial haplogroup with SNP-multiplexes; Phylogenetic reconstructions using PAUP*, MIGRATE, MrBAYES, NETWORK,...

Minimum requirements Candidates should hold a master's degree in the field of biological, chemical or life sciences. Practical experience of molecular biological lab work and computer literacy are essential, along with a high level of fluency in spoken and written English. Good communication and team-working skills are required and evidence of drive and self motivation. Experience and interest in mathematics/statistics would be desirable.

We offer: We offer a friendly and inspiring work atmosphere in an internationally renowned scientific team, access to brand-new scientific methods and IT-systems and efficient mentoring and support.

Please send your application to:

Prof. Walther Parson, PhD MSc Institute of Legal Medicine Innsbruck Medical University Muellerstrasse 44 A-6020 Innsbruck, Austria

T +43 (0)512 9003 70640 F +43 (0)512 9003 73640 E-Mail: walther.parson@i-med.ac.at

anita.brandstaetter@i-med.ac.at

LeidenU GeneIntrogression

1 PhD position (4 years) At the section Theoretical Biology of the Institute of Biology (Leiden University, the Netherlands)

This PhD project is aimed at studying effects of population structure and genetical mechanisms on introgression probabilities of modified genes. We use stochastic models that take inter-individual variation into account. The PhD will take part in a collaborative project, funded by the Duthc government, involving mathematicians, ecologists and molecular biologists.

We are looking for someone with a master degree in mathematics, physics, mathematical biology, or related field, and experience with stochastic modeling, preferably in population dynamics or population genetics.

For further information contact: Patsy Haccou, email:.p.haccou@ibl.leidenuniv.nl, tel: +31 71-5274917.

Patsy Haccou <p.haccou@biology.leidenuniv.nl>

LeidenU GeneIntrogressionCarrot

Graduate position Leiden

1 PhD position (second call)

In this PhD project the fitness of hybrids between crosses of wild and cultivated carrots will be determined under varying environmental conditions. In collaboration with others the PhD student will estimate with molecular techniques which parts of the genome have the highest fitness effects. The PhD student will also estimate the amount of gene flow between wild and cultivated carrot will on the basis of field surveys.

The candidate should have a degree in ecology (population dynamics), plant breeding or environmental biology, knowledge of modern molecular techniques, experience with growing plants, affinity with GIS, database manipulations and internet applications, drivers license and sufficient fluency in writing and speaking English

For more information contact: Dr. T.J. de Jong, email: t.j.de.Jong@ibl.leidenuniv.n, tel: +31 71-5275118 For the ERGO program see: www.nwo.nl/nwohome.nsf/pages/NWOA_6JNP94_Eng The full text of this grant is available from our website: http://biology.leidenuniv.nl/ibl/S11/docs/ERGOproject.pdf "T.J. de Jong" <T.J.de.Jong@biology.leidenuniv.nl>

London WaspEvolBiology

PhD in Evolutionary Biology and Behavioural Ecology available October 2007

Funding is available for a PhD student to study drifting behaviour in social wasps. The project will explore the costs and benefits of nest drifting behaviour in Polistes canadensis paper wasps using radio frequency identification (RFID) tagging technology to monitor internest movements. Drifting in this species has recently been identified as an alternative reproductive strategy, whereby drifting wasps may gain indirect fitness by helping raise related brood on several different nests (see Sumner et al. 2007 Current Biol. 17, 140-145).

The ideal candidate should have a strong background in evolutionary biology and ecology (empirical and theoretical), and a keen interest in social evolution and behaviour. Experience in molecular biology, field-work on insects, and behavioural observations are also highly desirable. The student will jointly supervised by Dr Seirian Sumner (ZSL) and Prof. Laurent Keller (Lausanne), and will be required to spend time in Lausanne University, Switzerland and the Institute of Zoology, Zoological Society of London (ZSL), and conduct fieldwork in Panama.

Interested candidates should email their CV and covering letter to Seirian Sumner (Seirian.Sumner@ioz.ac.uk) by 1st August 2007.

Dr Seirian Sumner Research Fellow Institute of Zoology Zoological Society of London Regent's Park London, NW1 4RY

Tel: +44 (0) 207 449 6617 Fax: +44 (0) 207 586 2870

Home number +44 (0) 208 986 4053 Mobile: +44 (0) 78 0573 6274

Web: http://www.zoo.cam.ac.uk/ioz/people/sumner.htm ZOOLOGICAL SOCIETY OF LONDON LIVING CONSERVATION Registered Charity no. 208728

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

MacquarieU 2 EvolBehaviour

PhD Scholarships in Cognitive Neuroethology

Two Macquarie University Research Excellence Scholarships (MQRES) for PhD research in Cognitive Neuroethology are available in the laboratory of Dr Andrew Barron at Macquarie University's Centre for the Integrative Study of Animal Behaviour (CISAB, http://galliform.bhs.mq.edu.au/~cisab/) (Sydney, Australia).

Possible research topics include:

1. Analysis of the neural mechanisms underlying the honeybee's symbolic dance language. Dance behaviour is the only clear example of symbolic communication in invertebrates and has become a classic study in animal behaviour, but the neural mechanisms generating this symbolic language system are completely unknown.

2. Neural mechanisms of reward processing and reward-seeking motivation in honeybees. Forager bees spend their lives seeking and collecting floral rewards to deliver to their nest mates. The aim of the project is to identify the neuromolecular basis of this reward-seeking drive, and to compare the mechanistic bases of reward seeking for individual versus colony benefit.

3. A comparative analysis of the mechanisms of queen control in social bees. In 'primitive' insect societies queens maintain control by attacking workers, but paradoxically largest societies are also most harmonious. In 'advanced' insect societies there has been a transition in the mechanism of queen control from assault to pheromonal signals. The project will explore how this transition has occurred and how advanced societies evolved a state of social harmony.

For further information and discussion regarding these projects, prospective applicants should contact Dr Andrew Barron (andy@galliform.bhs.mq.edu.au <mailto:andy@galliform.bhs.mq.edu.au>).

MQRES scholarships include a stipend currently AU$19,616 p.a. tax exempt (2007), allowances for relocation and thesis costs, international tuition fees and overseas health cover for a maximum of 3.5 years tenure. Additional support is available for research expenses and travel (visiting overseas laboratories and attending conferences). Casual teaching opportunities may also be available within the Department.

Applicants should have completed qualifications equivalent to a four-year Australian Bachelor degree with First Class Honours (such as a Masters degree with substantial thesis component). Experience in some of the following areas would be ideal: molecular biology, animal behaviour, neurobiology, behavioural ecology, neuroethology.

Further information on equivalence and other conditions for the scholarship are available from the Higher Degree Research Office, telephone: +61-2-9850 7663, e-mail: hdrschol@vc.mq.edu.au <mailto:hdrschol@vc.mq.edu.au>, or download from our website: www.research.mq.edu.au/students/-scholarships/pages/CISAB_CognitiveNeuroethology <http://www.research.mq.edu.au/students/-scholarships/pages/CISAB_CognitiveNeuroethology>
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Applications should be forwarded to:

The Scholarships Officer

Higher Degree Research Office

Cottage C4C

Macquarie University NSW 2109

AUSTRALIA

Andrew Barron <andrew.barron@mq.edu.au>

McGillU GuppyEvol

Graduate student opportunity: sexual selection and contemporary evolution in guppies

Prof. Andrew Hendry (biology.mcgill.ca/faculty/hendry/) in the Dept. of Biology at McGill University in Montreal, Canada, is looking for a graduate student (MSc or PhD) to study how sexual selection influences the contemporary evolution of guppies. This work will be part of a larger overall project titled: From Genes to Ecosystems: How do Ecological and Evolutionary Processes Interact in Nature? This overall project uses experimental introductions of guppies in Trinidad to study the fine scale evolution of traits - and how this evolution influences ecological processes (guppypool.umaine-biology.net/guppyFIBR.html). If entering into an MSc, the student would fit into this overall project by quantifying sexual selection and mate choice in the introduced populations which would then allow predictions regarding the evolution of male colour. If entering into a PhD, the student would do the above and also examine how mate choice evolves following introduction to the new environment. This would be the first study examining the evolution of mate choice in a contemporary population experiencing evolutionary change.

Preference will be given to students who have obtained whole or partial funding for their graduate studies (e.g., NSERC, NSF, EPA, FQRNT, SENACYT, CONACYT, CONICYT). Depending on his/her interests, the student might do their graduate work as a part of the Neotropical Environment Option (www.mcgill.ca/-neo/). The student would start graduate school in January 2008 but would ideally also start working on their project (with pay) in fall 2007.

Interested individuals should send their CV, transcripts (unofficial versions are OK), and a statement of interest, motivation, and potential funding to andrew.hendry@mcgill.ca. Consideration of applicants will begin immediately.

Andrew Hendry, Associate Professor Redpath Museum & Dept. of Biology McGill University 859 Sherbrooke St. W. Montreal, QC H3A 2K6 Canada Phone: 514-398-4086 ext. 00880# FAX: 514-398-3185 Email: andrew.hendry@mcgill.ca Website: http://www.biology.mcgill.ca/faculty/hendry/
Andrew Hendry <andrew.hendry@mcgill.ca>

MississippiStateU Genomics

Ecological genomics has been identified as a frontier in ecology and evolutionary biology. The Department of Biological Sciences at Mississippi State University recently has positioned itself to become a leader in ecological genomics research with plans to further expand the faculty in 2008. Faculty involved with the ecological genomics initiative at Mississippi State University seek graduate students interested in diverse areas ranging from landscape and community ecology to molecular evolutionary biology. Additional funding for Ph.D. students recently has become available for Fall 2007. Interested students should apply prior to July 31.Application materials are available online at: http://www.msstate.edu/dept/grad/ Ecological Genomics Faculty (http://www.msstate.edu/dept/-biosciences/bio.html)

Christopher Brooks (beginning Fall 2007), cpbrooks@gmail.com, quantitative ecology, disease ecology, spatial network theory, landscape ecology

Mark Welch (beginning Fall 2007), mark.e.welch@vanderbilt.edu, population genetics/genomics, speciation genetics, conservation genetics

Lisa Wallace, LisaWallace@biology.msstate.edu , plant systematics, population genetics, phylogeography, http://www2.msstate.edu/~lw404/)

Walter Diehl, wdiehl@biology.msstate.edu, evolutionary biology, comparative genomics, http:/-/www.msstate.edu/dept/biosciences/facu.html
Gary Ervin, gervin@biology.msstate.edu , plant ecology, wetlands ecology, invasive species, http://-www.msstate.edu/courses/ge14/)

mark.e.welch@vanderbilt.edu
mark.e.welch@vanderbilt.edu

OxfordUK PlantEvolGenetics

PhD studentship in Plant Sciences, Oxford UK

Plant evolutionary genetics

A PhD studentship is available to do a PhD in the area of plant evolutionary genetics at the department of Plant Sciences, Oxford UK. The PhD project can be devoted (but not restricted) to plant sex chromosome evolution, speciation or molecular adaptation.

The studentship is available only for UK citizens or students who did an undergraduate degree in a UK university. For details please contact Dmitry Filatov d.filatov@bham.ac.uk

Dmitry Filatov <d.filatov@bham.ac.uk>

SheffieldU PlantEvol

PhD Studentship: Climate change, environmenal variability and life- history evolution

A 3-year PhD studentship is available to examine how life-histories might evolve as climate changes in the coming decades. Both average climate and the variability of key weather variables are predicted to change in the coming decades, and this change would be expected to impact on growth and survival. We aim to predict how species might evolve in response to such changes. The study system is a series of dune annual communities, linking to a new long-term project in which a series of plots are being set up along an environmental transect from southern to northern Europe. The focus is to develop and parameterise models that predict plant growth and development as a function of key climatic variables. The models will be analysed within an adaptive dynamics framework to predict how growth characteristics will change with climate, and model predictions will tested using observational and experimental approaches.

The study will combine both field and modelling approaches, with the opportunity for field work in the UK, France and Spain.

Applicants should have a background in biology, ecology or environmental science. The studentship will offer opportunities for training in population and evolutionary modelling, as well as experimental design and analysis.

The project will be supervised by Prof Robert Freckleton and Dr Dylan Childs, both in the Department of Animal & Plant Sciences, University of Sheffield.

For more details contact Rob Freckleton (r.freckleton@sheffield.ac.uk).

Professor R Freckleton Department of Animal & Plant Sciences University of Sheffield Sheffield S10 2TN

Tel (work): 0114 2220017 Tel (mobile): 07788 742341 [new number]

http://www.shef.ac.uk/aps/index.html http:/-/www.shef.ac.uk/aps/contacts/acadstaff/-freckleton.html r.freckleton@sheffield.ac.uk
r.freckleton@sheffield.ac.uk

TrinityCollege HybridAsh

Graduate position Trinity College Dublin (TCD) & Teagasc invites applications to undertake an MSc/PhD research project entitled:

Identifying the scale of suspected hybrid ash (F. excelsior x F. angustifolia) in Ireland'

Ash is an important hardwood species for farm forestry in Ireland. The Irish government introduced substantial planting grants around 1992 for farmers to plant trees with an extra premium for planting hardwood species including ash. Consequently plants and seeds of several species were imported to fill the needs (from various sources including France, Czech Rep, Poland and the Netherlands). Many of these plantings developed poor morphology and growth. It was clear that the problem was due to the source of the material and that the imported material was probably hybrid ash derived from F. excelsior and F. angustifolia. Today, there are at least 100 afforested sites in which suspected hybrid ash was planted. There is a lack of understanding of hybrid ash in general, its occurrence in Ireland, and potential of it to interbreed with native ash. This proposal therefore aims to carry out a set of morphological and molecular DNA tests to characterise material from suspected sites and to assess the potential of these plantations to interbreed with indigenous ash.

This project will be jointly supervised by Dr Trevor Hodkinson (TCD) and Dr Gerry Douglas (Teagasc Kinsealy) and collaborate with Nathalie Frascaria-Lacoste, Universite Paris-Sud XI, Orsay, France. The student will receive an annual tax free stipend of 21,000 Euro for maintenance and to cover university fees. Fees are approximately 5,000 Euro for EU students and 10,000 Euro for non-EU students. There will be opportunities for extra money from teaching and demonstrating on undergraduate courses and invigilating examinations. The Graduate student will initially register for an MSc at TCD under the terms of the Walsh Fellowship Scheme and the work will be undertaken at Teagasc, Kinsealy Research Centre, and the Department of Botany TCD.

Applicants must have a first or upper second class Bachelors, or Masters, degree in a biological science or relevant subject. To apply or to obtain further information, please send a CV including research interests and contact details of two referees and a letter of motivation to trevor.hodkinson@tcd.ie and gerry.douglas@teagasc.ie by Friday 13th July 2007

– Dr Trevor Hodkinson Department of Botany School of Natural Sciences University of Dublin, Trinity College D2, Ireland

Phone: 353-1-8961128 Fax: 353-1-8961147 Email: trevor.hodkinson@tcd.ie

hodkinst@tcd.ie

TrinityCollege IrishBiodiversity

Job: Research Studentship Where: Botany School, Trinity College Dublin, Dublin 2, Ireland Status: 3 years (with the possibility of fee coverage for a fourth year) Closing Date for applications: Friday, 27th July 2007 Salary: ca. 16,500 per annum (plus research expenses + EU University registration fees covered for three or, if needed, four years) Start Date: October 2007

Details: The Irish Environmental Protection Agency, under its STRIVE Doctoral Scholarship programme, has recently agreed to fund a three year project on Irish biodiversity and systematics titled 'The genetic relationships, phylogeny and con-specificity of Irish Eriocaulon aquaticum (Hill) Druce (Pipewort) populations with those from Scotland and North America.' This project will involve multi-disciplinary research into the genetics and systematics of a rare native member of the Irish Flora.

The project aims to determine whether Irish, British and American material of Eriocaulon aquaticum are con-specific, to compare the genetic structure of Irish, British and American populations and to detail the reproductive biology of Irish material. Molecular DNA, morphological, cytological and anatomical techniques will be used to gather data which will then be analysed using phenetic (ordination, discriminant and possibly co-inertia analyses), phylogenetic (maximum parsimony and likelihood) and population genetic (diversity and differentiation) techniques.

Candidature: The successful candidate will- Possess a good honours undergraduate degree (at least a 2i or equivalent) in Botany, Biology or Environmental Sciences or a closely allied discipline or an appropriate Masters in these disciplines. Have, or be rapidly capable of developing, a high level of competency in field botany.

Enquiries to: Prof. J. Parnell (jparnell@tcd.ie)

Submission of applications: Candidates should submit a letter outlining their suitability for the position, a one-page summary of how they would approach the topic and a full curriculum vitae, to include the names, addresses and emails of two referees.

Send applications to: Prof. J. Parnell, Botany Department, Trinity College Dublin, Dublin 2, Ireland. Email: jparnell@tcd.ie by 27th July 2007.

– PLEASE NOTE THE NEW TELEPHONE AND FAX NUMBERS

John Parnell email: jparnell@tcd.ie Herbarium or John.parnell@tcd.ie School of Botany

Trinity College Dublin Tel: +353-1-8961269 Dublin 2 Fax: +353-1-8961147 Ireland

John Parnell <jparnell@tcd.ie>

UArkansas EnvGenomics

Ph.D. Graduate Assistantships, Environmental Genomics at the University of Arkansas and University of Nevada, Las Vegas

Two NSF-funded graduate research assistantships are anticipated to support Ph.D. candidates interested in functional genomics of adaptation to stressful environments. The project involves laboratory and field experiments designed to discover patterns of gene expression in populations of cactophilic Drosophila mojavensis. Our general goals are to uncover whole-genome patterns of gene expression in populations exposed to natural abiotic and biotic stress. Ultimately, we wish to pinpoint clusters of functionally interacting genes expressed throughout the life cycle in different environments, and predict limits of phenotypic plasticity and adaptation, particularly in response to stressful environments and long-term global climate change. Laboratory experiments will involve DNA microarrays to study gene expression changes due to different host cacti and environmental stresses, as well as differences in epicuticular hydrocarbons. Field-related work will include monitoring of wild flies, demography of wild populations, and analysis of hydrocarbon and RNA profiles. The positions are part of a collaborative project involving the Univ. of Arkansas, Fayetteville, and the Univ. of Nevada, Las Vegas. One research assistantship will be available at each institution. Please note that these positions are contingent upon receiving final funding approval from NSF.

Applicants must gain admission to the Ph.D. program in the Department of Biological Sciences at the University of Arkansas or the School of Life Sciences at UNLV. Application information is available at http://biology.uark.edu/1251.htm and http://-biology.uark.edu/1251.htm prospective.html. Stipends start at $22.8K/12 months; tuition and benefits are also covered. Supplemental funding is available on a competitive basis for applicants qualifying for Doctoral Fellowships at the Univ. of Arkansas (http://-biology.uark.edu/1255.htm). These positions are expected to begin January 2008 (spring semester); admission for the fall semester, 2007 is also possible. The deadline for spring semester applications is November 15, 2007.

To apply, please contact us for information and assistance.

William J. Etges Allen G. Gibbs Department of Biological Sciences School of Life Sciences University of Arkansas University of Nevada Fayetteville, AR 72701 USA Las Vegas NV 89154 USA 479-575-6358 702-895-3203 wetges@uark.edu allen.gibbs@unlv.edu http://comp.uark.edu/˜wetges/-wetges.html sols.unlv.edu/faculty/gibbs.html

UA-F and UNLV are equal opportunity/ affirmative action employers.

wetges@uark.edu wetges@uark.edu

UBonn PlantSimulations

PhD proposal

The project: In our research group we predict breeding values of self-pollinated crop-plants. In this project a “virtual” population of parental lines and their progenies will be simulated. Breeding values will be predicted based on restricted maximum likelihood (REML). Then main focus of the project will be the development of a Bayesian approach to predict breeding values. This project will have close collaboration with Mikko J. Sillanpää (Ph.D.), Department of Mathematics and Statistics, Rolf Nevanlinna Institute, University of Helsinki, Finland.

Provided: The chance to do research on an international level, The possibility to achieve a doctor’s degree.

Required: Diplom/MSc in Mathematics, Bioinformatics, Agriculture or related fields, Interests in biomathematics/biostatistics, programming work and quantitative genetics, Willing to participate in international collaborations, Language skills in English.

Preferred: Knowledge of plant breeding methodology, Familiar with programming in C/C++ language and in statistical environments like R, SAS, Matlab or AS-Reml.

Suitably qualified women candidates and handicapped persons are particularly encouraged to apply.

Additional information can be obtained from:

Dr. Andrea Bauer University of Bonn Department of Crop Science and Resource Conservation Chair of Plant Breeding Katzenburgweg 5 D-53115 Bonn Germany

Phone number: ++49-(0)228-732031 E-mail: a.bauer@uni-bonn.de.

Dr. Andrea M. Bauer University of Bonn Institute of Crop Science and Resource Conservation Chair of Plant Breeding Katzenburgweg 5 D - 53115 Bonn Germany Phone: ++49-(0)228-732031 Fax: ++49-(0)228-732045

Andrea Bauer <a.bauer@uni-bonn.de>

UHannover EvolBiol

New MSc-Program ‘Animal Biology and Biomedical Sciences The Graduate School for Biomedical Sciences Hannover at University of Veterinary Medicine Hannover Foundation (TiHo) offers a research- oriented Master of Science Program in “Animal Biology and Biomedical Sciences” for German and foreign students. This new modular Masters program presents a unique combination of biology and veterinary medicine, with a flexible, modular curriculum that allows you to tailor your study to match your particular interests. The program is grouped into three specialist areas focusing on - evolution, animal biodiversity and behaviour; - cellular, developmental and systems neurobiology; - infection biology.

During the first semester, all three areas will be covered. In the second semester, you will select courses of your choice from two of the three themes. The second year (semesters 3 + 4), your study will focus your studies on just one of these tracks.

Admission to the program requires a BSc degree in Biology, Biochemistry, Biomedicine or related subjects. We offer a fast -track route (without master thesis) to our PhD program for excellent students.

What you can expect TiHo is unique among institutions for higher education in Germany in its possibility to provide interdisciplinary courses with subjects ranging from Veterinary Sciences (e.g., what makes an organism a pathogen?) to modern Evolutionary and Conservation Genetics (evolutionary definition of conservation units), Behavioural Biology of Primates (e.g., acoustic communication and the origin of language), and selected topics in Physiology, Cell Biology and Neurobiology.

The University of Veterinary Medicine Hannover is Germany’s oldest independent establishment of veterinary education with - research priorities in infectious diseases, neuroscience, clinical research, animal health and food safety - six clinics, 15 institutes, two interdisciplinary departments - affiliated institutes and field stations for epidemiology and animal ecology - an animal farm for teaching and research and the animal welfare centre - the WHO Collaborating Centre ‘Veterinary Public Health - the EU Reference Laboratory for Classical Swine Fever - international partnerships and cooperative agreements with more than 30 universities

For further information please contact:

www.tiho-hannover.de/studium/gs/index.htm or:

Dr. Beate Poettmann Phone +49-511-953-8091, Fax +49-511-953-8053 Graduate School for Biomedical Sciences Hannover Stiftung Tieraerztliche Hochschule Hannover Buenteweg 2 D-30559 Hannover Germany

Stefan Koenemann <Stefan.Koenemann@tiho-hannover.de>

UHull InvasionGenetics

Department of Biological Sciences, University of Hull

MSc-studentship

A partially funded (tuition fees and project costs) MSc studentship is available at the Department of Biological Sciences at the University of Hull. For further information on the department see www.hull.ac.uk/biosci. Applicants are required to have a BSc in Biological Sciences or an equivalent undergraduate qualification. Experience in the application of molecular tools would be an advantage.

Title: Population genetic analysis of a recent fish invasion: the topmouth gudgeon Pseudorasbora parva.

Background Evolutionary factors play a crucial role during the invasion process, with recent empirical evidence confirming that post-introduction evolutionary processes often determine whether invasive species ultimately establish and disperse. Studies on genetic structure of invasive populations provide the basis for both understanding evolution during the establishment process and impact on native species. The MSc project will use a molecular approach (microsatellites) to study the invasion history of the topmouth gudgeon, Pseudorasbora parva, the most invasive fish in Europe. The candidate will work under supervision of Dr Bernd Hänfling (University of Hull) in collaboration with Drs Rob Britton and Rudy Gozlan (University of Bournemouth)

Informal enquiries and applications should be directed to Dr. Bernd Hänfling Telephone: 0044-1482-465804 Email: b.haenfling@hull.ac.uk Department of Biological Sciences, University of Hull, Hull, HU6 7RX, UK.

Applications (by mail or email) should include a cover letter, CV and names of two referees

Closing date for applications: Friday 27th July 2007

Dr. Bernd Haenfling University Research Fellow Molecular Ecology and Fisheries Genetics Lab University of Hull HU6 7RX

Tel: 0044-1482-46 5804 Fax: 0044-1482-46 5458 b.haenfling@hull.ac.uk

B.Haenfling@hull.ac.uk

UIllinois BeeConservation InvasivePathogens

Host-Parasite Interactions/Invasive Pathogens/Conservation Ecology 3-yr Graduate Student Research Assistantship

A Graduate Student Research Assistantship is available to develop research in ecology, behavior and/or evolution of insect pathogens, specifically to focus on the interactions between bumble bees, environment and pathogens and to participate in a multi-team effort to investigate causes of decline in North American bumble bees. The student will join the Nation's #1 ranked Department of Entomology (http://www.life.uiuc.edu/entomology/index.html) at the University of Illinois, and will have strong affiliation with the Illinois Natural History Survey (http://www.inhs.uiuc.edu/) located on the UIUC campus.

The research is multidisciplinary, and involves extensive fieldwork in both the midwestern and western U.S. to collect data on abundance, distribution and population structure of bumble bees, several species of which appear to be declining in abundance and distribution across the U.S. As bumble bees are among the Nation's most important wild pollinators, this is cause for concern– effective pollination is critical for the health of most terrestrial ecosystems. In addition to establishing the current status of targeted bumble bee species, we are developing experimental protocols for testing the potential role of pathogens in their population decline, and performing DNA sequencing of possible pathogens. The principal goal of the research to be developed by the student is to determine whether an insect pathogen, such as Nosema bombi, a naturally occurring microsporidium in European bumble bee populations, and found in commercially produced and wild populations in North America, is important in the decline of bumble bees in the U.S.

The research will be directed by Drs. Lee Solter (http://www.inhs.uiuc.edu/staff/index.php?action=list&user_name=lsolter) and Sydney Cameron (http://www.life.uiuc.edu/scameron/). We are looking for a student who is passionate about insects. If you are interested in applying for this graduate research opportunity, please do the following:

Go to our websites and look over our research programs; read the research statements and those of our students and find out if your interests coincide. If your interests match well with ours and with this project, please provide: 1. A letter stating why you want to apply for this position, and why you think you are the best person for this research. Include a broader perspective of why you want to go to graduate school and state your career objectives; 2. A curriculum vitae, including any honors research projects, other honors and awards, publications, presentations at meetings, courses, grades (can be informal record at this stage), overall GPA, GRE scores (%); 3. A list of lab techniques with which you have experience, such as molecular methods and statistical analysis, computer programming, mathematical skills, and other relevant expertise; 4. Names and contact information (e-mail, phone, address) for at least 3 people that can provide reference letters. We will be assessing applications during early July and will let you know whether you have been selected for the position soon thereafter. If selected, you will apply to the UIUC Department of Entomology (research programs of each of the faculty are listed on the department website) for Fall 2007 or Spring 2008. Information on admission to graduate school is available on the Department of Entomology website. Final acceptance is subject to approval by the faculty in the Dept of Entomology.

We expect to select a student who is highly motivated to becoming a career scientist, who enjoys being creative and productive, has independent initiative, likes problem-solving, works well with a team, and can work effectively under pressure. The student will join a team of students focused on the systematics, ecology and evolution of bees, and will be adding new research on the potential role of pathogens in pollinator decline. We expect to spend considerable time providing the student with resources and the infrastructure they need to succeed in the field.

Interested students should send all application materials as electronic pdf files to: Dr. Leellen Solter (lsolter@uiuc.edu)

For further information, e-mail Dr. Solter or Dr. Cameron

Application deadline is 1 July 2007

– Sydney A. Cameron Department of Entomology and Program in Ecology and Evolutionary Biology 320 Morrill Hall 505 S. Goodwin Ave. University of Illinois Urbana, IL 61801

Ph: 217-333-2340 Fax:217-244-3499 e-mail: scameron@life.uiuc.edu http://www.life.uiuc.edu/scameron Sydney Cameron <scameron@life.uiuc.edu>

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UIllinois InsectPathogenEvol

Host-Parasite Interactions/Invasive Pathogens/Conservation Ecology 3-yr Graduate Student Research Assistantship

A Graduate Student Research Assistantship is available to develop research in ecology, behavior and/or evolution of insect pathogens, specifically to focus on the interactions between bumble bees, environment and pathogens and to participate in a multi-team effort to investigate causes of decline in North American bumble bees. The student will join the Nation's #1 ranked Department of Entomology (http://www.life.uiuc.edu/entomology/index.html) at the University of Illinois, and will have strong affiliation with the Illinois Natural History Survey (http://www.inhs.uiuc.edu/) located on the UIUC campus.

The research is multidisciplinary, and involves extensive fieldwork in both the midwestern and western U.S. to collect data on abundance, distribution and population structure of bumble bees, several species of which appear to be declining in abundance and distribution across the U.S. As bumble bees are among the Nation's most important wild pollinators, this is cause for concern– effective pollination is critical for the health of most terrestrial ecosystems. In addition to establishing the current status of targeted bumble bee species, we are developing experimental protocols for testing the potential role of pathogens in their population decline, and performing DNA sequencing of possible pathogens. The principal goal of the research to be developed by the student is to determine whether an insect pathogen, such as Nosema bombi, a naturally occurring microsporidium in European bumble bee populations, and found in commercially produced and wild populations in North America, is important in the decline of bumble bees in the U.S.

The research will be directed by Drs. Lee Solter (http://www.inhs.uiuc.edu/staff/index.php?action=list&user_name=lsolter) and Sydney Cameron (http://www.life.uiuc.edu/scameron/). We are looking for a student who is passionate about insects. If you are interested in applying for this graduate research opportunity, please do the following:

Go to our websites and look over our research programs; read the research statements and those of our students and find out if your interests coincide. If your interests match well with ours and with this project, please provide: 1. A letter stating why you want to apply for this position, and why you think you are the best person for this research. Include a broader perspective of why you want to go to graduate school and state your career objectives; 2. A curriculum vitae, including any honors research projects, other honors and awards, publications, presentations at meetings, courses, grades (can be informal record at this stage), overall GPA, GRE scores (%); 3. A list of lab techniques with which you have experience, such as molecular methods and statistical analysis, computer programming, mathematical skills, and other relevant expertise; 4. Names and contact information (e-mail, phone, address) for at least 3 people that can provide reference letters. We will be assessing applications during early July and will let you know whether you have been selected for the position soon thereafter. If selected, you will apply to the UIUC Department of Entomology (research programs of each of the faculty are listed on the department website) for

Fall 2007 or Spring 2008. Information on admission to graduate school is available on the Department of Entomology website. Final acceptance is subject to approval by the faculty in the Dept of Entomology.

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Interested students should send all application materials as electronic pdf files to: Dr. Leellen Solter (lsolter@uiuc.edu)

For further information, e-mail Dr. Solter or Dr. Cameron

Application deadline is 1 July 2007

– Sydney A. Cameron Department of Entomology and Program in Ecology and Evolutionary Biology 320 Morrill Hall 505 S. Goodwin Ave. University of Illinois Urbana, IL 61801

Ph: 217-333-2340 Fax:217-244-3499 e-mail: scameron@life.uiuc.edu

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UMuenster EvolBiocomplexity

The recently founded Institute for Evolution and Biodiversity (IEB), part of the School of Biological Science, University of Muenster (Germany)

INVITES APPLICATIONS FOR THE MSc/SSP in "EVOLUTION AND BIOCOMPLEXITY" http://www.uni-muenster.de/Evolution/Teaching/ssp/ The "Special Study Program (SSP) in Evolution and Biocomplexity" is a specialisation within our existing MSc in Biology at the University of Muenster.

Currently we offer the following modules, each lasting 4 weeks (5 EC) and comprising a combination of lectures, practical work, field courses, lab courses, seminars and computer exercises:

* Host-parasite Coevolution (animals and plants) * Molecular Evolution and Evolutionary Bioinformatics * Experimental Molecular Evolution (Viruses) * Evolutionary and Ecological Genetics * Ecology and Evolution of Freshwater Organisms * The Major Transitions in Evolution: From Life's Origin to Human Evolution * Bernhard Rensch Summer-School in Evolutionary Biology * Design and Analysis of Experiments in Ecology and Evolution

Another integral part of this programme are research modules, experimental or theoretical projects of 6-8 weeks (10 EC), in any of the groups at the IEB (Limnology and Aquatic Ecology, Plant Evolutionary Ecology, Evolutionary Bioinformatics, Animal Evolutionary Ecology, Experimental Molecular Evolution. See www.uni-muenster.de/evolution/groups for details) or in the groups of our partner University in Groningen (www.rug.nl).

The top three students from each SSP cohort will be awarded the Annual Bernhard-Rensch Prize in Evolution and Biocomplexity. The prize is sponsored by the Volkswagen foundation and endowed with a total of 400EUR.

Students who are interested in earning an MSc with a specialisation on Evolution from the University of Muenster should send a statement of interest and their contact details to the course director, Prof. Thorsten Reusch [treusch@uni-muenster.de]. Applicants are advised to apply before mid July 2007.

Further details can be found at www.uni-muenster.de/evolution/ssp ABOUT THE IEB:

The School of Biological Sciences (FB 13) at the University of Muenster has built a tradition of excellence in evolutionary research and teaching. Bernhard Rensch, one of the key contributors to the modern synthesis, directed the Institute of Zoology for many years and helped establish the University as a centre for evolutionary study. Most recently Profs. Thorsten Reusch and Joachim Kurtz, formerly of the Max-Planck Institute for Evolution (Ploen), joined the IEB. In 2006 the School was one of three German Universities to be awarded a grant from the Volkswagen Foundation (http://www.volkswagenstiftung.de/foerderung/impulse/evolutionsbiologie.html) and this award provides funding for this curriculum.

ABOUT MUENSTER:

Muenster hosts many excellent scientific institutions such as a newly founded Max-Planck Institute for biomedical research, a Centre for Nanotechnology and a great number of specialised research areas ("SFBs"). Muenster is a dynamic city with a world-famous heritage centre and in the middle of the beautiful "Muensterland". It is very lively with many students (around 20% of the residents) and scholars. In addition, there is a the rich choice of social and cultural activities and excellent sporting facilities (see www.muenster.de for further details).

Prof. Erich Bornberg-Bauer (PhD), Institute for Evolution and Biodiversity School of Biol.Sciences, University of Muenster, Schlosspl.4 D48149 Germany Tel/Fax: +49(0)251-83-21630/21631 web: www.uni-muenster.de/evolution/ebb/ ebb@uni-muenster.de

UMunich EvolutionSystematics

!!Deadline 30th of June

Master Program in Evolution, Ecology and Systematics in Munich

The University of Munich (LMU) is launching a new, 2-year, international master program for highly motivated students from Germany and abroad with a background in biology or a related subject. The program starts in the winter semester 07/08 and all courses will be offered in English.

The EESlmu Master contains many innovative elements such as a mentoring program, integrated skills courses and individual research training. We also apply a feedback and revision system instead of simple grading. Thanks to funding by the Volkswagen Foundation, students can apply for their own research and travel money and for money to invite international speakers.

Application deadline is the 30th of June 2007.

For more information, please have a look at our website (http://www.eeslmu.de) or contact Pleuni Pennings by e-mail (pennings@lmu.de).

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Pleuni S. Pennings

* Program Coordinator of the Munich Graduate School for Evolution, Ecology, and Systematics

* Postdoc in theoretical evolutionary biology

Evolutionary Biology, Department Biologie II University of Munich (LMU) Großhaderner Str. 2 D-82152 Planegg-Martinsried

Tel: 0049 89 2180 74 234 http://www.biologie.uni-muenchen.de/ou/theopopgen/index.htm pennings@zi.biologie.uni-muenchen.de

pennings@zi.biologie.uni-muenchen.de

UMunich MolEvol

PhD position in bioinformatics/molecular evolution

A PhD position in bioinformatics/molecular evolution is available in the laboratory of Wolfgang Stephan at the University of Munich. The position is funded by the German Science Foundation (DFG) to study the evolution of RNA secondary structures based on DNA sequence comparisons. The position will be paid as BatIIa/2 (or equivalent) according to the German pay scale. Requirements are a master's degree (or Diploma) in bioinformatics (or related field) and a genuine interest in molecular evolution. The University of Munich has a strong, interactive group in evolutionary biology, including theoreticians and experimentalists working on both plant and animal systems. Our group is very international and the everyday working language is English. The LMU department of biology is housed in the new state-of-the-art BioCenter on the University of Munich High-Tech campus. More information is available on the web at:

http://www.zi.biologie.uni-muenchen.de/evol Applicants should send a PDF file with a statement of interest, curriculum vitae, and the contact information for at least two referees to:

stephan@zi.biologie.uni-muenchen.de

The University of Munich is an equal opportunity employer with an affirmative action program for the disabled.

rose@zi.biologie.uni-muenchen.de rose@zi.biologie.uni-muenchen.de

UNeuchatel EvolEntomology

ONE PhD POSITION IN ENTOMOLOGY AT THE UNIVERSITY OF NEUCHATEL, SWITZERLAND

Candidates will be given the opportunity to undertake a PhD on ecological interactions in alpine ecosystems, within the framework of the centres of interests of the laboratory of Evolutionary Entomology: Evolutionary Biology, Chemical Ecology, Tri-trophic interactions.

A possible PhD project would be to use species of the genus Oreina to test the basic principles of warning colour. These leaf beetles are brilliantly coloured in metallic greens, blues and reds, which appears to be a warning that they possess chemical defence. Learning by predators of unpalatable prey species is expected to produce strong purifying selection on warning colour, since only recognised patterns are avoided. Yet the genus Oreina is spectacularly polymorphic, showing geographic variation within species and multiple patterns within a population.

For more details about the laboratory of Evolutionary Entomology at the University of Neuchâtel please refer to http://www2.unine.ch/leae or contact Prof. Martine Rahier (tel. +41 32 718 3137, e-mail: martine.rahier@unine.ch).

Tasks (in addition to research): contributing to the practicals course in Entomology (2nd year) for the students following the Bachelor of Science in Biology.

The position is open from September 1st 2007 for students with a Master in the field of Evolutionary Ecology, Entomology or similar fields. Some knowledge of French is expected.

Applications (including CV, cover letter, one reference letter, the name and address of one additional referee) can be sent until July 20th 2007 to the following address:

- Prof. Martine Rahier Institut de biologie Case Postale 158 2009 Neuchâtel fax 032/718 30 01 e-mail: martine.rahier@unine.ch

Nicolas.Margraf@unine.ch

UPotsdam EvolEcolModelling

PhD Scholarships (University of Potsdam)

The Potsdam Graduate Initiative on modelling the response of populations, species and communities to global change is seeking highly qualified and motivated candidates for four PhD scholarships. The position is open from 01 July 2007 for up to 3 years.

The interdisciplinary research and education program deals with different ecological and evolutionary aspects of the response of populations, species, and communities to the global environmental change. The PhD projects combine recent developments in theoretical ecology as well as process-based and statistical ecological modelling. The projects will be supervised by two members of the Institutes of Biochemistry & Biology, Geoecology, and Physics at the University of Potsdam. They are integrated into the Potsdam Graduate School.

The four different topics of the PhD projects are: (1) Stay and adapt or flee and invade: how do life histories evolve under different scenarios of climate and landscape change Supervisors F. Jeltsch (Plant Ecology and Conservation Biology) & R. Tiedemann (Evolutionary Biology/Zoology)

(2) Propagation of variability patterns from individual populations to complex food webs - analysis of plankton time-series Supervisors U. Gaedke (Ecology & Ecosystem Modelling) & J. Kurths (Nonlinear Dynamics)

(3) Integrating dynamic processes into species distribution models to improve predictions for scenarios of environmental change Supervisors B. Schroeder (Landscape Ecology/Geoecology) & V. Grimm (Ecological Modelling)

(4) Using process-based statistical models to explain and predict range shifts under environmental change Supervisors F. Schurr (Plant Ecology and Conservation Biology) & W. Cramer (Global Ecology)

Applicants must have an above-average Master's degree or equivalent in Natural Sciences and a good background in modelling and statistics . The willingness, both to do interdisciplinary research and to actively participate in the activities of the Potsdam Graduate School, is a prerequisite for the application.

Applications, preferably in electronic form, should refer to one of the four projects and include a CV, copies of degree certificates, and possibly a letter of recommendation. They should be forwarded to the project leader, Prof. Dr. Florian Jeltsch, Institute of Biochemistry and Biology, Plant Ecology & Conservation Biology Group, Am Neuen Palais 10, Universitaet Potsdam, D-14469 Potsdam (email: jeltsch@uni-potsdam.de). For further information, please contact the coordinator of the Graduate Initiative, Dr. Boris Schroeder (Institute of Geoecology, University of Potsdam, Tel. +49 (0)331 977-2480, email: boris.schroeder@uni-potsdam.de). See also the web pages of the participating groups (http://www.bio.uni-potsdam.de/; http://www.uni-potsdam.de/u/Geooekologie/; http://www.uni-potsdam.de/u/Geooekologie/;). The closing date for applications is 18 June 2007.

boschroe@rz.uni-potsdam.de

URegensburg EvolBiol AntImmunity

PhD Position: Collective immunity in ant societies University of Regensburg (Germany)

The PhD project aims to study how ant colonies cope with the increased risk of disease transmission they face as many highly related individuals live together in close densities. The work will specifically address how ants recognise parasites and diseased group members, which behavioural and physiological parasite defences they show, and how they organise the performance of hygienic behaviour between group members. The project therefore combines two research fields, the evolution of insect societies and the study of innate immune systems.

Study methods are experimental infection (mostly with fungal insect pathogens), manipulation of colony structure, behavioural observations, measurement of physiological immune parameters, and gas chromatography - mass spectrometry. The invasive garden ant and a facultatively clonal ant are used as the main study organisms. Both study organisms and methods are established in the lab in Regensburg.

The PhD position is available from summer 2007, and will be supervised by Dr. Sylvia Cremer. The position is funded for three years by the German Science Foundation (according to 13 TV-L/2, i.e. equivalent to BAT IIa/2). It is based in the Evolution, Behaviour & Genetics group of the University of Regenburg, Germany (head of department: Prof. Dr. Jürgen Heinze). The department is active in various fields of evolutionary ecology and provides an international and interactive atmosphere.

Requirements for the position are: high motivation; background in evolutionary ecology, experimental design and statistics; team ability; fluency in English; ideally some experience with insect innate immunity or social insects.

Please send applications with CV, brief statement of research interest, and two references by email to sylvia.cremer@biologie.uni-regensburg.de. Applications are considered until the position is filled, but preferentially before July 20th.

Dr. Sylvia Cremer Evolution, Behaviour & Genetics Biology I University of Regensburg Universitaetsstrasse 31 D-93040 Regensburg Germany

Tel: +49 941 943 2152 Fax: +49 941 943 3304 email: sylvia.cremer@biologie.uni-regensburg.de

Printable version: http://www-evolution.uni-regensburg.de/staff/SylviaCremer/PhD_advertisment.pdf For more information see: http://www-evolution.uni-regensburg.de/staff/SylviaCremer/ and: http://www.biologie.uni-regensburg.de/Zoologie/Heinze/index_e.html SMCremer@bi.ku.dk

URennes WhereDoSpeciesAdapt

PhD theme in

Where do species respond to climate change? The role of endemism and of margins of environmental gradients.

offered within the competition for PhD fellowships at University of Rennes 1, France.

!!! Deadline for inscription: 29 June 2007 (and supervisors should be contacted before)

Obligatory dates for presentations by short-listed candidates: 10 / 11 / 12 July 2007.

Scientific background:

Contemporary ecology is implicitly based on the hypothesis that phenotypes of species respond to changes of their environment. These responses happen on the level of differentiation of populations within species as well as on the level of macroevolution of traits across species. Recent studies, however, indicate that this fundamental hypothesis often lacks support. Species exposed to changing climates, for instance, usually redistribute in space, they migrate with their climate (Ackerly 2003, Int. J. Plant Scie.). Species that stay will often be displaced by species that immigrate and are already well adapted to the novel climate. Consequently, the climate niche of species usually remains very rigid even across time periods of millions of years (for instance Prinzing et al. 2001 Proc. R. Soc. B). Adaptive responses of phenotypes are thus replaced by migrations and invasions. Overall, it is not obvious how phenotypes of species can respond to new climates.

Recently, several hypotheses have been proposed to resolve this paradox. These hypotheses propose that an adaptation or adaptive plasticity is likely to occur in particular situations:

(A) At the margin of climatic gradients. Two scenarios have been suggested. First, phenotypic responses appear at the margin where living conditions of established species become increasingly extreme, provided that species that are already well adapted to these conditions cannot immigrate from outside or (closer to the redaction in french?) where preadapted invasive species are not available from the outside. Second, the response appears at the margin where species face increasingly favorable conditions and can thus expand their range, leading to founder effects and increased phenotypic variability.

(B) As a function of endemism. Again, two scenarios have been suggested: First, endemics are more responsive as their genotypic adaptations to local conditions are not diluted by genotypes arriving from outside. Second, the endemics respond less, as they do not profit from an immigration of genotypes from regions with a climate resembling the novel conditions arising at the given locality.

These hypotheses will be studied for plant species, at the level of intraspecific differentiation of populations, and at the level of macroevolution of traits of traits across species. For the first level, we will use a system that is currently going through major environmental changes, with a well known history of colonization and a number of endemic species: the subantarctic Kerguelen Islands. In the field, the student will characterize climate and soil gradients, will sample different species, and culture plants for two generations in order to verify the heritability of the phenotype. In the lab, the student will measure vegetative and reproductive structure, characterize biochemical phenotypes and their response to environmental conditions (metabolomics, polyamines, growth regulators contributing to stress tolerance; e.g.; Hennion et al. 2006; Heat Shock Proteins will be studied in collaboration).

For the second, macroevolutionary, level we will profit from the regional flora that is best known in terms of phylogenetic relationships, life history traits, and distribution along environmental gradients; the flora of central Europe. The student will reconstruct characters of ancestors, i.e. their positions along environmental gradients and their degree of endemism, within habitats and regions. The student will identify macroevolutionary changes of life histories and certain physiological traits. Finally (s)he will test whether endemism of ancestors, or their position along environmental gradients, influence the evolution of the life history and ecophysiology of the descendants.

Salary / organizational background:

A PhD fellowship by the Ecole Doctorale Vie, Agro, Santé (<https://webmail.univ-rennes1.fr/util/go.php?url=http%3A%2F%2Fwww.vas.univ-rennes1.fr%2Fscripts%2Findex.php&Horde“3eb430ada6b2db40d288eeb
http://www.vas.univ-rennes1.fr/) for three years, approx. > 1040 Euros/month (which can luckily be backed by teaching assistance). Please note that candidates are selected by a committee of the Doctoral School, not by the supervisors of the theses (they can, however, contribute their opinion). Finally, travel costs will not be reimbursed by the Ecole

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

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UWindsor InvadingSpeciesGenetics

Great Lakes Institute for Environmental Research (GLIER), University of Windsor, Ontario.

Graduate Positions - Genetics of invading species. Ph.D. and MS positions are available to begin as early as September 2007 in the laboratory of Dr. Cristescu(http://cronus.uwindsor.ca/users/m/mcris/main.nsf).

The project involves analysis of hierarchical genetic structure of invasive tunicates at different spatial scales and aims to i) characterize spatial and temporal patterns of genetic structure during the establishment and subsequent spread of two invasive tunicates; ii) identify potential sources and vectors of invasions; and iii) address taxonomic problems related to color morphospecies. Ideal candidates will have prior experience with molecular genetics techniques (e.g. DNA sequencing) but students without prior experience will be considered provided they are interested in using molecular markers to understand species invasions. Priority will be given to Canadian candidates, however exceptional international students with outstanding GPA and with ability to work well in a collaborative research atmosphere will be considered.

Interested student should send their CV, a brief statement of research interest, and a list of 3 references to:

Dr. Melania Cristescu Great Lakes Institute for Environmental Research University of Windsor Windsor, Ontario Canada N9B3P4

Phone: 519-253-3000 x 3763 Email: mcris@uwindsor.ca

Melania E. Cristescu Assistant Professor University of Windsor Great Lakes Institute for Environmental Research 401 Sunset Ave Windsor Ontario Canada N9B 3P4

Phone: (519) 253-3000 Ext. 3763 FAX: (519) 971-3616 E-Mail: mcris@uwindsor.ca http://cronus.uwindsor.ca/users/m/mcris/main.nsf mcris@uwindsor.ca

UWyoming PlantEvol

Position: A Ph.D. research assistantship is available in the Weinig lab at the University of Wyoming to work in the area of evolutionary genetics/genomics.

Project: Genetic analysis of natural variation in the control of flowering timing and inflorescence architecture in Brassica rapa

Using Brassica rapa, we are examining genetic mechanisms that enable adaptation to seasonal climates. In particular, we are looking at how temperature and photoperiod interact to affect flowering time, inflorescence architecture, floral morphology, and fruit set directly as well as indirectly via effects on circadian rhythm. The circadian clock is 'set' in response to both temperature and photoperiod, but very little is known about the genetic underpinnings of temperature compensation, i.e., why the clock does not simply cycle faster under high relative to low temperatures. Moreover, there is little understanding of how natural variation in circadian rhythm affects plant performance in seasonal settings or of the genetic basis of quantitative reproductive traits.

Rob McClung, the PI on this grant, is focusing on the genetic characterization of temperature compensation. Another Co-PI on this grant, Rick Amasino, is heading up a large mutant screen. Our role will be to a) QTL map flowering time and floral morphological traits under variable simulated seasonal conditions, b) to evaluate attendant changes in mating system and fitness in a field setting, and c) screen some of the more interesting mutants in the field. We will also be performing studies of molecular evolution of candidate loci.

There is a substantial training component to this grant that includes the opportunity to visit labs of our collaborators to learn new techniques. The research assistantship is a good opportunity for a student to gain skills in population biological approaches, quantitative genetics and basic molecular genetic approaches in the framework of addressing evolutionary questions. As a graduate RA, the student would assist in ongoing QTL mapping and selection experiments while carrying out PhD research.

Inquiries may be directed to Cynthia Weinig (cweinig@umn.edu), Tel 612-624-1037.

cweinig@tc.umn.edu cweinig@tc.umn.edu

UtrechtU EvolBiol

PhD RESEARCHER IN BIOGEOLOGY

The Darwin Center for Biogeology is a virtual Dutch research institute, partially funded by the Netherlands Organization for Scientific Research (NWO), which aims at performing cutting-edge science in the central field of Biogeology where Biology and Earth Sciences meet. Its research mission is to understand the functioning of global, regional and local ecosystems, focusing on change and feedback at all time scales in and between biotic and abiotic components of a changing Earth.

We seek a candidate for a PhD position at Utrecht University within a recently funded program entitled:

Niche engineering and the evolution of biogeochemical cycles through time

Modern marine environments are characterized by complex faunal communities living in the sediment with densities and diversities that vary depending on sediment type, availability of oxygen and organic matter load arriving at the sea bottom. Some species play an extraordinary role in creating suitable environments for other taxa to live in. These keystone species, for example deep burrowing lugworms, are regarded as niche engineers. Through geological history, origination of such niche engineers is hypothesized to have lead to sudden bursts in evolution of other infaunal taxa.

This program is integrated in the Darwin Center for Biogeology, and will be performed in close cooperation with the Microbial Ecology group at the Netherlands Institute of Ecology (NIOO-KNAW, Yerseke). The program has 2 projects, each project carried out by a PhD student. Currently, we are looking for a candidate for the PhD position concerning the project:

The effects of bioirrigation on benthic foraminifera

The aim of this project is to study the effects of the presence of various types of niche engineers on the surrounding meiofauna, in particular the foraminiferal population, and on biogeochemical cycling. Bioturbation, burrow ventilation, bioirrigation and grazing are activities that may have a significant impact on the vertical distribution of benthic foraminifera in marine sediments. Alternatively, foraminifera seems to have a considerable impact on the bacterial population and, consequently, the biogeochemistry. The project will involve laboratory experiments with the coupled system biogeochemistry-bacteria-foraminifera in sediment cores with different imposed biogeochemical conditions, and with or without artificial bioirrigation. It also involves field sampling of marine sediments (Wadden Sea). This project will be supported by ongoing modeling work within the research groups of Stratigraphy/Paleontology at Utrecht University and Microbial Ecology group at NIOO-KNAW.

Qualifications: We are looking for a highly motivated individual with excellent communication skills who are interested in interdisciplinary research combining various fields of biogeology and an MSc in an appropriate field.

Terms of employment: We offer a full-time PhD position for 4 years, with monthly salary starting at 1956,- in the first year to 2502,- in the last year of appointment. We also offer a pension scheme, a collective health insurance and flexible employment conditions. Conditions are based on the Collective Employment Agreement of the Dutch Universities and are supplemented with a holiday allowance of 8 % per year and a year-end bonus of 3%.

For further details please contact: Dr. Mariëtte Wolthers (wolthers@geo.uu.nl) or Prof. Bert van der Zwaan (bzwaan@geo.uu.nl), You may also wish to visit the webpages of our Department at http://www.geo.uu.nl/ . How to apply: Applications, including a Curriculum Vitae, a statement of your research interests, and the names and addresses of 2 references, must be sent to: Faculty of Geosciences, Personnel Department, P.O. Box 80115, 3508 TC Utrecht, or submitted by e-mail to: peno@geo.uu.nl Please mention where you originally saw our advertisement and quote vacancy number 72082 in all communications. The position is open until filled.

wolthers@geo.uu.nl wolthers@geo.uu.nl

Vienna 6 PopGenomicsHybridization

PhD Program in Population Genetics at the VMU Vienna, Austria "Population Genomics of Natural Hybridization"

6 PhD positions in theoretical and experimental population genetics are available to found a new collaborative research program with projects in six research groups:

Empirical: # Measuring gene flow between Drosophila species by massive parallel sequencing (PI: Christian Schloetterer, christian.schloetterer@vu-wien.ac.at) # Measuring gene flow between hare species by massive parallel sequencing (PI: Franz Suchentrunk, Franz.Suchentrunk@vu-wien.ac.at) # Hybridization in camels (PI: Chris Walzer, Chris.Walzer@vu-wien.ac.at)

Theory: # The genomic signature of adaptive trait introgression (PI: Joachim Hermisson, joachim.hermisson@lmu.de) # Bayesian approaches to estimate population parameters from incomplete population genomic data (PI: Claus Vogl, Claus.Vogl@vu-wien.ac.at) # Development of new sequence alignment algorithms for massive parallel sequencing data (PI: Arndt von Haeseler, arndt.von.haeseler@univie.ac.at)

The program combines cutting-edge technologies (massive parallel sequencing) with state-of-the-art modelling and computational tools. The common aim is gain a deeper understanding of interspecific gene flow and the formation of species boundaries in hybrid zones of closely related species.

Prospective students could either have a background in theoretical, computational or experimental biology. The nature of the PhD program requests a strong desire for interdisciplinary and interactive research. In addition to a competitive salary, the program offers specifically designed courses on research methods and academic skills (all in English), a personal budget (travel money) and a labtop for every student, an annual retreat in the Austrian alps, etc, etc ...

Candidates are encouraged to contact the project advisors for additional details on individual PhD projects. For all details about the application procedure and further information about the PhD program consult the program webpage at:

http://i122server.vu-wien.ac.at/pop/PhD/phd_start.html The application deadline is the 3. August 2007, the prospective starting date of the PhD projects is the 1. January 2008.

hermisson@zi.biologie.uni-muenchen.de
hermisson@zi.biologie.uni-muenchen.de

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AgroParisTech MolAssistedSelection

A permanent position of assistant professor specialized in Molecular Assisted Selection and Association Genetics will soon be open at AgroParisTech (Paris France).

Applicants must be fluent in french so the rest of the message is written in this language.

Un poste de maitre de conference sera bientot mis a concours a AgroParisTech. Le profil est disponible aux adresses suivantes :

http://www.agroparistech.fr/spip.php?rubrique1034 (poste MC 01 105)

ou

http://moulon.inra.fr/SGV/jobs/ Les modalites de concours et toutes informations administratives sont disponibles a l'adresse :

http://www.agroparistech.fr/spip.php?rubrique645 Le concours se tiendra en 3eme session, pour laquelle les dates limites officielles de depot des dossiers par les candidats ne sont pas encore publiees par le ministere, mais cela risque d'etre en Aout ou debut septembre (nous esperons que ce ne sera pas plus tot).

Philippe BRABANT Professeur AgroParisTech : Génétique Evolutive et Amélioration des Plantes

Station de Génétique Végétale (UMR 320) Ferme du Moulon 91190 Gif sur Yvette France

Phone 33 (0 only in France) 1 69 33 23 77 Fax 33 (0 only in France) 1 69 33 23 40

email : brabant@moulon.inra.fr

brabant@moulon.inra.fr

AmericanMuseumNatHistory ResAssist EvolBiol

Research Assistant, Evolutionary Biology/Population Genetics/Conservation Genetics: Full-time

A laboratory research assistant to be based at The American Museum of Natural History is sought to work on conservation genetics projects beginning in mid-July. Experience with high-throughput molecular data collection, as well as data management and analysis, are essential. Applicants must have demonstrated proficiency with up-to-date approaches, including standard and alternative methods of DNA extraction including degraded tissues such as scat, bone and historical samples, standard skills for PCR and cloning, DNA sequencing and microsatellite optimization and analysis, and SNP analysis. Knowledge of automated DNA sequencer usage and troubleshooting is preferred. Applicants must hold a Bachelors or Masters degree in Evolutionary Biology, Population Genetics, Molecular Systematics, Molecular Ecology, Conservation Genetics or related field. Preference will be given to applicants with work experience (2-5 yrs.), data management skills, and proficiency with analytical software programs.

Interested applicants should send a cover letter detailing their experience and interests and CV, along with the names and contact information of 3 references to Dr. Howard Rosenbaum (hcr@amnh.org). Applicants must put (and ONLY put) the following term (as is) in the email subject line for applications to be considered: ConGenLabAsst

hcr@amnh.org

CNRS France EvolBiol

This advert concerns any scientist who wants to develop a project related to Life Sciences, some of the programmes being particularly interesting for evolutionary biologists.

Best regards,

Jean

CNRS ATIP PROGRAMMES (Actions Thématiques et Incitatives sur Programme) Call for Team leaders 2007-2008

The "Département des Sciences du Vivant" (Life Sciences Division) of the CNRS, offers an opportunity to scientists at the end of their postdoctoral training for developing an innovative independent research project while setting up their own group within a CNRS laboratory. Successful applicants will receive a three year grant (150 k for equipment and consumables), the possibility of hiring a postdoctoral fellow for two years, at least 50 m2 of lab space and, whenever possible, technical assistance. At the end of the three years, the ATIP team leaders may compete for a two year extension through the "ATIP Plus" programme. Eight programmes concern specific research areas (Biodiversity and ecosystem dynamics, Cell biology and Immunology, Developmental biology, Genetics, Microbiology, Systems biology, Neurobiology: from molecular to cognitive neurosciences, Structure-function relationships, Dynamics of biomolecules and their assemblies), and one (ATIP "Blanche") is open to any project of high scientific quality related to Life Sciences. Applications from scientists presently working in a foreign country are particularly encouraged. Applicants must be less than 40 years old, or have defended their PhD thesis within the last ten years (exception may be made for women with children). At the beginning of the ATIP contract, applicants need not hold a permanent position within a French research organisation such as CNRS, INSERM or University. In this case, the CNRS will hire the team leader, and salaries will range between 3,400 and 3,800 per month. However, he/she must apply for and obtain such a tenured position in order to be eligible for a possible two year extension ("ATIP Plus" programme). Applications for tenured positions are independent from the ATIP programme and have to be submitted in parallel. Applicants are not allowed to join a laboratory in which they have been PhD student or postdoctoral fellow for years. Application forms and more detailed information are available either directly or through the web site of the CNRS: http://www.cnrs.fr/infoslabos/atip/lifeatip.htm. Applications must be written in English and addressed before October 1st, 2007 to: Jean HOUMARD - Chargé de Mission CNRS - Département des Sciences du Vivant 3, rue Michel Ange - F-75794 Paris Cedex 16. E-mail: sdv-atipe@cnrs-dir.fr

Dr. Jean Houmard Chargé de mission Département Sciences du Vivant CNRS 3, rue Michel-Ange 75794 Paris cedex 16 Tél. 33 (0)1 44 96 40 29 Fax 33 (0)1 44 96 53 60

sdv-atipe@cnrs-dir.fr

CambridgeU BettleEvol

A post-doctoral research associate position is available to work with Dr Rebecca Kilner, studying a laboratory population of breeding burying beetles Nicrophorus vespilloides. The successful applicant will investigate how ageing influences the provision of parental care and how this, in turn, influences the extent of parent-offspring conflict and sibling rivalry. Candidates should therefore have a background in behavioural ecology and a strong interest in social evolution and life history theory. Experience in working with insects would be an advantage, but is not essential.

The position is funded by a Philip Leverhulme Prize and is available from 1 September 2007, for up to two years in the first instance. There is an initial probationary period of six months. Salary range: £24402 pa - £31840 pa.

For a standard application form, (PD18), please email Reception@zoo.cam.ac.uk Informal enquiries may be made to Dr Rebecca Kilner by email: rmk1002@hermes.cam.ac.uk Completed application forms together with a CV should be returned to the Departmental Administrator, Department of Zoology, Downing Street, Cambridge CB2 3EJ by the deadline, 30 June 2007. Applications can be emailed or sent through the post. Please quote: PF01262. Interviews are likely to held in mid/late July 2007.

–

Dr Rebecca Kilner Department of Zoology University of Cambridge Downing Street Cambridge CB2 3EJ UK

Tel: 01223 331766 Fax: 01223 336676 website: http://www.zoo.cam.ac.uk/zoostaff/bbe/Kilner/Rebecca1.htm rmk1002@hermes.cam.ac.uk rmk1002@hermes.cam.ac.uk

ComputerCraft Bioinformatics Taxonomist

Computercraft Corp. - Invertebrate Taxonomist

Invertebrate Taxonomist - Bethesda, MD USA

Computercraft seeks an Invertebrate Taxonomist to join the team of highly skilled and dedicated professional molecular biologists and systematists working onsite at the National Institutes of Health (NIH) in Bethesda, MD. Our scientists work with genomic experts at NIH's National Center for Biotechnology Information (NCBI) in the National Library of Medicine (NLM) to create and enhance a suite of databases and tools available to researchers worldwide. We are currently looking for an invertebrate taxonomist to help maintain the NCBI Taxonomy database for the Taxonomy Project at NCBI.

This technically challenging position requires a PhD with a broad knowledge of invertebrate systematics at the morphological and/or molecular level. Familiarity with the principles of phylogenetic systematics and zoological nomenclature is strongly desired. The successful candidate will be responsible for maintaining the nomenclature and classification of a portion of the taxonomy database. Database curation includes verifying taxon names, ensuring that classification is consistent with current consensus, and interacting with sequence annotators and submitters. Up to 50% of the candidate's time will be available for independent research. Opportunities for research collaboration exist within NCBI and NIH, as well as within other regional institutions, depending on research interests. Teamwork interaction, excellent verbal communication as well as written and organizational skills are essential for this position.

For consideration please submit cover letter, resume/CV, salary history, salary requirements, and U.S. employment eligibility (you must currently reside in the U.S. and be eligible to work). Please note that incomplete application cannot be considered.

Computercraft Attn: HR 8300 Greensboro Drive Suite 720 McLean VA 22102 703.288.4679 fax hr@computercraft-usa.com

For more information on Computercraft and our other biotechnology positions, please visit us at www.computercraft-usa.com

Computercraft offers a competitive salary and an excellent benefits package including PPO health insurance with 100% company paid premiums, 401K program with matching, paid time off and holiday pay, life insurance, flexible spending and disability coverage. We offer an excellent work life balance with a standard 40 hour work week and the chance to work alongside accomplished scientists at NIH/NCBI.

Computercraft is an equal opportunity employer.

Computercraft Corp. - Metagenome Bioinformatics

Scientist

Metagenome Bioinformatics Scientist - Bethesda, MD USA

Computercraft seeks a highly motivated individual to curate environmental sample sequences in GenBank and other related resources at the National Institutes of Health (NIH), National Center for Biotechnology Information (NCBI). These samples include sequences from more traditional site-directed environmental sample studies (rRNAs, and other loci) as well as more recent 'metagenomics' projects involving undirected whole-environment shotgun sequencing strategies.

The NCBI directed project aims to make these data more useful to the relevant research communities. The successful candidate will be in direct contact with all the current research and researchers in this field. Specifically, the individual will work with the external scientific groups that generate and study environmental sequence data, and with the various groups at the NCBI that are involved in the submission, classification and use of these sequences.

The successful candidate will work in the NCBI Taxonomy group and collaborate with experts in GenBank, Genomes, BLAST, and Probe database groups onsite at the NIH campus in Bethesda, Maryland. This is an opportunity for the right person to make a significant contribution to the scientific community.

Responsibilities:

Design a broad strategy to represent and manipulate environmental sequence data (site-specific and metagenomic).

Curate the nomenclature and classification of environmental sequences in the NCBI Taxonomy Database.

Assist in the development of submission tools, annotation guidelines, analysis and statistical software tools for environmental sequences.

Develop resources at the NCBI and contacts with the research community to best support these efforts.

Requirements:

Ph.D. in biology or related field Extensive experience with metagenome/environmental sample studies Excellent oral and written communication skills

For consideration please submit cover letter, curriculum vitae, salary history, salary requirements, and U.S. employment eligibility (you must currently reside in the U.S. and be eligible to work). Please note that incomplete application cannot be considered.

Computercraft Attn: HR 8300 Greensboro Drive Suite 720 McLean VA 22102 703.288.4679 fax hr@computercraft-usa.com

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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

CorvallisOR StatisticalGenetics

The USDA Forest Service, Pacific Northwest Research Station is looking to fill a Statistician (Biology) GS-1530-09 position ($43,731-$56,849 per year). This is a temporary, TERM position, located at the Forestry Sciences Laboratory in Corvallis, OR. The initial appointment is for 13 months, but may be extended up to four years. The vacancy announcement for this position will open June 11, 2007 and close June 28, 2007. The announcement will be posted at the USAJOBS website (http://www.usajobs.opm.gov), the U.S. Government's official site for jobs and employment information. The Announcement number for this position is: PNW-RMP-465-07D.

The Statistician position is with the Plant Genetics Team, and we study structure and function of molecular and adaptive genetic variation in native forests and grasslands, and the genetics issues associated with the management of genetic resources in natural stands, managed stands, and restoration efforts. Studies range from molecular genetics to quantitative and population genetics. Job duties include:

Assists scientists in the analyses of genetic studies involving bioinformatics as well population and quantitative genetic procedures. Executes and interprets statistical analyses on data for studies. Uses computational methods, including statistical, graphical, and other software packages as tools to accomplish analysis and interpretation. Assists scientists with experimental designs and mathematical and related analysis procedures. Reviews manuscripts prepared by scientists to insure the applicability of statistical methods, the accuracy of statistical results, and the reliability of presentation. May assist in the preparation of manuscripts. Researches and reviews statistical analyses, computer packages, and new data processing procedures for state-of-the-art methods and techniques. Disseminates information and advice on the use of these tools and capabilities. Consults with scientists on computer processing of statistical analyses by providing assistance with data organization, programming, and technical details necessary for data processing, by using statistical software packages. Assists users in developing solutions to related computer processing problems associated with statistical processing and analyses of data.

Questions regarding the duties of this position may be directed to Rich Cronn, rcronn@fs.fed.us, (541) 750-7291. If you would like to learn more about the Pacific Northwest Research Station, visit our website at http://www.fs.fed.us/pnw/about/programs/-rmp/forest-genetics.shtml . Rich Cronn, Research Geneticist US Forest Service, Pacific NW Research Station 3200 SW Jefferson Way, Corvallis, OR 97331 541-750-7291 phone * 541-750-7329 fax * rcronn@fs.fed.us

Richard Cronn <rcronn@fs.fed.us>

FribourgU JuniorGroupLeader Evol

Junior Group Leader in Ecology or Evolution

The Unit of Ecology & Evolution of the Department of Biology at Fribourg University, Switzerland, invites applications for a junior group leader position ("maitre-assistant") in the field of Ecology or Evolution.

We are seeking a highly motivated scientist with postdoctoral experience, a strong publication record, and the will to develop an independent research group within the Unit. Applications are invited from researchers in any area of Ecology and Evolution. Applicants will be expected to develop an externally funded and internationally recognized research program. Attached to the position is a 50% lab technician, funded by the university. Teaching duties include participation in undergraduate courses, and an advanced Master-level course in the applicant's research area. Undergraduate teaching in either German or French would be desirable, but English is also possible. Master-level teaching is in English.

The University of Fribourg provides excellent facilities and a stimulating intellectual and social environment. The Department of Biology comprises 14 research groups organized in three Units. The Unit of Ecology & Evolution consists of five groups studying plant population ecology, invasive plant species, community ecology in agricultural landscapes, and evolutionary genetics of subdivided populations (http://-www.unifr.ch/biol/ecology). Fribourg is a very pleasant and lively medium-sized town in the centre of Switzerland (less than one hour from Lausanne, Bern, and Neuchatel). The old town is charming and holds one of the finest remnant of medieval architecture in Europe. Students account for more than one fourth of the population.

The position is open starting 1 September 2007, and is limited to five years. Annual salary starts at about CHF 90'000 (ca. EUR 55'000). To apply, please send a CV with a list of publications, a brief (less than 1 page) statement of general research interests and planned research, as well as the names and e-mail addresses of two referees in a single pdf-file to Catherine Cuennet: catherine.cuennet@unifr.ch. The deadline for application is 30 June 2007.

For further information contact Louis-Felix Bersier, Unit of Ecology and Evolution, Ch. du Musee 10, CH-1700 Fribourg, Switzerland tel +41 26 300 8869; fax +41 26 300 9698; louis-felix.bersier@unifr.ch

tadeusz.kawecki@unifr.ch tadeusz.kawecki@unifr.ch

GeorgiaTech ResTech GenomeCenter

The School of Biology at the Georgia Institute of Technology seeks a Research Technician to help run its Genome Center. Faculty in the School of Biology are leaders in several cross-departmental programs, such as environmental systems microbiology and computational biology and bioinformatics. The ecology and evolution group in the School of Biology was recently ranked 8th in the country based on faculty productivity.

Required job duties: Direct and conduct the analysis of nucleic acid samples for the following determinations: Sequencing, AFLP, SNPs, Microarray-based analysis, capillary electrophoresis and phosphoimaging. Additional proficiency in quantitative Polymerase chain reaction and HPLC is highly desirable. Expected proficiency in all of the software that is used to set-up, Conduct sampling and interpretation of the various genomic-based analyses listed above. Mac and PC platform Proficiency required. Assist Director of Genome Center in grant writing to procure funds for additional instrumentation. Assist in the teaching and training of other students, technicians and staff that will be using the center.

For information see http://www.biology.gatech.edu/

and http://www.biology.gatech.edu/genomecenter/ To apply or to have questions addressed, please contact DR. PATRICIA SOBECKY at the address below:

>Patricia A. Sobecky, Ph.D. >Associate Professor >School of Biology >Georgia Institute of Technology >310 Ferst Drive >Atlanta, GA 30332-0230 > >404-894-5819 (office) Room 1242 ES&T Bldg >404-385-4440 (fax) or 404-894-0519 (fax)

Michael A D Goodisman

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

webpage: http://www.biology.gatech.edu/faculty/michael-goodisman/ profile: http://www.whistle.gatech.edu/archives/04/nov/08/spot.shtml spotlight: http://www.gatech.edu/profiles/goodisman.php email: michael.goodisman@biology.gatech.edu office: 404-385-6311 lab: 404-385-6312 fax: 404-894-0519

michael.goodisman@biology.gatech.edu michael.goodisman@biology.gatech.edu

Germany ForestGenetics

Research scientist in Forest Genetics at BFH

The Federal Research Centre for Forestry and Forest Products (BFH) is looking to fill the position of a research scientist at the Institute for Forest Genetics and Forest Tree Breeding in Grosshansdorf, Germany . The salary will be according to E13 (TVoD) (35.000 Euro - 51.000 Euro per year before taxes). This is a temporary position fixed for two years.

Job description: The Institute is increasingly applying molecular gene markers to address questions in population genetics of trees, to study genetic diversity and to work out guidelines for the conservation of forest genetic resources. Moreover, molecular gene markers are applied to identify the origin of forest reproductive material and are used as tools in quantitative genetics of trees.

The successful candidate is expected to perform a part of this work in cooperation with different national and international partners.

Required qualifications: PhD in forest science, biology or a similar field, doctoral thesis on a subject in population genetics or molecular biology, broad experience in development and application of molecular gene markers, as well as experience in analysis of population genetic data. Knowledge of the German language would be an advantage but is not a necessary requirement.

The BFH is interested in increasing the number of female employees and encourages women to apply. The BFH is an equal opportunity employer and handicapped candidates with minimum physical capabilities and equal qualifications will be given preference.

Application: To apply, please send a cover letter, CV with a list of publications, as well as the names and e-mail addresses of two referees. The applications need to be submitted via postal mail to Christine Meyer, BFH, Leuschnerstrasse 91, 21031 Hamburg, Germany. Applicants must put the following reference number (position: 140.2.0.1-12) in the subject line of the cover letter. The deadline for application submission is 13/07/07.

Questions regarding the duties of this position may be directed to Dr. Bernd Degen (phone ++49-(0)4102-696-101; E-mail: b.degen@holz.uni-hamburg.de). If you would like to learn more about the Institute for Forest Genetics and Forest Tree Breeding, visit our website at http://www.bfafh.de/inst2/indexe.htm Dr. Bernd Degen

Direktor und Professor BFH, Institut fuer Forstgenetik und Forstpflanzenzuechtung Sieker Landstrasse 2 D-22927 Grosshansdorf Germany Tel.: +49-4102-696-101 Fax.: +49-4102-696-200 E-mail: b.degen@holz.uni-hamburg.de http://www.bfafh.de/

b.degen@holz.uni-hamburg.de

HarvardU ResTech ArabidopsisEvolGenetics

Full Time Research Technician Position Harvard University Contact: Kathleen Donohue; kdonohue@oeb.harvard.edu

Full time research technician wanted to participate in research in evolutionary ecology and genetics of Arabidopsis thaliana. Research will combine work in the field, laboratory, and greenhouse. Duties include plant care; preparations for molecular and biochemical work; setting up and maintenance of field and greenhouse experiments and keeping supervisor informed of results; data collection and organization; instruction of others in basic laboratory techniques and procedures; general lab and clerical tasks; other related duties as required.

Available 1 August, 2007.

Please send CV and names of references to Kathleen Donohue: kdonohue@oeb.harvard.edu

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Kathleen Donohue Associate Professor Organismic and Evolutionary Biology Harvard University 22 Divinity Avenue Cambridge, MA 02138 USA

Tel: (617) 384-9768 Fax: (617) 495-9484 kdonohue@oeb.harvard.edu

Kathleen Donohue <kdonohue@fas.harvard.edu>

Lisbon EvolEpidemiology

Research Position in Evolutionary Biology at the Lisbon Epidemiology Consortium

The Lisbon Epidemiology Consortium (CEL) has been recently formed by the University of Lisbon (UL) and Instituto Gulbenkian de Ciência (IGC) to develop integrative approaches to epidemiology research, training and practice. Funded by a grant from the Portuguese Ministry of Science (http://www.eracareers.pt/)complemented by funds from the European Commission, CEL invites applications for eight positions:

1. Programme Manager - Contact: ggomes@igc.gulbenkian.pt 2. Mathematical Epidemiology - Contact: ggomes@igc.gulbenkian.pt 3. Evolutionary Biology - Contact: ggomes@igc.gulbenkian.pt 4. Statistical Epidemiology - Contact: ceaul@fc.ul.pt 5. Clinical Epidemiology - Contact: carmo.fonseca@fm.ul.pt 6. Biomedical Informatics - Contact: carmo.fonseca@fm.ul.pt 7. Statistical Physics - Contact: theresa@cii.fc.ul.pt 8. Dynamical Systems - Contact: cmaf@ptmat.fc.ul.pt

The post holders will have the opportunity to initiate their own research projects while contributing to the establishment of solid bonds between consortium research units. There are no teaching obligations, but there will be opportunities to contribute to graduate education.

Applicants should hold a PhD and demonstrate interdisciplinary interests and managerial skills. Candidates to posts 2-8 should show additional evidence of independent research and significant scientific accomplishments. An initial contract of 5 years will be offered to the successful candidates. For further details visit http://cel.igc.gulbenkian.pt . Deadlines are in August. For more details on each position follow the respective link.

Applications, including cover letter, CV, research plan and three letters of recommendation should be sent by email to the appropriate contact.

Gabriela Gomes <ggomes@igc.gulbenkian.pt>

MiamiU MolEvolTech

We seek a highly motivated Technician to join an active lab investigating population genetics, evolution and ecology of marine invertebrate species (http://www.bio.psu.edu/people/faculty/baums/). Responsibilities include DNA extraction, sequencing and genotyping as well as database entry and archiving, and general lab maintenance including ordering supplies and supervision of students. Active participation in lab meetings and discussions is expected.

Requires Bachelors degree or equivalent in an appropriate field of technology or science such as Biological Sciences, Molecular Biology, or Genetics, plus one year of work-related experience. Demonstrated research experience with DNA extractions, PCR, and sequencing; familiarity with genetic analyses of sequence and/or microsatellite data and facility with standard computer software programs required. Experience with microsatellites and gene sequencing is required. Candidates must have considerable experience with a variety of standard molecular techniques (DNA extraction, PCR, gel electrophoresis, DNA sequencing, microsatellites, etc.) so that he/she can work with minimal supervision. This is a fixed-term appointment funded for one year from date of hire with excellent possibility of re-funding. To apply, e-mail letter of application describing qualifications for the job and reason for interest, CV, and names and e-mail addresses of three references to baums@psu.edu. Women and minorities are encouraged to apply. Penn State is committed to affirmative action, equal opportunity, and the diversity of its workforce.

– Iliana B. Baums, Ph.D. Assistant Professor, Research Department of Biology The Pennsylvania State University 208 Mueller Laboratory University Park, PA, 16802

814.867.0491 (Office) 814.867.0492 (Lab) 814.321.3593 (Mob) 814.865.9131 (Fax)

http://www.bio.psu.edu/people/faculty/baums/ ibaums@rsmas.miami.edu ibaums@rsmas.miami.edu

MichiganStateU ResAssist DrosophilaGenetics

Research Assistant Job

I am looking for an active and well-organized person with relevant research experience to work as a laboratory manager and research assistant in the laboratory of Alexander Shingleton in the Department of Zoology at Michigan State University. My research involves the nutritional regulation of size, and the mechanism and evolution of allometry in Drosophila. The successful applicant will be joining a recently established laboratory and research program, so will have considerable influence over the future direction of their work.

REQUIRED: Bacholer's degree in genetics, developmental biology, molecular biology or related field.

DESIRED: One to three years of related and progressively more responsible or expansive work in area of genetics or developmental/ molecular biology; experience planning research methodology and developing, adapting, and updating research procedure; good understanding of Drosophila genetics; experience in a Drosophila development laboratory; experience with basic microscopy (dissecting, compound and confocal) and staining techniques (anti-body, in situ hybridization); experience with microscope imaging-software and statistical packages; good basic molecular biology skills (e.g. PCR, Western/Southern/Northern blotting, Microarray analysis).

BASIC FUNCTION: Assist in coordinating laboratory research activities; help plan, design and execute experiments on Drosophila development; use various molecular and microscopy techniques to obtain research data; analyze results using imaging and statistical packages; researche current literature to determine most economical, efficient and productive research methods.

CONDITIONS: Salary based on experience. This is a 12-month position, renewable indefinitely subject to funding.

Please apply by email with a letter expressing interest, your CV and names of three references to Alex Shingleton (shingle9@msu.edu). Earliest start date is expected to be August 1, 2007.

Alexander W. Shingleton Assistant Professor Ecology, Evolutionary Biology & Behavior Program Genetics Program

Department of Zoology Natural Sciences Building Michigan State University East Lansing, MI 48824

Tel: 517-353-2253 www.msu.edu/ ˜ shingle9 shingle9@msu.edu shingle9@msu.edu

OhioStateU DatabaseProgrammer

Title: Job for database programmer Job Location: Ohio State University (bmi.osu.edu)

Ground-up design of phylogeographic service like that used in Genomic Analysis and Geographic Visualization of the Spread of Avian Influenza (H5N1)

http://www.informaworld.com/openurl?genre=-article&issn=1063-5157&issue=2&spage=-321&volumeV

The Database Programmer is responsible for extending and building new components of a PostGIS enabled PostgreSQL database architecture. In addition, the position is responsible for reviewing and designing efficient query approaches for both spatial and standard SQL statements. Will need to be able to create SQL queries for the non-SQL versed user, and reformat/manipulate results. The successful candidates will have demonstrated strength in analyzing and troubleshooting data and processing issues. Assists in the resolution of database capacity issues, replication, and other distributed data issues.

You must have a desire to learn and understand the data in order to work with the "big picture" in mind. Finally, you should be able to work independently and confidently make decisions.

Minimum 2 years PostgresSQL and PHP experience.

Salary commensurate with experience

Please send CV and links to relevant examples of previous work. Contact: Daniel Janies, (danjanies@hotmail.com) for more information.

danjanies@hotmail.com

Oxford MRC Programmer

EUMODIC Scientific Programmer Bioinformatics Group MRC Mammalian Genetics Unit Oxfordshire, U.K.

Scientific Programmer

From £19,238 pa

The MRC Mammalian Genetics Unit one of the participants in the EU Eumodic project (www.eumodic.org). The project aims to carry out comprehensive first-line phenotyping of a large number of gene knockout lines in four major phenotyping centres across Europe and bring together this data in a central database, EuroPhenome.

We are seeking a software engineer to lead the software development of the EuroPhenome database, including refinement of its data capture functions and adding new functionality to its user interface for data annotation. In addition, you will be involved in the research and development of data mining and knowledge extraction interfaces to EuroPhenome alongside subsequent integration with phenotype ontologies. You will also assist in the development and maintenance of associated websites.

We are looking for someone with a strong background in database integration, ideally the use of XML for phenotype data exchange combined with knowledge of the storage and representation of phenotype data.

You will be based in the MGU Bioinformatics Group and will interact with related groups across Europe. There will be opportunities to attend project meetings in Europe (maximum of 3 per year). We can offer a competitive salary, 30 days holiday and a generous pension scheme.

This post is funded until 31 January 2011.

For further information on the post please contact Dr John Hancock (j.hancock@har.mrc.ac.uk) or Dr Ann-Marie Mallon (a.mallon@har.mrc.ac.uk).

For an application form please email oxford.recruitment@ssc.mrc.ac.uk or contact 01793 301156 quoting reference number 2007-318/MGU Scientific Programmer.

Closing date for applications: 15 June 2007

The MRC is an Equal Opportunities Employer

Dr John M. Hancock Head of Bioinformatics, MRC Mammalian Genetics Unit, Harwell, Oxfordshire OX11 0RD, U.K.

E-mail: J.Hancock@har.mrc.ac.uk Telephone: +44 (0)1235 84 1014 Fax: +44 (0) 1235 84 1210 WWW: http://informatics.har.mrc.ac.uk/ Personal Page: http://informatics.har.mrc.ac.uk/jmhwww/ j.hancock@har.mrc.ac.uk j.hancock@har.mrc.ac.uk

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PennStateU ResTech FruitFlyPopGenet

Pennsylvania State University

DEPARTMENT OF Entomology

Research Technologist

Phylogenetic and Population Genetics of true fruit flies (Tephritidae)

A research technologist position is available in the McPheron laboratory in the department of Entomology at the Pennsylvania State University. The McPheron lab is exploring the phylogenetic relationships of related Anastrepha species using mitochondrial and microsatellite DNAs. We seek an enthusiastic individual to participate in our genetics projects and to oversee various lab activities. The successful candidate should be motivated, organized and careful, with excellent oral and written communication skills, and be able to work largely independently. Salary will range from $24,000 to $28,000 per annum depending on experience and will include benefits.

Job responsibilities will include performing basic molecular techniques (DNA extraction, PCR, sequencing, genotyping) as well as general lab management (including some supervision of undergraduate researchers). Opportunities for independent research projects will also likely exist.

Minimum qualifications are a M.S./M.A. or B.A./B.S. (with experience) degree in biology (or a related field), and demonstrable experience conducting research in a broadly-defined) genetics or molecular biology lab. The candidate should be familiar with genetic analysis software such as MEGA, DNASP, Arlequin, and PAUP. Preference will be given to those candidates with significant laboratory experience that includes troubleshooting and optimizing molecular biology protocols, and/or those who have previously worked with fruit flies or other small invertebrates.

Review of applications will begin June 8, 2007 and continue until the position is filled. Informal inquires about the position are welcome and can be directed to Raul Ruiz (rur132@psu.edu). To apply, send your resume or CV, and include a cover letter (describing your interest in the position and any relevant expertise). Also, arrange to have at least two professional letters of reference sent by email/fax/mail to:

Raul Ruiz Department of Entomology The Pennsylvania State University 501 ASI Bldg University Park, PA 16802 tel: 814-865-3345 fax: 814-865-3048 email: rur132@psu.edu web: http://www.ento.psu.edu/mcpheronlab/ rur132@psu.edu

Prague ResAssist SexEvol

Marie Curie Early Stage Training Fellow (Fixed-term)

Institute of Vertebrate Biology, Academy of Sciences and Charles University in Prague, Czech Republic

Salary: approx 1,900 Euro per month plus additional allowances as per Marie Curie Early Stage fellowships

The postholder will work with Prof. Jan Zima in Prague to investigate the evolutionary balance between sexual and asexual reproduction in the ostracod Eucypris virens using molecular genetic approaches. Applicants must have a good grounding in evolutionary biology and experience of laboratory methods in molecular ecology. Sound knowledge of English is essential. This post is available from September 2007 for a period of 9 months.

This is a component project of a Marie Curie Research Training Network (for details, see http://www.evirens.group.shef.ac.uk/index.htm). The official working language of the network is English.

In accordance with Marie Curie mobility regulations, this fellowship is available to EU nationals only, except for the Czech nationals or other nationals who will have resided/worked in the Czech Republic for more than 12 months in the 3 years prior to starting the fellowship. Applicants who already have a PhD are not eligible. Further details can be found in the Marie Curie Early Stage training handbook (see sections 5.4 - 5.8) and FAQs available at http://ec.europa.eu/research/fp6/mariecurie-actions/action/stage_en.html . Closing Date: June 22, 2007

Contacts: Prof. Jan Zima Institute of Vertebrate Biology Academy of Sciences of the Czech Republic Kvetna 8 CZ - 603 65 Brno Czech Republic

Tel : +420-5 4342 2554 Fax: +420-5-4321 1346 jzima @ ivb.cz

Dr. Ruza Bruvo Department of Animal and Plant Sciences The University of Sheffield Western Bank Sheffield S10 2TN r.bruvo @ sheffield.ac.uk

Tel. +44 (0)114 22 20113

r.bruvo @ sheffield.ac.uk r.bruvo @ sheffield.ac.uk

TREEEditor maternitycover

Editor, Trends in Ecology & Evolution (6-10 months' maternity cover)

We are seeking to appoint an editor to cover maternity leave onTrends in Ecology & Evolution, which is one of the leading international review journals dealing with all aspects of ecology and evolution. The role will be based in the Holborn office in London and is for a period of six-ten months with an anticipated starting date of 1st September 2007 (applicants must have EU work permit). You will be acquiring, managing and developing the very best editorial content, making use of a network of contacts in academia, as well as exploiting information gathered at international conferences, to ensure the title maintains its market-leading position. You will be keen to develop new streams of content in-line with new developments, as well as to exploit the opportunities offered by on-line and interactive services.

This is an exciting and challenging role and you will need a PhD and post-doctoral experience in a relevant discipline and have confidence in your scientific judgement. Good interpersonal skills are essential because the role involves networking in the wider scientific community as well as collaborations with other parts of the business.

For this position, previous publishing experience is not necessary but preferred - we will make sure you get the training and development you need. This is an ideal opportunity to stay close to the cutting edge of scientific developments in the field whilst developing a new career in a dynamic publishing environment. For further information, please contact Katrina Lythgoe, Editor of Trends in Ecology & Evolution, e-mail: k.lythgoe @elsevier.com.

To apply, please send your CV and a covering letter, including your salary expectations by 28th June 2007 to Emma Bowers, HR Administrator, Elsevier Limited The Boulvevard, Langford Lane, Kidlington, Oxford, OX5 1GB. Alternatively, please e-mail: e.bowers@elsevier,com

This email is from Elsevier Limited, a company registered in England and Wales with company number 1982084, whose registered office is The Boulevard, Langford Lane, Kidlington, Oxford, OX5 1GB, United Kingdom.

"Lythgoe, Katrina (ELS-LON)" <K.Lythgoe@elsevier.com>

UAarhus EvolGenetics

FACULTY OF SCIENCE

DEPARTMENT OF BIOLOGICAL SCIENCES

Associate Professor in Evolutionary Genetics

A position as Associate Professor in Evolutionary Genetics is available at the Department of Biological Sciences, Section for Ecology and Genetics, from January 1, 2008.

The candidate is expected to become an integrated part of a research team at the Section for Ecology and Genetics, seeking to integrate empirical and theoretical approaches to tackle problems within evolutionary biology. The candidate should have a strong international research profile and be willing and able to cooperate across borders of research fields, and he/she is expected to be experienced in the use of molecular techniques on evolutionary genetic problems.

Furthermore, the applicant should document teaching and tutoring qualifications at all levels (BSc, MSc, PhD).

Applications must be in English and include a curriculum vitae, a complete list of publications, a statement of future research plans and information about research activities, teaching qualifications and management experience, all in 4 copies (see http://www.nat.au.dk/default.asp?id=7838&la=UK <http://www.nat.au.dk/default.asp?id=7838&la=UK> for the recommended level of detail). If the applicant wants other material to be considered in the evaluation (publications and other documentation of research and teaching qualifications, as well as management experience) such material must be clearly specified and must either be enclosed in hardcopy (3 copies) or must be available electronically.

The Faculty refers to the Ministerial Order No. 170 of 17.03.2005 ((http://www.au.dk/da/21-05.htm) on the appointment of teaching and research staff at the universities under the Ministry of Science, Technology and Innovation.

Salary depends on seniority as agreed between the Danish Ministry of Finance and the Confederation of Professional Unions.

Applications should be addressed to The Faculty of Science, University of Aarhus, Ny Munkegade, Building 1520, DK-8000 Aarhus C, Denmark, and marked 212/5-???

The deadline for receipt of all applications is June 25, 2007, at 12,00 noon.

For more information contact the head of the department Jørgen Bundgaard, Institute of Biological Sciences, Build. 1540, Ny Munkegade, 8000 Aarhus C., Denmark; phone: 89423266; E-mail: biojb@biology.au.dk <mailto:biojb@biology.au.dk>

Volker Loeschcke <volker.loeschcke@biology.au.dk>

UBalearicIslands ResTech ArthropodEvol

Hi,

The Joan Ponss Lab at the IMEDEA (a Research Institute of to Centro Superior de Investigaciones Científicas, CSIC, and also part the University of Balearic Islands, UIB) on the sunny Majorca, Balearic Islands (SPAIN) has an opening for a Research Technician. In short, our lab focusses on evolutionary biology on arthropods (http://www.imedea.uib.es/ ˜ jpons/JPWPhome.htm). The successful applicant will be involved in various aspects of our research but mainly in our DNA barcoding project (www.pancoding.org). Lab tasks include DNA extraction, PCR-based genotyping, sequencing, data analysis, and maintaining our DNA and specimen collection. This individual will also be responsible for general lab management such as ordering supplies, maintaining equipment and organized lab.

Minimum qualifications are a Bachelor's degree in biology or a related field. Prior laboratory experience is desired, but not necessarily required. Training will be provided. We seek for an individual who pays attention to detail and good organizational skills.

We offer a two year contract, and a gross salary of 14000-17000 Euros per year upon qualifications.

To apply, please send a resume and contact information for three references to Joan Pons (joan.ponspons@uib.es).

Informal inquiries are also encouraged.

Joan

–

– Joan Pons PhD IMEDEA (CSIC-UIB) Miquel Marqués, 21 Esporlas, 07190 Illes Balears, SPAIN

email joan.ponspons@uib.es web http://www.imedea.uib.es/ ˜ jpons/JPWPhome.htm web http://www.pancoding.org phone +34 971 173425 fax +34 971 1731844

vieajpp8@uib.es

UCollegeLondon ChairSystemsBiology

UCL Faculty of Life Sciences

Chair of Systems Biology

UCL is pleased to invite applications for a new Chair in Systems Biology.

UCL is seeking applicants with an international research profile in Systems Biology. The successful applicant will lead an active research group in an area that may include; biophysics, cell and developmental biology, cell signaling, transcriptional control, or systems physiology.

UCL is a multi-disciplinary research-led university that has strengths in Life and Medical Sciences, Engineering, Physics, Chemistry and Engineering. The new Chair of Systems Biology will provide leadership in the development of a cross-departmental Centre for Systems Biology at UCL. This Chair will also be expected to help coordinate efforts to respond to national and international funding initiatives to advance Systems Biology research at UCL.

The Chair will also play a central role in CoMPLEX, the UCL Centre for Mathematics and Physics in the Life Sciences and Experimental Biology, which hosts a Doctoral Training Programme that attracts PhD students of the highest calibre from across the disciplines.

Salary is negotiable on the professorial scale.

Informal enquiries may be made to Professor Peter Mobbs, Dean of the Faculty of Life Sciences, tel: +44 (0) 20 7679 0879; email: p.mobbs@ucl.ac.uk

Further particulars and application details for the post can be downloaded from the Physiology website at http:// www.physiol.ucl.ac.uk/vacancies/ or obtained from Liz Hancock, tel: +44 (0) 20 7679 1351; email: e.hancock@ucl.ac.uk

We particularly welcome female applicants and those from an ethnic minority, as they are currently underrepresented within UCL at this level.

Closing date: Friday 22nd June 2007

ucbhpom@ucl.ac.uk ucbhpom@ucl.ac.uk

UEastAnglia Biodiversity

The School of Biological Sciences at the University of East Anglia (Norwich, UK) invites applications for a faculty position in biodiversity, at the lectureship level.

For non-UK readers, a lectureship position is equivalent to an Assistant Professorship in North America, with a three-year probationary period, after which the position is made permanent. Applications from any nationality are welcome, and biodiversity is to be interpreted in its broadest sense, as detailed below.

Details are below.

Dr. Douglas W. Yu School of Biological Sciences, University of East Anglia Norwich, Norfolk NR4 7TJ UK, 44-(0)1603-593-835 http://bioweb2.bio.uea.ac.uk/faculty/YuD.aspx http://homepage.mac.com/dougwyu/index.html office hours Tues 2:00 to 4:00

University of East Anglia, Norwich, U.K. Lectureship in Biodiversity

School of Biological Sciences

Lectureship in Biodiversity Ref: ATR761

Academic 2: £27,466 to £32,796 per annum or Academic 3: £34,813 to £40,335 per annum

The School of Biological Sciences at UEA is consistently rated to be one of the best academic communities of its kind in the UK for both research and teaching. We invite applications for the post of Lecturer in Biodiversity, tenable from 1 September 2007. Applicants must have a strong publication record and the ability or potential to lead a research group funded by competitive, external research grant funding, as well as to teach undergraduate and postgraduate (Ph.D. and M.Sc.) students. Biodiversity is to be interpreted in its broadest sense, potentially encompassing (without being restricted to) behavioural ecology, comparative and phylogenetic studies, conservation biology, evolutionary biology, molecular ecology, and population biology. To complement the School's existing research strengths, applicants with an interdisciplinary research outlook, and especially those with a strong interest in molecular, behavioural, genetic or evolutionary approaches, will be at an advantage.

Informal enquiries can be made to Andrew Bourke (e-mail a.bourke@uea.ac.uk or tel 01603 591868). More information about the School of Biological Sciences UEA can be found at http:// www.uea.ac.uk/bio/ Closing date: Friday 29 June 2007.

Interview date: Week commencing 16 July 2007.

Further particulars and an application form can be obtained from the University's web page at: http://www.uea.ac.uk/hr/jobs/ or by e-mail at: hr@uea.ac.uk or by calling the answerphone on 01603 593493 or by mail to the Human Resources Division, University of East Anglia, Norwich NR4 7TJ, U.K.

douglas.yu@uea.ac.uk

UGloucestershire TeachingEvolBiol

Lecturer/Senior Lecturer Biology University of Gloucestershire, UK The main focus of this post will involve teaching within the undergraduate Biology Field. You will be expected to contribute to a variety of areas of biology and ecology but expertise in one or more of the following areas would be an advantage: parasitology, population ecology, invertebrate biology. You will also be expected to engage in other developments within the Department and participate in field course teaching. You will be expected to engage actively in research and knowledge transfer activity. In addition, research supervision is expected of staff with appropriate qualifications and experience. For further information, see http://www.glos.ac.uk/jobs/index.cfm?jobRef=A292 or contact Dr Adam Hart, ahart@glos.ac.uk

Adam Hart PhD, MA (Cantab), PGCHE

Senior Lecturer in Biological Sciences Field Chair in Environmental Science and Management, and Biology Associate Editor Ecological Entomology

Department of Natural & Social Sciences University of Gloucestershire Francis Close Hall, Swindon Road, Cheltenham GLOS GL50 4AZ, UK Email ahart@glos.ac.uk NOTE CHANGE IN NUMBER Tel +44 (0) 1242 714670

"HART, Adam" <ahart@glos.ac.uk>

UMissouriColumbia Bioinformatics

Tenure Track Position in Bioinformatics and Computational Biology

The University of Missouri-Columbia invites applications for a tenure track faculty position in Bioinformatics and Computational Biology. The candidate will be hired into the Food for the 21st Century Animal Reproductive Biology Group. This is an established interdisciplinary reproductive biology group that is poised to make discoveries from genomic information gathered from agricultural species. This recruitment will build on a strong tradition of interaction between physical, biological and agricultural sciences on this campus. An ongoing campus initiative is coupled to community and state efforts to enhance research, education, and economic development in bioinformatics and computational biology. Of particular interest are the areas of:

* Systems biology (e.g. gene networks, modeling protein-protein interactions, and complex behavior at the sub-cellular and cellular levels) * Genome and sequence analysis including, comparative genomics, gene prediction and sequence annotation * EST analysis including predicting function from primary sequence * Database and browser applications

Recruitment will be at the Assistant, Associate or Full Professor level, depending on qualifications. Applicants must have a doctoral degree, postdoctoral experience, and evidence of outstanding research potential. It is expected that the successful candidate will participate in the core functions of the Reproductive Biology Cluster of the Food for the 21st Century program (http://cafnr.missouri.edu/arbg), and establish an internationally recognized research program via both independent and interdisciplinary collaborations, train graduate students, and contribute to the undergraduate or graduate instructional program. Successful candidates will be provided with excellent start-up funds, support, and a salary commensurate with experience. Columbia has the residential advantages of a medium-sized university city, excellent cultural opportunities, and easy access to St. Louis and Kansas City. Information about the

Division of Animal Sciences can be found at the departmental link (http://www.asrc.agri.missouri.edu/). Questions and applications can be directed to: Dr. Jerry Taylor, Chair of the Search Committee at taylorjerr@missouri.edu. An application must include curriculum vitae with a complete list of publications and grant support, a concise summary of research interests and future plans, and the names of four individuals prepared to write letters of recommendation. To ensure full consideration, applications should be received by October 1, 2007. The University of Missouri is an Affirmative Action, Equal Opportunity employer.

Jeremy Taylor Professor and Wurdack Chair in Animal Genomics S135 ASRC University of Missouri 920 East Campus Drive Columbia, MO 65211-5300 Voice: (573) 884-4946 Fax: (573) 882-6827 E-mail: taylorjerr@missouri.edu <mailto:taylorjerr@missouri.edu> http://animalgenomics.missouri.edu <http://animalgenomics.missouri.edu

"Things are never so bad they can't be made worse"

taylorjerr@missouri.edu

USheffield EvolGenetics

A Marie Curie fellowship (duration two years) is available as part of a project titled Molecular Adaptation in Ecologically Relevant Organisms, MAERO. The aim of this Transfer of Knowledge program is to create local expertise in the analysis of sequence and molecular marker data to identify loci that have evolved adaptively in natural populations. The fellow will lead a team comprising themselves and 3 other postdocs, in developing and testing methods that distinguish the effects of selection and demography on genetic variation. The fellow will mainly study molecular adapatation in range margin populations of Arabidopsis lyrata. The other team members will study natural populations of Soay sheep, littorina winkles and passerine birds. Applicants should hold a PhD in a relevant discipline such as evolutionary/population genetics, molecular evolution, computational biology or bioinformatics. The post is very generously salaried and offers an excellent opportunity for a motivated scientist to develop the skills/publication record required for research independence.

In order to fulfill the European Commission's mobility criteria for this post, please be aware that all applicants must NOT (a) have been employed in the UK for more than 12 months in the last three years (b) be a UK national unless they have resided in a non-EU country for at least 4 of the last 5 years.

The Department of Animal and Plant Sciences (http://www.shef.ac.uk/aps/index.html) is one of the largest whole organism biology departments in the UK and was ranked 5* (the highest possible grade) in the last Research Assessment Exercise. The department is widely regarded as a dynamic and exciting work place. Furthermore, Sheffield is an excellent place to live as it is affordable, culturally stimulating and located on the edge of Peak District National Park. Further details and application packs on the post can be found at http://www.sheffield.ac.uk/jobs/research.html, under job reference R4022. Informal enquiries or requests for further details can be made to Jon Slate (j.slate@shef.ac.uk), Roger Butlin (r.k.butlin@shef.ac.uk) or Terry Burke (t.a.burke@shef.ac.uk).

The closing date is June 20th 2007.

Dr Jon Slate Dept. Animal & Plant Sciences University of Sheffield Tel: 0114 2220048 Fax: 0114 2220002 Web: http://www.jon-slate.staff.shef.ac.uk/

Jon Slate <j.slate@sheffield.ac.uk>

UStThomas VisitorTeachingEvol

BIOLOGY: VISITING PROFESSOR

The University of St. Thomas Department of Biology is seeking applicants for a one-year Visiting Professor position for 2007-2008. Teaching responsibilities will include introductory level courses in (a) Diversity and Adaptation, and (b) Genetics, Evolution and Ecology, with the possibility of also teaching upper-level courses in the candidate's area of expertise. Applicants should have a Ph.D. or be an advanced graduate student. Previous experience teaching equivalent courses is preferred, but not required. Ideally, applicants should also be currently located in the Upper Midwest region of the United States.

Applications should be made electronically through the UST Human Resources web site (http://www.stthomas.edu/hr/ <http://www.stthomas.edu/hr/) and should include a cover letter, a current C.V., and a statement of teaching philosophy. Candidates should also arrange to have three letters of recommendation sent to: Dr. Simon K. Emms, Chair, Department of Biology, OWS 390, 2115 Summit Avenue, St.

Paul, MN 55105. Review of applications will begin immediately and continue until the position is filled.

Inspired by Catholic tradition, the University of St. Thomas educates students to be morally responsible leaders who think critically, act wisely, and work skillfully to advance the common good. The successful candidate will possess a commitment to the ideals of this mission statement.

Established in 1885, the University of St. Thomas is Minnesota's largest private university with an enrollment of 11,000 students studying in a wide range of liberal arts, professional, and graduate programs. The University of St. Thomas is located in the major metropolitan area of Minneapolis and St. Paul. It is within this context of Catholic intellectual tradition and the rich resources of the dynamic, urban Twin Cities that St. Thomas seeks to accomplish our mission of developing individuals who combine career competency with cultural awareness and intellectual curiosity.

The University of St. Thomas has a strong commitment to the principles of diversity and inclusion, to equal opportunity policies and practices, and to the principles and goals of affirmative action; and, in that spirit, seeks a broad spectrum of candidates who have demonstrated a commitment to these principles. The University strongly encourages nominations of, as well as applications from, women, persons of color, and persons with disabilities.

The University of St. Thomas is an affirmative action and equal opportunity employer. Women, persons of color, and persons with disabilities are encouraged to apply.

Simon K. Emms, Chair, Department of Biology, OWS 390, University of St. Thomas, St. Paul, MN 55105

skemms@stthomas.edu 651 962-5228

"Emms, Simon K." <SKEMMS@stthomas.edu>

USussex EvolBiol

The University of Sussex has recently undergone a major expansion in evolutionary biology with the appointment of Francis Ratnieks and Jeremy Field, working on the evolution of social insects. We are looking to capitalise on this momentum and to make another appointment in the near future. We are looking for evolutionary biologists from any field of the subject who will complement our existing strengths. More information about the evolution group, which forms part of the Centre for the Study of Evolution, can be found at http:// www.lifesci.sussex.ac.uk/CSE/. Expressions of interest and enquiries can be sent to Adam Eyre-Walker (a.c.eyre- walker@sussex.ac.uk), David Waxman (d.waxman@sussex.ac.uk) or Joel Peck (j.r.peck@sussex.ac.uk).

A.C.EYRE-WALKER@SUSSEX.AC.UK A.C.EYRE-WALKER@SUSSEX.AC.UK

Valencia Bioinformatics ResContract

Research Contract, Bioinformatics Department CIPF, Valencia (Ref.: CI02/2007)

A research contract for a biostatistician is available in the Department of Bioinformatics, CIPF, Valencia.

Requirements:

- A degree in Mathematics, Statistics, or related fields. - Experience in statistical analysis of large datasets in the field of biomedicine. - Knowledge of programming languages such as R or C/C++. - Good oral and written English level. - Background in population genetics is highly desirable.

Job Description:

- Conducting statistical analysis and consulting, mostly involving DNA polymorphisms (mainly SNPs)and microarray data. - Providing statistical support to the team. - Developing bioinformatic/biostatistic software. - Teaching short courses on biostatistics and data analysis.

We offer:

- The CIPF is dedicated to international excellence in biomedical research and to translating new knowledge into improved medical practice. - The successful candidate will join a new, rapidly expanding team with access to cutting edge technology in an environment of scientific excellence. - Work contract liked to the project GENOMA ESPAÑA for INB.

Please send your CV, cover letter and contact information of two referees to (Management(gerencia@cipf.es) and to HR (recursoshumanos@cipf.es). Please state the reference number as the subject of your e-mail.

Joaquin Dopazo <jdopazo@cipf.es>

Vienna EvolBiol PopGenet

Evolutionary Biology and Population Genetics continues to grow in the Vienna research area. Following recent recruitments and the foundation of a PhD program in population genetics (http://i122server.vu-wien.ac.at/pop/PhD/phd_start.html), the VMU Wien offers two group leader positions, two postdoctoral positions, and three PhD positions.

Details about the positions and the host institution can be found at: http://i122server.vu-wien.ac.at/pop/opportunities.html Group leader in functional genetics We are searching for a dynamic and enthusiastic scientist with an excellent track record and a proven ability to attract extramural funding. Candidates should have a strong interest to use Drosophila genetics to study the functional implications of natural variation. The starting date of this tenure-track position is negotiable. Applications need to be received by 16.7.07 to receive full consideration. The application should be emailed to Christian Schlötterer as a single pdf containing CV, list of publications, research plan, and the names of three reviewers with contact details.

Group leader in evolutionary genomics We are searching for a dynamic and enthusiastic scientist with an excellent track record and a proven ability to attract extramural funding. Candidates should pursue genomic approaches to characterize evolutionary processes in natural populations. While preference is given to researchers working with Drosophila, other animal models are also considered. The starting date of this tenure-track position is negotiable. Applications need to be received by 16.7.07 to receive full consideration. The application should be emailed to Christian Schlötterer as a single pdf containing CV, list of publications, research plan, and the names of three reviewers with contact details.

Postdoc position in intron evolution We are searching for a postdoc in Drosophila genetics, preferentially with a strong background in EvoDevo. Knowledge of evolutionary genetics and/or genome evolution would be a bonus. The candidate is expected to collaborate with a bioinformatics PhD student. The position is available for two years with the possibility of extension. The starting date is negotiable. Applications need to be received by 16.7.07 to receive full consideration. The application should be emailed to Christian Schlötterer as a single pdf containing CV, list of publications, research interests, and the names of two reviewers with contact details.

Postdoc position in Drosophila population genetics We are searching for a postdoc in population genetics aiming to disentangle the genomic traces of demography and selection. Candidates pursuing either empirical or theoretical approaches are being considered. The position is available for two years with the possibility of extension. The starting date is negotiable. Applications need to be received by 16.7.07 to receive full consideration. The application should be emailed to Christian Schlötterer as a single pdf containing CV, list of publications, research interests, and the names of two reviewers with contact details.

PhD positions In addition to the PhD program on population genetics, we offer three PhD positions in the following research areas: ecological genetics, population genetics, evolutionary genomics, bioinformatics. Applications should be emailed to Christian Schlötterer as a single pdf containing CV, list of publications, research interests, and names of two reviewers with contact details.

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

phone: +43-1-250775603 fax: +43-1-250775693 http://i122server.vu-wien.ac.at/pop/pop_gen.html christian.schloetterer@vu-wien.ac.at christian.schloetterer@vu-wien.ac.at

Vienna EvolBiol PopGenetUCambridge SeniorResTech ButterflyAdaptation

Applicants are sought for a Senior Research Technician to work in the Department of Zoology, University of Cambridge. Our laboratory studies the genetic basis of adaptation in the Lepidoptera (butterflies and moths). The postholder will work on projects studying the molecular basis of butterfly colour patterns, insecticide resistance in a globally important moth pest and the genetics of the interaction between a butterfly and a sex ratio- distorting bacteria. The post holder will provide support for all of these projects including insect rearing, laboratory management and molecular biology experiments.

Please see our group webpage at www.heliconius.org for more information about our research, and the job particulars for Ref. No. PF01881 at http://www.zoo.cam.ac.uk/zooone/administration/-vacancy.html Chris Jiggins Department of Zoology University of Cambridge Downing Street Cambridge CB2 3EJ Tel: (+44)(0)1223 769021 Fax: (+44)(0)1223 336676 Home: 01223 578 371 http://www.heliconius.org/ Chris Jiggins <c.jiggins@zoo.cam.ac.uk>

WageningenU Summer SNPmining

SNP Database Mining on mallards and wild boars

Single nucleotide polymorphisms (SNPs) are an abundant form of genome variation which can benefit a wide range of genetic disciplines. The use of SNPs in population genetics and host-parasite interaction studies has dramatically increased through the availability of large genomic databases and a panel of automatic mining software packages.

We are looking for motivated MSc students from EU countries with a background in bioinformatics and database management. You will develop a SNP set for a host-parasite interaction study on the mallard (Anas platyrhynchos) or the wild boar (Sus scrofa scrofa) at Wageningen University, The Netherlands.

Applications will be evaluated from the 1st of July, up until the positions have been filled.

If interested, please contact: Dr. Pim van Hooft Lecturer Wageningen University Resource Ecology Group Droevendaalsesteeg 3a building 'Lumen', building number 100 (central wing, first floor), room 1.320 6708 PB Wageningen The Netherlands E-mail: pim.vanhooft@wur.nl Tel: +31-317-484320 Fax: +31-317-484845

robert.kraus@wur.nl robert.kraus@wur.nl

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AFLP lineage sorting

Dear all,

Authors of phylogenetic studies (incl. myself) often claim that AFLP overcome the problem of incomplete lineage sorting by combining many independent loci. Are there published studies addressing this e.g. with simulations of AFLP data on species trees and evaluation of the resulting phylogenies, or any other citeable data/rationale supporting or rejecting this claim?

With many thanks Kristina

Kristina Sefc Department of Zoology University of Graz Universitätsplatz 2 8010 Graz Austria

kristina.sefc@uni-graz.at

Batch Genbank

Dear EvolDir Colleagues,

I am wondering if there was some software(s) that could be used for downloading several, for example, 100 sequences at the same time from GenBank? I mean I know the accession numbers of these sequences (for example EF100000 to EF102000), but it is almost impossible for me to download these sequences one by one.

So, your kind reply to jinyong.hu@googlemail.com is highly appreciated and will be great helpful for me and for those with similar problems!

Looking forward to your kind reply!

jinyong

jinyong.hu@googlemail.com

Batch Genbank answers

Dear EvolDir Colleagues,

Many thanks to all the people sending their kind reply concerning my question on batch downloading sequences from GenBank. I think all your suggestions are very useful and work well. Among them, the simplest way is just type like "EF100000:EF102000[ACCN]" for the users, like me, who are not familiar with scripts. Or you can do some scripting with perl or R or other softwares like bioedit, macvector....

Here I attached the answers to my question. Hearted thanks are give to the colleagues helping me and also to evoldir providing such a good platform to communicate.

Have a nice time and good luck for your work and life!!

Sincerely yours,

Jinyong

Dear Jinyong and all other users of GenBank,

there is an easy (but not well known) way to achieve this without any additional software. In your example, just type the following term into the GenBank search field:

EF100000:EF102000[ACCN]

Please note the colon between the first and last sequence and the final term in square brackets.

Yours Martin.

Dr. Martin Wiemers Department für Populationsökologie Fakultät für Lebenswissenschaften Universität Wien Althanstr. 14 A-1090 Wien Austria Tel. +43 1 4277 57403 e-mail: martin.wiemers@univie.ac.at http://www.univie.ac.at/population-ecology/ http://www.ncbi.nlm.nih.gov/entrez/batchentrez.cgi?db=Nucleotide should probably work

Go to NCBI home page and select CoreNucleotide or just Nucleotide from the Search pull down menu and just type in EF100000, EF102000, ... as many as you want and then click on Go. Once you get the records you can save it in any format you want. You don't need a script for this I would think. Good luck. Raja Georgetown University - Show quoted text -

if you have some familiarity with Perl, I'd recommend to take a look at BioPerl (www.bioperl.org). It comes with variety of example scripts that probably already do what you want, or will be easy to modify.

For running the example scripts you in fact don't even need to know Perl, though for modifying the scripts you obviously do. You might simply ask your question on the bioperl mailing list, though.

-hilmar

Bioedit can do this (under File->retrieve from GenBank or GenPept), although it's a bit clunky because you can't just enter a range of accession numbers - you have to enter each as a separate number, with a carriage return in between. What I usually do is use Excel to make a list (if you enter the first number and then "drag down" the cells, it will give you a sequential list of #s), save it as text, and then cut and paste the list into the window in Bioedit.

Don't forget to click on the ticky box for "accession" not "gi" or it won't find anything.

For really long lists it will take a while to download so be patient - my suspicion is that the bottleneck is at the GenBank end, not the program.

Bioedit is free and runs on Windows - if you do a google search you should find it multiple places - I got it here: http://www.mbio.ncsu.edu/BioEdit/bioedit.html Hope that helps, Regards, Laura

– Laura B. Geyer, PhD Smithsonian Tropical Research Institute geyerl@si.edu lbgeyer@gmail.com (preferred)

>From the US: Smithsonian Tropical Research Institute Attn: Laura Geyer - Naos Unit 948 APO AA 34002-0948

703/487-3770 ext. 8730

Internationally: Instituto Smithsonian de Investigaciones Tropicales Att: Laura Geyer - Naos Apartado 0843 - 03092 Balboa, Ancón Panamá, República de Panamá

(+507) 212-8730

Fax: (+507) 212-8790 or (+507) 212-8791

Dear Jinyong,

http://www.ncbi.nlm.nih.gov/entrez/batchentrez.cgi?db=Nucleotide please follow the instructions at the website above.

Good luck!

Renyi

Hi Jinyong,

The best way to do this is Batch Entrez: http://www.ncbi.nlm.nih.gov/entrez/batchentrez.cgi?db=Nucleotide Hope this helps, Dave Arde

– David H. Ardell Linnaeus Centre for Bioinformatics, Box 598, SE-751 24 Uppsala, Sweden T:+46(0).18.471.6694 F:+46(0).18.471.6698 http://www.lcb.uu.se/ ~ dave I've used Geneious (www.geneious.com) for kind of task you've described. It works well, and it has a number of flexible output options.

Kind regards - Rich

Rich Cronn, Research Geneticist US Forest Service, Pacific NW Research Station 3200 SW Jefferson Way, Corvallis, OR 97331 541-750-7291 phone * 541-750-7329 fax * rcronn@fs.fed.us

I've used R with the packages "ape" and "seqinr" to batch download sequences

— / —

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

BioinformaticsText online

I was told that my recent book "Bioinformatics and the cell: modern computational approaches in genomics, proteomics and transcriptomics" is freely downloadable at:

http://www.springerlink.com/content/xp0371/ in most universities and major research institutions.

(I learned this, not from the publisher, but from a Canadian colleague who accidentally browsed to this link.)

Best Xuhua

Dr. Xuhua Xia CAREG and Biology Department University of Ottawa 30 Marie Curie, P.O. Box 450, Station A Ottawa, Ontario Canada K1N 6N5 Tel: (613) 562-5800 ext 6886 Fax: (613) 562-5486 URL: http://dambe.bio.uottawa.ca Xuhua.Xia@uottawa.ca Xuhua.Xia@uottawa.ca

Classification Life

Dear colleagues,

New updated version (v.5.6) of original classification of living organisms containing four kingdoms (Monera, Protista, Vegetabilia and Animalia), 60 phyla and 253 classes, is presented. This classification incorporated as much as possible recent taxonomical data from different sources.

Any suggestions are welcome. Please leave your comments on the Nature Precedings page of classification: http://precedings.nature.com/documents/241/version/1 The Web-page of classifications with some explanations: http://herba.msu.ru/shipunov/os/os-en.htm Russian page: http://herba.msu.ru/shipunov/os/os-ru.htm With best wishes,

Alexey Shipunov University of Idaho

Alexey Shipunov <dactylorhiza@gmail.com>

Evol textbook

Dear evoldir members

Last week I asked about references for a good introduction book in evolution. I got many answers and here is a summary of the book selections received. Many thanks to all of you for the suggestions.

Most teachers in evolution seem to use:

- The books from Doug Futuyma - 'Evolutionary Biology' and his new one 'Evolution'. The book 'Evolution' is a readily recognized descendant of the author's previous textbook, Evolutionary Biology. However, it is much shorter and is exclusively directed toward an undergraduate audience (description from Amazon). If you order a teacher version of the book 'Evolution' it comes along with a CD that contains powerpoint lectures for each chapter.

- The other highly recommended textbook is the one from Freeman & Herron, Evolutionary Analysis (4th edition). This book comes with quite a few instructor resources, including a CD with every graphic and picture from the book to facilitate creating powerpoints.

Other highly recommended textbooks for an introduction in evolution are:

- The new textbook 'Evolution', by Nicholas H. Barton, Derek E.G. Briggs, Jonathan A. Eisen, David B. Goldstein, Nipam H. Patel - coming out soon and being highly recommended (check the link <http://www.evolution-textbook.org/> http://www.evolution-textbook.org/>)

- 'Evolution: an introduction' by Stephen C. Stearns & Rolf F.Hoekstra

- 'Evolution' by Mark Ridley

Finally other books that were suggested:

- 'What Evolution Is' by Ernst Mayr

- A Very Short Introduction to Evolution (Oxford University Press, 2003) by Brian Charlesworth and Deborah Charlesworth.

- 'Discovering Evolutionary Ecology' by Mayhew, Oxford Univ Press, 2006

I hope this helps

I got a few powerpoint lectures, thank you very much!!! Some other evoldir members asked me for those lectures, I suppose I can forward the link to them? Those who want the link please send me a personal email at karine.vandoninck@mpl.ird.fr

Have a nice day

Karine VAN DONINCK

Karine VAN DONINCK <karine.vandoninck@mpl.ird.fr>

Evol textbook coursenotes

I was one who provided links to Powerpoint lectures from my Genetics 500 lecture course. I'm happy to share them, of course with the stipulation that the lectures and their contents cannot be used commercially/for profit. Since I will be retired soon (11 days, but who's counting), I'd be pleased to see others get some use of the lectures. This is a general genetics course, and includes a few lectures on population/evolutionary genetics (not evolution in general). It is for undergraduates, but the lectures might be used as a starting point for a beginning graduate course.

Incidentally, I'm retiring from teaching but will continue to do research.

Enjoy!

Bill

>Dear evoldir members > >Last week I asked about references for a good introduction book in >evolution. I got many answers and here is a summary of the book selections >received. Many thanks to all of you for the suggestions. > >Most teachers in evolution seem to use: > >- The books from Doug Futuyma - 'Evolutionary Biology' and his new one >'Evolution'. The book 'Evolution' is a readily recognized descendant of the >author's previous textbook, Evolutionary Biology. However, it is much >shorter and is exclusively directed toward an undergraduate audience >(description from Amazon). If you order a teacher version of the book >'Evolution' it comes along with a CD that contains powerpoint lectures for >each chapter. > >- The other highly recommended textbook is the one from Freeman & Herron, >Evolutionary

Analysis (4th edition). This book comes with quite a few >instructor resources, including a CD with every graphic and picture from the >book to facilitate creating powerpoints. > > > >Other highly recommended textbooks for an introduction in evolution are: > >- The new textbook 'Evolution', by Nicholas H. Barton, Derek E.G. Briggs, >Jonathan A. Eisen, David B. Goldstein, Nipam H. Patel - coming out soon and >being highly recommended (check the link ><http://www.evolution-textbook.org/> http://www.evolution-textbook.org/>) > >- 'Evolution: an introduction' by Stephen C. Stearns & Rolf F.Hoekstra > >- 'Evolution' by Mark Ridley > > > >Finally other books that were suggested: > >- 'What Evolution Is' by Ernst Mayr > >- A Very Short Introduction to Evolution (Oxford University Press, 2003) by >Brian Charlesworth and Deborah Charlesworth. > >- 'Discovering Evolutionary Ecology' by Mayhew, Oxford Univ Press, 2006 > > > >I hope this helps > > > >I got a few powerpoint lectures, thank you very much!!! Some other evoldir >members asked me for those lectures, I suppose I can forward the link to >them? Those who want the link please send me a personal email at >karine.vandoninck@mpl.ird.fr > > > >Have a nice day > > > >Karine VAN DONINCK > > > > >Karine VAN DONINCK <karine.vandoninck@mpl.ird.fr>

–

C. William Birky, Jr. Professor of Ecology and Evolutionary Biology Member, Graduate Interdisciplinary Program in Genetics

Department of Ecology and Evolutionary Biology Biological Sciences West The University of Arizona Tucson, AZ

office: 520-626-6513 lab: 520-626-5108 http://eebweb.arizona.edu/faculty/birky/home.html Bill Birky <birky@u.arizona.edu>

Evol textbook coursenotes 2

Dear colleagues,

Less than 24 hours after I posted the offer to provide people with my genetics lecture notes, I have 10 requests. The interest is gratifying, and especially from those people who already found the notes and liked them. Last semester was the first time I put all of my lectures on Powerpoint and it is good that somebody else may get some use out of them.

Since the course web site for the genetics course includes some material provided by another lecturer, and won't be up indefinitely anyway, I am going to move my sections of it to my own web site later today. When this process is completed, I'll make the URL available to everybody via links on my personal web site at http://eebweb.arizona.edu/faculty/birky/home.html and also on my laboratory web site at http://eebweb.arizona.edu/faculty/birky/BirkyLab.html. I hope to finish this by late afternoon but it might take until the end of tomorrow.

Later I may also add links to pdf files of some lectures on the evolution of sex and the nature of species I gave in our evolution core course for graduate students.

Thanks for your interest,

Bill –

C. William Birky, Jr. Professor of Ecology and Evolutionary Biology Member, Graduate Interdisciplinary Program in Genetics

Department of Ecology and Evolutionary Biology Biological Sciences West The University of Arizona Tucson, AZ

office: 520-626-6513 lab: 520-626-5108 http://eebweb.arizona.edu/faculty/birky/home.html Dear colleagues,

As promised in a message earlier today, I have created a new web page at http://eebweb.arizona.edu/faculty/birky/CourseMaterials.html. This page is also accessible from my home page (URL below) and from my lab page. It has links to Powerpoint files for the lectures I gave in our general genetics course this past semester, including three lectures in population and evolutionary genetics. You can also download .pdf files of handouts from some of my lectures given to our introductory evolution course for new graduate students, and a computer simulation of random drift. There is also a manual version of the simulation which is fun to do in class and can help students understand the concept of stochastic changes in gene frequencies.

I hope these will be helpful.

Bill –

C. William Birky, Jr. Professor of Ecology and Evolutionary Biology Member, Graduate Interdisciplinary Program in Genetics

Department of Ecology and Evolutionary Biology Biological Sciences West The University of Arizona Tucson, AZ office: 520-626-6513 lab: 520-626-5108 http://eebweb.arizona.edu/faculty/birky/home.html Bill Birky <birky@u.arizona.edu>

Evolution textbook

Dear Evoldir members,

Can anyone suggest me a good introducing textbook to evolution?

And if the teaching experts of evoldir have powerpoint courses on evolution, for master students in biology and if they do not mind sharing it. I would be pleased to have a look at it. As I am starting in September as a teacher and have several courses to prepare, it is always helpful to get some nice examples and good references from colleagues.

Many thanks

All the best

Karine VAN DONINCK

Karine VAN DONINCK <karine.vandoninck@mpl.ird.fr>

Experimental Treefinder

A new experimental TREEFINDER version is online at:

www.treefinder.de TREEFINDER is a software to compute phylogenetic trees from molecular sequences.

New features are:

- general model selection and testing, using - paired sites tests with information criterion - parametric bootstrap test with information criterion - output of sitewise information criteria - two more information criteria: HQ and CAIC - experimental simulated information criterion of my own: SimIC - one more cost function for rate smoothing: NPRS-LOG

I would appreciate expert comments about the SimIC. This is an AIC-like information criterion, but using an estimated "effective" number of parameters as a penalty. The effective number of parameters is estimated by parametric bootstrap as the gain in likelihood that is due to fitting the noise of simulated data. It's described in the manual. For one thing I am not sure whether the approach is new - sorry, I have here no access to most of the literature. Second, the effective number of parameters often appears to differ significantly from the true number of parameters. This raises the question whether or not the traditional information criteria such as AIC and BIC, when based on naive parameter counts, are applicable in phylogenetics at all.

Please note that I am still not being paid for my work and that I had no income for years.

Gangolf Jobb

Gangolf Jobb <gangolf@treefinder.de>

Freeze-drying lyophilizing PlantTissue

Hello I would appreciate advice on how to freeze-dry (lyophilize) plant tissue samples for maximum preservation of DNA quality when storing the freeze-dried samples at room temp. We currently use a Labconco Lyophilizer and freeze-dry the prefrozen (at -80C) leaf samples in batch mode in coin envelopes or plastic tubes at about -10C shelf temp and -40C collector temp. for 3 to 7 days and store them sealed with a desiccant at room temp. There are problems with DNA degradation especially in the tube-dried samples (desiccant is outside the small tubes). I recently read about the need for secondary drying at a temperature higher than ambient and a time 1/3 to 1/2 that required for primary drying. What in your estimation is a safe shelf temperature for secondary drying and a safe duration? Do you think that our primary freeze-drying conditions are optimal- or at least good enough? If you have a really good, tested freeze-drying (Lyophilizing) protocol for plant tissue samples or any other related helpful advise I'd much appreciate a note from you.

Sincerely

Heidi Schwaninger

Heidi R. Schwaninger, Ph. D. Molecular Geneticist New York State Agricultural Experiment Station USDA/ARS Plant Genetic Resources Unit 630 W. North Street Geneva, NY 14456-0462

Office: 315 787 2431 FAX: 315 787 2339 E-mail: Heidi.Schwaninger@ars.usda.gov

"Schwaninger, Heidi" <Heidi.Schwaninger@ARS.USDA.GOV>

Freezing Plant Tissue

Hello I would appreciate advice on how to freeze dry plant tissue samples for maximum preservation of DNA quality when storing the dry samples at room temp. We currently freeze dry the prefrozen (at -80C) leaf samples in batch mode in coin envelopes or plastic tubes at about -10C shelf temp and -40C collector temp. for 3 to 7 days and store them sealed with a desiccant at room temp. There are problems with DNA degradation especially in the tube-dried samples (desiccant is outside the small tubes). I recently read about the need for secondary drying at a temperature higher than ambient and a time 1/3 to 1/2 that required for primary drying. What in your estimation is a safe shelf temperature for secondary drying and a safe duration? Do you think that our primary drying conditions are optimal- or at least good enough? If you have a really good, tested freeze drying protocol for plant tissue samples or any other related helpful advise I'd much appreciate a note from you.

Sincerely

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Office: 315 787 2431 FAX: 315 787 2339 E-mail: Heidi.Schwaninger@ars.usda.gov

“Schwaninger, Heidi” <Heidi.Schwaninger@ARS.USDA.GOV>

HostParasite questions

Dear EvolDir community, Does anybody know of examples in host-parasite systems where there is low species diversity within a genus that have the ability to infect 100s of host species in many genera from one taxonomic Order?

Thanks, Greg

Department of Plant Pathology and Microbiology University of California Riverside, Ca 92521 gdouhan@ucr.edu

gdouhan@ucr.edu

Lion feeding behaviour

Hi colleagues, I am currently supervising an undergrad dissertation comparing feeding aggression and ecology in wild versus captive (safari park) lions Panthera leo. Despite popular press and media I am astonished just how little research has been done (judging from our searches). Does anyone have anything up to date on these aspects of lion behaviour, or point me in a suitable direction? Thanks, Roger

Roger Davies Dept of Biological Science University of Chester Parkgate Rd Chester CH1 4BJ UK

r.davies@chester.ac.uk

Micro Stats advice

Dear all,

I'm involved in a PhD project on the use of stable isotopes, morphological data and microsatellite alleles to determine the possible origin of migratory birds, namely two thrush species We now have three categories of data from UK and continental breeding populations and birds in the UK in winter. These data categories are: (1) wing length , (2) stable isotope ratio values for carbon, deuterium and nitrogen and (3) genotypes at about 6 microsatellite loci.

The aim would be to infer the origin of a bird in the UK in winter given wing length (and age-class and sex), stable isotope values (C, D and N) and alleles at each microsatellite locus, by comparison with data for UK and continental breeding birds of that species.

Plan A at the moment is just to do a standard discriminant type of analysis, but maybe there are much better ways to combine the data, such as a Bayesian approach. Other data such as ringing recovery patterns, differences in UK winter and summer population sizes etc could be used to inform priors.

Any advice on how to combine these three types of data? Are there programmes combining quantitative and genotypic data? Any help is appreciated.

Best wishes, Kirsten

Dr. Kirsten Wolff Reader in Evolutionary Genetics University of Newcastle School of Biology and Psychology Division of Biology Ridley Building, room 457, Newcastle NE1 7RU, UK phone: (+44) 0191 222 5626 fax: (+44) 0191 222 5229

http://www.staff.ncl.ac.uk/kirsten.wolff/ http://www.bioprofiles.co.uk/ http://www.ncl.ac.uk/biology/ kirsten.wolff@newcastle.ac.uk

Molecular dating

Dear All,

I am trying to run Multidivtime in Windows on a dataset resulting in a tree with 224 nodes, 24 more than allowed in the original, downloadable version of the software.

Efforts to produce a working version recompiled with an increased MAXNODES specification have so far failed.

Does anyone here have a working version of Multidivtime that can work with > 200 nodes that they might be willing to share?

Many thanks,

Wolfgang Wüster – Dr. Wolfgang Wüster - Lecturer School of Biological Sciences University of Wales Bangor LL57 2UW Wales, UK

Tel: +44 1248 382301 Fax: +44 1248 371644 E-mail: w.wuster@bangor.ac.uk http://sbsweb.bangor.ac.uk/ ~ bss166/ Herpetological Journal: http://sbsweb.bangor.ac.uk/ ~ bss166/HJ/ w.wuster@bangor.ac.uk

Museum DNAextraction

Dear all,

we want to extract DNA from bird museum skins (toe pads) that are on average 100 yrs old. Does any of you has experience with such old tissue? And what is the best way of extracting DNA? Do you have any suggestions and tips on how to do this and which DNA extraction kit is best for this?

We thought about using one of the following two DNA extraction kits (but I am also glad for other suggestions):

- Sigma: GenElute Mammalian Genomic DNA Miniprep Kit (for mammalian tissue, but we ourself used it successfully on bird blood in EtOH) or - Qiagen: DNeasy Blood & Tissue Kit

It would be of great help to hear your opinions and experiences.

Best regards,

Julia Schroeder

Julia Schroeder

Animal Ecology Group CEES University of Groningen PO Box 14 9750 AA Haren The Netherlands tel ++31 (0)50-3632025 j.schroeder@rug.nl

Museum DNAextraction answers

Dear all,

Thank you very much for sharing your experience concerning my question of how to extract DNA from >100yr toe pads of birds. They were all extremely helpful.

Below are all the answers I got.

Julia Schroeder

I'm the sequencing technician in Irby Lovette's lab and was forwarded your ancient DNA request by one of our postdocs.

I've done a ton of ancient DNA work on toe-pads from 50-150 yr old bird toe-pads. I use the qiagen kit for extraction, with a few protocol modifications.

On the first day, I chop up the toe-pad as much as possible with a razor blade, and add it to 40ul proteinase and 160 buffer ATL. This digests overnight in a 55 degree incubator on a shaker. The next morning, I vortex the samples and if they still haven't digested fully, I add another 20ul proteniase and let them digest another 4 or 5 hours.

On the second day, I add the AL buffer and ethanol as the protocol states, and if there are still chunky bits in the tube, I centrifuge and add just the supernatant to the column. If there is no chunky stuff, add the whole thing as normal.

The only other protocol change is the elution amount. I elute with 50ul of the elution buffer, and repeat with another 50ul into a second tube. I don't bother checking DNA yields with gels or spectrophotometry because I don't like "wasting" any DNA from scarce samples, and our ancient DNA samples do not move back and forth between our low-contamination room and the normal lab.

If you have any questions, feel free to contact me and I'll do my best to give advice.

-Amanda Talaba

I used the QIAamp tissue kit kit, supplemented with DTT, for extraction from feathers and also a few toe pads. My samples consisted mostly of feathers from 30-40 years old museum skins, but I also extracted from a few toe pads, and some of my material was up to 100 years old. Not surprisingly, older material yielded DNA of worse quality. I attached two papers on genotyping and sequencing errors that were observed in experiments with the old DNA, maybe you find these useful.

Best regards, Kristina

Kristina Sefc Department of Zoology University of Graz Universitätsplatz 2 8010 Graz

To extract from museum skin or feathers, I digest overnight at 55C with Proteinase K, DDT, and SDS. The next day I do a short phenol/chloroform extraction then put through a modified version of the Qiagen DNA minikit.

Cheers Hayley Lawrence

I extract DNA from 80-year old museum skins and have successfully used a modification of the DNeasy Tissue kit that was first suggested to me by Tasha Belfiore of UC- Berkeley.I first perform several washes of the samples in 100% EtOH for ˜24 hours, which gets rid of any PCR inhibitors, such as the gasoline and butane that were used to prepare the skins I've worked with. I can provide the entire protocol if you are interested.

Have you seen the following paper by Mundy et al. Skin from feet of museum specimens as a non-destructive source of DNA for avian genotyping. The Auk. 1997. 114(1): 126-129? That may also be of help.

Lynne Mullen Hoekstra Lab Ecology, Behavior, and Evolution Division of Biological Sciences University of California, San Diego 9500 Gilman Drive, MC 0116 La Jolla, CA 92093-0116 Tel (858) 822-0170 Fax (858) 534-7108 email lynne@ucsd.edu <mailto:lynne@ucsd.edu>

I've worked quite a bit with toe pads from bird museum skins. I did my work in Rob Fleischer's lab at the Smithsonian Institution. Maybe someone from his lab has already contacted you. But if not, I'll try to track down an electronic copy of the entire protocol so I can email it to you. But we didn't use a kit– we made our own extraction solution and did phenol/chloroform extraction followed by Centricon purification. I had really good luck with the procedure, but the key is to design really small, overlapping fragments for PCR (<200 bp or even smaller). I noticed that I had less success with samples that came from museums in tropical locations– likely the DNA was degraded more from the heat and humidity prior to the invention of air conditioning.

I'll be in touch in a few days with the protocol.

Dawn

Dawn Reding Graduate Student Ecology, Evolution, and Organismal Biology 253 Bessey Hall Iowa State University

I extracted DNA from a toe pad of a bird museum sample from, the 1950s. I just give you the details of my protocol:

I used the Qiagen DNeasy Tissue Kit and performed all steps in a separated lab only for ancient DNA samples.

I took 0.0076g of the toe pad and cut it a bit (as possible :-))

+ 180μl ATL-Buffer

+ 20μl proteinase K

30" vortex

55C water bath for overnight

during the next day I added 3 times 20μl proteinase K until everything was digested

the 3rd day:

+ 5μl RNA (to increase the crop of DNA)

+ 240μl AL-buffer

vortex

incubate for 10' 70C

+240μl EtOH 96%, vortex, put in on the column and follow the washing procedure in the protocol.

— / —

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

OpenJournal records

Perhaps, an interesting for the whole community? Found in NATURE|Vol 447|31 May 2007.

Open journals? records to give reviewers their due

SIR ? Sydney Brenner and Richard Robert?s request in Correspondence (Nature 446, 725; 2007) for authors to conserve records of their work and make them freely accessible is of great importance to historians of science. However, unlike an artist?s preparatory sketches or a novelist?s drafts, scientific papers describing major discoveries have gone through the process of peer review. Reviewers often make significant contributions in shaping discoveries. They suggest new experiments, propose novel interpretations and reject some papers outright. Clearly, this is also important ?behind the scenes? work by scientists usually at the forefront of their discipline, and is an intrinsic part of the scientific process. It is well worth keeping a record of such work, for no history of science will be complete and accurate without it. I therefore propose that journals? records should be made publicly available after an adequate lapse of time, including the names of reviewers and the confidential comments exchanged between editors and reviewers. The Nobel Foundation makes all its records available after 50 years, as do many governmental and other institutions. This delay may be reduced for scientific journals to, perhaps, 15 or 20 years. This is also likely to have a positive impact on the peer-review process itself. The scientific community and future historians will gain from this transparency and from full knowledge of all the events that have contributed to a great discovery. Ariberto Fassati Wohl Virion Centre and MRC?UCL Centre for Medical Molecular Virology, Division of Infection and Immunity, University College London Medical School, 46 Cleveland Street, London W1T 4JF, UK

Matthias Stoeck <Matthias.Stoeck@unil.ch>

PLoSCompBiol retraction

Dear Colleagues,

This to inform you that we must retract Hall, B.G. and S. Salipante. 2007. Measures of clade confidence do not correlate with accuracy of phylogenetic Trees. PLoS Comp. Biol 3: (3) e51 .

As a result of a bug in the Perl script used to compare estimated trees with true trees, the clade confidence measures were sometimes associated with the incorrect clades. The error was detected by the sharp eye of Professor Sarah P. Otto of the University of British Columbia. She noticed a discrepancy between the example tree in Figure 1B and the results reported for the gene nuoK in Table 1. At her request I sent her all ten nuoK Bayesian trees. She painstakingly did a manual comparison of those trees with the true trees and concluded that for that data set there was a strong correlation between clade confidence and the probability of a clade being true. She suggested to me the possibility of a bug in the Perl script. Dr. Otto put in considerable effort, and I want to acknowledge the generosity of that effort.

I have now corrected the script and re-analyzed the trees in Tables 1-6. The results show that there are strong correlations between clade confidence and the probability that a clade is valid for Bayesian posterior probabilities and for Maximum Likelihood bootstrap percentages and weaker correlations for Maximumn Likelihood aLRT values.

The major conclusion of our paper, as given in its title, is therefore invalid and the paper must be retracted. Because of the importance of measures such as bootstrap percentages and posterior probabilities to the field of phylogenetics, it is important to retract that conclusion as quickly and publicly as possible.

It is important to stress that the responsibility for the necessity of retracting our paper is entirely mine, and that my co- author Stephen J. Salipante bears none of the responsibility. I wrote the Perl script and failed to check its accuracy sufficiently. Sincerely,

Barry G. Hall

"Barry G. Hall" <barryghall@gmail.com>

Plant Range Dynamics answers

Dear Evoldir members

Here is the collection of answers I got for the Plant range dynamics question I made to Evoldir. Thank you for all of you that anwser.

Best regards Filipe Alberto

Dear Evoldir members

I would like to ask for relevant references with evidence that show plant range dynamics on mountains in relation to climate oscillations (during glaciations). I am interested on vertical (altitude) range contractions and expansions caused by Pleistocene glaciations.

Thank you

Filipe Alberto, PhD CCMAR-CIMAR University of Algarve campus de Gambelas 8005-139 Faro, Portugal http://www.ualg.pt/ccmar/maree/ Filipe Alberto <falberto@ualg.pt>

Dear Filipe, some of the best work is of J R Flenley 1998 Climate Change 39:177 - other references in this pdf of mine. (Hewitt Nature 2000, Hewitt Fiz 2004,) Sincerely Godfrey

refs: Flenley JR (1998) Tropical forests under the climates of the last 30,000 years. Climatic Change 39, 177-197. Hewitt G (2000) The genetic legacy of the Quaternary ice ages. Nature 405, 907-913. Hewitt GM (2004) Genetic consequences of climatic oscillations in the Quaternary. Philosophical Transactions of the Royal Society of London Series B-Biological Sciences 359, 183-195. Hewitt GM (1996) Some genetic consequences of ice ages, and their role in divergence and speciation. Biological Journal of the Linnean Society 58, 247-276.

Godfrey M Hewitt PhD DSc FRES FLS Professor Emeritus

Biological Sciences, UEA Norwich NR4 7TJ, UK tel +44 1603 592182 work tel +44 1603 458142 home fax +44 1603 592250 work email g.hewitt@uea.ac.uk <mailto:g.hewitt@uea.ac.uk>

Hi, please find attached a couple of papers on the topic. Figure 2 of the Davis & Shaw paper comes probably closest to what you are looking for, whereas the other two may help you with finding further references.

Cheers, Arndt

refs: Walther GR, Beissner S, Burga CA (2005) Trends in the upward shift of alpine plants. Journal of Vegetation Science 16, 541-548. Davis MB, Shaw RG (2001) Range shifts and adaptive responses to Quaternary climate change. Science 292, 673-679.

Dr. Arndt Hampe Postdoctoral fellow Equipe de Génétique UMR Biodiversité, Gènes & Communautés (INRA) 69 Route d'Arcachon F-33612 Cestas Cedex France Tel. +33 (0)5 57122837 Sec. +33 (0)5 57122843 Fax. +33 (0)5 57122881 arndt@pierroton.inra.fr http://www.pierroton.inra.fr/-biogeco/genetique/personnel/Hampe/Hampe- en.html

Dear Filipe,

See papers by Connie Millar and colleagues. I emailed you some references. If the papers don't address range dynamics, I know that she has data on that issue for Sierra Nevada conifers of California.

Ellen Simms

refs: Notes: response to your evoldir query

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FN ISI Export Format VR 1.0 PT J AU Millar, CI King, JC Westfall, RD Alden, HA Delany, DL AF Millar, Constance I. King, John C. Westfall, Robert D. Alden, Harry A. Delany, Diane L. TI Late Holocene forest dynamics, volcanism, and climate change at Whitewing Mountain and San Joaquin Ridge, Mono County, Sierra Nevada, CA, USA SO QUATERNARY RESEARCH AB Deadwood tree stems scattered above treeline on tephra-covered slopes of Whitewing Mtn (3051 in) and San Joaquin Ridge (3122 in) show evidence of being killed in an eruption from adjacent Glass Creek Vent, Inyo Craters. Using tree-ring methods, we dated deadwood to AD 8151350 and infer from death dates that the eruption occurred in late summer AD 1350. Based on wood anatomy, we identified deadwood species as Pinus albicaulis, R monticola, P lambertiana, R contorta, R jeffreyi, and Tsuga mertensiana. Only P albicaulis grows at these elevations currently; P lambertiana is not locally native. Using contemporary distributions of the species, we modeled paleoclimate during the time of sympatry to be significantly warmer (+3.2 degrees C annual minimum temperature) and slightly drier (-24 mm annual precipitation) than present, resembling values projected for California in the next 70-100 yr. (c) 2006 University of Washington. All fights reserved. SN 0033-5894 PD SEP PY 2006 VL 66 IS 2 BP 273 EP 287 UT ISI:000241874000007 ER

PT J AU Millar, CI Westfall, RD Delany, DL King, JC Graumlich, LJ TI Response of subalpine conifers in the Sierra Nevada, California, USA, to 20th-century warming and decadal climate variability SO ARCTIC ANTARCTIC AND ALPINE RESEARCH AB Four independent studies of conifer growth between 1880 and 2002 in upper elevation forests of the central Sierra Nevada, California, U.S.A., showed correlated multidecadal and century-long responses associated with climate. Using tree-ring and ecological plot analysis, we studied annual branch growth of krummholz Pinus albicaulis; invasion

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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

Plant range dynamics

Dear Evoldir members

I would like to ask for relevant references with evidence that show plant range dynamics on mountains in relation to climate oscillations (during glaciations). I am interested on vertical (altitude) range contractions and expansions caused by Pleistocene glaciations.

Thank you

Filipe Alberto, PhD CCMAR-CIMAR University of Algarve campus de Gambelas 8005-139 Faro, Portugal http://www.ualg.pt/ccmar/maree/ Filipe Alberto <falberto@ualg.pt>

PlantMicro question

Hi all, I have a new microsatellite marker obtained from a dicot's enriched genomic library, (AAAG)25, that shows only one allele per individual. This microsatellite is highly polymorphic (at least compared to the rest I isolated) and is the only one in a set of 12 that shows no heterozygotes. I Blasted the sequence and the closest hits to the flanking regions were mitochondrial NADH dehydrogenase genes of other plants. Being so variable, its mitochondrial origin is unlikely and I am thinking it is actually a NUMT. However, it is really puzzling that it shows only one allele per individual. I hope someone can give me some light about this microsatellite. Thanks,

Alejandro anettel@nature.berkeley.edu

Sequence how many clones answers

Dear All

I would like to thank everyone who contributed to the huge response regarding my recent query concerning ?How many clones should I sequence ? below?

?When cloning and identifying individual alleles of mixed PCR products, a key question is how many clones do I have to sequence to ensure that I have approached a good probability (eg 95%) that I have identified all different copies. In the past when I have been isolating two heterozygotic copies of a nuclear marker, simply sequencing five colonies always identified the two variants. But how many colonies would I have to sequence if there were 3, 4, 5, ... 20 etc...??

Many solutions have been supplied and I have taken the liberty of reproducing most contributions below. Some favour experimental approaches such as SSCP, others, standard probability solutions, binomial calculations and R scripts, poisson distribution, accumulation curves, online calculators and repeated warnings of recombinant cloning issues. Thank you for the comprehensive response and please take what you would like to from the following collation.

Sincere apologies to any contributors that I may not have replied directly to and please note that some contributions have not been reposted due to txt/.html conversion issues/duplication/attachment problems.

Hopefully, we should be able to better gauge how many sequencing reactions we should now be expending on complex cloning mixtures.

With very best wishes and thanks

Si

Dear Si Creer,

If the two copies are present in equal numbers in your pcr mix, this is easy to calculate. The probability to obtain sequences of both copies, is (1 - probability that all sequenced clones are identical): 1 - 2*(0.5)n , with n=the number of sequenced clones.

If you want to have 0.95 probability of having sequenced both copies, 1 - 2*(0.5)n=0.95 -> n=5.3

This means that you will have to sequence 6 clones to have a >95 % probability. With 5 sequenced clones, the probability to have both copies is 1-2*(0.5)5 = 0.9375.

Duur

Duur Aanen Laboratory of Genetics Wageningen University and Research Center The Netherlands Tel. +31(0)317 482706 Mobile: +31 (0)6 10327948 Fax: +31 (0)317 483146 http://www.gen.wur.nl/uk/staff/-postdocs/duur+aanen/ Dear Si,

calculating the probability of missing one of the two alleles under the assumption that the two alleles are amplified and cloned with the same probability is very easy. Sort of white and black balls picked out of a sack (with replacement). I kind of remember the number of clones to be six if you want to go under 5% of probability of missing one of the two alleles in an heterozygote. But you can calculate this based on the ploidy of your system.

But do the assumptions hold ? I am not sure. This is a starting point, nevertheless.

cheers francesco

Francesco Nardi, Dr.

Dept. of Evolutionary Biology University of Siena

Master in Bioinformatics University of Siena

via Aldo Moro 2 - 53100 Siena Italy

Ph.: +39.0577.234420 (lab. 4398) Fax.: +39.0577.234476

Here is a quick and easy way:

Assuming you have a diploid organism and thus two PCR products in equal or near proportions and have one sequence already in the bag, then the chance that you pull the wrong one (probability of a miss) next time is 0.5 and the chance that you do so the next time as well is 0.5 x 0.5..........

So as you have set the acceptable probability of a miss at 0.05, so all you have to do is keep pushing the buttons on your calculator to multiply 0.5 by itself until the answer on the display is <0.05. If you have kept count of the number of times you pressed the button, then that is how many clones you need to sequence.

This method works for any probability level or any fractional representation of what you are after in the mixture. It is standard library screening question and can be solved with a fancy formula using logs and other horrid stuff. My way is easier if you can keep count.

Hope this helps

Geoff

Dr Geoffrey K. Chambers

Reader in Cell and Molecular Biosciences

School of Biological Sciences Victoria University PO Box 600 Wellington 6140 NEW ZEALAND

Ph: +64-(0)4-463-6091 Fax: +64-(0)4-463-5331

E-Mail: Geoff.Chambers@vuw.ac.nz

Please visit my Personal Home Page on the SBS website: http://www.vuw.ac.nz/sbs Hi Si This may help Tom Gilbert Bower MA, Spencer M, Matsumura S, Nisbet RER and Howe CJ 2005. How many clones need to be sequenced from a single forensic of ancient DNA sample in order to determine a reliable consensus sequence? Nucleic Acids Research 33, 8, 2549-2556.

Hi Si,

You could always plot the cumulative number of clones analysed against the number of different sequences identified. As the curve begins to level off (i.e. you are identifying fewer new alleles), you know that you are approaching the maximum number of different sequences contained

— / —

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

Sequencing costs

Dear All

in an era when DNA sequencing should be getting cheaper, we have been hit by a doubling of prices by our favoured supplier (from £1 to £2 to run a sample (not including tax)). Another supplier that recently offered sequencing at £0.50 a sample has also just increased theirs to £2.

In order to help drive down costs, it would probably be helpful to circulate details of the cheapest suppliers amongst the community. So if you can recommend a company, then please let me know. If results are interesting then I will send out another email to evoldir with a summary.

My aim is to find a 50 pence / 50 cent company!

I am primarily interested in companies that run out PCR products (I have a PCR machine but not a sequencer, after all). To try to categorise things, please pay attention to:

1) Cost to electrophorese sample only a) Individual tubes b) 48 well or 96 well plates (usually supplied as precipitated products)

2) Cost to do PCR reactions, clean up and run c) Individual tubes d) Plates.

3) Location of company

4) General reliability / turn-around time

I understand that there are many local services but often they are restricted to a particular set of users, so not of use to the general public - please do not reply with details of these.

Thanks, Angus

– Dr. Angus Davison

Institute of Genetics The University of Nottingham Queen's Medical Centre Nottingham NG7 2UH angus.davison@nott.ac.uk www.molluscs.org tel 0115 823 0322 (int. 30322) fax 0115 823 0313

Angus.Davison@nottingham.ac.uk Angus.Davison@nottingham.ac.uk

Software PGEToolbox

Dear All,

PGEToolbox is a Matlab-based program for analysis of polymorphism and divergence data in population genetics and evolution. It computes basic statistics of DNA sequence variation and carries out neutrality tests, such as Tajima's D test, Fu & Li's tests and Fay & Wu's H test. The significance of tests is determined from the distribution of the statistics obtained by coalescent simulation. The toolbox performs McDonald-Kreitman test (and several extensions), and also contains functions for handling SNP genotype and haplotype data. The latest version of the program can be obtained from:

http://bioinformatics.org/pgetoolbox/ All the best,

James

– James J. Cai, Ph.D.

The Petrov Lab Dept. of Biological Sciences Stanford University Stanford, CA 94305 USA

e-mail: jamescai@stanford.edu phone: 1-650-736-2249

jamescai@stanford.edu jamescai@stanford.edu

Software Simprot v1 01

Dear EvolDir members

We are releasing a new version of our protein alignment simulation package, Simprot. Version 1.01 incorporates new features and improvements to the older version. Simprot is a cross-platform application that runs on Windows and Linux (pre-compiled version with gcc 4.1 on Fedora Core 5). The program allows for several models of amino acid substitution (PAM, JTT and PMB), allows for gamma distributed sites rates according to Yang's model, and implements a parameterised Qian and Goldstein distribution model for insertion and deletion.

New features and improvements:

- root sequence input - from a sequence file or directly on the interface - ability to simulate multiple protein segments with distinct evolutionary histories, either different parameters or different phylogenetic trees or both - automatic detection of taxa when different trees are used to simulate multiple segments

The program has been developed in C/C++ and was published on BMC Bioinformatics:

http://www.biomedcentral.com/1471-2105/6/236 To download Simprot go to

http://www.uhnresearch.ca/labs/tillier/-software.htm#3 A Windows installation package and a Linux tarball are available. As the distributed Linux version is precompiled, if you require a precompiled executable to another distribution/system configuration just contact us on the email address listed in the program's documentation.

Best regards

Elisabeth Tillier and Paulo Nuin

pnuin@uhnres.utoronto.ca pnuin@uhnres.utoronto.ca

Software msatcommander

I have been working for some time with the fine folks from Savannah River Ecology Lab on a software package for microsatellite array searching, primer design, and 5' tagging (m13, CAG, or custom tag sequences) for polymorphism testing (see Glenn and Schable, Methods in Enzymology, 2005). We had a version for locating repeat arrays that some of you may have used (msatcommander <=0.4.5) and some scripts (msatprimer) for automated primer design and tagging using results output from msatcommander.

These have now been integrated into an "all-inclusive" application with a GUI. Changes/features in the most recent version (0.8.1) include:

+ addition of primer design functionality using Primer3 as the design engine + addition of primer tagging functionality (also uses Primer3) + addition of a function to combine microsatellite arrays within a user-specified range (in bp) + addition of length-qualifications for located microsatellite arrays

Prior to downloading and/or using the program, please look at the FAQ. Both the FAQ and downloads may be found at the website:

http://code.google.com/p/msatcommander/ OSX (10.4 or greater) and Windows XP executables are available. Linux users can download a tarball of the source or check the source out from the Subversion repository (be sure to check the README.UNIX). Running the program on Linux has been *very* lightly tested. Additional information regarding features, etc. may be found on the website. I also have a program note in press that describes and formally announces the software.

If you have suggestions for the program or think you have identified a problem and/or bug, please send an email to:

msatcommander-discuss@googlegroups.com

Email sent to this address will be archived and is searchable by the general public.

Thanks go to Travis Glenn, Nick Crawford, Bettina Harr, Julie Glenn, Olga Tsyusko, Abigail Fusaro, Nancy Schable, Jennifer Ness, and Maureen Peters for providing extremely helpful suggestions and/or comments regarding the software in its various, earlier forms. These individuals have also been kind enough to test earlier releases.

cheers, Brant

Brant C. Faircloth Bobwhite Genetics Project The University of Georgia 180 East Green Street Athens, GA 30602

email: brant@uga.edu tel: +1.706.542.3932 fax: +1.706.542.8356 mobile: +1.706.201.6110 http://gallus.forestry.uga.edu/genetics/ brant@uga.edu brant@uga.edu

Variance Covariance Matrices

Hi all,

I have a list of trees (from a Bayesian analysis) and I would like to get the variance-covariance matrices for all of them to use in comparative analyses. While I know how to get the matrix for a single tree (say in R), I am having trouble automating it for a list of trees. So I hoping that there is a program that might already do this. If the program generated matrices under multiple models (e.g. Brownian motion, Ornstein-Uhlenbeck) that would be a bonus, but just Brownian would be a start.

Thanks in advance for your help!

Stacey Smith

Dept. Biology Duke University

sds21@duke.edu

PostDocs

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DukeU YeastQuantTraits

NIH-funded postdoctoral positions are available in my laboratory at Duke University Medical Center (Durham, NC) to study quantitative (complex) traits in S. cerevisiae; for example, see Nature 416:326-330 (2002) and PLoS Genetics 2(2):e13 (2006).

http://www.duke.edu/web/microlabs/mccusker/ Applicants should have 0 to (at most) 2 years of postdoctoral experience and a strong background in at least one of three areas - yeast genetics, quantitative/population genetics and/or genomics/informatics - and a desire to expand into the other listed areas. While not a requirement, eligibility for NIH fellowships/training grants or other fellowship funding will be viewed positively. Start dates are flexible.

Applicants should email their curriculum vitae (in pdf format) and the names/email addresses of three references to John McCusker <mccus001@mc.duke.edu>.

–

John H. McCusker, Assoc. Prof. Dept. of Molecular Genetics & Microbiology, 3020 Duke University Medical Center Durham, NC 27710

http://www.duke.edu/web/microlabs/mccusker/ phone: (919) 681-6744 fax: (919) 684-8735 e-mail: mccus001@mc.duke.edu

PLASMID REQUESTS: PLEASE CHECK WEB SITE

John McCusker <mccus001@mc.duke.edu>

ESF ThermalAdaptation

****** 3rd CALL ******

The Objective of the ESF Programme “Thermal adaptation in ectotherms: Linking life history, physiology, behaviour and genetics” (ThermAdapt; http://www.esf.org/thermadapt) is to foster a multidisciplinary European network of scientists working on thermal adaptation. We particularly aim to integrate research at multiple levels of investigation, including genetics, physiology, ecology, behaviour or theory. Interested persons or groups are encouraged to join our activities. These include advertising their expertise via our web site, and participation in various activities to be announced separately and regularly over the next 5 years such as workshops, training courses, short and long exchange grants, exchange of specimens and expertise, sharing of facilities, and scientific collaboration of any kind.

We here Call for Applications for a number of

Short Visit Exchange Grants (< 15 days)

broadly related to the scientific objectives of the Programme (deadline 30 September 2007). Short Visits may serve for planning collaborative research projects, brief data gathering or data analysis (see http://www.esf.org/thermadapt under Grants for application guidelines and forms).

Similar calls are planned to occur repeatedly over the next 5 years. We advise applicants to contact potential labs of interest early to jointly prepare the application. Grant applications will be chosen by the Steering Committee based on scientific quality, and priority will be given to applicants who come from or intend to visit countries supporting the programme (Austria, Belgium, Czech Republic, Denmark, Estonia, Finland, Germany, Hungary, Netherlands, Portugal, Slovenia, Spain, Switzerland), but other European nations can be involved.

If you wish to be included in the ThermAdapt e-mail list to receive regular updates on Programme activities, please send an email to edegott@esf.org.

For further inquiries contact:

Ellen Degott (ESF office liaison; Email: edegott@esf.org) Wolf Blanckenhorn (chair; Email: wolf.blanckenhorn@zm.uzh.ch) Mauro Santos (co-chair; Email: mauro.santos@uab.es)

APPLICATIONS ARE SUBMITTED ONLINE UNDER http://www.esf.org/thermadapt Dr. Wolf Blanckenhorn Zoological Museum, University of Zurich-Irchel Winterthurerstrasse 190 CH-8057 Zurich Phone: +41 44 635.47.55 Fax: +41 44 635.47.80 e-mail: wolf.blanckenhorn@zm.uzh.ch http://www.unizh.ch/-zoolmus/zmneu/englisch/forschung_e/ blanckenhorn_wolf_e.html http://www.esf.org/thermadapt wolfman@zm.uzh.ch wolfman@zm.uzh.ch

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MPI Ploen MolGeneticBioinformatics

MPI Evolbiol. - Postdoctoral research Position in molecular genetics/bioinformatics

The Max-Planck-Institute for Evolutionary Biology, Ploen (near Hamburg, Kiel, Lübeck), Germany, is seeking a molecular biologist to join the department of evolutionary ecology.

She/he will work with a team in an integrative project involving immunological, parasitological, population genetic and behavioral approaches. Details about the departments's research activities can be found under: http://www.mpil-ploen.mpg.de/ The department's major goal is to understand the evolutionary ecology of sexual reproduction and its role in enhancing immune function in the offspring. The specific goal for this position is to identify the molecular correlates of immune challenge and pathogen defence and to explain the functional significance of MHC diversity in the wild.

The successful candidate should have a strong background in evolutionary biology and is expected to study MHC loci in the model organism three-spined stickleback (Gasterosteus aculeatus). He/she is expected to have experience in state of the art molecular techniques, e.g. cloning and sequencing, real-time PCR, expression profiling, but also in using bioinformatic tools as well as library and genome screening and should be enthusiastic to do strong research in a team.

As a Max Planck Institute we can offer labs and technical equipment at the highest standards. The candidate will collaborate with the team including PhD students and postdocs working on the immunogenetics, immunology, population genetics, parasitology and behavioural ecology both in the lab and in the field.

Salary will be according to the guidelines of the Max-Planck-Society, about 42 000 Euro per year. This postdoctoral research position is for a two years term and can be extended.

The MPI for Evolutionary Biology has three departments: evolutionary ecology, evolutionary genetics and evolutionary theory. Plön is a small touristic village located in a beautiful lake district with major cities nearby.

Please send your application including a CV, a list of publications and the contact information of three references by e-mail () within 3 weeks after appearance (or until position is filled).

Prof. Dr. Manfred Milinski, Director Max-Planck-Institute for Evolutionary Biology (former Max-Planck-Institute of Limnology) Department of Evolutionary Ecology August-Thienemann-Strasse 2 D-24306 Ploen, Germany Phone: +49-(0)4522 763 254 Fax: +49-(0)4522 763 310 email: milinski@mpil-ploen.mpg.de

Prof. Manfred Milinski Executive Director Max-Planck-Institute for Evolutionary Biology (former Max-Planck-Institute of Limnology) Department of Evolutionary Ecology August-Thienemann-Strasse 2 D-24306 Ploen, Germany

direct: +49-(0)4522 763 254 Sec: +49-(0)4522 763 253 Fax: +49-(0)4522 763 310 email: milinski@mpil-ploen.mpg.de http://www.mpil-ploen.mpg.de/ milinski@alpha1.mpil-ploen.mpg.de milinski@alpha1.mpil-ploen.mpg.de

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Montpellier GrapePopGenet

We are offering a 2 year post-doc position in INRA, Montpellier, France, for the fine mapping of LD in grapevine (Vitis vinifera). We are looking for candidates with skills in population genetics, but if possible also able to use genomic tools (sequence search and handling) and ready to work on the lab (SSR and SNP genotyping).

Thanks very much in advance.

Agnes Doligez

Nouvelle adresse email ? partir du 1er janvier 2007 : New email address from January 1st 2007: doligez@supagro.inra.fr

Agn?s DOLIGEZ UMR 1097 DGPC (Diversit? et G?nome des Plantes Cultiv?es) Equipe G?n?tique Vigne INRA, b?t 21 2 place Viala 34060 Montpellier Cedex 01, France T?l: + 33 4 99 61 25 03 Fax: + 33 4 99 61 20 64 E-mail: doligez@supagro.inra.fr

Agn?s Doligez <doligez@supagro.inra.fr>

Porto Portugal HumanAdaptiveEvol

Postdoctoral Position Human Genetics, IPATIMUP, Porto, Portugal

A Postdoctoral position is available in the Group of Genetics, Evolution and Pathology, directed by Jorge Rocha, at the Institute of Molecular Pathology and Immunology of the University of Porto (IPATIMUP), Porto, Portugal. Our research team is particularly interested on aspects of human genetic variation linked to adaptive evolution and their implications in health and disease. We aim to use serine protease inhibitors as models to analyze the impact of natural selection on current health patterns of human populations through the use of both experimental and theoretical tools. We have found previously evidences for a signature of natural selection among one of these genes and since serine protease inhibitors are known to be enrolled in many biological functions, including immune response and reproduction, they represent good candidates for natural selection. The successful candidate is expected to collaborate closely with Susana Seixas in the project Looking for evidences of human adaptation in the proteolysis universe: the case-study of serine protease inhibitors which has been financed by the Portuguese Funding Agency (Fundação para a Ciência e a Tecnologia) and the European Funding for Regional Development (FEDER). This project integrates works of molecular biology, population genetics and comparative genomics and benefits from the expertise of Anna Di Rienzo from the Department of Human Genetics of the University of Chicago who is the project consultant. We seek for creative and highly motivated applicants who have a PhD in Biomedical Sicences and a strong interest in research field of the project. A significant background in the fields of Population or Evolutionary Genetics is appreciated and computational skills are desirable. Applicants should send a CV, a motivation letter and two references letters to:

Susana Seixas BPD Grant IPATIMUP Rua Dr. Roberto Frias s/n, 4200-465 PORTO PORTUGAL or e-mail: sseixas@ipatimup.pt

– Susana Seixas Genetics, Evolution and Pathology Unit IPATIMUP Rua Dr. Roberto Frias, s/n 4200-465 Porto, PORTUGAL Tel.: +351225570700 Fax : +351225570799 http://www.ipatimup.pt

sseixas@ipatimup.pt

RutgersU MosquitoPopGenetics

Multiple postdoctoral positions are available at the Rutgers Center for Vector Biology to join a team of researchers working on diverse aspects of mosquito biology. Candidates are invited with training in vector field ecology, molecular biology, population genetics, mathematical modeling, risk assessment, and/or biological control. Most projects in the Center involve one or more faculty from other Departments and Centers at the Rutgers University (Ecology, Evolution, and Natural Resources; Human Ecology; Environmental Sciences; Institute of Marine and Coastal Sciences; Mathematics). Candidates must have a relevant doctoral degree. Ability to work collaboratively in a goal-oriented team environment is required. Excellent written and verbal communication skills are important and strong analytical skills are preferred. Positions are available IMMEDIATELY. Send inquires to Prof. Dina Fonseca at dinafons@rci.rutgers.edu. Send applications consisting of curriculum vitae, a short statement of research interests, and contact information for three references to carolt@rci.rutgers.edu (refer to this announcement in the subject line). Information on the Center and its activities can be obtained at our webpage: http://vectorbio.rutgers.edu/. Applications will be reviewed as they are received.

Dina M. Fonseca, PhD Associate Professor Center for Vector Biology Rutgers University 180 Jones Avenue New Brunswick, NJ 08901 Phone:(732) 932-3146

and

Randy Gaugler, PhD Professor II and Director Center for Vector Biology Rutgers University 180 Jones Avenue New Brunswick, NJ 08901 Phone:(732) 932-9341

dinafons@rci.rutgers.edu

SheffieldU PlantEvol

Post-doctoral Research Assistant: Forecasting the ecological and evolutionary consequences of environmental change

The post holder will work on a project funded by the Leverhulme Trust and will be responsible for setting up and conducting a large-scale field study on the population and community dynamics of dune annual plants. The study will be conducted at 15 sites along a North-South transect from Scotland to Morocco and involve regular monitoring and experimental manipulations. The project aims to use the environmental variation along this transect as a surrogate climate gradient. The data from the study will be used to ask questions about how climate affects population dynamics, community structure and the evolution of species in changing environments.

The successful applicant should be experienced in organising and managing a large-scale field project, including the management of teams of field assistants. Familiarity with dune annuals is desirable, as is experience in experimental design and the analysis of ecological data.

This work will be undertaken at the University of Sheffield under the supervision of Prof Freckleton. There will also be collaboration with Prof Andrew Watkinson (University of East Anglia) and Prof M Rees (Sheffield).

The post is tenable from October 2006 for 1 year, renewable for up to a further 4 years, subject to the funding constraints of a cash- limited budget.

For more details pleas contact Rob Freckleton (r.freckleton@sheffield.ac.uk)

Professor R Freckleton Department of Animal & Plant Sciences University of Sheffield Sheffield S10 2TN

Tel (work): 0114 2220017 Tel (mobile): 07788 742341 [new number]

http://www.shef.ac.uk/aps/index.html http://www.shef.ac.uk/aps/contacts/acadstaff/freckleton.html

StAndrewsU BirdAdaptation

University of St Andrews

Research Fellow in Animal Behaviour

£26,915 pa

A behavioural scientist is required to join the group of Professor Peter Slater, on a BBSRC-funded project to investigate how birds adapt their songs to the environment. The project is a laboratory-based one and will focus on the impact of environmental noise on the song learning of birds and their song performance later in life.

Information about the acoustic communication research group can be found at http://biology.st-andrews.ac.uk/bmac/ The position is available immediately on a fixed term until 31 Jan 2010.

Please quote ref: SK273/07 Closing date: 20 July 2007

Application forms and further particulars are available from Human Resources, University of St Andrews, College Gate, North Street, St Andrews, Fife KY16 9AJ, (tel: 01334 462571, by fax 01334 462570 or by e-mail Jobline@st-andrews.ac.uk. The advertisement and further particulars and a downloadable application form can be found at http://www.st-andrews.ac.uk/employment/.

The University is committed to equality of opportunity.

Dr. Henrik Brumm University of St Andrews School of Biology Bute Building St Andrews, Fife KY16 9TS U.K.

Phone: +44 1334 463615 Fax: +44 1334 463600

http://biology.st-and.ac.uk/staff/brumm-h.html Henrik Brumm <henrik.brumm@st-andrews.ac.uk>

StanfordU VertebratePopGenetics

Stanford Postdoctoral Position in Vertebrate Population Genetics and Genomics

A postdoctoral position is available as part of an NIH-funded Center of Excellence in Genomic Science at

Stanford University. The Center primarily focuses on the understanding of patterns of genetic adaptation following colonization and adaptation of new environments, using threespine sticklebacks and humans as model systems. The approach is integrative, employing QTL mapping, quantitative and evolutionary genetics, genomics, transgenics, and molecular population genetics. The project is a collaborative effort of a number of faculty including David Kingsley (PI), Richard Myers, Will Talbot, and Dmitri Petrov at Stanford. The postdoctoral fellow will primarily work on development of statistical methods for the identification of targets of selection from patterns of molecular polymorphisms. He/she will also collaborate closely with other members of the team and will help define which data will be acquired in the project.

The following papers provide a background for the project:

Shapiro et al. (2004) Genetic and developmental basis of evolutionary pelvic reduction in threespine sticklebacks Nature 428: 717-723.

Colosimo et al. (2005) Widespread parallel evolution in sticklebacks by repeated fixation of ectodysplasin alleles Science 307: 1928-1933.

Conditions: The position is available immediately and we will accept applications until the position is filled. Initially the position is for one year but can be extended to up to 5 years. Starting salary will be commensurate with experience.

Education: Ph.D. in Population Genetics, Genome Biology, Bioinformatics or related fields. Applicants with experience in computational biology, comparative genomics, and statistical genetics are especially encouraged to apply. Computational competence and strong population genetics background are essential.

Instructions: Applicants should submit a cover letter, curriculum vitae or resume, and a list of three or more references including telephone numbers and email address to Dmitri Petrov at dpetrov@stanford.edu. Please e-mail at the same address for additional information.

– Dmitri A. Petrov Associate Professor Department of Biological Sciences Stanford University Stanford, CA 94305-5020

dpetrov@stanford.edu http://petrov.stanford.edu (650) 736 1169 (office) (650) 736 2249 (lab)

dpetrov@stanford.edu

TexasAMU LabManager

A postdoctoral position is available in Dr. Gus Cothran's laboratory in the Department of Veterinary Integrative Biosciences. The position will primarily be to manage a genotyping laboratory that performs identity and parentage testing for domestic animals as well as diagnostic typing of genes associated with specific traits of interest to the animal breeders. The laboratory has primarily focused on horses but we are moving into increased testing of dogs, cats and cattle. Testing involves both microsatellite typing and SNP typing. In addition, the person in this position will have the opportunity to work in research in equine genomics, equine population/conservation genetics, or research of their own choosing if it fits within the capabilities of the lab.

Qualifications: A highly competent motivated PhD is sought with a solid background in genetics and expertise in molecular biology techniques for the DNA polymorphisms. Experience in the specific techniques employed in the lab (msat and snp genotyping) are preferred but not required. Proficiency in written and spoken English required. There will be supervisory duties involved with the position and some communication with clients will be needed. Please submit curriculum vitae, summary of research experience, and contact information of three references to Gus Cothran, Ph.D., Department of Veterinary Integrative Biosciences, College of Veterinary Medicine, Texas A&M University, College Station, TX, email: gcothran@cvm.tamu.edu.

E. Gus Cothran, Ph.D. Equine Genetics Lab. VIBS, CVM Texas A&M University TAMU 4458 College Station, TX 77843-4458 (979) 845-0229

dtriant@cvm.tamu.edu dtriant@cvm.tamu.edu

UBristol SoilNematodeEvol

A postdoctoral research fellow is required to initiate an 18 month 'Proof of Concept' study to investigate the interactions between pathogenic bacteria and nematode worms, both commonly found co-occurring in the soil. The research fellow will join a multidisciplinary team of microbiologists, disease ecologists and molecular biologists at UWE Bristol (UK), The Center for Infectious Disease Dynamics (CIDD), Penn State University USA and The School of Veterinary Science, University of Bristol (UK). For further details and to apply for this job please follow this link http://info.uwe.ac.uk/-vacancies/job_details.asp?ref=R/11237RWS Closing date: June 15th 2007

Informal enquires can be made to Sarah Perkins, via email: sep18@psu.edu

Sarah Perkins Center for Infectious Disease Dynamics 208 Mueller Laboratory Penn State University University Park Pennsylvania 16802 Tel: (814) 863-2099 http://www.cidd.psu.edu/people/bio_perkins.html sep18@psu.edu

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UBritishColumbia SpeciationModels

A postdoctoral position is available in the group of Michael Doebeli (Department of Zoology and Department of Mathematics, University of British Columbia) to investigate mathematical models of speciation due to host-pathogen interactions.

An international research team consisting of Detlef Weigel, Jeff Dangl, Jonathan Jones and Michael Doebeli is investigating the molecular basis of pathogen recognition and its links to speciation in plants, particularly Arabidopsis. Michael Doebeli's group contributes by developing mathematical models for the evolutionary dynamics of pathogen recognition, which will be used to study how divergence in recognition systems can lead to reproductive isolation and speciation. The theoretical work will be very closely linked to the experimental work of the other three groups. Applicants should have excellent analytical skills and a strong interest in connecting theory to experimental model systems and empirical data. UBC offers an outstanding research environment with a strong group in Ecology and Evolution and a strong group in Mathematical Biology.

The earliest start date for the position is October 1, 2007, and the position is initially for one year but can be extended to three years. Salary is in the range of CAD $40-45K (plus benefits) per year, depending on qualifications. Applicants should send a CV, contact details of three referees, and a cover letter describing their interest in the position to doebeli@zoology.ubc.ca (preferred) or by normal mail to Michael Doebeli, Department of Zoology, University of British Columbia, 6270 University Boulevard, Vancouver, BC V6T 1Z4, Canada.

Dr. Michael Doebeli Department of Zoology University of British Columbia 6270 University Boulevard Vancouver B.C. Canada V6T 1Z4

email: doebeli@zoology.ubc.ca phone: (604) 822-3326 fax: (604) 822-2416

web: http://www.math.ubc.ca/ ˜ doebeli doebeli@zoology.ubc.ca doebeli@zoology.ubc.ca

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UBurgundy Ambrosia artemisiifolia evol

A post-doctoral research associate position in Evolutionary Biology is available to work with Pr François Bretagnolle and Bruno Chauvel, in the Biology and Management of Weed (BGA) Laboratory of the University of Burgundy, ENESAD and INRA The project consists in using phenotypic and microsatellites markers to compare introduced invasive and introduced historical non invasive populations of Ambrosia artemisiifolia in France.

Ambrosia artemisiifolia was recurrently and independently introduced in France at the end of the 19th and at beginning of the 20th. Some populations, after a lag phase, started to expand considerably although others remained stable and persist in localised populations. Moreover some historical populations have been collected in large number of individuals in herbarium collections. This situation allows comparing the genetic structure of invasive and historical non invasive populations based on phenotypic and neutral markers. Moreover, the existence of consistent herbarium collections of invasive and non invasive populations that still persist allows detecting evolutionary patterns through the time by the comparative analysis of neutral variation between ancient and actual DNA. The Weed Biology and Management laboratory in Dijon is the only INRA site dealing with weeds. Its activities focus on weeds biology, their management and the conservation of the biodiversity of weed species and communities in agricultural landscape. For detailed information about the research team visit http://www.dijon.inra.fr/bga/-umrbga/eng_presentation.php The candidates should have a strong interest in evolutionary biology of invasive species and a solid experience of laboratory methods in molecular ecology.

The position is funded by EGIDE and is available from now (ultimate dead line 31 December 2007) and for 12 months in the first instance. The net salary is 2000 / month.

Applicants should send a complete CV and names of three references via email to Prof. F. Bretagnolle (breta@dijon.inra.fr), or to UMR BGA Biologie et Gestion des Adventices' 17 rue Sully, BP 65510,. 21065 Dijon. France.

Best regards

François BRETAGNOLLE UMR BGA Biologie et Gestion des Adventices' 17 rue Sully, BP 65510,. 21065 Dijon. France Phone. (33) 3 80 69 32 67 - Fax (33) 3 80 69 32 62 breta@dijon.inra.fr

breta@dijon.inra.fr

UCBerkeley ComparativeBiomechanics

Post-doctoral Scientist Integrative Organismal Biology

A postdoctoral position is available in the Patek laboratory to examine the evolution and biomechanics of the mantis shrimp's raptorial strike. This integrative and comparative research links biomechanical analyses and field work with phylogenetic comparative analyses and modeling. We are looking for a candidate with experience in one or more of these areas. A Ph.D. is required.

The appointment will be for 12 months with the possibility for renewal. The annual salary range for this position will be commensurate with experience. The start date is flexible, preferably between September 2007 and January 2008. The University of California, Berkeley is an Equal Opportunity Employer.

Review of applications will begin on June 30, 2007 and will continue until the position is filled. Please email a letter explaining your interest/qualifications for the position, a curriculum vitae, research statement, up to three pdf reprints, and contact information of three references to: Dr. Sheila Patek Assistant Professor patek@berkeley.edu

Sheila Patek Assistant Professor Department of Integrative Biology University of California, Berkeley Berkeley, CA 94720-3140

Website: http://ist-socrates.berkeley.edu/ ~ patek/ patek@berkeley.edu patek@berkeley.edu

UCD Dublin FishPopStructure

Post-Doctoral Position: “Genotypic and phenotypic characterisation of deep-sea fish population structure”

Applications are invited for a 1-year postdoctoral position in the School of Biology & Environmental Science at UCD Dublin, working with Dr Stefano Mariani at the Marine Biodiversity, Ecology & Evolution Group: http://www.ucd.ie/zoology/marbee/ The research is funded by the Irish Research Council for Science, Engineering & Technology (IRCSET) and forms part of a EUROCORE/EURODEEP coordinated project supported by the European Science Foundation. The project, entitled “Genotypic and phenotypic characterisation of deep-sea fish population structure(GP-DEEP)” is aimed at unravelling the patterns of population structuring in a number of bathyal fish species across continental slopes, seamounts and trenches between the Azores and north-western Norway, by employing genetic (microsatellites) phenotypic (otolith microchemistry) and physical (oceanographic modelling) methods. The work is closely connected with partners in Norway (IMR Bergen & Oslo University), Portugal (DOP, Azores) and the UK (FRS Marine Lab, Aberdeen). The ideal candidate should possess a PhD in empirical population genetics or evolutionary biology, though we welcome applicants from other disciplines such as ecology or marine biology. Proficiency in molecular laboratory techniques is essential. A strong commitment to timely publication and interdisciplinary research is critical. The appointee will join a research team that together comprises 14 PhD students, 3 Postdoctoral fellows and 3 Lecturers, working on a broad range of topics from comparative genomics, molecular phylogenetics and population genetics, to fisheries science, community ecology and ecosystem management.

Application procedure: Please send a 1-page covering letter and a CV no longer than 3 pages, plus names and emails of three people who can be contacted for references, to: stefano.mariani@ucd.ie Closing date for applications: 30th June 2007 (interviews in mid July). Project start date: September 2007. Salary: around 38,000 per annum. Contract is initially for 12 months, with possibility of extension. Committed to Equal Opportunities.

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

Best,

Stefano Mariani

Dr Stefano Mariani MARine Biodiversity, Ecology & Evolution UCD School of Biology & Environmental Science Science and Education Research Centre (West) University College Dublin Belfield Dublin 4 Republic of Ireland tel. +353.1.716.2347 fax. +353.1.716.1152 http://www.ucd.ie/zoology/marbee/stefano_mariani.html stefano.mariani@ucd.ie

UCaliforniaMerced CoralReefGenomics

Position: Postdoctoral scholar on Coral Reef Genomics. University of California, Merced

Description: The University of California is creating a dynamic new university campus and campus community in Merced, California, which opened in August 2005 as the tenth campus of the University of California and the first American research university built in the 21st century. The campus is located at the base of the Sierra Nevada foothills, near Yosemite and the San Francisco Bay Area.

A full-time postdoctoral position is available as part of ongoing NSF- funded projects to look at the functional genomics of coral symbiosis and health in the Caribbean species Montastraea faveolata and Acropora palmata. cDNA microarrays as well as several thousand ESTs are now available for these two species. Additional EST sequencing is being done by DOE?s Joint Genome Institute for these corals and their dominant dinoflagellate symbionts. BAC libraries are also available for both coral species. Primary research questions will focus on, but are not limited to, developmental biology of corals, mechanisms of cell communication between host-symbiont, maintenance of symbiosis, breakdown of symbiosis (i.e. bleaching), response to disease, comparative genomics of syntenic regions. The successful candidate will be part of a multidisciplinary research team and a member of the Quantitative Systems Biology Group in the School of Natural Sciences.

Questions regarding the exact duties and responsibilities may be addressed to: mmedina@ucmerced.edu. Additional information about the School of Natural Sciences and the University of California at Merced can be found at http://www.ucmerced.edu . Conditions: The position is initially available in September 2007 for one year. Continuation is contingent on performance and availability of funds. Starting salary $34,000 or commensurate with experience according to the UC pay scale. The position includes generous benefits. The University of California at Merced is an affirmative action/equal opportunity employer with a strong institutional commitment to the achievement of diversity among its faculty, staff, and students.

Education: Ph.D. in Genome Biology, Marine Biology, Bioinformatics or related fields. Applicants with experience in comparative genomics, and/or microarray analysis are especially encouraged to apply.

Instructions: Applicants should submit online a cover letter, curriculum vitae or resume, and a list of three or more references including telephone numbers and email address http://jobs.ucmerced.edu/n/academic/position.jsf?positionId60

For additional information, please contact Mónica Medina mmedina@ucmerced.edu.

Deadline: Until a suitable candidate is identified.

Monica Medina Assistant Professor and Founding Faculty School of Natural Sciences University of California, Merced P.O. Box 2039 Merced CA 95344 tel: 209-228-7863 fax: 209-228-4053 mmedina@ucmerced.edu http://qsb.ucmerced.edu/faculty/mmedina/lab/ Monica Medina <mmedina@ucmerced.edu>

UCaliforniaMerced CoralReefGenomics 2

Position: Postdoctoral scholar on Coral Reef Genomics. University of California, Merced

Description: The University of California is creating a dynamic new university campus and campus community in Merced, California, which opened in August 2005 as the tenth campus of the University of California and the first American research university built in the 21st century. The campus is located at the base of the Sierra Nevada foothills, near Yosemite and the San Francisco Bay Area.

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Education: Ph.D. in Genome Biology, Marine Biology, Bioinformatics or related fields. Applicants with experience in comparative genomics, and/or microarray analysis are especially encouraged to apply.

Instructions: Applicants should submit online a cover letter, curriculum vitae or resume, and a list of three or more references including telephone numbers and email address http://jobs.ucmerced.edu/n/academic/position.jsf?positionId60

For additional information, please contact Mónica Medina mmedina@ucmerced.edu.

Deadline: Until a suitable candidate is identified.

Monica Medina Assistant Professor and Founding Faculty School of Natural Sciences University of California, Merced P.O. Box 2039 Merced CA 95344 tel: 209-228-7863 fax: 209-228-4053 mmedina@ucmerced.edu http://qsb.ucmerced.edu/faculty/mmedina/lab/ Monica Medina <mmedina@ucmerced.edu>

UCaliforniaRiverside EvolGenomics

Postdoctoral position in Evolutionary Genomics, University of California, Riverside

A fulltime postdoctoral position is available in the laboratory of Renyi Liu in the Department of Botany & Plant Sciences at the University of California, Riverside. The primary focus of the research is to investigate the evolutionary mechanisms underlying the diversification and adaptation of plants and bacteria, and the origin and evolution of complex systems.

Candidates should have a Ph.D. degree in evolutionary genetics/genomics, bioinformatics/computational biology, or related disciplines. Computational competence and strong background in evolutionary and/or molecular genetics are essential. Familiarity with Unix/Linux environment and databases is desirable. Experience in analyzing sequence and gene expression data is preferred.

The start date is flexible and can be as early as September 1, 2007. The position has guaranteed funding for two years. Continuation is contingent on performance and availability of funding. Salary is commensurate with experience and qualifications.

Interested individuals should send a CV, contact details of three referees, and a cover letter describing their interest in the position to rliu.biocomp@gmail.com.

The University of California, Riverside has an active career partner program, and is an Affirmative Action equal opportunity employer committed to excellence through diversity.

rliu.biocomp@gmail.com

UCaliforniaRiverside QuantGenet

POSTDOCTORAL POSITION: QUANTITATIVE GENETICS/GENOMICS Two postdoctoral positions are available in the laboratory of Professor Shizhong Xu, Department of Botany and Plant Sciences, University of California, Riverside to develop statistical methods for mapping quantitative trait loci (QTL) and for microarray data analysis. Candidates should have an interest in quantitative genetics/genomics, good programming skills, and be comfortable dealing with very large data sets. The positions are available immediately and will remain open until suitable candidates are located. For immediate consideration, please send applications via email (include a cover letter outlining your interests, complete CV, and contact information for three individuals willing to provide references) to Shizhong Xu at xu@genetics.ucr.edu or Department of Botany and Plant Sciences, University of California, Riverside, CA 92521. Shizhong Xu, Ph.DProfessor of Genetics and StatisticsDepartment of Botany and Plant

SciencesUniversity of CaliforniaRiverside, CA 92521Tel: (951)-827-5898Fax: (951)-827-4437E-mail: xu@genetics.ucr.edu

shxu@ucr.edu shxu@ucr.edu

UConnecticut SouthAfricanProteaceae

If anyone interested in this positon will be at the Botany/Plant Biology 2007 meetings in Chicago, please look me up. If you are interested in this position but won't be in Chicago, please e-mail me.

Kent

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Post-doctoral Fellow I-Anticipated

Department of Ecology & Evolutionary Biology

University of Connecticut

Evolutionary radiations in South African Proteaceae

The Department of Ecology & Evolutionary Biology at the University of Connecticut invites applications for an anticipated position as Post-doctoral Fellow I on a project investigating evolutionary radiations in white proteas (Protea sect. Exsertae). The successful applicant will be primarily responsible for establishing common gardens, monitoring individual performance, measuring a suite of morphological/physiological traits, and supervising field assistants. The successful applicant may also be involved in laboratory analyses using AFLPs and microsatellites. Extended travel to the Cape region of Southern Africa will be required for field work and experiments.

This is a one year, grant funded position. Continuation of this position may be possible for a maximum of two additional years if performance is satisfactory and grant funding is available.

Qualifications: Ph.D. in biology or a closely related field. Experience with experimental ecology is required. Experience in some combination of plant population ecology, plant physiological ecology, statistical modeling, and AFLP/microsatellite analysis is desired.

Electronic submission of applications is preferred. They should be submitted to Dr. Kent Holsinger (kent@darwin.eeb.uconn.edu). Paper applications should be addressed to Dr. Kent Holsinger, Department of Ecology & Evolutionary Biology, U-3043, University of Connecticut, Storrs, CT 06269-3043 USA. Applications should include a brief statement (1-2 pages) summarizing previous scientific work and experience, a curriculum vitae, and the names and addresses of up to three individuals able to evaluate the applicants qualifications for the position. The position is expected to be available on 1 September 2007 (pending final approval of funding). Review of applications will begin on 16 July 2007 and continue until the position is filled.

– 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

kent@darwin.eeb.uconn.edu kent@darwin.eeb.uconn.edu

UEdinburgh HIVevolution

University of Edinburgh School of Biological Sciences Postdoctoral Research Fellow

An evolutionary or computational biologist is required to join the group of Professor Andrew Leigh Brown (http://homepages.ed.ac.uk/eang09/LeighBrownGroup.html), on an MRC-funded position to analyse time-resolved phylogenies from HIV sequence data to infer the structure of the transmission network in the UK population for epidemiological models. A PhD and a background in one of molecular evolution, epidemiological modelling or computational biology is required; experience in viral evolutionary analysis would be helpful.

Fixed Term: 2 years 6 months

Salary: £32,795 - £39,160

Closing date: 27th June 2007

Website: www.jobs.ed.ac.uk Ref: 3007496

A.Leigh-Brown@ed.ac.uk A.Leigh-Brown@ed.ac.uk

UEdinburgh InfluenzaEvol

University of Edinburgh School of Biological Sciences Postdoctoral Research Fellow

An evolutionary or computational biologist is required to join the groups of Professor Andrew Leigh Brown (http://homepages.ed.ac.uk/eang09/LeighBrownGroup.html), and Dr Andrew Rambaut (http:// tree.bio.ed.ac.uk/) to analyse the evolution of human and avian influenza genomes as part of an interdisciplinary consortium at 3 Universities in Scotland funded by the Scottish Funding Council. A PhD and a background molecular evolution, or computational biology is required; experience in viral evolutionary analysis would be helpful.

Fixed Term: 2 years

Salary: £30,012 - £32,796

Closing date: 14th June 2007

Website: www.jobs.ed.ac.uk Ref: 3007482

Andrew Rambaut Institute of Evolutionary Biology University of Edinburgh Ashworth Laboratories Edinburgh EH9 3JT EMAIL - a.rambaut@ed.ac.uk TEL - +44 131 6508624

a.rambaut@ed.ac.uk a.rambaut@ed.ac.uk

UKansas EvolGenetics

Postdoc in Evolutionary Genetics at the University of Kansas

A 3 year post-doctoral position is available to work with John Kelly at the University of Kansas. The position is funded through a recently renewed IRACDA grant to KU from the National Institute of Health (http://www2.ku.edu/~iracda/). The position involves both research and teaching components, although the teaching commitment does not begin until the second year of the appointment. The topic of the research project is open, but should be related to our currently funded projects on the model plants species Mimulus guttatus. The central questions involve the maintenance of genetic variation in quantitative traits, the evolutionary consequences of epistasis, the genetic basis of adaptation, and the evolution of plant mating systems.

The annual salary is in the range of $39,000-41,000. The position can begin as early as August 1, 2007. This NIH program is available only to US citizens and permanent residents.

Anyone that is interested should contact me by telephone (785-864-3706) or email (jkk@ku.edu).

Sincerely, John Kelly Dept. Ecology and Evolutionary Biology University of Kansas

“Kelly, John K” <jkk@ku.edu>

UOttawa EvolBiol

Postdoctoral Fellowship in Evolutionary Biology University of Ottawa, Canada

The evolutionary biology group (http://www.science.uottawa.ca/~hrund050/evolution) in the Department of Biology at the University of Ottawa wishes to nominate a candidate for a Vision 2010 Postdoctoral Scholarship (http://www.etudesup.uottawa.ca/Default.aspx?tabid=3D2247). Research topics are open but are expected to build on, and complement, the strengths of the group in one or more of the following areas: the ecology and genetics of adaptation and diversification (R. Kassen), sexual selection and speciation (H. Rundle), the diversification of angiosperms (R. Sargent), and evolutionary medicine (S. Findlay). The position is for two years and can begin as early as January 01, 2008. The total stipend is CDN $50,000 per annum, which may include a maximum research allowance of $5,000. Fellowships are open to Canadian and international candidates.

Applications should include a cover letter, a curriculum vitae, a short (1 page) description of proposed research, and the names and contact information (including e-mail) of three referees. All application materials must be submitted as PDF’s in a single email to both Rees Kassen (rkassen@uottawa.ca) and Howard Rundle (hrundle@uottawa.ca), to whom queries may also be addressed. Evaluation of applications will begin on July 15, 2007. Application deadline for the fellowship is Aug. 31, 2007.

Located at the confluence of English and French

Canada, Ottawa is a rich and vibrant national capital of approximately 1 million inhabitants (http://www.ottawatourism.ca). The city offers a wide range of cultural activities in the visual and performing arts, as well as easy access to green spaces and wilderness. The University of Ottawa is located next to the historic Rideau Canal, steps from Parliament and within easy access to a wide range of research facilities of interest to evolutionary biologists including the Canadian Museum of Nature, the National Wildlife Research Center, Health Canada, and Environment Canada.

Howard D. Rundle Assistant Professor - Professeur adjoint Canada Research Chair - Chaire de recherche du Canada Department of Biology - Département de biologie University of Ottawa - Université d'Ottawa 30 Marie-Curie (277 Gendron) Ottawa, Ontario, K1N 6N5, CANADA

Office: +1 613-562-5800 x2835; Fax: +1 613-562-5486; Lab: +1 613-562-5800 ×6837 Email: hrundle@uottawa.ca; Skype: howarddrundle http://www.science.uottawa.ca/ ˜ hrund050 hrundle@uottawa.ca hrundle@uottawa.ca

UParisSud GeneticsAndEvolution

A CNRS postdoctoral position is available in the group Fundamental Quantitative Genetics (INRA-University Paris Sud-CNRS-AgroParisTech) in Gif-sur-Yvette, France, on the topic: "Genetics and evolution of metabolic systems: heuristic modelling for flux prediction and optimization". All details about the project are on the site: https://www2.cnrs.fr/DRH/post-docs07/index.php?pid=-1&action=view&idW7&lang=en Dominique de Vienne Professeur, Université Paris-Sud Directeur de l'UMR de Génétique Végétale INRA-UPS-CNRS-AgroParisTech Ferme du Moulon 91190 Gif-sur-Yvette, France Tel : 01 69 33 23 60 Fax : 01 69 33 23 40 devienne@moulon.inra.fr

devienne@moulon.inra.fr

UParisXI DNABarcoding classification

Postdoctoral fellowship on Classification methods for DNA barcoding.

DNA Barcoding consists in assigning an individual to a given species according to the sequence of this individual at a given locus (for the animals, often a fraction of the COI mitochondrial DNA gene). The technique consists first in sequencing a sample of reference individuals for which the taxonomic status is unambiguous. This reference sample is then used as a training data set for a classification algorithm, which aims at assigning newly sampled individuals to a given species on the basis of their DNA sequence only.

The postdoctoral fellow will work in particular in the development and comparison of the efficiency of various classification algorithms in this context. These algorithms include classical phylogenetic methods (e.g. neighbour joining, maximum likelihood), statistical classification methods (e.g. CART, Random Forest, neural networks, kernel and SVM methods) and coalescent-based methods. Methods that take advantage of recent advances in statistical learning and inference and in population genetics will be favoured in particular. The comparisons will be carried out on simulated data sets and also on well-characterized experimental data sets. In particular, the impact on the efficiency of the different methods of events like gene flow between species or population expansions will be investigated. The contribution of additional information at nuclear loci will also be considered. Finally the question of the detection of new species might also be addressed.

The position is opened for one year with a possible extension of nine months. It should start in September 2007. The salary will be around 1800 euros/month. The postdoctoral fellow will be mainly located at the Unite Mathematiques et Informatique Appliquees of the INRA - Jouy-en-Josas, near Paris, in strong interactions with two other laboratories (see below). A strong background in mathematics, statistics and computer science is requested for this position. An experience in interacting with biologists, especially population geneticists, will be a plus.

Interested candidates are invited to submit by email to C. Laredo and F. Austerlitz (see addresses below) the following elements.

- a CV with a list of publications - two or three relevant publications - an application letter - the names and e-mail addresses of three referees.

Supervisors:

Catherine Laredo, INRA, Unite Mathematiques et Informatique Appliquees, Centre de Recherche de Jouy-en-Josas, F-78352 JOUY-EN-JOSAS, France. Tel : +33 1 34 65 22 26, FAX : +33 1 34 65 22 17, Email: Catherine.Laredo@jouy.inra.fr http://w3.jouy.inra.fr/-unites/miaj/index.php3 and Laboratoire Probabilites et modeles Aleatoires, UMR 7599, Universites Paris VI et VII, 75013 Paris, France

Frederic Austerlitz, Laboratoire Ecologie, Systematique et Evolution, U.M.R. C.N.R.S./U.P.S./E.N.G.R.E.F. 8079, Universite Paris-Sud XI, Betiment 360, F-91405 Orsay cedex, France. tel: + 33 1 69 15 77 20, fax: + 33 1 69 15 46 97, email: Frederic.Austerlitz@u-psud.fr http://www.ese.u-psud.fr/ Collaborators:

Olivier David (INRA, Unite Mathematiques et Informatique Appliquees)

Brigitte Schaeffer (INRA, Unite Mathematiques et Informatique Appliquees)

Michel Veuille (Departement Systematique et Evolution, Museum National d'Histoire Naturelle, Paris)

Raphael Leblois (Departement Systematique et Evolution, Museum National d'Histoire Naturelle, Paris)

Frederic.Austerlitz@u-psud.fr Frederic.Austerlitz@u-psud.fr

USouthDakota FishEvol

Scientific Data Curator

We are seeking a scientist to help compile comparative morphological data from the scientific literature on fish evolution. This person will lead data curation and ontology development as part of a team comprised of scientists and software developers, in order to develop a novel system for the analysis of developmental and phenotypic diversity data using ontologies. This NSF funded project (3 years) is led by Paula Mabee (University of South Dakota) in collaboration with Monte Westerfield (Zebrafish Information Network), the National Evolutionary Synthesis Center (www.nescent.org <http://www.nescent.org/>) and the National Center for Biomedical Ontology. For more information about the project, see the following:

* https://www.nescent.org/phenomap/Main_Page

* Mabee et al. (2007) Phenotype ontologies: the bridge between genomics and evolution. Trends Ecol Evol. doi:10.1016/j.tree.2007.03.013

Job description: The incumbent will curate evolutionary morphological data from the literature on fishes, annotating anatomical features using terms from ontologies, to populate a database that will be integrated with the existing developmental and genomic database of zebrafish; contribute new terms, definitions, and relationships to the ontologies where needed and work with the broader community to ensure consistency; review the data that is submitted to the database by expert morphologists and communicate with them regarding homology relationships among entities; provide and solicit input regarding the nature of characters, character states, homologies, and phylogenetic relationships; and work closely with software developers at NESCent to develop the curatorial interfaces, the database, and the web interface to the system being developed as needed.

Required qualifications:

* Ph.D. degree in biological sciences with expertise in comparative vertebrate anatomy and evolution

Preferred qualifications:

* Ph.D. degree in biological sciences with expert knowledge of comparative anatomy and evolution of fishes * Ability to communicate well and work as part of a distributed research team * Experience using or creating ontologies

How to apply: Please send cover letter, resume, and the contact information for three references to the project PI, Dr. Paula Mabee (pmabee@usd.edu). Further inquiries about the position may be directed to Dr. Mabee by email, or by phone at +1-605-677-6171.

"Mabee, Paula" <Paula.Mabee@usd.edu>

UTexasArlington EvolGenomics

UT Arlington Postdoc in Evolutionary Genomics

A postdoctoral position is available in the laboratory of Esther Betran, Ph.D., located in the newly remodeled facilities of the Genome Biology Group at the University of Texas at Arlington (http://biology.uta.edu/-genome_group/index.htm)

The NIH funded research focuses on the origin of new genes and their role in genome evolution.

Several projects are under development in the lab to answer essential questions in the field of new gene origination: functional and evolutionary study of young retrogenes, de novo formation of promoter regions, patterns on the formation of new genes and genes domesticated from transposable elements. For a summary of research, please see: http://www3.uta.edu/faculty/betran/publications.html We seek a highly trained, enthusiastic, innovative post-doctoral researcher with ability to think independently and to work cooperatively. Candidates should have a Ph.D. degree in Drosophila genetics, evolutionary genetics, computational biology, or related disciplines with desire to conduct comparative genomic analyses. Candidates with theoretical, computational or experimental background are welcome.

Salary commensurate with qualifications and experience.

Our lab enjoys vibrant interactions with other members of the new and rapidly expanding Genome Biology Group. Additionally, the lab is benefiting greatly from the new Genomics Facilities and new lab space.

The University of Texas at Arlington, the second largest institution in The University of Texas system, is a full service research and teaching university with over 25,000 students. The University is located in the city of Arlington in the center of the Dallas-Ft. Worth Metroplex, one of the leading centers of aerospace, electronics, and telecommunications activity in the U.S. Excellent recreational, entertainment, and cultural facilities, major airport, modern shopping complexes and professional sports organizations are located in Arlington and the surrounding area. Other of the main advantages of the Metroplex area is the inexpensive cost of living.

To apply for this position please send a CV, a letter of interest and names of two potential referees to betran@uta.edu

For more information please visit: http://www3.uta.edu/faculty/betran UTA is an equal opportunity/affirmative action employer

BETRAN@uta.edu BETRAN@uta.edu

UTexasArlington HerpetologyEvol

THE UNIVERSITY OF TEXAS AT ARLINGTON POST-DOCTORAL POSITION

An NSF-supported, three-year, post-doctoral fellowship is available to study herpetological diversity of Mexico at The University of Texas at Arlington. Applicants should be highly motivated, independent scientists with a sound knowledge of Neotropical herpetology. Desired qualifications include fluency in Spanish, experience conducting fieldwork under difficult conditions, photographic expertise, and leadership abilities in heading up field parties of 6 to 12 persons. Responsibilities will include organization of field trips into remote regions of Mexico for 2-4 weeks at a time, the collection and documentation of scientific materials, and identification and incorporating these materials into permanent collections. Salary is between $28,000 and $32,000. Review of applications is ongoing and will continue until a candidate is selected. The starting date is September 2007.

Applicants must have a PhD in Biology or related field. Applicants should send electronic copy of CV and names (and e-mail addresses) for two referees to:

Jon Campbell Department of Biology UT-Arlington Arlington, TX 76019

E-mail: Campbell@uta.edu

esosorum@sbcglobal.net

UWuerzburg 2 Bioinformatics

PhD/Postdoc position(s) in bioinformatics/phylogenetics

Two 3 year PhD (or one Postdoc) position(s) in bioinformatics/phylogenetics are available in the department of bioinformatics at the University of Wuerzburg. The positions are funded by the German Research Foundation (DFG) to study the evolution of rRNA internal transcribed spacer 2 primary sequences and their secondary structures. The positions will be paid as BatIIa/2 (or equivalent) according to the German pay scale. Requirements are a master's degree (or diploma) in biology or bioinformatics (or related fields) and a genuine interest in phylogeny and RNA structures.

The department of bioinformatics located at the biocenter consists of interactive groups focussing on statistics and mathematical biology, evolutionary biology and phylogenetics, proteomics and genomics, sequence analysis, function and structure prediction, as well as on networks and pathway analysis.

More information about the department/biocenter is available on the respective web sites at:

http://bioinfo.biozentrum.uni-wuerzburg.de/ http://www.biozentrum.uni-wuerzburg.de/ Relevant literature and project related information can be found on the ITS2 Database:

http://its2.bioapps.biozentrum.uni-wuerzburg.de/
Applicants should send a PDF file with a statement of interest, Curriculum vitae and the contact information for at least two referees to:

matthias.wolf@biozentrum.uni-wuerzburg.de

The University of Wuerzburg is an equal opportunity employer with an affirmative action program for the disabled.

Dr. Matthias Wolf Department of Bioinformatics Biocenter University of Wuerzburg D-97074 Wuerzburg Germany

phone: +49(0)931/888-4562

fax: +49(0)931/888-4552

mail: <mailto:matthias.wolf@biozentrum.uni-wuerzburg.de> matthias.wolf@biozentrum.uni-wuerzburg.de

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Matthias Wolf <Matthias.Wolf@biozentrum.uni-wuerzburg.de>

UWyoming MicrobialGenomicsEvol

University of Wyoming College of Agriculture - Academic Vacancy

POST-DOCTORAL RESEARCH ASSOCIATE - #4604

Molecular Biology

A position for a postdoctoral researcher in microbial genomics, ecology, and evolution in the Ward Research Group at the University of Wyoming is currently available. The position has guaranteed funding for two years. Applicants should have good molecular biology skills, a willingness to participate in field work, a familiarity with statistics, and an interest in the application of genetic and genomic tools to investigate the relationships between microbes and their habitat, and the evolution of relevant traits. Previous experience with the cultivation of prokaryotes, microbial physiology, and/or microscopy would be an advantage, but not essential. For more details on research in the Ward Research Group, please see http://uwacadweb.uwyo.edu/-uwmolecbio/Faculty/N_Ward.asp. Salary commensurate with experience and qualifications.

To apply, please send a cover letter, CV, contact information for three references, and PDF copies of two papers describing your recent research to nlward@uwyo.edu. Review of applications will begin June 15, 2007 and will continue until a suitable applicant is identified.

NWard@jcvi.org

UWyoming PlantEvol

Position: A 3-yr post-doctoral fellowship is available in the Weinig lab at the University of Wyoming to work in the area of evolutionary genetics/genomics.

Project: Genetic analysis of natural variation in the control of flowering timing and inflorescence architecture in Brassica rapa

Using Brassica rapa, we are examining genetic mechanisms that enable adaptation to seasonal climates. In particular, we are looking at how temperature and photoperiod interact to affect flowering time, inflorescence architecture, floral morphology, and fruit set directly as well as indirectly via effects on circadian rhythm. The circadian clock is 'set' in response to both temperature and photoperiod, but very little is known about the genetic underpinnings of temperature compensation, i.e., why the clock does not simply cycle faster under high relative to low temperatures. Moreover, there is little understanding of how natural variation in circadian rhythm affects plant performance in seasonal settings or of the genetic basis of quantitative reproductive traits.

Rob McClung, the PI on this grant, is focusing on the genetic characterization of temperature compensation. Another Co-PI on this grant, Rick Amasino, is heading up a large mutant screen. Our role will be to a) QTL map flowering time and floral morphological traits under variable simulated seasonal conditions, b) to evaluate attendant changes in mating system and fitness in a field setting, and c) screen some of the more interesting mutants in the field. We will also be performing studies of molecular evolution of candidate loci. There is a substantial training component to this grant that includes the opportunity to visit labs of our collaborators to learn new techniques.

Qualifications: I am primarily interested in an individual who is enthusiastic and who has a background in evolutionary genetics and some experience using basic PCR-based approaches.

Inquiries should be directed to Cynthia Weinig (cweinig@umn.edu) Tel: 612 624-1037.

Cynthia Weinig Assistant Professor University of Minnesota Department of Plant Biology 250 Biosciences Center 1445 Gortner Ave. St. Paul, MN 55108 Tel: 612-624-1037 Fax: 612-625-1738 E-mail: cweinig@umn.edu

cweinig@tc.umn.edu cweinig@tc.umn.edu

UZurich SexualSelection

A postdoctoral position is available from 1st September, or as arranged, in the Zoological Museum of the University of Zurich, Switzerland. The successful applicant will join an active research group working on postcopulatory sexual selection in the yellow dung fly. The precise research topic(s) within this broad theme will substantially depend on the interests and background of the applicant.

Applicants must have a completed Ph.D. Postdoctoral experience would be advantageous. A knowledge of, or a willingness to learn, German would also be advantageous. A small amount of teaching, in either English or German, will be required. The position will be offered for two years in the first instance, with the possibility of annual renewal to a maximum of six years.

Please send a curriculum vitae, publication list and a one-page statement of research interests to zmdirektion@zm.uzh.ch. Applications should be sent before the 18th July 2007.

Enquiries to Prof. Paul Ward, Zoological Museum of the University of Zurich, Winterthurerstr. 190, CH-8057 Zurich, Switzerland. Email: pward@zm.uzh.ch. Prof Paul I Ward Direktor Zoologisches Museum der Universität Zürich Winterthurerstrasse 190 CH 8057 Zürich Switzerland Phone +41 44 635 4760 Fax +41 44 635 4780 email: pward@zm.uzh.ch

Direktionssekretariat: Rosemarie Keller Mail: zmdirektion@zm.uzh.ch Phone +41 44 635 4761

pward@zm.uzh.ch pward@zm.uzh.ch

UppsalaU ComputationalGenet

We are seeking researchers interested in joining our Computational Genetics program in Uppsala, Sweden.

We are interested in understanding the genetics underlying complex traits taking a computational approach. Projects are often, but do not necessarily have to be, inspired by problems or opportunities that advent from experimental data. We encourage scientists to form and develop their projects to suit their interests and abilities within the framework of existing funding. We also support grant proposals from individuals that wish to pursue individual projects. The project portfolio in the group will thus vary, but we usually have ongoing projects in the field of statistical and computational methods in genetics, genetic modeling, exploratory analyses of experimental datasets and experiments to validate interesting biological findings.

A common theme in our research is epistasis. We are actively developing models, algorithms and tools for large scale screening and interpretation of the genetic effects of epistatic QTL in regulating complex trait expression. Our tools have mostly been used to study the importance of epistasis in phenotypic evolution using data from divergent crosses between domesticated animals.

We aim to integrate researchers with different backgrounds both within and across traditional scientific disciplines. We do, however foresee that you have a relevant scientific education (Ph.D. degree or similar) and an interest in Quantitative-, Population- and Evolutionary Genetics. A strong mathematical / statistical background and programming experience is an advantage

If you want to learn more about us, please visit http://www.computationalgenetics.se or contact Örjan Carlborg (orjan.carlborg@lcb.uu.se). When you are interested in working with us, please send us a CV, list of publications and a short description of what interests you in the field of complex trait genetics and what you can contribute to in an interdisciplinary group working on this topic. We look forward to hear from you!

Salary and conditions of future employment(s) are under the terms of the current agreement for academic scientists employed in the public sector. We are looking for several candidates and positions will remain open until suitable candidates have been found. Positions can start 1 Aug, 2007 at the earliest.

Please feel free to spread this advert to others that might be interested!

Örjan Carlborg Linnaeus Centre for Bioinformatics, Uppsala University BMC, Box 598 SE-75124 Uppsala Sweden Email: orjan.carlborg@lcb.uu.se Phone: +46-18-4716691 Mobile: +46-70-4250387 Fax: +46-18-4716698 Web: http://www.orjancarlborg.com orjan.carlborg@lcb.uu.se orjan.carlborg@lcb.uu.se

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WageningenU Celegans genomics

C. elegans Post-doc position

On gene-environment interactions in Caenorhabditis elegans using genetical genomics

Job description It is widely documented that environmental changes will induce differential expression of genes, yet it is unknown how these patterns of environment-induced expression plasticity are inherited and how they differ between genetically divergent individuals of a biological species. We use recombinant inbred lines of the nematode C. elegans and measure genome-wide gene expression (genetical genomics) at different environmental conditions. Using statistical analysis tools developed for quantitative trait locus (QTL) mapping, we aim to detect genes with genetically determined differences in their plastic response to environmental changes. Our previous results show that differential responses of different genotypes to environmental changes are widespread. The candidate will study the heritable component of plasticity of gene transcription regulation to enhance our understanding of the environmental forces that drive evolutionary adaptation. Recent papers of our group include:

Kammenga JE, Doroszuk A, Riksen JAG, Hazendonk E, Spiridon L, Petrescu AJ, Tijsterman M, Plasterk RHA, Bakker J (2007) A C. elegans wild-type defies the temperature-size rule owing to a single nucleotide polymorphism in tra-3. PLoS Genetics 3: 358-366.

Kammenga JE, Herman M, Ouborg NJ, Johnson L, Breitling R (2007) Microarray challenges in ecology. Trends Ecol. Evol. 22: 273-279.

Li Y, Alvarez OA, Gutteling EW, Tijsterman M, Fu J, Riksen JAG, Hazendonk E, Prins P, Plasterk RHA, Jansen RC, Breitling R, Kammenga JE (2006) Mapping determinants of gene expression plasticity by genetical genomics in C. elegans. PLoS Genetics 2: e222.

Gutteling EW, Riksen JAG, Bakker J, Kammenga JE (2007) Mapping phenotypic plasticity and genotype-environment interactions affecting life history traits in Caenorhabditis elegans, Heredity, 98: 28-37.

Gutteling EW, Doroszuk A, Riksen JAG, Prokop Z, Reszka J, Kammenga JE (2007) Environmental influence on the genetic correlations between life-history traits in Caenorhabditis elegans. Heredity, 98: 206-213.

Requirements â PhD degree in Biology, genetical and/or biotechnological sciences â experience in genetic mapping and knowledge of bioinformatics or high throughput gene expression profiling is required â excellent writing (English) and communication skills â accurate, systematic worker

Organization Wageningen University and Researchcentre, Laboratory of Nematology

Conditions of employment Estimated maximum salary per month: â¬3597, $-Durationofthecontract : 3years$

Additional information can be obtained from

Dr. Jan E. Kammenga, Laboratory of Nematology, Wageningen University, Binnenhaven 5, 6709 PD, Wageningen, The Netherlands, Tel: +31 317 482998/482197, Fax: +31 317 484254, email: Jan.Kammenga@wur.nl

No rights can be obtained from this notification.

Jan.Kammenga@wur.nl

WorkshopsCourses

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Lisbon ConGen Sep19-21 errors

Dear colleagues, I recently sent an e-mail advertising for an ESF-funded workshop in Lisbon (19-21 sept 2007). There has been a PROBLEM with the web page LINK I gave and data may have been lost. If you have ALREADY APPLIED, could you send me an e-mail (chikhi@cict.fr) just to mention that and I will check that your data have not been lost.

If you have NOT APPLIED YET, and wish to, the CORRECT LINK is: http://www.igc.gulbenkian.pt/-node/view/91 You will then need to look for the "ESF Conservation genetics and Fragmentation" workshop and click on "Application" to fill the application. Otherwise, you can also go the IGC main page (http://-www.igc.gulbenkian.pt/) and click on the "Workshops and Conferences" link. Look for the "ESF Conservation genetics and Fragmentation" workshop and click on "Application" to fill the application.

A preliminary program is available by clicking directly on "ESF Conservation genetics and Fragmentation".

I apologize for the inconvenience. Due to this problem the DEADLINE for applications has been EXTENDED to the 30th of June.

Below is a copy of the previous mail containing more information on the workshop, Lounès Chikhi

Dear evoldir members, A ESF ConGen (http://-www.esf.org/congen/) funded workshop entitled "Population genetics modelling and habitat fragmentation: separating recent and ancient events for efficient conservation" will be held at the Instituto Gulbenkian de Ciências in Oeiras (http://www.igc.gulbenkian.pt/) from the 19 to 21 Sept 2007.

The aim of the workshop is to bring together specialists from different areas related either to conservation biology and population genetics, including statistical modelling. We shall discuss the current needs of conservation biologists in connection with the achievements and limitations of current population genetics methods. Discussions will revolve around case studies, and ongoing theoretical work to unravel the past demography of species. One aim is to show conservation biologists the existence of tools that can be applied to infer the past of endangered species and that this knowledge can be used to improve conservation strategies. Another aim is to show theoreticians that interesting inference problems still need to be addressed in conservation biology. Case studies, theoretical work and software related presentations will all be represented during the workshop. Current invited speakers are (in alphabetical order):

D. Balding, M. Beaumont C. Bessa-Gomes, B. Crouau-Roy M. Currat, L. Excoffier P. Garnier-Géré, B. Goossens D. Hudson, C. Lavigne R. Nielsen, U. Radespiel I. Togan, L. Vigilant

The Workshop aims at favouring discussion between participants and is thus open to up to 25 participants in addition to the invitees mentioned above. Local costs (meals and lodging close to the Instituto Gulbenkian de Ciências) will be taken care of for *all 25* participants. Moreover, a limited number of grants will be given to participants to reimburse partly flight tickets.

The selection of participants will be based on scientific criteria and on the need to maintain a balance between theoretical and case studies. Participants coming from ConGen contributing countries will be favoured in the selection process (Austria, Belgium, Croatia, Czech Republic, Denmark, Finland, France, Hungary, Netherlands, Norway, Spain, Sweden, Turkey). A couple of self funded participants may also be accepted depending on the number of applications.

Applications should be submitted online through the following website: http://www.igc.gulbenkian.pt/-node/view/23 Note that there is more than one workshop/course on this page and that you should click on the right "Application" link. A preliminary program will soon be available on the same site (clicking on the Workshop name).

The DEADLINE for registration is 15/06/2007. BEFORE APPLYING: please remember to name any file you upload with your name.

If you have any problem with the application, please do not hesitate to contact me, best wishes, Lounès Chikhi

Organizer: Lounès Chikhi (chikhi@cict.fr – chikhi@igc.gulbenkian.pt) CNRS, Université Paul Sabatier, Toulouse, France Instituto Gulbenkian de Ciências, Oeiras, Lisboa, Portugal

Workshop location: http://www.igc.gulbenkian.pt/ chikhi@cict.fr chikhi@cict.fr

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Montana ConservationGeneticDataAnalysis Sep11-16 3

*********LAST CALL***********

2nd Conservation Genetics Data Analysis Course Recent Approaches for Estimation of Population Size, Structure, Gene flow, Landscape Genetics, Selection Detection & Bioinformatics

11 - 16 September, 2007, Flathead Lake Biological Station, Montana

Objective: To provide training in conceptual and practical aspects of data analysis for the conservation genetics of natural and managed populations. Emphasis will be on interpretation of output from recent novel statistical approaches and software programs. The course also will allow daily discussions among young researchers and top-researchers to help develop the next generation of conservation geneticists, and to identify developments needed to improve data analysis approaches. This course will cover analysis methods including the coalescent, Bayesian, approximate Bayesian, and likelihood-based approaches.

Who should apply: Ph.D. students, post-docs, and population biologists with a background of at least one semester university-level course in population genetics and a course in population ecology. Applicants must have a basic background in population genetic data analysis, including testing for Hardy-Weinberg proportions and gametic disequilibrium. Participation will be limited to 28 people allowing efficient instruction with hands-on computer exercises during the course. Priority will be given to persons with their own data to analyze (for example graduate students at the end of their degree program). Deadline for application is 15 June, 2007

Course/Workshop Format: For each subject, we provide 30-45 minutes of background, theory, discussion and introduction to concepts. Immediately following, we will conduct data analyses together for 30-60 minutes using relevant software programs and real data sets. Evening hands-on computer sessions and housing together of instructors and students in the same location will allow for extensive exchange and facilitate learning.

Instructors:

Oscar Gaggiotti, University Joseph Fourier in Grenoble, France Gordon Luikart, Center for Investigation of Biodiversity and Genetic Resources at the University of Porto (CIBIO), Portugal & University of Montana Albano Beja-Pereira, Center for Investigation of Biodiversity and Genetic Resources at the University of Porto (CIBIO), Portugal David Lynn, Simon Fraser University, Burnaby (Vancouver), Canada Mark Miller, Utah State University, Logan, USA Jonathan Pritchard, University of Chicago, Logan, USA Mike Schwartz, US Forest Service, Missoula, USA David Tallmon, University of Alaska, Juneau, USA Robin Waples, Northwest Fisheries Science Center of the National Marine Fisheries Service, Seattle, USA

Location: The course will be held at the beautiful Flathead Lake Biological Station near Glacier National Park (see ?Location? at http://popgen.eu/-congen2007/, click ?Site Map? then ?Location Map?). The International airport is 40 miles drive north of the Biological Station (see http://www.iflyglacier.com/).

Application and cost: For detailed information see http://popgen.eu/congen2007/. Accommodations and meals are included in the registration fee. Cost: $US 1,100 per person (plus $200 if payment arrives after June 15) will cover all meals, lodging, transportation to and from the airport, and a visit to Glacier National Park. Up to two reduced-cost scholarships could be available for candidates with no funding.

congen@popgen.eu

NewtonInstitute Phylogenetics Sep3-7

** Extended Deadline **

Isaac Newton Institute for Mathematical Sciences, Cambridge, UK

EMBO Workshop on Current Challenges and Problems in Phylogenetics

(3 September to 7 September 2007)

in association with the Newton Institute programme entitled Phylogenetics (3 September to 21 December 2007)

Sponsored by: European Molecular Biology Organisation (EMBO)

Principal Organiser: Professor Vincent Moulton (University of East Anglia)

Organisers: Dr Brent Emerson (University of East Anglia), Professor Daniel Huson (Tuebingen University) and Professor Mike Steel (University of Canterbury)

Theme of Workshop: Phylogenetic trees and networks are central to modern molecular evolutionary biology, with applications ranging from the origin of viruses (e.g. HIV, influenza) to modelling plant and animal radiations. As biologists attempt to reconstruct larger slices of the tree of life' using increasingly complex data, and incorporating more accurate models of molecular evolution, mathematics (and its sister fields, statistics and computer science) is increasingly being seen as an essential tool.

This workshop will showcase some of the recent achievements, challenges and new problems that arise in using mathematical approaches to understand molecular evolution. Topics covered will include: phylogenomics, molecular epidemiology, genetic biodiversity and phylogeography, processes of reticulate evolution (such as horizontal gene transfer), haplotype mapping by perfect phylogeny, population genetics in phylogeny, and metagenomics.

In addition this workshop will launch (and set the agenda for) a 4-month workshop of collaboration and research at the Isaac Newton Institute for Mathematical Sciences in a program on Phylogenetics, which will bring mathematicians and biologists together to develop new approaches in molecular phylogenetics.

Invited Speakers: J Felsenstein (Washington), O Gascuel (LIRMM), J Hein (Oxford), J Kim (Pennsylvania), W Martin (Heinrich-Heine), A Mooers (Simon Fraser), L Pachter (UC Berkeley), A Rodrigo (Auckland), A von Haeseler (Duesseldorf) and T Warnow (Texas).

Location and Cost: The workshop will take place at the Newton Institute and accommodation for participants will be provided in a single study bedroom with shared bathroom at Wolfson Court. The workshop package, costing 450GBP, includes accommodation, breakfast and dinner from dinner on Sunday 2 September to breakfast on Saturday 8 September 2007, and lunch and refreshments during the days that lectures take place. Participants who wish to attend but do not require the workshop package will be charged a registration fee of 90GBP. Self-supporting participants are very welcome to apply.

Further Information and Application Forms are available from the WWW at:

<http://www.newton.cam.ac.uk/programmes/PLG/-plgw01.html> ** Closing Date for the receipt of applications is 30 June 2007 **

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– Prof. Mike Steel Director, Biomathematics Research Centre University of Canterbury, Christchurch, NZ. http://www.math.canterbury.ac.nz/ ˜ mathmas/ M.Steel@math.canterbury.ac.nz

UAarhus EvolTheory Sep23-28

Please find below and attached an invitation to attend a phd course in evolutionary theory and applications to held at the Molslaboratory, 40 km north of Aarhus. Volker Loeschcke, Professor in Evolutionary Genetics (Dept. of Biological Sciences, Section for Ecology and Genetics, Univ. of Aarhus, Aarhus, Denmark)

Ph.D. course: Evolutionary theory and its applications

Aim: The power of evolutionary approaches to very different disciplines from economy over philosophy to medicine is getting increasing attention among scientists while at the same time the validity of evolutionary explanations concerning the origin of life and the forces that shape its diversity has been under attack - a significant proportion of the populations of western (and other) countries is not satisfied by the answers that biologists provide and feel comfortable with non-scientific based ideas as intelligent design or creationism. On this background, it is timely to improve the knowledge on evolutionary concepts and the evolutionary approach among students in biology and other disciplines with interest in evolutionary thinking. Thus we invite PhD students in biology and related fields to participate in a course that provides the opportunity to refresh knowledge on central elements in evolutionary theory and to discuss the concept of evolution in a broad perspective. The course shall familiarize the participants with ?thinking evolution? and encourage them to include this thinking in reflection on their own project.

Prerequisites: Reading of the following literature:

1. John Maynard Smith and Eörs Szathmáry, The origins of life ? From the Birth of Life to the Origins of Language, Oxford 1999 ?

2. Further readings will be announced later and a collection of papers will be given to the participants in due time before the start of the course.

Organizers and contact: Kai Finster (kai.finster@biology.au.dk <mailto:kai.finster@biology.au.dk>) or Volker Loeschcke (volker.loeschcke@biology.au.dk <mailto:volker.loeschcke@biology.au.dk>).

Lecturers: Eörs Szathmáry, Dirk Fabricius, Louis Klostergaard, Henrik Knudsen.

Lecturers? background:

1. Eörs Szathmáry: Current affiliation: Professor of biology and head of the Department of Plant Taxonomy and Ecology of Eötvös Loránd University, Budapest, where he is also the chairman of the PhD programme in theoretical biology and ecology. http://www.colbud.hu/fellows/szathmary.shtml 2. Dirk Fabricius: studied Law and Psychology, now Professor of Criminal Law, Criminology and Psychology of Law at the Johann Wolfgang Goethe-University, Frankfurt/Main, Germany since 1996. See www.dfabricius.de <http://www.dfabricius.de> for further information 3. Louis Klostergaard: Studied Philosophy of Science and Bioethics at the Department of Philosophy, now Ass. Professor at the Department for Studies of Science and Science Education at Aarhus University. For further information see http://person.au.dk/en/louis@si 4. Henrik Knudsen: Studied History of Ideas and History of Science at the Department for Studies of Science and Science Education, now Post.Doc. at the Department for Studies of Science and Science Education. For further information see http://person.au.dk/en/henrik.knudsen@si Organizers: Kai Finster and Volker Loeschcke

Organizer?s background:

Kai Finster: Research interests in microbial ecology and microbial physiology with special focus on anaerobic processes such as methanogensis and sulfate reduction. Since 2003 affiliated with the marslab (www.marslab.dk <http://www.marslab.dk/>) at the faculty of natural sciences, university of Aarhus. Involved in the development of an instrument that permits biological experiments under proxy Mars conditions. General interest in the diversity and adaptions of living things and their capacity to deal with extremes.

Volker Loeschcke: Research interests in evolutionary genetics and environmental stress, climate change and biodiversity. Works at the section of Ecology and Genetics, Dept. of Biology, Aarhus University and is head of the Center of Environmental Stress Research (ACES) (www.biology.au.dk/aces <http://www.biology.au.dk/aces>). In his work he tries to combine studies on variation at the DNA level with variation in phenotype and function.

Prior to the course all those that are interested to attend the course should forward a short CV (maximum 2 pages) by email to Kai Finster with c.c. to Volker Loeschcke or. In case we receive more than 20

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

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UColoradoBoulder MORPH Dec14-16

Investigating the Evolution of Plant Form: Conceptual Integration from the Molecular to the Ecological

A Molecular and Organismic Research in Plant History (MORPH) sponsored minicourse

December 14th - 16th, 2007 at the University of Colorado, Boulder

This intensive minicourse and workshop will provide an opportunity for a select group of doctoral students and distinguished investigators in plant evolutionary developmental biology to interact. The goal will be to address current methodological and conceptual hurdles associated with the study of the evolution of plant form. In particular, participants will focus on the integration of developmental information across molecular, organismic, and ecological levels of plant biology. In addition to presentations by the faculty, each student will outline critical issues associated with his/her own evolutionary developmental research for discussion by all participants.

Faculty include: Scott Armbruster Spencer Barrett Peter Crane Pamela Diggle Michael Donoghue Peter Endress William Friedman Larry Hufford Vivian Irish Amy Litt Michael Purugganan

The deadline for application is September 1, 2007.

MORPH will cover all reasonable costs (registration, air fare, hotel accommodations, and meals) for successful applicants.

More information is available on the MORPH website: http://www.colorado.edu/eeb/MORPH Sincerely,

Rob Baker MORPH RA

Dept. of Ecology and Evolutionary Bio Ramaley N122 Campus Box 334 University of Colorado Boulder, CO

80309

"Robert L. Baker" <Robert.Baker@Colorado.EDU>

Vienna EvolEcolGenetics Sep15-16 2

*****DEADLINE APPROACHING: JUNE, 19th*****************

ESF sponsored exploratory workshop on

Ecological genetics: understanding the functional consequences of natural variation in adaptation

Vienna 15.-16.9. 2007 Note: this is immediately after the European Drosophila Research Conference (http://www.imp.ac.at/EDRC2007/)

Synopsis

It is well established that natural populations harbor huge amounts of molecular variation. The neutral theory of molecular evolution suggested that the effect of most of mutations is so small that they can be considered as neutral. Recent evidence, however, demonstrated that a large proportion of natural variation seems to be involved in adaptation to the environment. Population genetics has developed powerful tools to identify genes under selection, but the functional validation of such ecologically important variants requires new functional approaches suitable to measure effects that are important in the wild, but difficult to score in the laboratory. Conversely, there is increasing evidence that natural variation in structural or regulatory genes have major effects, which were only recognized through the comparison of different naturally occurring variants.

This workshop provides a platform for both functional biologists and population geneticists with the aim to develop concepts and new tools to study the functional consequences of natural variation, in particular in the context of ecology.

The invited speakers cover a broad range of topics and approaches, ranging from theoretical population genetics and quantitative genetics to developmental biology. The impact of environmental and genetic variation on phenotypic traits will be covered. It will be discussed how the knowledge of well-studied model organisms, such as D. melanogaster, yeast and A. thaliana, can be extended to less studied organisms.

Speakers

Patricia Beldade Jean David Jean-Michel Gibert Greg Gibson Joachim Hermisson Martin Jaekel Volker Loeschcke Artyom Kopp Sergey Nuzhdin Leonie Ringrose Christian Schlötterer Karl Schmid Lars Steinmetz

The workshop will be open to a limited number of additional participants, in particular functional biologists are encouraged to participate. Applications including CV and motivation statement should be sent to jmg@i122server.vu-wien.ac.at until June, 19th.

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

phone: +43-1-250775603 fax: +43-1-250775693 http://i122server.vu-wien.ac.at/pop/pop_gen.html christian.schloetterer@vu-wien.ac.at christian.schloetterer@vu-wien.ac.at

Instructions

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

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

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

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

Afterward

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